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## Massimo Alberti Bambagiotti, ${ }^{\text {a }}$ Bruno Bruni, ${ }^{\text {b }}$ Massimo Di Vaira ${ }^{\text {b }}$ and Valerio Giannellini ${ }^{\text {a }}$

${ }^{\text {a }}$ Dipartimento di Scienze Farmaceutiche, Universitá di Firenze, Via U. Schiff 6, I-50019 Sesto Fiorentino, Firenze, Italy, and
${ }^{\mathbf{b}}$ Dipartimento di Chimica, Universitá di Firenze, Via della Lastruccia 3, I-50019 Sesto Fiorentino, Firenze, Italy

Correspondence e-mail: massimo.divaira@unifi.it

## Key indicators

Single-crystal X-ray study
$T=180 \mathrm{~K}$
Mean $\sigma(\mathrm{C}-\mathrm{C})=0.003 \AA$
$R$ factor $=0.022$
$w R$ factor $=0.047$
Data-to-parameter ratio $=9.1$

For details of how these key indicators were automatically derived from the article, see http://journals.iucr.org/e.
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## $(R)$-(-)-Mepivacaine hydrochloride enantiomer: a low-temperature study

Low-temperature structural data are reported for the anaesthetic ( $2 R$ )-( - )-2-(2,6-dimethylphenylaminocarbonyl)-1-methylpiperidinium chloride, $\mathrm{C}_{15} \mathrm{H}_{23} \mathrm{~N}_{2} \mathrm{O}^{+} \cdot \mathrm{Cl}^{-}$, which complement existing room-temperature data for the $S$ enantiomer. Crystal packing is largely controlled by infinite $\mathrm{N}-\mathrm{H} \cdots \mathrm{Cl}$ hydrogen-bonded chains.

## Comment

As part of a study of solid-state structural relationships between mepivacaine and its solvates (Giannellini et al., 2005), the structure of the $(R)-(-)$ enantiomer of mepivacaine hydrochloride, (I), has been refined using 180 K diffraction data. The room-temperature structure of the $(S)-(+)$ enantiomer was already known (Csöregh, 1992). No phase transitions are recorded in the course of the 111 K temperature decrease from measurements of the previous study. There is a slightly anisotropic cell-volume reduction, $1.1 \%$ overall, the (moderately) largest linear contraction being in the (crystallographic b) direction of the infinite $\mathrm{N}-\mathrm{H} \cdots \mathrm{Cl} \cdots \mathrm{H}-\mathrm{N}$ chains. Results (Fig. 1, and Tables 1 and 2) are presented using the same labelling criteria of the previous study, for convenience. There is close agreement with the previous results, possibly with a smaller spread of values for chemically equivalent bond distances in the present case.

(I)

## Experimental

Crystals of ( $R$ )-(-)-mepivacaine hydrochloride, suitable for X-ray work, were kindly supplied by Monica Jacobsson (Astra Zeneca R\&D, Sweden) and were used as received.

## Crystal data

$\mathrm{C}_{15} \mathrm{H}_{23} \mathrm{~N}_{2} \mathrm{O}^{+} \cdot \mathrm{Cl}^{-}$
$M_{r}=282.80$
Orthorhombic, $P_{2} 2_{1} 2_{1} 2_{1}$
$a=9.7378$ (10) $\AA$
$b=10.5790(9) \AA$
$c=15.2761(15) \AA$
$V=1573.7$ (3) $\AA^{3}$
$Z=4$
$D_{x}=1.194 \mathrm{Mg} \mathrm{m}^{-3}$
$\mathrm{Cu} K \alpha$ radiation
Cell parameters from 952
reflections
$\theta=6-58^{\circ}$
$\mu=2.10 \mathrm{~mm}^{-1}$
$T=180$ (2) K
Elongated prism, colourless
$0.80 \times 0.30 \times 0.30 \mathrm{~mm}$

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Figure 1
A view of the structure of the protonated molecule, showing the atomic numbering scheme. Displacement ellipsoids are drawn at the $30 \%$ probability level and H atoms are shown as small spheres of arbitrary radii.

