## 126. Structural Aspects of the Enantioselectivity of Tartrates with α-Amino-alcohol Salts

Part II

## Crystal Structures of (1*R*,2*S*)-Norephedrine Hydrochloride and (1*R*,2*R*)-Norpseudoephedrine Hydrochloride

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(6.IV.89)

Enantioselective host-guest complexes between  $\alpha$ -amino-alcohol salts and chiral tartrates can not be crystallised up to now. To study structural aspects of their enantioselectivity, crystal structures of the components were determined. Norephedrine was used as a reference guest  $\alpha$ -amino-alcohol. (1*R*,2*S*)-Norephedrine hydrochloride (monoclinic, space group *P*2<sub>1</sub>, *Z* = 4, *a* = 8.455, *b* = 10.331, *c* = 12.570 Å,  $\beta$  = 107.45°) and (1*R*,2*R*)-norpseudoephedrine hydrochloride (monoclinic, space group *P*2<sub>1</sub>, *Z* = 2, *a* = 5.493, *b* = 8.052, *c* = 11.986 Å,  $\beta$  = 104.62°) both adopt *M*-synclinal conformations with respect to the ammonium and hydroxy groups. Rather short intramolecular N···O distances indicate interaction between ammonium and hydroxy groups.

**Introduction.** – Chiral tartaric-acid diesters show remarkable enantioselectivity with salts of  $\alpha$ -amino-alcohols [1][2] and are among the simplest known ionophores. Their enantioselectivity has been studied extensively by partition experiments in liquid phases [3]. Since the molecular complexes between tartaric-acid diesters and  $\alpha$ -amino-alcohols could not be crystallised, crystal-structure analyses of the components have been accomplished in order to obtain information on structural aspects of enantioselectivity. The structures of the tartaric-acid diester hosts have been already discussed in [4]. Here, we describe the structures of  $\alpha$ -amino-alcohol guests, and molecular-modeling studies of the host-guest complexes will be presented later [5]. Our investigations of stereoselective behaviour made use of *erythro*-norephedrine  $\cdot$  HCl (1) and *threo*-norpseudo-ephedrine  $\cdot$  HCl (2) as reference guest molecules. Their (1*R*)-enantiomers are preferred by (*S*,*S*)-tartaric-acid diesters.



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**Force-Field Calculations.** – The diastereoisomers of norephedrine, *erythro*-norephedrine, and *threo*-norpseudoephedrine can, in principle, adopt three different conformations about the central C(1)-C(2) bond (*Fig. 1*). The relative potential energies of these rotamers were calculated using the force-field program MMP2 [6].

(1R,2S)-Norephedrine (erythro)



Fig. 1. Newman projections of possible rotamers for (1R,2S)-norephedrine and for (1R,2R)-norpseudoephedrine. Numbers at each rotamer indicate relative potential energies (kcal · mol<sup>-1</sup>)

Unfortunately, this force field has no parameters for ammonium groups, therefore, the bases of the  $\alpha$ -amino-alcohols were used instead. For the (1R,2R)-enantiomer of norpseudoephedrine, potential energies suggest a clear preference of the *M*-synclinal arrangement, with energies of  $1.74 \text{ kcal} \cdot \text{mol}^{-1}$  higher for the *P*-synclinal and of 4.42 kcal  $\cdot \text{mol}^{-1}$  higher for the s-trans- arrangement. For the (1R,2S)-enantiomer of norephedrine, however, the calculations showed no significant differences (*Fig. 1*). Both calculations are of course hampered by the use of the bases. Possible influences of dipolar interactions in the salts used for the experiments in solution might shift the minimum-energy conformation to a different arrangement.

**Crystallographic Investigations.** – The nonconclusive results of the force-field calculations led us to look at the crystal structures of both optically active diastereoisomers. A crystal-structure analysis of racemic *erythro*-norephedrine  $\cdot$  HCl (1) was published some time ago [7]. The racemic substance crystallizes in the non-centrosymmetric space

group  $P2_1$  with two enantiomeric molecules in the asymmetric unit. Both enantiomers have identical synclinal arrangements (torsion angles O–C(1)–C(2)–N –64.8° and –57.7°) but different conformations. One molecule has a torsion angle C(4)–C(1)–C(2)–N of 172.7° – an s-*trans*-arrangement of Ph ring and ammonium group – the other molecule has an s-*cis*-arrangement, with a torsion angle of 63.6°. A s-*cis* arrangement must be more stable than the s-*trans*-conformer because of dipole interactions.

