Structural Studies of Tryptophan Metabolites by X-ray Diffraction Method. III. The Crystal and Molecular Structure of 5-Methoxyindole-3-acetic Acid

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The crystal structure of 5-methoxyindole-3-acetic acid (5-MIAA) has been solved by application of the direct method with symbolic addition procedure. 5-MIAA, colorless transparent prism, is monoclinic, space group C2/c, with lattice parameters: a=34.461(9) Å, b=6.150(5) Å, c=9.480(5) Å, $\beta=96.14(2)$ °, Z=8. The molecules are hydrogen-bonded into dimers related by the center of symmetry, which are held together in an infinite double-layered sheet structure perpendicular to the a-axis with N-H···O hydrogen bond between indole nitrogen and carboxyl oxygen atoms. The methyl groups of adjacent molecules contact to each other by van der Waals forces. The conformation of the side-chain is quite distinguishable from that of indole-3-acetic acid. The dihedral angle between carboxyl and indole planes is 59.5 ° in this molecule, whereas that is 90.0 ° in indole-3-acetic acid, and the carboxyl group sticks out to be perpendicular to the indole plane.

5-MIAA, one of the final products in a metabolic pathway of tryptophan, is excreted into urine, through 5-hydroxyindole-3-acetaldehyde, etc.¹⁾ As a series of structural investigation of tryptophan metabolites,²⁻⁴⁾ the authors describe here the crystal and molecular structure of 5-MIAA in order to obtain the substantial information about the stereospecific conformation of individual metabolites suitable for performing the related enzyme action in living cells.

Experimental

The sample was purchased from the Sigma Co., and preliminary oscillation and Weissenberg photographs using the suitable crystal showed it to be monoclinic with space group as Cc or C2/c from systematic absent spectra, (hkl) with h+k=2n+1 and (h0l) with l=2n+1. The space group was determined finally as C2/c from the statistical distribution of normalized structure factors (E).5) The unit cell dimensions were determined with the Rigaku Denki automatic four circle diffractometer at room temperature. The density was measured by the floatation method in a benzene-carbon tetrachloride mixture. The crystallographic data are shown in Table 1. Intensities of 951 independent reflections having the number of counts over three times of standard deviation were measured with the diffractometer using Ni-filtered Cu-K α radiation, by means of $\omega/2\theta$ scan technique (crystal dimension: $0.10 \times 0.10 \times 0.35$ mm), and adjusted to the absolute scale by the program for Wilson's statistics. A Σ_2 list was then computed using 270 reflections with the normalized structure factors E, greater than 1.2.

Determination and Refinement of Structure

Phases for the reflections were determined by means of the symbolic addition procedure. To specify the origin for nonprimitive space group C2/c, two reflections with large E-values were chosen to have positive sign. ⁶⁾ The signs of other reflections having many Σ_2 interactions were specified by symbols a, b and c, respectively. This starting set is summarized in Table 2. By hand calculation, the phases of additional 219 reflections were determined in terms of the starting sign and symbols. Of the three-dimensional E maps calculated with possible two combinations (a=b=+, c=- and a=b=-, c=+), the former one revealed reasonable positive peaks which correspond to all non-hydrogen

TABLE 1. CRYSTAL DATA OF 5-MIAA

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C_{11}H_{11}NO_3, MW. 205.22

Colorless and transparent prisms, Monoclinic a=34.461(9), b=6.150(5), c=9.480(5) Å \beta=96.14(2)^{\circ} V=1997.3 ų, Z=8, F(000)=864 \mu (for Cu-K\alpha)=9.67 cm<sup>-1</sup> D_m=1.363 g/cm³, D_x=1.365 g/cm³ Absent spectra; (hkl):h+k=2n+1 (h0l):l=2n+1 Space group; C2/c
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Table 2. Starting set of 5-MIAA chosen for symbolic addition procedure

h	k	l	Phase	E
8	2	3	+	3.118
31	1	-1	+	3.325
3	1	2	a	4.152
6	2	5	b	3.067
22	2	-4	c	3.465

atoms. These positional parameters were refined by successive Fourier syntheses and block-diagonal least-squares method, first with the isotropic thermal parameters for all the non-hydrogen atoms, and then with the anisotropic temperature factors. At this stage, *R*-value was dropped to 0.120, and the difference Fourier synthesis was computed in order to find the position of eleven hydrogen atoms. (see Fig. 1). The

