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Journal of Chemical Crystallography

Resolution of the (1R,2S) Enantiomer of cis-Cyclohexane-1,2-dicarboxylic Acid in the Brucinium Salt 2,3-Dimethoxy-10-oxostrychnidinium (1R,2S)-2-carboxycyclohexane-1-carboxylate Dihydrate. --Manuscript Draft--

Manuscript Number:	JOCC2357R1			
Full Title:	Resolution of the (1R,2S) Enantiomer of cis-Cyclohexane-1,2-dicarboxylic Acid in the Brucinium Salt 2,3-Dimethoxy-10-oxostrychnidinium (1R,2S)-2-carboxycyclohexane-1-carboxylate Dihydrate.			
Article Type:	Original Research			
Keywords:	brucine; cis-cyclohexane-1,2-dicarboxylic acid; proton-transfer compound; hydrogen bonding			
Corresponding Author:	Graham Smith, PhD Queensland University of Technology Brisbane, Queensland AUSTRALIA			
Corresponding Author Secondary Information:				
Corresponding Author's Institution:	Queensland University of Technology			
Corresponding Author's Secondary Institution:				
First Author:	Graham Smith, PhD			
First Author Secondary Information:				
Order of Authors:	Graham Smith, PhD			
	Urs D. Wermuth, PhD			
	Michael L. Williams, PhD			
Order of Authors Secondary Information:				
Abstract:	The structure of the 1:1 brucinium salt of cis-cyclohexane-1,2-dicarboxylic acid, 2,3- dimethoxy-10-oxostrychnidinium (1R,2S)-2-carboxycyclohexane-1-carboxylate dehydrate, has revealed the resolved (1R,2S) enantiomer of the acid. Crystals of the compound are orthorhombic, space group P212121, with unit cell dimensions a = 8.1955(3), b = 12.4034(3), c = 29.9073(9)Å, and Z = 4. The asymmetric unit comprises the brucinium cation, the hydrogen cis-cyclohexane-1,2-dicarboxylate cation, in which the carboxylate group is disordered over two sites (58, 42%), and two water molecules of solvation, one of which occupies two 50% sites. The classic undulating brucinium cation substructures are present, with the anion and the water molecules occupying the interstitial cavities and are hydrogen-bonded to them in a two-dimensional network structure.			
Response to Reviewers:	 Article JOCCxxxx Replies and Actions taken post-Review for the Article. Minor corrections have also been made where indicated by the Reviewers. Also, I have completed a re-refinement of the structure paying attention to the handling of the disorder in the carboxylate group of the cyclohexane-1,2-carboxylate (CHDC) monoanion and in so doing I have rectified the problem of the high difference residual in the original structure. There has been little change to the original Discussion except in those points pertaining to the disorder and the numerical values contained in the text and tables. All figures except Fig. 2 remain unchanged from the original submission. (1) The revised manuscript has been uploaded. (2) The revised Fig. 2 as been uploaded. 			
	 (3) The revised CIF has been submitted to the CSD replacing the original deposited 			

CIF (CCDC 838579)
Responses are as below:
Reviewer #1.
Points (1)-(4).
The structure shows no signs of major structural problems, the only oddity is the rotationally disordered carboxyl group of the CHDC monoanion. On the matter of space group ambiguity the above is not going to be the reason. The disorder affects only two carboxyl O atoms in a total formula of 43 non-H atoms. Furthermore the space group options are limited with brucine structures with the requirement of chirality, the known space groups being limited to four in total: P1, P21, C2 and P212121, the latter providing probably 60% of the total.
On these counts I therefore reject a mis-assigned space group or crystal class as being the causative factor in the resultant higher-than-expected R factors.
However, in the structure, although the brucinium cation is thermally stable with small, almost isotropic displacement parameters (Ueq ca. 0.03-0.04), the values for the atoms of the CHDC anion are invariably larger and irregularly anisotropic (0.04-0.10). This I would suggest is the major contributing factor to the problem and the higher-than-expected refinement residual. Supporting this contention is the observation that the CHDC anions in a number of structures I have determined recently (there are very few examples of cis-CHDC salts
in the crystallographic literature) (three examples are in fact contained in a JOCC paper which I am working on at the moment, two of which have significant conformational disorder in the CHDC ring).
Reviewer #2.
The modelling of the disordered carboxylate group. I have addressed this matter applying DANG constraints to both the major and minor components of the disordered carboxyl group. In addition I have refined the O-atoms with the incorporation of a split carboxyl O (O15A) with an S.O.F. of 0.12 which now absorbs the electron density which contributed to the abnormally large residual electron density (1.07 eÅ-3). This residual now is more satisfactory at 0.54 eÅ-3. The Refinement residual is not changed significanty (R = 0.068)

(a) Cover Page

Resolution of the Chiral (1*R*,2*S*) Enantiomer of *cis*-Cyclohexane-1,2-dicarboxylic Acid in the Brucinium Salt 2,3-Dimethoxy-10-oxostrychnidinium (1*R*,2*S*)-2carboxycyclohexane-1-carboxylate Dihydrate.

