

The Crystal Structure of γ -Aminobutyric Acid Hydrochloride: A Refinement

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The crystal structure of γ -aminobutyric acid hydrochloride originally determined by Tomita [*Jap. J. Brain Physiol.* (1965). **61**, 1–4], has been refined. The general form of the molecule is confirmed as being 'fully-trans'. The structure now reveals a bifurcated hydrogen bond between an amino hydrogen and two chlorine atoms.

Introduction

The crystal structure of γ -aminobutyric acid hydrochloride, $C_4H_9NO_2 \cdot HCl$ (GABA.HCl) was first determined by Tomita (1965) from two projections, the reported residual factors for these being 0.22 (*h0l*) and 0.38 (*0kl*). In the light of the recent interest (Steward & Player, 1973) in the structural aspects of physiological activity of γ -aminobutyric acid (GABA) and its analogues it was considered necessary to obtain more accurate data for GABA.HCl than were provided by the previous determination.

Experimental

Platelet crystals of GABA.HCl were grown from ethanol solution trimmed to *circa* $0.2 \times 0.4 \times 0.4$ mm and stored in a desiccator. All reflexion data were collected using a Stoe-Güttinger diffractometer with Ni-filtered copper *K* radiation (1.5418 \AA) and a pulse-height analyser.

A redetermination of the cell constants from a least-squares refinement using the 2θ values of 24 *h0l* and 26 *hk0* reflexions gave $a = 9.040$ (3); $b = 6.528$ (2), $c = 5.900$ (3) \AA , $\beta = 99.82$ (3) $^\circ$. There were no systematic absences on the *b*-axis zero layer, but on the *c*-axis zero layer systematic absences occurred for *0k0* when $k = 2n + 1$: these are consistent with the previously reported space group $P2_1$. The calculated density, 1.332 g cm^{-3} , with $Z = 2$ compares well with density measured by the flotation method, 1.33 g cm^{-3} . The melting point of the crystals was found to be in the range $132\text{--}136^\circ\text{C}$.

Intensity data were collected from the *hnl* and *hkn* ($n = 0, 1, 2$) layers, to a limit of $\sin \theta/\lambda = 0.58$. 417 independent reflexions were measured of which 4 were systematically absent and 46 deemed 'unobserved' *i.e.* having integrated intensity less than 100 counts above background. The remaining 367 reflexions were regarded as 'observed'.

Data processing and structure refinement were effected using the X-RAY 70 suite of programs (Stewart, Kundell & Baldwin, 1970) implemented on the CDC

6600 and 7600 computers at the University of London Computer Centre. Atomic scattering factor data were taken from *International Tables* (Lonsdale, 1962).

The general form of the structure was confirmed by a *y*-axis Patterson projection. Refinement was started with the final coordinates reported by Tomita (1965) and these gave a residual factor [$R = \sum ||F_o| - |F_c|| / \sum |F_o|$] of 0.179. Three cycles of isotropic full-matrix least-squares refinement were carried out, minimizing the function $\sum [w(|F_o| - |F_c|)^2]$ with weights assigned according to the following scheme:

$$w = X \cdot Y,$$

if $\sin \theta > 0.4$, $X = 1$, else $X = (\sin \theta)/0.4$.

if $F_o < 9.0$, $Y = 1$, else $Y = 9.0/F_o$.

The largest reflexion measured, 020, was considered to be suffering from extinction and was assigned zero weight. $R = 0.105$ for the observed reflexions and $R = 0.115$ for all measured reflexions were obtained with these conditions. Final atomic parameters are given in Table 1. Bond lengths and angles are listed in Table 2.*

Table 1. Fractional atomic coordinates and isotropic temperature factors

	<i>x</i>	<i>y</i>	<i>z</i>	$U \times 100 \text{ \AA}^2$
Cl(1)	0.0620 (3)	0.25	0.2138 (5)	3.7 (1)
O(1)	0.726 (1)	0.726 (3)	0.148 (1)	4.2 (3)
O(2)	0.518 (1)	0.737 (4)	-0.115 (2)	4.5 (3)
C(1)	0.580 (1)	0.755 (7)	0.085 (2)	3.4 (3)
C(2)	0.497 (1)	0.745 (6)	0.289 (2)	3.6 (3)
C(3)	0.329 (1)	0.733 (7)	0.210 (2)	3.7 (3)
C(4)	0.246 (1)	0.765 (7)	0.420 (2)	3.9 (3)
N	0.082 (1)	0.744 (6)	0.332 (2)	4.0 (3)

Discussion of structure

The arrangement of the molecules in the unit cell is shown in Fig. 1. Each C–C bond length is within

* A table of structure factors has been deposited at the National Lending Library, England (Supplementary Publication No. SUP. 30174). Copies may be obtained through The Executive Secretary, International Union of Crystallography, 13 White Friars, Chester CH1 1NZ, England.