Crystal Structure of (1R,2S)-Norephedrine  $\cdot$  HCl (1). The optically active erythronorephedrine  $\cdot$  HCl (1) crystallizes in the same space group P2<sub>1</sub> as the racemic substance, also with two molecules per asymmetric unit. Both molecules have *M*-synclinal conformations with torsion angles O–C(1)–C(2)–N of –61.2° and –70.5°, respectively (see *Figs. 2* and 3), and the same s-*trans*-arrangement of Ph ring and ammonium group as one of the molecules in the racemic crystal (torsion angles C(4)–C(1)–C(2)–N 175.2° and 165.2°).



Fig. 2. Newman projection along the C(1)-C(2) bond of one of the two independent molecules in the crystal structure of (1R,2S)-norephedrine  $\cdot$  HCl (1)

All H-atoms of the ammonium and the hydroxy groups are involved in H-bonds to Cl<sup>-</sup> anions, every anion accepting four H-bonds (*Fig. 3*). The N···O distances are rather short, 2.741 Å and 2.881 Å, suggesting interaction between ammonium N- and hydroxy O-atoms. No intramolecular H-bond, however, exists between these groups (*cf. Table 2*).



Fig. 3. ORTEP Stereoview of the (1R, 2S)-norephedrine  $\cdot$  HCl (1), showing the H-bonds to Cl-atoms

Crystal Structure of (1R,2R)-Norpseudoephedrine  $\cdot$  HCl (2). The optically active threo-norpseudoephedrine  $\cdot$  HCl (2) also crystallizes in the space group  $P2_1$ , but in this case with only one molecule per asymmetric unit. The preference of an *M*-synclinal arrangement (torsion angle O–C(1)–C(2)–N –54.7°) suggested by the force-field calculation is confirmed by the structure analysis. Fig. 4 shows the conformation in a Newman projection along the central C(1)–C(2) bond.



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Fig. 4. Newman projection along the C(1)-C(2) bond in the crystal structure of (1R,2R)-norpseudoephedrine  $\cdot$  HCl (2)



Fig. 5. ORTEP Stereoview of (1R,2R)-norpseudoephedrine · HCl (2), showing the H-bonds to Cl-atoms

The s-*trans*-arrangement of Ph and ammonium groups (torsion angle  $C(4)-C(1)-C(2)-N-176.8^{\circ}$ ) is the same as for *erythro*-norephedrine. Also the H-bonding scheme is very similar. Again, the four donor H-atoms of ammonium and hydroxy groups form H-bonds to Cl<sup>-</sup> anions (*Fig. 5*). The interaction between ammonium N- and hydroxy O-atoms shortens the N···O distance to 2.709 Å, without formation of an intramolecular H-bond.

**Discussion.** – The results suggest, that a s-*cis*-arrangement of hydroxy and ammonium groups is the preferred conformation for both *erythro*- and *threo*-norephedrine. In the case of *erythro*-norephedrine, the energy difference between *M*- and *P*-synclinal arrangements seems to be small, so that crystal-packing influences might suffice to tilt the balance. A similar situation exists for the arrangement of the Ph with respect to the ammonium group. In the crystal structure of racemic *erythro*-norephedrine, s-*cis*- and s-*trans*-arrangements are observed. Again, crystal-packing forces could decide between the two arrangements.

**Experimental.** – Reflection intensities for both compounds were measured at r.t. with a four-circle diffractometer (*Enraf-Nonius CAD4*, graphite monochromatized  $MoK_{\alpha}$  radiation). Crystal data for 1 and 2 are given in *Table 1*. Full lists of coordinates and isotropic displacement parameters as well as H-positions are deposited with the *Cambridge Structural Data Centre* and are available from the authors.

	1	2
Formula	$C_0ONH_{13} \cdot HCl$	C <sub>o</sub> ONH <sub>13</sub> · HCl
Space group	P2,	P2, 13
Crystal system	monoclinic	monoclinic
a [Å]	8.455(2)	5.438(3)
b [Å]	10.331(4)	8.052(2)
	12.570(3)	11.986(4)
β	107.45(2)	104.61(4)
V [Å <sup>3</sup> ]	1047.4	507.8
Z	4	2
$\rho$ [g · cm <sup>-3</sup> ]	1.19	1.23
$\theta$ [°]	28	30
h max c s	-1111	-77
k	013	011
1	016	016
Reflections		
measured	2662	1578
used $(l > 3\sigma)$	2041	1328
R factor	0.029	0.031

Table 1. Crystal Data for (IR,2S)-Norephedrine  $\cdot$  HCl (1) and (IR,2R)-Norpseudoephedrine  $\cdot$  HCl (2)

Both structures were solved by direct methods (SHELX-S86 [8]) and refined by full matrix least-squares analysis. For both structures, the positions of all H-atoms were taken from difference *Fourier* maps, and refined isotropically. The final *R* factors were 0.029 for 1 and 0.031 for 2, using weights  $1/\sigma^2$  in both cases. Some details of the molecular geometry are given in *Tables 2–4*.