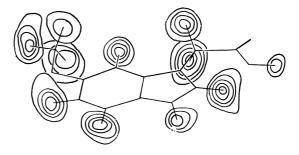


Fig. 1. The location of hydrogen atoms from a threedimensional difference Fourier map. Contours from 0.2 e. Å⁻³ at intervals of 0.2 e. Å⁻³.

Table 3. Observed and calculated structure factors for 5-MIAA

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final refinement by block-diagonal least-squares method was carried out with anisotropic temperature factors for all non-hydrogen atoms and with isotropic temperature factors for all hydrogen atoms to reduce R-value to 0.078. The electron density map is illustrated in Fig. 2. The observed and calculated structure factors obtained by the last cycle of refinement are given in Table 3, and the atomic coordinates and

thermal parameters with their estimated standard deviations in Table 4. In the structure factor calculation of 5-MIAA, the atomic scattering factors cited in "International Tables for X-ray Crystallography" (1962)?) were used, and all the numerical calculations were carried out on an NEAC-2200-700 computer of computation center of this University, using the UNICS programs.

Table 4. The final atomic coordinates and thermal parameters with their estimated standard deviations in parentheses $(\times 10^4$ for non-hydrogen atoms, $\times 10^3$ for hydrogen atoms)

	×	*	Z	B_{11}	\mathcal{L}_{22}	\mathcal{L}_{33}	\mathcal{B}_{12}	B_{13}	B_{23}
i	0.4508(2)	0.5029(12)	0.0775(7)	0.0009(1)	0.0242(23)	0.0098(9)	0.0015(7)	0.0010(4)	0.0004(24)
	0.4109(2)	0.4994(13)	0.1347(8)	0.0006(1)	0.0306(26)	0.0131(10)	-0.0003(7)	0.0023(4)	-0.0051(27)
	0.4063(2)	0.6864(12)	0.2365(7)	0.0006(1)	0.0267(23)	0.0095(8)	-0.0007(6)	0.0010(4)	-0.0006(25)
	0.3720(2)	0.7048(12)	0.3115(6)	0.0006(1)	0.0276(24)	0.0080(8)	0.0000(6)	0.0009(4)	-0.0013(24)
	0.3386(2)	0.5771(12)	0.3149(7)	0.0007(1)	0.0288(25)	0.0103(9)	0.0003(7)	0.0012(4)	-0.0047(25)
	0.3112(2)	0.6368(12)	0.4051(7)	0.0006(1)	0.0307(25)	0.0108(9)	-0.0008(7)	0.0015(4)	-0.0011(26)
	0.3170(2)	0.8290(13)	0.4873(7)	0.0007(1)	0.0358(28)	0.0114(10)	0.0003(8)	0.0022(4)	-0.0055(27)
	0.3493(2)	0.9536(13)	0.4864(7)	0.0009(1)	0.0325(28)	0.0112(10)	0.0003(8)	0.0017(5)	-0.0046(27)
	0.3770(2)	0.8946(12)	0.3940(7)	0.0006(1)	0.0294(25)	0.0101(9)	-0.0003(7)	0.0008(4)	-0.0001(25)
	0.4292(2)	0.8582(13)	0.2750(7)	0.0008(1)	0.0323(27)	0.0113(10)	-0.0003(8)	0.0012(4)	-0.0003(28)
	0.2682(2)	0.3487(14)	0.3301(8)	0.0008(1)	0.0372(31)	0.0171(13)	-0.0024(8)	0.0030(5)	-0.0061(33)
	0.4125(2)	0.9845(11)	0.3714(6)	0.0009(1)	0.0324(22)	0.0127(9)	-0.0021(6)	0.0014(4)	-0.0086(23)
	0.4713(1)	0.3326(9)	0.1087(5)	0.0009(1)	0.0413(21)	0.0153(8)	0.0036(6)	0.0036(3)	0.0167(21)
	0.4611(1)	0.6541(9)	0.0072(5)	0.0009(1)	0.0336(19)	0.0175(8)	0.0026(5)	0.0039(3)	0.0131(21)
	0.2770(1)	0.5327(9)	0.4182(5)	0.0008(1)	0.0418(21)	0.0143(7)	-0.0031(5)	0.0033(3)	-0.0103(21)
				В					
	0.496(2)	0.332(15)	0.074(8)	6.19					
	0.409(2)	0.344(11)	0.188(6)	2.01					
	0.387(2)	0.506(13)	0.045(7)	3.06					
	0.459(2)	0.897(12)	0.246(7)	3.02					
	0.424(2)	1.116(12)	0.416(7)	3.65					
	0.335(2)	0.428(11)	0.260(6)	1.75					
	0.293(2)	0.886(12)	0.535(7)	2.73					
	0.353(2)	1.098(11)	0.545(7)	2.59					
	0.285(2)	0.181(14)	0.353(8)	4.33					
	0.265(2)	0.381(13)	0.232(8)	4.21					
	0.241(2)	0.331(12)	0.342(7)	3.11					

