

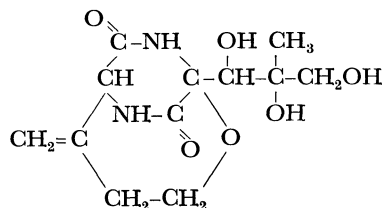
The Crystal and Molecular Structure of Bicyclomycin, a New Antibiotic

Yoji TOKUMA, Shigetaka KODA, Toshio MIYOSHI, and Yukiyoishi MORIMOTO

Research Laboratories, Fujisawa Pharmaceutical Co., Ltd., Higashiyodogawa-ku, Osaka 532

(Received August 27, 1973)

The molecular structure of a new antibiotic, Bicyclomycin ($C_{12}H_{18}O_7N_2$), has been elucidated by X-ray diffraction analysis. Bicyclomycin crystallizes from aqueous solution in two forms, an orthorhombic and a monoclinic systems. The crystal data for the former are $a=11.72$, $b=12.72$, $c=8.80$ Å and the space group $P2_12_12_1$, while those for the latter are $a=10.27$, $b=10.91$, $c=6.67$ Å, $\beta=101.4^\circ$, and the space group $P2_1$. The crystal structure of the former was solved by the direct method and refined by least-squares method to a final R factor of 0.07 for 1623 reflections. The established structure is



The diketopiperazine ring is folded into a boat form. The conformations of the side chain are all *gauche* or nearly so. All the oxygen and nitrogen atoms participate in two intramolecular and four intermolecular hydrogen bonds.

A new antibiotic Bicyclomycin was obtained from the culture filtrate of *Streptomyces sapporonensis* which was isolated from a soil sample collected at Sapporo City. Bicyclomycin has an antibacterial activity against Gram-negative bacteria and exhibits no cross resistance to major antibiotics for human use.¹⁾ Chemical and spectroscopic investigations²⁾ suggested several functional groups in the molecule, but the precise stereochemistry of the structure remained to be unknown. X-Ray diffraction study was thus undertaken to establish the whole structure of the molecule.

Experimental

Bicyclomycin crystallizes from aqueous solution in two forms, colorless prisms and plates. Oscillation and Weissenberg photographs uniquely identified the space groups as $P2_12_12_1$ for the former and $P2_1$ for the latter. The unit cell dimensions were determined by the least-squares calculation using the high angle spots of $CuK\alpha_1$ and $CuK\alpha_2$ on zero-layer Weissenberg photographs superimposed by the Al wire patterns for calibration. The densities were measured by a floatation method in a chloroform-carbon tetrachloride mixture for the orthorhombic crystal and a benzene-carbon tetrachloride mixture for the monoclinic one, respectively.

Crystal data were summarized in Table 1. The intensity data for the orthorhombic modification were collected from the multiple-film equi-inclination Weissenberg photographs for the layer lines 0 to 8 on the a axis and 0 to 6 on the c axis, respectively using the Ni-filtered $CuK\alpha$ radiation. The intensities were estimated visually by comparison with a calibrated film strip. Corrections were made for Lorentz and polarization factors and spot sizes. A total of 1623 intensities was recorded, but 74 of these were too weak to be measured. Structure factor magnitudes $|F|$ and normalized structure factor magnitudes $|E|$ were derived by the Wilson's method. The values of the statistical average, $\langle |E| \rangle$ and $\langle |E|^2 - 1 \rangle$, were 0.867 and 0.778, respectively, as compared with 0.886 and 0.736, the theoretical values for noncentrosymmetric space groups.

Structure Determination

The structure of Bicyclomycin was solved using the symbolic addition technique applied to noncentrosymmetric structures.³⁾ The Eq. (1) was used to define 30 phases ($|E| \geq 1.5$) in terms of initial set of phases listed in Table 2. From multiple indications, it soon became obvious that $2b \simeq 0$, $2c \simeq \pi$, and $2\phi \simeq \pi$. As for the value a , there were no confirmative indications.

