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N,*N*′-Bis(2-hydroxycyclohexyl)-*N*,*N*′-bis(2-hydroxyethyl)ethane-1,2-diaminium dichloride

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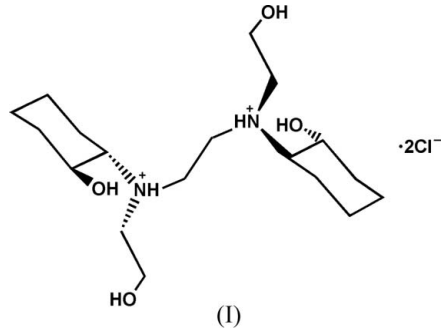
The achiral *meso* form of the title compound, $C_{18}H_{38}N_2O_4^{2+}\cdot 2Cl^-$, crystallizes to form undulating layers consisting of chains linked *via* weak hydroxyalkyl C—H···Cl contacts. The chains are characterized by centrosymmetric hydrogen-bonded dimers generated *via* N—H···Cl and hydroxycycloalkyl O—H···Cl interactions. *trans*-*N*-Alkyl bridges subdivide the chains into hydrophilic segments flanked by hydrophobic cycloalkyl stacks along [001].

Comment

Work on solid-state structures of reinforced β-amino alcohols, where cyclohexyl bridges are fused onto pendent hydroxyethyl groups, has suggested these compounds are able to self-assemble (de Sousa *et al.*, 2010). Relatively simply amino alcohols, such as diethanolamine, weakly assemble into tubular stacks through the linking of ring motifs (Bernstein *et al.*, 1995) *via* N—H···O hydrogen bonds, defining internal cavities of a predominantly hydrophilic nature. Tubular stacks are preferentially formed by stronger O—H···O intermolecular hydrogen bonds favoured in *anti* conformations adopted by β-amino alcohols with fused cyclohexyl bridges (de Sousa *et al.*, 2010). In these compounds the cyclohexyl bridge, between the amine N atom and a single hydroxy O-atom donor, promotes stronger intermolecular O—H···O hydrogen bonds that link the ring motifs into elaborate tubular stacks in the reinforced diethanolamine derivative 2-[(2-hydroxyethyl)amino]cyclohexanol (CyEA). The hydrophilic inner cores in this structure arise from the stereospecificity of the intermolecular O—H···O hydrogen bonds, which are dependent on the cyclohexyl conformation defining the surrounding hydrophobic outer surface. The selective enhancement of the intermolecular interactions within the hydrophilic inner core, *via* *N*-alkyl substitution of the amino group or *C*-alkyl substitution of the hydroxyalkyl pendents, may prompt controlled self-assembly of β-amino alcohols.

The solid-state structures of the hydrochloride salts of enantiomers of the *C*-alkylated amino alcohol nebivolol (Tuchalski *et al.*, 2006) and the *N*-substituted amino alcohol triethanolammonium chloride (Light & Gale, 2003; Mootz *et al.*, 1990; Vollbrecht *et al.*, 1997) largely suggest that conventional O—H···Cl and N—H···Cl interactions stabilize the crystallization of these compounds (Steiner, 1998). These interactions, often characteristic of ion pairs, accommodate the anion in distorted geometries: trigonal pyramidal (Linden *et al.*, 1994; Koman *et al.*, 2000; Henkel *et al.*, 1999; Bi & Aggarwal, 2008), tetrahedral (Nash *et al.*, 1988; Furneaux *et al.*, 1997; Henkel *et al.*, 1997*a*,*b*), trigonal planar (Zukerman-Schpector *et al.*, 2005), square pyramidal (Nash *et al.*, 1990; Huerta *et al.*, 2004) and T-shaped (Chang *et al.*, 2005). The halide anion, a strong hydrogen-bond acceptor, typically interacts with four donors, and the above-mentioned geometries, observed in the solid state, include weaker C—H···Cl interactions. Halides are among the strongest hydrogen-bond acceptors, and analysis of the hydrogen-bonding motifs described by O—H···Cl, N—H···Cl and weaker interactions permits investigation of the chloride ion as a suitable template for the self-assembly of amino alcohols.



