

Planar Structure and Antibacterial Activity of Korormicin Derivatives Isolated from *Pseudoalteromonas* sp. F-420

KAZUHIRO YOSHIKAWA*[†], KYOKO ADACHI, FUMIKO NISHIDA
and KENICHI MOCHIDA^{††}

Marine Biotechnology Institute Co. Ltd.,
3-75-1 Heita, Kamaishi, Iwate 026-0001, Japan

(Received for publication May 14, 2003)

Korormicin (**1**, Fig. 1) is an antibiotic produced by a marine bacterium, *Pseudoalteromonas* sp. F-420, collected from the Palauan sea.¹⁾ Total synthesis studies by two independent laboratories have described the stereochemistry of the compound as 5*S*,3'*R*,9'*S*,10'*R*.^{2,3)} Compound **1** was first characterized by its specific inhibitory activity against Gram-negative marine bacteria.^{1,4)} The target molecule of **1** was found to be Na⁺-translocating NADH-quinone reductase (Nqr).^{4,5)} Nqr is widely distributed among Gram-negative marine bacteria, and functions as a primary Na⁺ pump.⁶⁾ Compound **1** acts as a noncompetitive inhibitor for a substrate ubiquinone-1, with the inhibition constant of 82 μ M.⁵⁾ By using a korormicin-resistant mutant of *Vibrio alginolyticus*, KR2, Gly140 on NqrB, one of the subunits of the Nqr complex, was shown to be essential to the binding of **1**.⁷⁾ This amino acid residue Gly140 is well conserved among Gram-negative pathogens on which the *nqr* operon is found in the genome sequence. Korormicin could be used as an antibiotic not only against marine bacteria, but against any bacterium using the primary sodium pump to maintain life.

During a fermentation study of the strain F-420, we found some minor compounds detected in the HPLC chromatogram in a step of the purification of **1**. In this report, we describe our isolation of some compounds that were derivatives of **1**.

When a subculture of *Pseudoalteromonas* sp. F-420 (deposited as FERM P-16084), 0.2 ml, had an OD₆₅₀ of 0.5, it was transferred to 100 ml of Marine Broth 2216 (Becton, Dickinson Co., Franklin Lakes, NJ, USA) culture medium supplemented with 1% (w/v) maltose and 0.16% NaHCO₃ in a 1-liter Erlenmeyer flask with baffles. Incubation was

done on a rotary shaker (110 rpm) at 30°C for 20 hours. Cells were collected from the 9.9-liter culture and were extracted with 500 ml of aqueous ethanol by using an ultrasonic cell disrupter. Then the extract was concentrated to dryness and was resolved in an aliquot of ethyl acetate. Solvent extraction, silica gel column chromatography, and size-exclusion chromatography for the separation of the antibacterial compounds were by the methods described in our previous paper.¹⁾ A bioactive fraction was then further purified by using a reversed-phase HPLC (Capcell Pak C-18, Shiseido, Tokyo, Japan: 15 mm×250 mm column, 5 ml/minute flow rate), eluting with 80% methanol at ambient temperature. Under these conditions, **1** (163.83 mg in total) was eluted at 23.1 minutes when monitored with A₂₃₃. Compounds, **1a** (7.30 mg), **1b** (13.25 mg), **1c** (3.89 mg), **2** (10.69 mg), and **3** (12.78 mg) were isolated, eluting at 13.4, 17.3, 31.8, 23.8, and 21.9 minutes, respectively.

Their MS were recorded with a JEOL JMS-SX102 mass spectrometer. The NMR spectra were measured by using a Varian Unity 500 NMR spectrometer, and the data were recorded in DMSO-*d*₆ at 500 MHz for ¹H, and at 125 MHz for ¹³C. The IR spectrum was obtained from a KBr pellet by using a JASCO FT-IR 7000 spectrophotometer. Optical rotations were found by using a Horiba SEPA-300 polarimeter.