$$\varphi_h \simeq \langle \varphi_k + \varphi_{h-k} \rangle_{kr} \quad (1)$$

Thus, various combinations of symbolic phases for

TABLE 1. CRYSTAL DATA

Crystal system	orthorhombic	monoclinic
Molecular formula	$C_{12}H_{18}O_7N_2$	$C_{12}H_{18}O_7N_2 \cdot H_2O$
Unit cell constants	$a=11.72(1)$ Å $b=12.72(1)$ $c=8.80(1)$	$a=10.27(1)$ Å $b=10.91(1)$ $c=6.67(1)$ $\beta=101.4(1)^\circ$
V	1312 Å ³	732 Å ³
D_m	1.54	1.46
D_c	1.53 g/cm ³	1.45 g/cm ³
Z	4	2
Absent spectra	$h00$ when h is odd, $0k0$ when k is odd, $00l$ when l is odd.	$0k0$ when k is odd.
Space group	$P2_12_12_1$	$P2_1$

TABLE 2. INITIAL SET OF PHASES

Reflection	Phase	$ E $
0 3 7	$\pi/2$	2.56
0 9 4	$\pi/2$	2.73
5 0 8	0	3.29
4 2 10	a	2.67
5 10 4	b	2.69
10 4 1	c	2.78
4 5 8	ϕ	2.57

the use of the tangent formula were assigned as follows:

$$a = \pi/6, 3\pi/6, 5\pi/6, -\pi/6, -3\pi/6, -5\pi/6$$

$$b = 0, \pi$$

$$c = \pi/2, -\pi/2$$

$$p = \pi/2, -\pi/2.$$

For each of the 48 sets with 185 phases ($|E| \geq 1.50$), six cycles of tangent refinement were carried out. Only four sets of them converged characteristically at lowest R' index,³⁾ defined by

$$R' = \frac{\sum_{kr} ||E_h|_{\text{obs}} - |E_h|_{\text{calc}}|}{\sum_{kr} |E_h|_{\text{obs}}} \quad (2)$$

Further eight cycles of tangent refinement for each of these four sets of 391 phases ($|E| \geq 1.20$) converged at the same R' index of 0.26.

Three dimensional E -maps with 391 terms were then calculated for these sets. The 21 largest peaks appeared on the respective four E -maps; each of them was found to give the same molecular structure. There was only one unique set, however, to which the other three were related by a mirror symmetry or by a translation. Assuming all the atoms to be nitrogen atom, structure factor calculation based on these 21 atoms gave an R factor of 0.25 for all reflections, and the corresponding Fourier synthesis showed no spurious peaks. All the 21 non-hydrogen atoms were assigned to 12 carbon, 7 oxygen and 2 nitrogen atoms, respectively on the basis of this Fourier map and the partial structure known from chemical and spectroscopic investigations.²⁾

The atomic coordinates and isotropic thermal parameters for the 21 atoms were refined by block-diagonal

least-squares method for four cycles. The function minimized was $\sum w(|F_o| - |F_c|)^2$. Then, anisotropic temperature factors for all non-hydrogen atoms were introduced, and two more cycles of refinement reduced the R factor to 0.09. A difference map calculated at this stage revealed all the 18 hydrogen atoms. Setting the isotropic temperature factor of each hydrogen atom

TABLE 4. THE ANISOTROPIC TEMPERATURE FACTORS^{a)} AND THEIR ESTIMATED STANDARD DEVIATIONS IN PARENTHESES (multiplied by 10^4)

Atom	B_{11}	B_{22}	B_{33}	B_{12}	B_{13}	B_{23}
C(1)	24(2)	36(3)	15(4)	-24(4)	-10(6)	-5(6)
C(2)	21(2)	34(2)	19(4)	-5(4)	10(6)	12(5)
C(4)	16(2)	20(2)	7(3)	3(4)	3(5)	2(5)
C(6)	24(2)	26(2)	33(4)	23(4)	-12(6)	-6(5)
C(7)	27(3)	40(3)	31(4)	22(5)	-30(7)	6(6)
C(8)	22(2)	42(3)	18(4)	3(4)	-14(6)	-17(6)
C(10)	22(2)	22(2)	8(4)	16(4)	-3(6)	7(5)
C(13)	15(2)	16(2)	19(4)	1(3)	14(6)	-5(5)
C(15)	16(2)	26(2)	24(4)	-1(4)	3(6)	-7(5)
C(17)	17(2)	52(3)	79(6)	-12(5)	3(7)	-15(8)
C(18)	40(3)	24(2)	58(5)	-3(5)	-13(8)	-18(6)
C(20)	31(3)	71(4)	92(7)	-10(6)	34(9)	-58(10)
N(3)	17(2)	26(2)	8(3)	-3(3)	-6(5)	5(4)
N(9)	28(2)	33(2)	5(3)	-7(4)	-22(5)	-24(5)
O(5)	22(2)	21(2)	34(3)	13(3)	8(5)	13(4)
O(11)	28(2)	44(2)	71(4)	-34(4)	-13(5)	11(5)
O(12)	41(2)	62(2)	18(3)	-42(4)	0(5)	35(5)
O(14)	27(2)	17(1)	44(3)	11(3)	23(5)	-8(4)
O(16)	25(2)	40(2)	28(3)	8(3)	-16(5)	17(4)
O(19)	60(3)	22(2)	84(5)	-14(4)	27(7)	12(5)
O(21)	31(2)	49(2)	10(3)	10(4)	8(5)	-12(4)