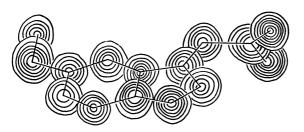
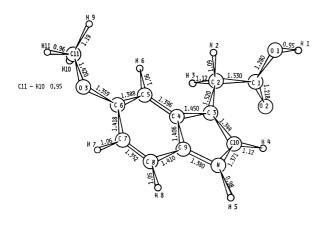


Fig. 2. Electron-density map for 5-MIAA viewed along b-axis.
Contours are drawn at intervals of 0.2 e. Å⁻³.

Description and Discussion of the Structure

The final bond lengths and angles are shown in Fig. 3, where the average standard deviations for non-hydrogen atoms are about 0.009 to 0.011 Å and 0.6 to 0.7°, respectively. The deviation from a regular trigonal angle of C(2)-C(3)-C(10) is about 11°, which is also observed in serotonin creatinine sulfate (about 6°)⁵⁾ and melatonin (about 5°).²⁾ This may be explained by the fact that the *cis*-orientation of C(3)-C(10) bond with respect to C(1)-C(2) bond around C(2)-C(3) bond causes bond angle C(2)-C(3)-C(10) to be larger by the repulsion between C(10) and C(1). The angle of C(3)-C(6)-C(5) is also about 11° larger than that of C(3)-C(6)-C(7), as well as melatonin C(3)0° or 5-methoxy-C(3)1°. This may be also explainable by similar



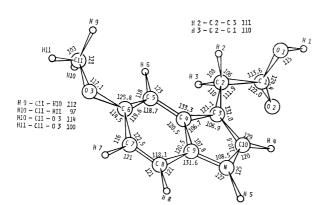


Fig. 3. The final bond lengths and angles of 5-MIAA.

reason described above, provided the special orientation of methoxy group around C(5)-C(6) bond is effective. The planarity of the two parts of the molecule, indole ring and carboxyl group, was examined by the equation of the least-squares plane. Equation for indole ring;

0.39119X - 0.54044Y + 0.74491Z = 4.74731.

Equation for carboxyl group and α-carbon atom;

0.31420X + 0.44497Y + 0.83862Z = 6.83928.