(I)

The title compound, (I), can be viewed as a chirally substituted derivative of ethylene diamine (Fig. 1). An inversion centre at $(\frac{1}{2}, \frac{1}{2}, \frac{1}{2})$ pairs cyclohexyl (*S*,*S*) groups bonded to

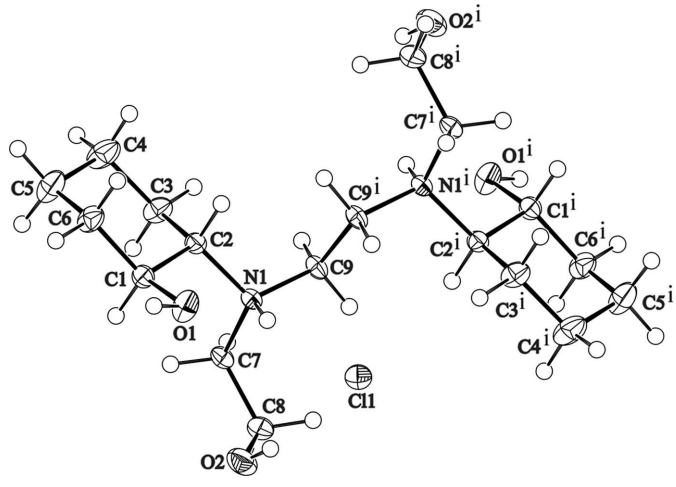


Figure 1
The molecular structure of (I), showing the atomic numbering scheme. Displacement ellipsoids are drawn at the 50% probability level. [Symmetry code: (i) $-x+1, -y+1, -z+1$.]

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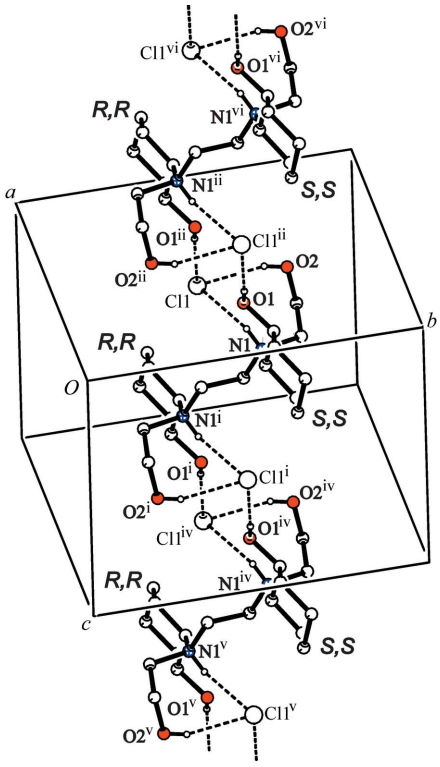

Figure 2
The intermolecular O—H···Cl and N—H···Cl interactions in (I) (dashed lines), forming chains along [001]. [Symmetry codes: (i) $-x+1, -y+1, -z+1$; (ii) $-x+1, -y+1, -z$; (iv) $x, y, z+1$; (v) $-x+1, -y+1, -z+2$; (vi) $x, y, z-1$.]

an *R* amine N atom at (*x*, *y*, *z*) with (*R*,*R*) cyclohexyl groups bonded to an *S* amine N atom at ($-x+1, -y+1, -z+1$), affording the achiral diastereomer of (I). The CyEA fragments of (I) occur in distorted *syn* conformations, with torsion angles N1—C2—C1—O1 = 53.12 (13)° and N1—C7—C8—O2 = 72.17 (14)° for the hydroxycyclohexyl and hydroxyethyl pendents, respectively. The hydroxyalkyl torsion angles in (I) show larger deviations from the strain-free values (de Sousa *et al.*, 1991; Kemp & Vellacio, 1980) compared with the *syn* conformer [58.98 (10) and −65.06 (13)°] reported for CyEA (de Sousa *et al.*, 2010).

