## Structure Reports

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## Key indicators

Single-crystal X-ray study
$T=298 \mathrm{~K}$
Mean $\sigma(\mathrm{C}-\mathrm{C})=0.007 \AA$
$R$ factor $=0.067$
$w R$ factor $=0.162$
Data-to-parameter ratio $=17.4$

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

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# $N, N^{\prime}, N^{\prime \prime}$-Tricyclohexylguanidinium chloride 

In the title crystal structure, $\mathrm{C}_{19} \mathrm{H}_{36} \mathrm{~N}_{3}{ }^{+} \cdot \mathrm{Cl}^{-}$, the central C atom of the $N, N^{\prime}, N^{\prime \prime}$-tricyclohexylguanidinium ion and the chloride ion both lie on positions of site symmetry 3 . Weak $\mathrm{N}-\mathrm{H} \cdots \mathrm{Cl}$ hydrogen bonds $[\mathrm{N} \cdots \mathrm{Cl}=3.539$ (3) $\AA$ ] link anions and cations, forming a three-dimensional network.

## Comment

Guanidines are strong bases that find applications in a large number of organic reactions widely employed in organic synthesis, including carbon-carbon bond formation and transesterification of vegetable oils (Horvath, 1996; Gobbi \& Frenking, 1993; Vargas et al., 1998). Coupled with the increasing emphasis on the development of environmentally friendly catalysts, the heterogenization of these bases is a desirable goal (Tanatani et al., 1998; Sercheli et al., 1999). Here we report the the crystal structure of the title compound, (I).

(I)

The title compound comprises an $N, N^{\prime}, N^{\prime \prime}$-tricyclohexylguanidinium cation and a chloride anion (Fig. 1). C 1 and Cl 1 both lie on positions of site symmetry 3 . In the $N, N^{\prime}, N^{\prime \prime}-$ tricyclohexylguanidinium cation, the sum of the angles at atom C 1 comfirms the $s p^{2}$ hybridization of this atom. The unique cyclohexyl group is in a chair conformation. In the crystal structure, anions and cations are linked by intermolecular N $\mathrm{H} \cdots \mathrm{Cl}$ hydrogen bonds, forming a three-dimensional network (Table 2).

## Experimental

A DMF solution ( 10 ml ) of $N, N^{\prime}, N^{\prime \prime}$-tricyclohexylguanidine ( $0.1 \mathrm{mmol}, 0.31 \mathrm{~g}$ ) was added dropwise to a stirred aqueous solution $(10 \mathrm{ml})$ of hydrochloric acid $(0.2 \mathrm{mmol}, 0.07 \mathrm{~g})$ at 253 K . The reaction

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mixture was filtered and the filtrate allowed to stand for approximately two weeks until colorless single crystals formed.

## Crystal data

| $\mathrm{C}_{19} \mathrm{H}_{36} \mathrm{~N}_{3}{ }^{+} \cdot \mathrm{Cl}^{-}$ | Cell parameters from 2136 <br> reflections |
| :--- | :--- |
| $M_{r}=341.96$ | $\theta=2.5-24.1^{\circ}$ |
| $\mathrm{Cubic}, P 2_{1} 3$ | $\mu=0.19 \mathrm{~mm}^{-1}$ |
| $a=12.6411(5) \AA$ | $T=298(2) \mathrm{K}$ |
| $V=2020.02(14) \AA^{3}$ | Block, colorless |
| $Z=4$ | $0.34 \times 0.28 \times 0.12 \mathrm{~mm}$ |
| $D_{x}=1.124 \mathrm{Mg} \mathrm{m}$ |  |
| Mo K radiation |  |
|  |  |
| Data collection |  |
| Bruker APEX area-detector | 1221 independent reflections |
| $\quad$ diffractometer | 1146 reflections with $I>2 \sigma(I)$ |
| $\varphi$ and $\omega$ scans | $R_{\text {int }}=0.040$ |
| Absorption correction: multi-scan | $\theta_{\max }=25.2^{\circ}$ |
| $\quad(S A D A B S ;$ Bruker, 2002) | $h=-15 \rightarrow 11$ |
| $T_{\min }=0.931, T_{\text {max }}=0.972$ | $k=-15 \rightarrow 14$ |
| 10792 measured reflections | $l=-13 \rightarrow 15$ |
|  |  |

## Refinement

Refinement on $F^{2}$
$R\left[F^{2}>2 \sigma\left(F^{2}\right)\right]=0.067$
$w R\left(F^{2}\right)=0.162$
$S=1.29$
1221 reflections
70 parameters
H -atom parameters constrained


Figure 1
The structure of (I) with displacement ellipsoids drawn at the $30 \%$ probability level and H atoms shown as spheres of arbitary radii. In the cation, only the symmetry-unique atoms are labelled, the others being related by three-fold rotation $\left(\frac{3}{2}-z, 2-x, y-\frac{1}{2}\right.$ and $\left.2-y, \frac{1}{2}+z, \frac{3}{2}-x\right)$.

Data collection: SMART (Bruker, 2002); cell refinement: SAINT (Bruker, 2002); 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, 2002); software used to prepare material for publication: SHELXL97.

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