Graham Smith*

Science and Engineering Faculty, Queensland University of
Technology, G.P.O. Box 2434, Brisbane, Qld. 4001, Australia.
Telephone: (07) 3864 2293; Fax. (07) 3864 1804; e-mail: <u>g.smith@qut.edu.au</u>.

Urs D. Wermuth

Science and Engineering Faculty, Queensland University of Technology, G.P.O. Box 2434, Brisbane, Qld. 4001, Australia.

Michael L. Williams

School of Biomolecular and Physical Sciences, Griffith University Nathan, Qld. 4111, Australia.

(b) Index Abstract

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Figure for insertion in Index Abstract: (CHDCBRUAbs.TIF)



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(c,d). Title: Authors and Affiliations

Title

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Authors and Affiliations

Graham Smith*

Science and Engineering Faculty, Queensland University of
Technology, G.P.O. Box 2434, Brisbane, Qld. 4001, Australia.
Telephone: (07) 3864 2293; Fax. (07) 3864 1804; e-mail: <u>g.smith@qut.edu.au</u>.

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School of Biomolecular and Physical Sciences, Griffith University Nathan, Qld. 4111, Australia.

Abstract

The structure of the 1:1 brucinium salt of *cis*-cyclohexane-1,2dicarboxylic acid, 2,3-dimethoxy-10-oxostrychnidinium (1*R*,2*S*)-2carboxycyclohexane-1-carboxylate dihydrate, has revealed the resolved (1*R*,2*S*) enantiomer of the acid. Crystals of the compound are orthorhombic, space group $P2_12_12_1$, with unit cell dimensions a = 8.1955(3), b = 12.4034(3), c =29.9073(9)Å, and Z = 4. The asymmetric unit comprises the brucinium cation, the hydrogen *cis*-cyclohexane-1,2-dicarboxylate cation, in which the carboxylate group is disordered over two sites (58, 42%), and two water molecules of solvation, one of which is occupies two 50% occupancy sites. The classic undulating brucinium cation substructures are present with the anion and the water molecules occupying the interstitial cavities and are hydrogen-bonded to them in a two-dimensional network structure.

Key Words: brucine; *cis*-cyclohexane-1,2-dicarboxylic acid; proton-transfer compound; hydrogen bonding.

Running Title:

brucinium (1R,2S)-2-carboxycyclohexane-1-carboxylate dihydrate

Resolution of the Chiral (1*R*,2*S*) Enantiomer of *cis*-Cyclohexane-1,2dicarboxylic Acid in the Brucinium Salt 2,3-Dimethoxy-10oxostrychnidinium (1*R*,2*S*)-2-carboxycyclohexane-1-carboxylate Dihydrate.

by

Graham Smith^{*}, Urs D. Wermuth and Michael L. Williams Introduction

Cyclohexane-1,2-dicarboxylic acid may exist in two diastereoisomeric forms, one *trans* [(1*R*,2*R*) or (1*S*,2*S*)], the other *cis* [(1*R*,2*S*) or (1*S*,2*R*)]. Whereas the *trans*-isomer forms separable *dl* pairs, with the *cis*-isomer, the *dl* pairs are inseparable because the two enantiomeric forms have a low interconversion potential, hence forming racemic pairs [1]. Quinine and cinchonidine have been used for the resolution of the *trans*-form of the acid [2] but brucine has not, although it has been used on a hit-or-miss basis for the resolution of racemic carboxylic acids, first by Emil Fischer in 1899 [3] with the *N*-benzoyl derivatives of the amino acids alanine, glutamic acid and aspartic acid. The crystal structures of a number of these chiral salts have been determined, e.g. *N*-benzoyl-D- α -alanine [4]; (*S*)-3-[2,4--dimethyl-5-(ethoxycarbonyl)-1*H*-pyrrol-3-yl]butanoic acid [5]; α -D-glucuronic and β -Dgalacturonic acids [6]; *N*-phthaloyl-L- α -alanine [7]; L-glyceric acid [8] and (*S*)malic acid and (2*R*,3*R*)-tartaric acid [9]. The crystalline product from our 1:1 stoichiometric reaction of cyclohexane-1,2-dicarboxylic anhydride with brucine in aqueous ethanol was the hydrated title salt $C_{23}H_{27}N_2O_4^+ C_8H_{11}O_4^-$. 2H₂O (**1**) (scheme 1) and the structure is reported here.