$R_2^2(16)$ and $R_2^2(10)$ hydrogen-bonded dimers have been previously reported for *syn* and *anti* CyEA enantiomeric pairs (de Sousa *et al.*, 2010). These ring motifs are observed for O—H···O and N—H···O interactions where the hydroxycyclohexyl O atom acts as a hydrogen-bond acceptor. In the presence of the chloride ion, acting as an additional strong hydrogen-bond acceptor, these interactions are not observed in the structure of (I). Hydroxycyclohexyl atom O1 and hydroxyethyl atom O2 interact with acceptors $Cl1^{ii}$ [symmetry code: (ii) $-x+1, -y+1, -z$] and Cl1 *via* atoms H10 and H12, respectively, to generate an $R_4^2(20)$ motif (Bernstein *et al.*, 1995) (Table 1 and Fig. 2) centred at ($\frac{1}{2}, \frac{1}{2}, 0$) when combined with interactions $O2^{ii}$—$H12^{ii}$···$Cl1^{ii}$ and $O1^{ii}$—$H10^{ii}$···Cl1. Combining symmetrically equivalent interactions N1—H11···Cl (Table 1) and $N1^{ii}$—$H11^{ii}$···$Cl1^{ii}$ with hydroxycyclohexyl interactions $O1^{ii}$—$H10^{ii}$···Cl1 and O1—H10···$Cl1^{ii}$, respectively, generates an $R_4^2(14)$ motif. $R_4^2(20)$ and $R_4^2(14)$ motifs observed in the structure of (I) may be viewed as enlarged $R_2^2(16)$ and $R_2^2(10)$ motifs, in which O—H···O and N—H···O interactions are replaced by O—H···Cl and N—H···Cl counterparts upon inclusion of the halide. The latter interactions play a predominant role in assembling molecules of (I) into chains along [001] (Fig. 2). Chain motifs $C_2^1(13)$ and $C_2^1(10)$, defined along the ethylene backbone, join $R_4^2(20)$ and $R_4^2(14)$ dimers, respectively. The [001] motif is therefore best represented as a chain of rings, *viz.* $C_2^1(13)R_4^2(20)C_2^1(10)$-$R_4^2(14)$.

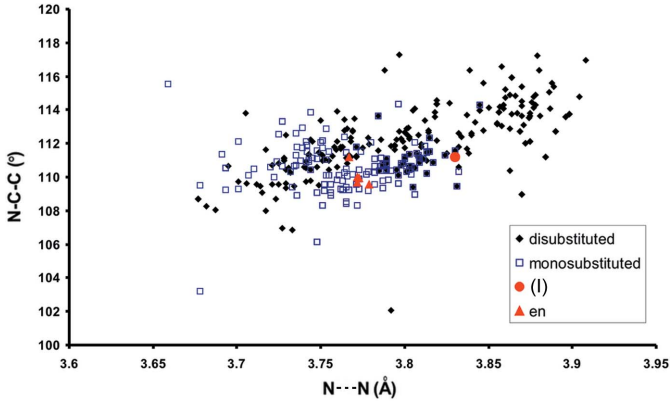

Figure 3
A plot of N—C—C bond angle *versus* N···N separation for (I) (filled circle), ethylammonium dichloride [CSD refcodes EDAMCL04 (Dickman, 2007), EDAMCL06 (Gabro *et al.*, 2009), EDAMCL03 (Kooijman *et al.*, 2006) and EDAMCL05 (Seidel, 2008)] and ethylammonium dinitrate (CSD refcode KOHMID; George *et al.*, 1991) (filled triangles), and substituted ethylenediamine derivatives (open squares and solid diamonds).