a) The anisotropic temperature factor is in the form:
 $\exp\{-(B_{11}h^2 + B_{22}k^2 + B_{33}l^2 + B_{12}hk + B_{13}hl + B_{23}kl)\}.$

TABLE 3. THE FRACTIONAL ATOMIC COORDINATES AND THEIR ESTIMATED STANDARD DEVIATIONS IN PARENTHESES

Atom	x	y	z
C(1)	0.1686(3)	0.2872(3)	0.2093(4)
C(2)	0.2539(3)	0.2885(3)	0.3436(4)
C(4)	0.3899(3)	0.3824(3)	0.1740(4)
C(6)	0.2563(3)	0.5317(3)	0.2167(5)
C(7)	0.1437(4)	0.4891(4)	0.1549(5)
C(8)	0.0988(3)	0.3887(4)	0.2235(4)
C(10)	0.3371(3)	0.3203(3)	0.0399(4)
C(13)	0.5216(3)	0.3802(3)	0.1637(4)
C(15)	0.5869(3)	0.4369(3)	0.2948(4)
C(17)	0.7150(4)	0.4338(4)	0.2601(6)
C(18)	0.5495(4)	0.5514(3)	0.3199(5)
C(20)	0.0006(4)	0.3870(5)	0.3001(6)
N(3)	0.3527(3)	0.3412(3)	0.3188(3)
N(9)	0.2323(3)	0.2819(3)	0.0654(3)
O(5)	0.3575(2)	0.4898(2)	0.1452(3)
O(11)	0.1035(3)	0.1967(3)	0.2230(4)
O(12)	0.2311(3)	0.2516(3)	0.4675(3)
O(14)	0.5587(2)	0.2740(2)	0.1537(3)
O(16)	0.5610(3)	0.3868(3)	0.4359(3)
O(19)	0.5455(4)	0.6134(3)	0.1831(4)
O(21)	0.3845(3)	0.3150(3)	-0.0840(3)

TABLE 5. THE FRACTIONAL ATOMIC COORDINATES FOR HYDROGEN ATOMS AND THEIR X-H BOND LENGTHS (X=C, N, or O)

Atom	Bonded to	x	y	z	X-H (Å)
H(1)	N(3)	0.405	0.353	0.395	0.92
H(2)	C(6)	0.258	0.605	0.192	0.96
H(3)	C(6)	0.255	0.520	0.327	0.98
H(4)	C(7)	0.156	0.472	0.049	0.96
H(5)	C(7)	0.081	0.550	0.171	1.08
H(6)	N(9)	0.191	0.266	-0.009	0.84
H(7)	O(11)	0.034	0.209	0.157	1.01
H(8)	C(13)	0.536	0.412	0.071	0.93
H(9)	O(14)	0.522	0.238	0.214	0.82
H(10)	O(16)	0.612	0.343	0.467	0.86
H(11)	C(17)	0.753	0.484	0.341	1.06
H(12)	C(17)	0.733	0.344	0.243	1.17
H(13)	C(17)	0.730	0.464	0.166	0.93
H(14)	C(18)	0.614	0.587	0.392	1.09
H(15)	C(18)	0.473	0.554	0.384	1.06
H(16)	O(19)	0.469	0.587	0.136	1.05
H(17)	C(20)	-0.043	0.459	0.314	1.05
H(18)	C(20)	-0.028	0.326	0.338	0.91

The mean standard deviation in atomic coordinates is 0.08 Å, and that of the distance X-H is 0.09 Å.