INSERT 1 Schematic of 1 is given here (CHDCBRU.eps)

The molecular structure of 1

Experimental

Preparation. The title compound **1** was synthesized by heating together under reflux for 10 min., 1 mmol quantities of brucine tetrahydrate and cyclohexane-1,2-dicarboxylic anhydride in 50 mL of 50% ethanol-water. After concentration to *ca.* 30 mL, partial room temperature evaporation of the hot-filtered solution gave colourless plates of **1** (m.p. 101 $^{\circ}$ C) from which a specimen was cleaved for the X-ray analysis.

Crystallography.

X-ray diffraction data were acquired for **1** at 180(2) K on an Oxford Diffraction Gemini-S Ultra CCD-detector diffractometer employing graphite crystal monochromatized Mo $K\alpha$ radiation ($\lambda = 0.71073$ Å). Data collection and reduction was completed using CrysAlis PRO [10] with data corrected for absorption (multi-scan, CrysAlis PRO [10]). The structure was solved using direct methods (SIR92 [11]) and refined with SHELXL97 [12] operating within WinGX [13]. The carboxylate group at C1 of the anion was found to be rotationally disordered over three sites with the occupancy of the four oxygen atoms being determined as O11A (0.58), O12A (0.38), O15A (0.12) and O13A, and O14A both 0.42), all components subsequently being refined isotropically.

5

Water molecules O3W and O4W were found to have 50(1)% occupancy. Hydrogen atoms potentially involved in hydrogen-bonding interactions were located by difference methods but their positional and isotropic thermal parameters were constrained in the final refinement cycles. Other H atoms were included in the refinement at calculated positions and treated as riding with C-H = 0.93-0.98Å and $U_{iso}(H) = 1.2U_{eq}(C)$. In the absence of a heavy atom and because the known absolute structure for the strychnidin-10-one cage was invoked [14] [giving the overall absolute structure classification as C7(*S*), C8(*S*), C12(*S*), C13(*R*), C14(*R*), C16(*S*), N19(*S*) for the brucinium cation], the Friedel pairs (2868) being merged in the final cycles of refinement. General crystallographic details are given in Table 1. The atom numbering scheme employed for the brucinium cation species (Fig. 1) [15] follows the original Robinson convention for strychnine [16].

Results and Discussion

In the structure of compound **1**, protonation has occurred as expected at N19 of the brucine cage (Fig. 1), the invoked Peerdeman absolute configuration [14] for the seven chiral centres in the brucinium cation allowing the assignment of the configuration of the *cis*-anion component as (1R,2S)-2-carboxycyclohexane-1-carboxylate. In this anion, the carboxylate group has an atypical (for this anionic species) rotational disorder giving four oxygen atoms sites for the two groups [O11A, O12A (S.O.F = 0.58(1)) and O13A, O14A (S.O.F. = 0.42(1))].

INSERTS 2, 3:

Figure 1 (Atom numbering scheme for the cation, anion and water species in the asymmetric unit of 1) CHDCBRU1.TIF

Figure 2 (The cation-anion-water hydrogen-bonding interactions) CHDCBRU2.TIF

The brucinium cations form the previously described head-to-tail overlapping, undulating sheet host substructures [4,6-9] with a dimeric repeat period in 1 along the direction of propagation (a 2_1 screw axis: the *b* cell dimension) of 12.4034(3)Å [16] (Figs. 2, 3). This value is consistent with those for similarly structured brucine compounds (range 12.366-12.660 Å) [4, 17]. The monoanion and the three water molecules [two of which (O2W and O3W) have a site occupancy of 0.50(1)], occupy the interstitial spaces between the brucine substructures and are hydrogen-bonded to them (Table 1, Fig. 2), giving a two-dimensional structure (Fig. 4). Interactions include brucine aminium N-H...O(carboxyl), water O-H...O(brucine carbonyl), and strong carboxylic acid O-H...O(water) hydrogen bonds. In addition, the water molecules are inter-associated, with all giving hydrogen-bonding interactions, with the exception of one of the H atoms of water molecule O3W (H32W) which has no reasonable acceptor in the structure. The water stabilization of brucinium carboxylates is quite common, e. g. the Nbenzoylalaninate [4] (a 4.5-hydrate); the glycerate [8] (a 4.75--hydrate); the dihydrogen citrate [18] (a trihydrate), and the (S)-malate [9] (a pentahydrate).

