Acta Crystallographica Section E

## **Structure Reports**

**Online** 

ISSN 1600-5368

## A. Sivalakshmidevi, K. Vyas, \*\* S. Mahender Rao<sup>b</sup> and G. Om Reddy<sup>b</sup>

<sup>a</sup>Discovery Research, Dr. Reddy's Laboratories, 7-1-27, Ameerpet, Hyderabad 500 016, India, and bCustom Chemical Services, Dr. Reddy's Laboratories, 7-1-27, Ameerpet, Hyderabad 500 016, India

Correspondence e-mail: vyask@drreddys.com

#### **Key indicators**

Single-crystal X-ray study T = 298 KMean  $\sigma(C-C) = 0.007 \text{ Å}$ R factor = 0.068wR factor = 0.068 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.

# A monoclinic polymorph of venlafaxine hydrochloride

Venlafaxine hydrochloride,  $[(\pm)-N,N-dimethyl-2-(1-hydroxy$ cyclohex-1-yl)-2-(4-methoxyphenyl) ethylamine chloride, C<sub>17</sub>H<sub>28</sub>ClNO<sub>2</sub>] is found to crystallize in both orthorhombic and monoclinic crystal systems. The molecular structures in the two polymorphs differ in the conformations of the substituents at the ethylamine group. In the monoclinic crystal structure, the molecules translated along the a axis are linked by Cl ions through O-H···Cl and N-H···Cl hydrogen bonds to form infinite one-dimensional chains.

Received 12 August 2002 Accepted 4 September 2002 Online 13 September 2002

DRL Publication No. 230

#### Comment

Venlafaxine hydrochloride,  $[(\pm)-N,N-dimethyl-2-(1-hydroxy$ cyclohex-1-yl)-2-(4-methoxyphenyl) ethylamine chloride, C<sub>17</sub>H<sub>28</sub>ClNO<sub>2</sub>] is used as an antidepressant and an anxiolytic. Recrystallization of the compound for purification yielded crystals of two different morphologies, viz. blocks (form I) and needles (form II), as observed under the microscope. They were separated manually and characterized by different solid-state techniques such as differential scanning calorimetry, infrared spectroscopy, powder X-ray diffraction and single-crystal X-ray diffraction. These polymorphic forms were patented along with their characteristic physicochemical data (Rao et al., 1999,, 2002). Recently, the crystal structure of form I has been reported in the orthorhombic space group Pca2<sub>1</sub> byVega et al. (2000). In this paper we report the structure of form II and compare it with that of form I.

Form II of venlafaxine hydrochloride is found to crystallize in the monoclinic space group  $P2_1/n$ . The structure of the molecule in the monoclinic form is shown in Fig. 1. All the bond lengths (Table 1) show normal values (Allen et al., 1987) and agree well with the corresponding values observed for the orthorhombic polymorph (Vega et al., 2000). In both polymorphs, the cyclohexane ring adopts a chair conformation. An intermolecular hydrogen bond links the N atom of the dimethylammonium group of the venlafaxine cation to the chloride anion. The chloride ion is also involved in another

DOI: 10.1107/S160053680201588X

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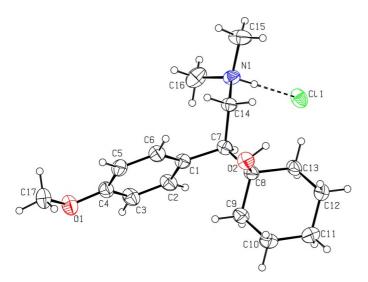


Figure 1
A perspective view of venlafaxine hydrochloride. Displacement ellipsoids are drawn at the 30% probability level.

hydrogen bond, with the O atom of the hydroxyl group of the cation translated one unit along the a axis. These hydrogen bonds (Table 2), which stabilize the crystal structure (Fig. 2), lead to chains of molecules along the short a (= 5.797 Å) axis. An identical hydrogen-bonding scheme constitutes the molecular chain in the orthorhombic polymorph, along the short b (= 5.881 Å) axis (Vega et al., 2000). Hence the two polymorphic modifications have the same lattice stabilization mechanism. However, careful comparison of the torsion angles (Table 3) reveals that the molecules differ by 3 to  $6^{\circ}$  in the rotations about the bonds N1—C14, C1—C7 and C7—C14. Hence these two forms of venlafaxine hydrochloride are conformational polymorphs (Bilton et al., 1999).

### **Experimental**

Crystals of form II of venlafaxine hydrochloride suitable for X-ray diffraction were grown from a mixture of methanol and ethyl acetate (1:8).