The deviations of the individual atoms from the best planes are given in Table 5. The H(1) atom lies almost on the plane through four atoms, C(1), O(1), O(2) and α -carbon C(2), whereas C(2) and O(3) are on the plane through indole ring, except C(11) atom which is slightly deviated. It is of interest to compare the molecular conformation of this compound with that of indole-3-acetic acid (IAA).⁹⁾ Relevant torsion angles¹⁰⁾ of IAA and 5-MIAA are given in Table 6 in order to elucidate the difference of conformation. The torsion angle C(10)-C(3)-C(2)-C(1) is in the region of anti-clinal in IAA, but syn-periplanar in 5-MIAA. (see Figure 4). The dihedral angle between the two

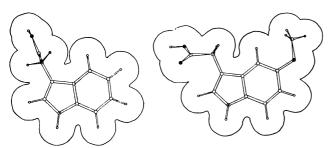
Table 5. Deviations of atoms from the least-squares planes through the indole ring and carboxyl group $(\text{in } \mathring{\mathbf{A}})$

Indol	e group	Acid group		
Atom	Distance	Atom	Distance	
C (3)	-0.0157	O(1)	0.0019	
C (4)	0.0117	O (2)	0.0021	
C(5)	0.0146	C(1)	-0.0056	
C (6)	-0.0159	C (2)	0.0016	
\mathbf{C} (7)	0.0011			
C (8)	-0.0143	*C (3)	-1.2325	
$\mathbf{C}(9)$	0.0278	*C (4)	-1.4799	
N	-0.0017	*C (10)	-2.2417	
C (10)	-0.0072	*H(1)	0.0025	
*C(1)	-0.1715			
*C (2)	-0.0247			
*C (11)	0.1036			
*O(1)	-1.2203			
*O(2)	0.6575			
*O(3)	0.0126			

Atoms with asterisk were excluded from the least-squares calculations. The mean deviation from the indole ring is 0.0122 Å and from the acid group is 0.0028 Å.

Table 6. Comparison of torsion angles between 5-MIAA and IAA

Bond sequence	IAA	5-MIAA
C(10) - C(3) - C(2) - C(1)	97.7°	6.0°
C(3)-C(2)-C(1)-O(1)	173.6	119.2
C(3)-C(2)-C(1)-O(2)	-11.7	-61.9
C(2)-C(1)-O(1)-H(1)	-175.2	-179.7
O(2)-C(1)-O(1)-H(1)	-0.5	-0.8
C(5)-C(6)-O(3)-C(11)		-1.1



Indole-3-acetic acid

5-Methoxyindole-3-acetic acid

Fig. 4. Comparison of conformation between 5-MIAA and IAA projected to indole ring plane.

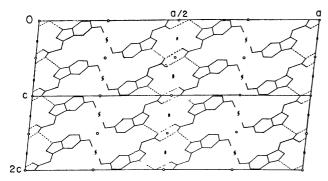


Fig. 5. The crystal structure of 5-MIAA viewed down along b-axis.

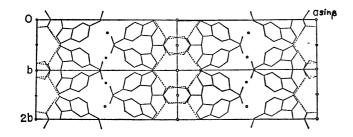


Fig. 6. The crystal structure of 5-MIAA viewed down along c-axis.

planes, one through carboxyl group and the other through indole ring, is 59.5° in 5-MIAA, while that is 90.0° in IAA. These facts may reflect that IAA and 5-MIAA are the final products of tryptophan metabolites in different metabolic pathways.1,11) The molecular arrangements in crystals viewed along b- and c-axes are shown in Figs. 5 and 6. Between the two adjacent molecules related by the center of symmetry, a dimer was formed at carboxyl end with O-H···O hydrogen bond. This dimer was also connected by hydrogen bond N-H(5)... O(2) around diad axis to make the infinite sheet elongated toward b- and c-axes. The methyl groups have very short contact to each other around the screw diad axis. (3.596 Å) In crystals, the polar part of the molecules is held together by hydrogen bond and the nonpolar part, by van der Waals forces. Therefore, it seems that the molecules are arranged into a double layered sheet structure perpendicular to a-axis with N-H···O hydrogen bonds between indole nitrogen and carboxyl oxygen atoms.

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