[illegible]

$\langle\sigma\rangle=0.3^\circ$ $\langle\sigma\rangle=0.006\text{ \AA}$
Fig. 2. Bond distances and angles.

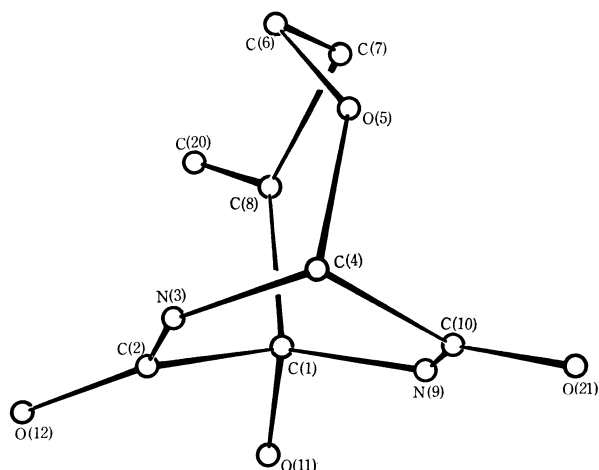


Fig. 3. A part of the molecule showing the cage type of ring system.

The diketopiperazine ring is folded into a boat conformation. Bridging the axial bonds of C(1) and C(4) in the ring, four atoms, O(5), C(6), C(7), and C(8), constitute the two eight-membered rings together with >C-CO-NH-C< moieties of the six-membered ring and thus establish the cage type of ring system. These features are shown in Fig. 3. There exists an approximate two fold axis going through the center of the diketopiperazine ring and the middle point of the C(6)–C(7) bond.

Atoms C(1), C(2), N(3), and O(12) are coplanar within 0.03 Å (amide plane I) and those C(1), C(4), N(9), C(10), and O(21) are also coplanar within 0.03 Å (amide plane II). The dihedral angle between amide plane I and II is 144°. The moiety, C(1), C(8), C(7), and C(20) involving the methylene group, displays the good planarity (methylene plane). The equations of the best planes and the deviations of respective atoms from the planes are listed in Table 7.

The distances, C(2)–N(3) (1.36 Å) and C(10)–N(9) (1.34 Å) significantly shorter than that of C–N single

TABLE 7. SOME OF THE LEAST-SQUARES PLANES AND THE DEVIATION OF ATOMS FROM THE PLANES (Å)

1) Amide plane I

$$0.4088X - 0.8604Y - 0.3045Z = -2.888$$

C (1)	–0.008	O (12)	0.011
C (2)	0.026	C (4)*	0.105
N (3)	–0.010	H (1)*	–0.09

2) Amide plane II

$$0.4286X - 0.8493Y + 0.3084Z = -1.690$$

C (1)	0.002	C (10)	0.031
C (4)	–0.010	O (21)	–0.010
N (9)	–0.011	H (6)*	–0.25

3) Methylene plane

$$0.4823X + 0.2134Y + 0.8496Z = 3.295$$

C (1)	–0.003	C (20)	–0.004
C (7)	–0.003	H (17)*	–0.06
C (8)	0.010	H (18)*	0.04

In the above equations, X , Y , and Z are the rectangular coordinates in Å unit.

Asterisks indicate atoms not included in the calculation of the plane.

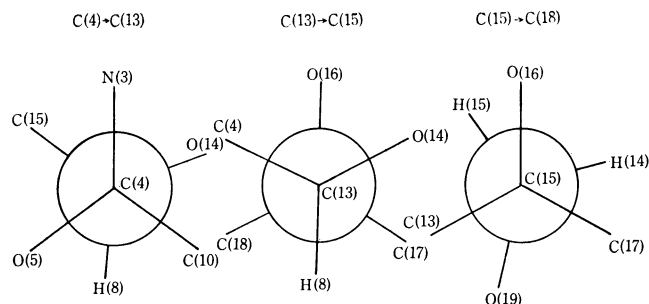


Fig. 4. Newman projections about C(4)–C(13), C(13)–C(15), and C(15)–C(18) bonds.

bond length (1.47 Å), indicate some double bond character; similar shortening of the bond length has been reported in diketopiperazine⁶⁾ and in many peptides.⁷⁾ The distance C(1)–O(11) (1.39 Å) seems to be shorter than that of the corresponding single bond length.