Table 2. Bond lengths (\AA) and bond angles ($^\circ$)

O(1)–C(1)	1.32 (2)
O(2)–C(1)	1.22 (2)
C(1)–C(2)	1.53 (2)
C(2)–C(3)	1.52 (2)
C(3)–C(4)	1.56 (2)
C(4)–N	1.49 (2)

In addition, possible hydrogen bonds:

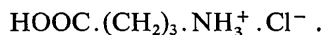
N—Cl ^(i-iv)	3.29 (4), 3.38 (4), 3.18 (1), 3.26 (1)
O(1)–Cl	3.11 (1)

O(1)–C(1)–O(2)	122 (1)
O(1)–C(1)–C(2)	112 (1)
O(2)–C(1)–C(2)	124 (1)
C(1)–C(2)–C(3)	111 (1)
C(2)–C(3)–C(4)	110 (1)
C(3)–C(4)–N	107 (1)

In addition, possible hydrogen bonds:

C(4)–N—Cl ^(i-iv)	100 (2), 91 (2), 103 (1), 123 (1)
C(1)–O(1)–Cl	120 (1)

experimental error of the expected value. The N–C(4) bond length (1.49 \AA) is longer than the standard value, suggesting the presence of a charged NH_3^+ group. In addition, the two C–O bond lengths (1.32, 1.22 \AA) are consistent with an uncharged carboxyl group. In the crystalline state the molecule appears to exist, therefore, as:



There are three amino and one carboxyl hydrogen atom available for hydrogen bonding. However, this structure refinement reveals that in addition to the carboxyl hydrogen that is suitably located for hydrogen bonding, there are four possible N–Cl distances consistent with hydrogen bonding. Of these, Clⁱ and Clⁱⁱⁱ (Fig. 1.) are arranged tetrahedrally (within 10°) about the amino group. If hydrogen atoms are placed along these N–Cl bonds at a distance of 1.05 \AA from the nitrogen, the position of the third amino hydrogen may be calculated, assuming an approximately tetrahedral configuration for the amino group. The distance of this hydrogen atom from both Clⁱ and Cl^{iv} (Fig. 2) is within the sum of the van der Waals radii of 3.0 \AA (Pauling, 1939), and bifurcation of the hydrogen bond may be deduced (Donohue, 1968).

The molecule is held by the network of hydrogen bonds in the 'fully-trans' conformation with the plane of the GABA.HCl molecule nearly normal to the *b* axis. This conformation is different from the 'gauche' conformation found in the free acid, γ -aminobutyric acid (Steward, Player & Warner, 1973).

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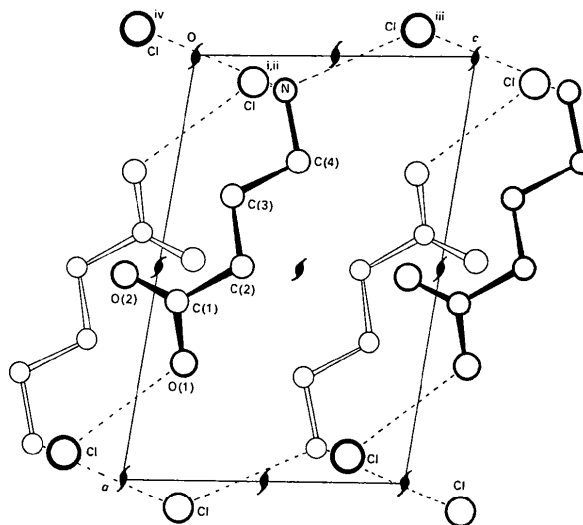


Fig. 1. Arrangement of GABA.HCl molecules in the unit cell viewed along the *y* axis.

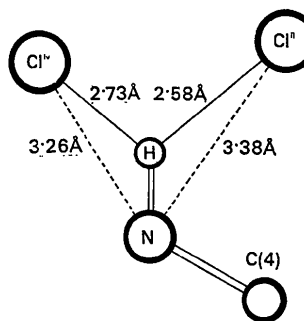


Fig. 2. Schematic diagram of the proposed bifurcated hydrogen bond.

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