## Data collection

Oxford Diffraction Xcalibur 3 CCD diffractometer
$\omega$ scans
Absorption correction: multi-scan
(SADABS; Sheldrick, 1986)
$T_{\text {min }}=0.331, T_{\text {max }}=0.533$
6079 measured reflections
2201 independent reflections
1989 reflections with $I>2 \sigma(I)$
$R_{\text {int }}=0.030$
$\theta_{\text {max }}=59.0^{\circ}$
$h=-10 \rightarrow 9$
$k=-11 \rightarrow 9$
$l=-15 \rightarrow 16$

## Refinement

Refinement on $F^{2}$
$R\left[F^{2}>2 \sigma\left(F^{2}\right)\right]=0.022$
$w R\left(F^{2}\right)=0.047$
$S=0.96$
2201 reflections
242 parameters
Only coordinates of H atoms refined
$w=1 /\left[\sigma^{2}\left(F_{o}{ }^{2}\right)+(0.0218 P)^{2}\right]$
where $P=\left(F_{o}{ }^{2}+2 F_{c}{ }^{2}\right) / 3$

Table 1
Selected bond lengths ( $\AA$ ).

| $\mathrm{N} 1-\mathrm{C} 1^{\prime}$ | $1.494(2)$ | $\mathrm{N} 8-\mathrm{C} 9$ | $1.437(2)$ |
| :--- | :--- | :--- | :--- |
| $\mathrm{N} 1-\mathrm{C} 2$ | $1.495(2)$ | $\mathrm{C} 9-\mathrm{C} 14$ | $1.396(2)$ |
| $\mathrm{N} 1-\mathrm{C} 6$ | $1.508(2)$ | $\mathrm{C} 9-\mathrm{C} 10$ | $1.399(2)$ |
| $\mathrm{C} 2-\mathrm{C} 7$ | $1.526(2)$ | $\mathrm{C} 10-\mathrm{C} 11$ | $1.389(3)$ |
| $\mathrm{C} 2-\mathrm{C} 3$ | $1.528(3)$ | $\mathrm{C} 10-\mathrm{C} 16$ | $1.505(3)$ |
| $\mathrm{C} 3-\mathrm{C} 4$ | $1.523(3)$ | $\mathrm{C} 11-\mathrm{C} 12$ | $1.379(3)$ |
| $\mathrm{C} 4-\mathrm{C} 5$ | $1.512(3)$ | $\mathrm{C} 12-\mathrm{C} 13$ | $1.380(3)$ |
| $\mathrm{C} 5-\mathrm{C} 6$ | $1.499(3)$ | $\mathrm{C} 13-\mathrm{C} 14$ | $1.391(2)$ |
| $\mathrm{C} 7-\mathrm{O} 7$ | $1.231(2)$ | $\mathrm{C} 14-\mathrm{C} 15$ | $1.507(3)$ |
| $\mathrm{C} 7-\mathrm{N} 8$ | $1.335(2)$ |  |  |

Table 2
Hydrogen-bonding geometry ( $\AA{ }^{\circ},{ }^{\circ}$ ).

| $D-\mathrm{H} \cdots A$ | $D-\mathrm{H}$ | $\mathrm{H} \cdots A$ | $D \cdots A$ | $D-\mathrm{H} \cdots A$ |
| :--- | :--- | :--- | :--- | :--- |
| $\mathrm{~N} 1-\mathrm{H} 1 \mathrm{~N} \cdots \mathrm{Cl}$ |  |  |  |  |
| $\mathrm{N} 8-\mathrm{H} 8 \mathrm{~N} \cdots \mathrm{Cl}$ | $0.905(17)$ | $2.182(18)$ | $3.0140(16)$ | $152.5(16)$ |

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


Figure 2
A view of the packing in the proximity of the $b c$ face, showing the system of hydrogen bonds (dashed lines) in the structure. Only the H atoms directly involved in hydrogen bonding are shown.

Although the structure of the $(S)-(+)$ enantiomer was known (Csöregh, 1992), that of the present $(R)-(-)$ enantiomer was determined $a b$ initio and the assignment of absolute configuration was checked (Flack, 1983). The material does not diffract strongly and it was deemed that collecting data at $\theta$ higher than $58^{\circ}$ would not yield improvement. In the refinement, H -atom positions, initially assigned geometrically, were allowed to refine, with $U_{\text {iso }}(\mathrm{H})=1.2 U_{\mathrm{eq}}(\mathrm{C}, \mathrm{N})$ or $1.5 U_{\text {eq }}\left(\mathrm{C}_{\text {methyl }}\right) . \mathrm{C}-\mathrm{H}$ bond distances: secondary $\mathrm{CH}_{2}=0.94(2)-$ 1.01 (2) Å, methyl $\mathrm{CH}_{3}=0.90(2)-1.04(2) \AA$, tertiary $\mathrm{CH}=$ 0.93 (3) $\AA$, aromatic $\mathrm{CH}=0.92$ (2) -0.98 (2) $\AA$ and $\mathrm{N}-\mathrm{H}=0.84(2)-$ 0.90 (2) $\AA$.

Data collection: CrysAlis CCD (Oxford Diffraction, 2001); cell refinement: CrysAlis CCD; data reduction: CrysAlis RED (Oxford Diffraction, 2001); 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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