The conformation of the side chain is presented by the Newman projections down the C(4)–C(13), C(13)–C(15), and C(15)–C(18) bonds. As shown in Fig. 4,

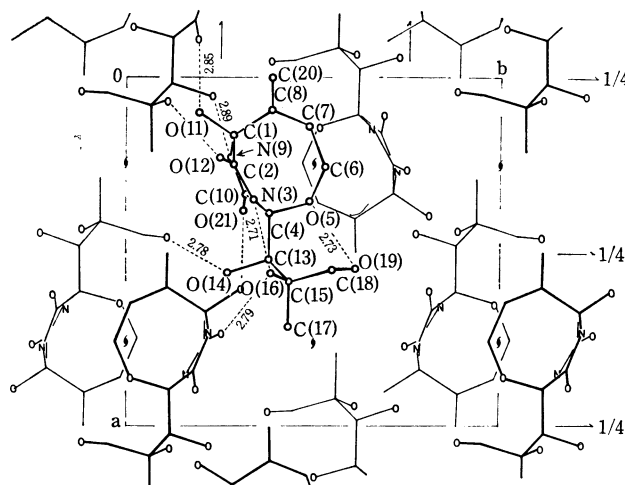


Fig. 5. The crystal structure viewed along the c axis. The hydrogen bonds are indicated by dashed lines.

TABLE 8. INTER- AND INTRAMOLECULAR HYDROGEN BONDS (D–H...A)

Donor	H	Acceptor	D...A (Å)	H...A (Å)	D–H...A (°)
I) Intermolecular					
N (9)	H (6)	O(14) ^I	2.89	2.07	166
O(11)	H (7)	O(21) ^I	2.85	1.89	156
O(14)	H (9)	O(19) ^{II}	2.78	1.99	161
O(16)	H(10)	O(12) ^{III}	2.79	1.93	178
II) Intramolecular					
N (3)	H (1)	O(16)	2.71	1.91	144
O(19)	H(16)	O (5)	2.73	1.80	146

Roman numerals as superscripts denote the following transformations relative to the reference molecule at x, y, z :

I	$-1/2 + x,$	$1/2 - y,$	$-z,$
II	$1 - x,$	$-1/2 + y,$	$1/2 - z,$
III	$1/2 + x,$	$1/2 - y,$	$1 - z,$

all the conformations are *gauche* or nearly so.

All the oxygen and nitrogen atoms in the molecule participate in two intramolecular and four intermolecular hydrogen bonds. Two oxygen atoms, O(16) and O(19), in the side chain participate in intramolecular hydrogen bonds, N(3)–H(1)···O(16) and O(19)–H(16)···O(5). These hydrogen bonds are of particular contribution to retain the molecular frameworks.

The crystal structure viewed along the *c* axis is shown in Fig. 5. The hydrogen bonds are indicated by dashed lines and detailed features of these hydrogen bonds are listed in Table 8.

The authors are indebted to Professor Masao Kakudo and Dr. Tamaichi Ashida, Institute for Protein Research, Osaka University, for discussions and suggestions in the progress of this work and for permitting us to use original program, TANG.

References

- 1) T. Miyoshi, N. Miyairi, H. Aoki, M. Kohsaka, H. Sakai, and H. Imanaka, *J. Antibiotics*, **25**, 569 (1972).
 - 2) T. Kamiya, S. Maeno, M. Hashimoto, and Y. Mine, *ibid.*, **25**, 576 (1972).
 - 3) J. Karle and I. L. Karle, *Acta Crystallogr.*, **21**, 849 (1966).
 - 4) "International Tables for X-ray Crystallography," Vol. III, Kynoch Press, Birmingham (1962), p. 202.
 - 5) "Universal Crystallographic Computation Program System (UNICS)," ed. by T. Sakurai, The Crystallographic Society of Japan, Tokyo (1967).
 - 6) R. Degeilh and R. E. Marsh, *Acta Crystallogr.*, **12**, 1007 (1959).
 - 7) R. E. Marsh and J. Donohue, "Advances in Protein Chemistry," Vol. 22, ed. by C. B. Anfinsen, Jr., M. L. Anson, J. T. Edsall, and F. M. Richards, Academic Press, New York and London (1967), p. 235.
-