INSERTS 4 and 5:

Figure 3 (the undulating brucine substructure) (CHDCBRU3.TIF) Figure 4 (packing of 1 in the unit cell) CHDCBRU4.TIF)

Conclusion

This work provides another example of the molecular selectivity of brucine in

forming stable salts having the classic brucine host substructures, and also

represents the first reported structure of a resolved enantiomer of cis-

cyclohexane-1,2-dicarboxylic acid or its salt as a guest molecule.

Supplementary material

CCDC 838579 contains the supplementary crystallographic data for compound 1 from this paper. These data can be obtained free of charge from The Cambridge Crystallographic Data Centre *via* http:// www.ccdc.cam.ac.uk/data_request/cif_ or by e-mailing data_request@ccdc.cam.ac.uk, or by contacting The Cambridge Crystallographic Data Centre, 12 Union Road, Cambridge CB2 1EZ, UK.

Acknowledgements.

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Table 1. Crystal data for compound 1.

Compound	1
CCDC reference	838579
Molecular formula	$C_{31}H_{42}N_2O_{10}$
M _r	603.67
Temperature (K)	180(2)
Wavelength (λ)	0.71073
Crystal system	orthorhombic
Space group	P212121
a (Å)	8.1955(3)
<i>b</i> (Å)	12.4034(3)
<i>c</i> (Å)	29.9073(9)
$V(\text{\AA}^3)$	3040.14(16)
Ζ	4
$D_{\rm c} ({\rm g}{\rm cm}^{-3})$	1.317
$\mu (\text{mm}^{-1})$	0.098
<i>F</i> (000)	1288
Instrument	Oxford Diffraction
	CCD
Reflections total, θ_{max} (°)	11479, 28.7
Crystal size (mm)	0.40 x 0.30 x 0.28
Collection range:	
h	-10 to 7
k	-9 to 15
<i>l</i>	-24 to 39
Reflections (independent)	3953
Reflections $[F^2 > 2 \sigma(F^2)]$	3378
R _{int}	0.0287
$R1^{a} [F^{2} > 2\sigma(F^{2})]$	0.0684
$wR2^{a}$ (all data)	0.2007
S ^a	1.04
n_p	399
Transmission factors	0.990/0.908
(max/min)	
Residuals (max/min) ($e\dot{A}^{-3}$)	0.544/-0.385

^a $R1 = (\Sigma |F_{o}| - |F_{c}|) / \Sigma |F_{o}|; wR2 = \{\Sigma [w(F_{o}^{2} - F_{c}^{2})^{2}] / \Sigma [w(F_{o}^{2})^{2}]\}^{\frac{1}{2}}; S = \{\Sigma [w(F_{o}^{2} - F_{c}^{2})^{2}] / (n-p)\}^{\frac{1}{2}}.$

D-HA	D-H	HA	DA	∠ DHA
N19-H19O11A	0.91	1.69	2.583(6)	168
N19-H19O13A	0.91	1.78	2.657(10)	162
O22A-H22AO1W ⁱ	0.91	1.77	2.601(7)	151
O1W-H11WO25 ⁱⁱ	0.92	1.83	2.753(6)	173
O1W-H12WO2W	0.80	2.05	2.631(10)	130
O2W-H21WO12A	0.88	1.78	2.686(15)	178
O2W-H22WO3W	0.90	1.68	2.582(13)	180
O3W-H31WO14A ⁱⁱⁱ	0.90	2.41	3.015(18)	127

Table 2. Hydrogen-bonding interactions (Å/ °) for 1

Symmetry codes: (i) x + 1, y, z; (ii) -x + 1, $y + \frac{1}{2}$, $-z + \frac{11}{2}$; (iii) x - 1, y, z.

Figures

Figure 1. Atom numbering scheme for the cation, anion and the two water molecules of solvation, two of which (O2W,O3W) have 50% occupancy. The carboxylate group is also disordered over two sites. Inter-species hydrogen bonds are shown as dashed lines and non-hydrogen atoms are shown as 30% probability ellipsoids [26].

- Figure 2. The cation-anion-water hydrogen-bonding environment in 1 showing the head-to-tail overlap of the brucinium cations in the substructure extending along *b*. For symmetry codes, see Table 2.
- **Figure 3**. The convoluted brucinium cation host substructures with interstitial guest anions and water molecules removed.
- Figure 4. A perspective view of 1 in the unit cell viewed down the approximate *a* axial direction. The minor disordered component of the carboxylate group is omitted for clarity.

molecule scheme Click here to download Figure: CHDCBRU.eps











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