			D····A	Н…А	D-H…A
1 (Molecul	e 1)				
N(1)–H(1)	Cl(1)	(1-x, 0.5+y, 2-z)	3.261(3)	2.49(3)	166(3)
N(1)-H(2)	Cl(2)	(2-x, 0.5+y, 2-z)	3.218(3)	2.42(3)	142(3)
N(1)-H(3)	Cl(1)		3.175(3)	2.16(3)	168(3)
N(1)–H(2)	<b>O</b> (1)		2.742(3)	2.33(3)	105(3)
O(1)–H(1)	Cl(2)		3.061(2)	2.29(4)	168(4)
1 (Molecul	e 2)				
N(2)–H(1)	<b>Cl(1)</b>	(1-x, y=0.5, 2-z)	3.173(3)	2.37(3)	160(3)
N(2)–H(2)	Cl(2)		3.136(3)	2.25(4)	161(3)
N(2)-H(3)	Cl(2)	(2-x, y-0.5, 2-z)	3.159(3)	2.36(3)	150(3)
N(2) - H(2)	O(2)		2.881(3)	2.64(3)	96(3)
O(2)–H(2)	Cl(1)	(2-x, y-0.5, 2-z)	3.151(3)	2.44(3)	164(4)
2					
N-H(3)	Cl	(x-1, y, z)	3.261(2)	2.47(3)	158(3)
N-H(2)	Cl		3.332(2)	2.60(4)	156(3)
N-H(1)	Cl	(1-x, y-0.5, 1-z)	3.166(2)	2.37(3)	155(3)
N-H(2)	0		2.710(2)	2.40(4)	105(3)
O-H	Cl	(1-x, 0.5+y, 1-z)	3.139(2)	2.23(3)	168(3)

Table 2. *H-Bond Geometry for* **1** and **2**. D...A: Distance donor to acceptor atom, H...A: distance H to acceptor atom, D-H...A: angle donor-donor H-acceptor atom [\*]. E.s.d. (in parentheses) refer to the last digit.

Table 3. Bond Lengths [Å] for 1 and 2 (e.s.d. in parentheses)

	1 (Molecule 1)	1 (Molecule 2)	2
C(1)–C(2)	1.523(3)	1.527(4)	1.520(3)
C(1)-C(4)	1.515(4)	1.496(4)	1.504(3)
C(1)-0	1.417(3)	1.412(3)	1.426(3)
C(2)-C(3)	1.510(4)	1.497(5)	1.518(3)
C(2)–N	1.506(3)	1.480(4)	1.492(3)
C(4) - C(5)	1.382(4)	1.396(5)	1.393(4)
C(4) - C(9)	1.378(4)	1.372(4)	1.385(3)
C(5)-C(6)	1.380(5)	1.372(5)	1.375(4)
C(6)-C(7)	1.369(6)	1.374(7)	1.377(4)
C(7)–C(8)	1.371(6)	1.349(7)	1.378(4)
C(8)-C(9)	1.391(5)	1.383(6)	1.380(3)

,	1 (Molecule 2)	2
110.6(2)	111.7(2)	110.1(2)
105.2(2)	106.0(2)	105.7(2)
114.0(2)	113.7(2)	112.7(2)
113.9(2)	114.7(2)	113.0(2)
107.2(2)	109.2(2)	108.8(2)
110.0(2)	109.8(3)	109.3(2)
119.0(2)	119.2(3)	121.2(2)
121.7(3)	122.8(3)	120.8(2)
119.2(3)	118.0(3)	117.9(9)
120.4(3)	120.6(3)	120.9(2)
120.3(3)	119.8(4)	120.5(3)
119.9(3)	120.8(4)	119.5(2)
120.2(4)	119.7(4)	120.1(2)
120.0(3)	121.2(4)	121.2(2)
	110.6(2) $105.2(2)$ $114.0(2)$ $113.9(2)$ $107.2(2)$ $110.0(2)$ $119.0(2)$ $121.7(3)$ $119.2(3)$ $120.4(3)$ $120.3(3)$ $119.9(3)$ $120.2(4)$ $120.0(3)$	110.6(2) $111.7(2)$ $105.2(2)$ $106.0(2)$ $114.0(2)$ $113.7(2)$ $113.9(2)$ $114.7(2)$ $107.2(2)$ $109.2(2)$ $110.0(2)$ $109.8(3)$ $119.0(2)$ $119.2(3)$ $121.7(3)$ $122.8(3)$ $119.2(3)$ $118.0(3)$ $120.4(3)$ $120.6(3)$ $120.3(3)$ $119.8(4)$ $119.9(3)$ $120.8(4)$ $120.2(4)$ $119.7(4)$ $120.0(3)$ $121.2(4)$

Table 4. Bond Angles [°] for 1 and 2 (e.s.d. in parentheses)

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