The mean planes through the *syn* CyEA fragments in (I) are separated by 2.0 Å, compared with the previously reported $R_2^2(16)$ counterparts (3.2 Å; de Sousa *et al.*, 2010). However, the tubular stacks are segmented by the *trans* ethylene bridge between CyEA fragments. An inner hydrophilic core is segmented into hydrophilic pockets that separate adjacent $R_4^2(20)$ and $R_4^2(14)$ inversion centres (9.55 Å). Chains of hydrophilic segments describing the dimeric hydrogen-bonding ring motifs are flanked by hydrophobic columns of stacked cyclohexyl rings. A survey of the Cambridge Structural Database (CSD; Version 5.31; Allen, 2002) indicates that the *trans* conformation of ethylenediamine is subject to distortion in mono- and disubstituted derivatives of this compound (Fig. 3). Variations in N—C—C bond angle and ethylene chain length, as measured by N···N distance, are pronounced for substituted ethylenediamine compounds compared with the recent structures of ethylenediammonium dichloride (Dickman, 2007; Gabro *et al.*, 2009; Kooijman *et al.*, 2006; Seidel, 2008) and ethylenediammonium dinitrate (George *et al.*, 1991). The N1—C9—$C9^{i}$ bond angle [111.56 (12)°] is less than the calculated average bond angle (112.2°) for disubstituted ethylenediamine derivatives, comparing favourably with the value observed in ethylammonium dinitrate (111.19°) which exhibits nitrate hydrogen-bond bifurcation. However, the ethylene chain length as measured by the N1···$N1^{i}$ distance [3.830 (2) Å]

compares with the calculated average length (3.82 Å). The conformations adopted in the hydrogen-bonded chain are largely influenced by O—H···Cl and N—H···Cl interactions; C—H···Cl contacts (Table 1) are of lesser significance. A very weak interaction, C7—H7*A*···Cl1^{iii} (Table 1), of the hydroxyethyl pendent links adjacent [001] chains to form undulating layers along (011) in the solid state.

In conclusion, the influence of the chloride ion upon the hydrogen-bonding interactions of (I) confirms its role as a template for the assembly of β-amino alcohols bearing cyclohexyl pendents. Segmentation of the hydrophilic inner core is less desirable for the controlled synthesis of porous materials (Ishida *et al.*, 2003). Congruency of *N*-alkyl chain conformation, linking CyEA molecules, with hydrogen-bond orientation is necessary for achieving a central hydrophilic core in synthesizing larger supramolecular amino alcohol structures.

Table 1
Hydrogen-bond geometry (Å, °).

D—H···*A*	*D*—H	H···*A*	*D*···*A*	*D*—H···*A*
O1—H10···Cl1^{ii}	0.78 (2)	2.40 (2)	3.1819 (11)	178.6 (19)
N1—H11···Cl1	0.877 (16)	2.411 (16)	3.2239 (12)	154.4 (13)
O2—H12···Cl1	0.806 (19)	2.34 (2)	3.1089 (12)	160.0 (18)
C7—H7*A*···Cl1^{iii}	0.99	2.78	3.5834 (13)	139
C9—H9*A*···Cl1^{i}	0.99	2.68	3.4830 (14)	138

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

Experimental

Chemicals were used as obtained, *viz*. ethanolamine and magnesium sulfate from Merck, cyclohexene oxide and 1,2-dibromoethane from Aldrich, and potassium carbonate from Saarchem.