Compound **1a**. A colorless oil; FAB-MS *m/z* 406 (M+H)⁺, 428 (M+Na)⁺; HR-MS *m/z* (M+H)⁺: Calcd for C₂₃H₃₆NO₅: 406.2593, Found, 406.2596; [α]_D²⁶ -42.4 (*c* 0.19, EtOH); IR ν_{\max} (KBr) cm⁻¹ 3450, 2930, 2860, 1765, 1695, 1655, 1540, 1460, 1380, 1325, 1205, 1110, 1050, 995, 945; UV $\lambda_{\max}^{\text{EtOH}}$ nm (log ϵ) 232 (4.55).

Compound **1b**. A colorless oil; FAB-MS *m/z* 420 (M+H)⁺, 442 (M+Na)⁺; HR-MS *m/z* (M+Na)⁺: Calcd for C₂₄H₃₇NO₅Na: 442.2569, Found, 442.2571; [α]_D²⁶ -24.1 (*c* 0.67, EtOH); IR ν_{\max} (KBr) cm⁻¹ 3455, 2930, 2860, 1765, 1695, 1655, 1540, 1460, 1380, 1325, 1205, 1110, 1050, 995, 945; UV $\lambda_{\max}^{\text{EtOH}}$ nm (log ϵ) 232 (4.59).

Compound **1c**. A colorless oil; FAB-MS *m/z* 448 (M+H)⁺, 470 (M+Na)⁺; HR-MS *m/z* (M+Na)⁺: Calcd for C₂₆H₄₁NO₅Na: 470.2882, Found, 470.2876; [α]_D²⁶ -28.2 (*c* 0.25, EtOH); IR ν_{\max} (KBr) cm⁻¹ 3470, 2930, 2860, 1740, 1655, 1540, 1460, 1400, 1055; UV $\lambda_{\max}^{\text{EtOH}}$ nm (log ϵ) 233 (4.43).

Compound **2**. A colorless oil; FAB-MS *m/z* 513, 515

[†] Present address: Central Research Laboratories, Nippon Suisan Kaisha, Ltd., 559-6 Kitano-machi, Hachioji, Tokyo 192-0906, Japan.

^{††} Present address: Kyowa Hakko Kogyo Co., Ltd., 1-6-1 Otemachi, Chiyoda-ku, Tokyo 100-8185, Japan.

* Corresponding author: yoshi3@nissui.co.jp

Table 1-1. NMR chemical shifts for compounds **1**, **1a~c**, **2**, and **3**.