#### Crystal data

$C_{17}H_{28}NO_2^+\cdot Cl^-$	$D_x = 1.197 \text{ Mg m}^{-3}$
$M_r = 313.87$	Cu K $\alpha$ radiation
Monoclinic, $P2_1/n$	Cell parameters from 24
a = 5.797 (6)  Å	reflections
b = 26.074 (7)  Å	$\theta = 6.4-23.7^{\circ}$
c = 11.722 (3)  Å	$\mu = 1.97 \text{ mm}^{-1}$
$\beta = 100.72 (5)^{\circ}$	T = 298.2  K
$V = 1741 (2) \text{ Å}^3$	Needle, colourless
Z = 4	$0.40 \times 0.10 \times 0.10 \text{ mm}$

#### Data collection

Rigaku AFC-7S diffractometer	$R_{\rm int} = 0.078$
$\omega$ –2 $\theta$ scans	$\theta_{\rm max} = 70.1^{\circ}$
Absorption correction: ψ scan	$h = 0 \rightarrow 6$
(North et al., 1968	$k = 0 \rightarrow 31$
$T_{\min} = 0.843, T_{\max} = 0.996$	$l = -14 \rightarrow 14$
3564 measured reflections	4 standard reflections
3304 independent reflections	every 150 reflections
3304 reflections with $I > 1.3\sigma(I)$	intensity decay: 0.3%

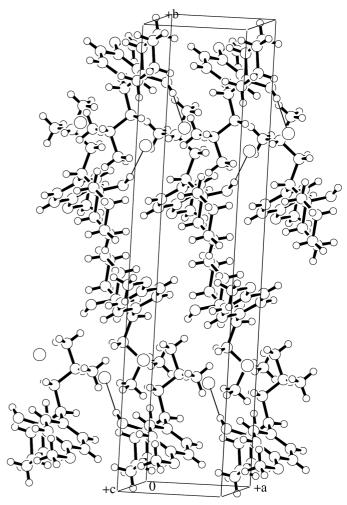


Figure 2 Packing of the molecules.

#### Refinement

refinement

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Refinement on F	$w = 1/[\sigma^2(F_o) + 0.00016 F_o ^2]$
R = 0.068	$(\Delta/\sigma)_{\text{max}} = 0.001$
wR = 0.068	$\Delta \rho_{\text{max}} = 0.40 \text{ e Å}^{-3}$
S = 1.48	$\Delta \rho_{\min} = -0.33 \text{ e Å}^{-3}$
1816 reflections	Extinction correction: Zachariasen
199 parameters	(1967)
H atoms treated by a mixture of	Extinction coefficient: 0.0000022 (7)
independent and constrained	

**Table 1** Selected geometric parameters  $(\mathring{A}, \circ)$ .

O1-C4	1.363 (6)	N1-C15	1.486 (6)
O1-C17	1.426 (7)	N1-C16	1.487 (7)
O2-C8	1.442 (5)	N1-C14	1.495 (6)
C4-O1-C17	117.0 (4)	O1 - C4 - C5	125.4 (4)
C14-N1-C16	113.3 (4)	O2-C8-C9	106.3 (3)
C15-N1-C16	110.6 (4)	O2-C8-C13	110.2 (3)
C14-N1-C15	109.7 (4)	O2-C8-C7	108.7 (3)
O1-C4-C3	115.8 (4)	N1-C14-C7	114.4 (3)

## organic papers

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

$D-H\cdots A$	D-H	$H \cdot \cdot \cdot A$	$D \cdot \cdot \cdot A$	$D-H\cdots A$
O2-H27···Cl1 <sup>i</sup>	0.91 (5)	2.33 (5)	3.213 (5)	164 (4)
N1-H28···Cl1	0.92 (6)	2.13 (6)	3.040 (5)	169 (5)

Symmetry code: (i) 1 + x, y, z.

**Table 3** Comparison of some torsion angles (°) in form I and form II.

Angle	form I	form II
C16-N1-C14-C7	58.8 (5)	62.0 (5)
C15-N1-C14-C7	-177.0(4)	-173.9(4)
C2-C1-C7-C8	-107.3(4)	-101.8(5)
C2-C1-C7-C14	129.1 (4)	133.0 (4)
C6-C1-C7-C8	71.7 (5)	77.0 (5)
C6-C1-C7-C14	-51.9(5)	-48.3(5)
C1-C7-C14-N1	-88.9(4)	-95.1(4)
C8-C7-C14-N1	144.7 (3)	137.6 (4)

H atoms bound to carbons were fixed geometrically, with C-H = 0.95 Å, and refined using a riding model. H atoms bound to O and N were refined isotropically.

Data collection: MSC/AFC Diffractometer Control Software (Molecular Structure Corporation, 1994); cell refinement: MSC/AFC Diffractometer Control Software; data reduction: teXsan (Molecular

Structure Corporation, 1995); program(s) used to solve structure: *SIR*92 (Altomare *et al.*, 1993); program(s) used to refine structure: *teXsan*; molecular graphics: *ORTEP*3 for Windows (Farrugia, 1999); software used to prepare material for publication: *teXsan*.

The authors acknowledge Dr A. Venkateswarlu and Dr K. Anji Reddy for their interest and encouragement in this work.

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