The reagent 2-[(2-hydroxyethyl)amino]cyclohexanol was synthesized as reported previously (de Sousa *et al.*, 2010). A suspension of 2-[(2-hydroxyethyl)amino]cyclohexanol (0.6 g, 3.77 mmol) and potassium carbonate (0.2633 g, 1.89 mmol) in dried dimethylformamide (10 ml) was allowed to reflux, followed by dropwise addition of an anhydrous 1,2-dibromoethane (0.3596 g, 1.89 mmol) dimethylformamide solution (4 ml) over 30 min. The reaction was allowed to reflux for a further 72 h before the solvent was removed under reduced pressure to yield an orange–brown viscous oil. The oil was dissolved in chloroform (30 ml) and solid KBr removed by filtration. The chloroform solution was washed with deionized water (3 × 20 ml) and dried over magnesium sulfate. Filtration and removal of solvent down to dryness produced a clear orange oil which was characterized by NMR and FAB–MS to be the desired product. Addition of concentrated HCl to an ethanolic solution of this product afforded the dihydrochloride salt as an off-white powder that crystallized upon cooling from hot absolute ethanol (yield 31%). ^{1}H NMR (D_2O, 300 MHz): δ 3.73–3.37 (6H, *m*, 2CH, $2CH_2$), 2.84–2.23 (10H, *m*, 2CH, $4CH_2$), 2.03–1.51 (8H, *m*, $4CH_2$), 1.29–0.99 (8H, *m*, $4CH_2$); ^{13}C NMR ($CDCl_3$, 300 MHz): δ 70.54, 69.59, 67.17, 64.31, 60.81, 59.69, 52.69, 51.68, 51.58, 46.80, 34.38, 25.91, 25.84, 24.79, 23.09, 22.15; MS, *m*/*z* (FAB): 345 (M^+, 100%).

Crystal data

$C_{18}H_{38}N_2O_4^{2+}\cdot 2Cl^-$
M_r = 417.40
Monoclinic, $P2_1/c$
a = 9.6668 (3) Å
b = 11.7616 (4) Å
c = 9.5471 (3) Å
β = 97.210 (2)°
V = 1076.89 (6) Å^3
Z = 2
Mo $K\alpha$ radiation
μ = 0.33 mm^{-1}
T = 173 K
0.30 × 0.22 × 0.10 mm

Data collection

Bruker APEXII CCD area-detector diffractometer
Absorption correction: integration [face-indexed correction using *XPREP* in *SHELXTL* (Sheldrick, 2008)]
T_{min} = 0.918, T_{max} = 0.969
13823 measured reflections
2668 independent reflections
2233 reflections with $I > 2\sigma(I)$
R_{int} = 0.050

Refinement

$R[F^2 > 2\sigma(F^2)]$ = 0.034
$wR(F^2)$ = 0.086
S = 1.06
2668 reflections
128 parameters
H atoms treated by a mixture of independent and constrained refinement
$\Delta\rho_{max}$ = 0.40 e Å^{-3}
$\Delta\rho_{min}$ = −0.22 e Å^{-3}

PLATON (Spek, 2009) indicated that there was a minor twinning problem and the TwinRotMax function was used to generate an HKLF 5 file (Sheldrick, 2008) for use in the final refinement. This file therefore contains the non-overlapped reflections from the major twin component, but not from the minor component, plus the overlapped reflections from both twin components; details are in the `_refine_special_details` section of the CIF. Final refinement gave a twin volume fraction of 0.1187 (14) for the major twin component. H atoms were visible in the difference map and those bonded to C atoms were positioned geometrically and allowed for as riding, with C—H = 1.00 (CH) or 0.99 Å (CH_2). The coordinates of the H atoms involved in hydrogen bonding were refined freely. For all H atoms, U_{iso}(H) = 1.2U_{eq}(C,N,O).

Data collection: *APEX2* (Bruker, 2005); cell refinement: *APEX2*; data reduction: *SAINT-Plus* (Bruker, 2005); program(s) used to solve structure: *SHELXS97* (Sheldrick, 2008); program(s) used to refine structure: *SHELXL97* (Sheldrick, 2008); molecular graphics: *SHELXTL* (Sheldrick, 2008) and *PLATON* (Spek, 2009); software used to prepare material for publication: *SHELXTL*.

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Supplementary data for this paper are available from the IUCr electronic archives (Reference: FG3200). Services for accessing these data are described at the back of the journal.

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