(1)¹H-NMR

Compound	1 ^a	1a	1b	1c	2	3
Position						
4	7.26 (1H, s)	7.37 (1H, s)	7.37 (1H, s)	7.37 (1H, s)	7.38 (1H, s)	7.45 (1H, s)
6	1.76 (2H, q)	1.75 (2H, q)	1.75 (2H, q)	1.75 (2H, q)	1.74 (2H, q)	1.420 (3H, s) ^g
7	0.74 (3H, t)	0.75 (3H, t)	0.75 (3H, t)	0.75 (3H, t)	0.75 (3H, t)	1.423 (3H, s) ^g
8	1.37 (3H, s)	1.40 (3H, s)	1.40 (3H, s)	1.40 (3H, s)	1.40 (3H, s)	
NH	9.83 (1H, s)	9.86 (1H, s)	9.86 (1H, s)	9.86 (1H, s)	9.83 (1H, s)	9.83 (1H, s)
2a'	2.39 (1H, dd)	2.40 (1H, dd)	2.39 (1H, dd)	2.40 (1H, dd)	2.40 (1H, dd)	2.39 (1H, dd)
2b'	2.59 (1H, dd)	2.61 (1H, dd)	2.61 (1H, dd)	2.61 (1H, dd)	2.60 (1H, dd)	2.61 (1H, dd)
3'	4.84 (1H, ddd)	4.84 (1H, ddd)	4.84 (1H, ddd)	4.84 (1H, ddd)	4.83 (1H, ddd)	4.83 (1H, ddd)
3'-OH	5.09 (1H, d)	5.11 (1H, d)	5.11 (1H, d)	5.11 (1H, d)	5.10 (1H, br)	5.10 (1H, d)
4'	5.30 (1H, dd)	5.31 (1H, dd)	5.31 (1H, dd)	5.31 (1H, dd)	5.26 (1H, d)	5.31 (1H, dd)
5'	5.92 (1H, dd)	5.93 (1H, dd)	5.93 (1H, dd)	5.93 (1H, dd)	5.91 (1H, dd)	5.93 (1H, dd)
6'	6.46 (1H, dd)	6.47 (1H, dd)	6.47 (1H, dd)	6.47 (1H, dd)	6.42 (1H, dd)	6.47 (1H, dd)
7'	5.70 (1H, dt)	5.71 (1H, dt)	5.71 (1H, dt)	5.71 (1H, dt)	5.71 (1H, dt)	5.71 (1H, dt)
8'	2.26 (2H, dd)	2.28 (2H, dd)	2.28 (2H, dd)	2.27 (2H, dd)	2.29 (2H, dd)	2.28 (2H, dd)
9'	2.90 (1H, dt)	2.91 (1H, dt)	2.91 (1H, dt)	2.91 (1H, dt)	3.50 (1H, m)	2.91 (1H, dt)
9'-OH					5.10 (1H, br)	
10'	2.87 (1H, ddd)	2.88 (1H, ddd)	2.88 (1H, ddd)	2.88 (1H, ddd)	4.05 (1H, m)	2.88 (1H, ddd)
11'	1.48 (2H, m)	1.47 (2H, m)	1.47 (2H, m)	1.47 (2H, m)	1.80 (2H, m)	1.47 (2H, m)
12'	1.38 (2H, m)	12-14(2H,m) ^c	12-14(2H,m) ^d	12-14(2H,m) ^e	1.46 (2H, m)	12-14(2H,m) ^h
13'	12-14(2H,m) ^b	12-14(2H,m) ^c	12-14(2H,m) ^d	12-14(2H,m) ^e	12-14(2H,m) ^f	12-14(2H,m) ^h
14'	12-14(2H,m) ^b	12-14(2H,m) ^c	12-14(2H,m) ^d	12-14(2H,m) ^e	12-14(2H,m) ^f	12-14(2H,m) ^h
15'	12-14(2H,m) ^b	12-14(2H,m) ^c	12-14(2H,m) ^d	12-14(2H,m) ^e	12-14(2H,m) ^f	12-14(2H,m) ^h
16'	1.22 (2H, m)	0.85 (3H, t)	12-14(2H,m) ^d	12-14(2H,m) ^e	1.24 (2H, m)	12-14(2H,m) ^h
17'	1.24 (2H, m)		0.85 (3H, t)	12-14(2H,m) ^e	1.26 (2H, m)	12-14(2H,m) ^h
18'	0.83 (3H, t)			12-14(2H,m) ^e	0.84 (3H, t)	0.84 (3H, t)
19'				0.85 (3H, t)		

^aData from reference 1).

b-h, interchangeable.

(M+H)⁺; HR-MS *m/z* (M+H)⁺: Calcd. for C₂₅H₄₁⁸¹BrNO₅: 516.2168, Found, 516.2141; [α]_D²⁶ -36.1 (*c* 0.45, EtOH); IR *v*_{max} (KBr) cm⁻¹ 3448, 2928, 2858, 1763, 1694, 1653, 1541, 1458, 1383, 1328, 1207, 1110, 1031, 948; UV λ_{max}^{EtOH} nm (log ε) 234 (4.47).

Compound **3**. A colorless oil; FAB-MS *m/z* 420 (M+H)⁺, 442 (M+Na)⁺; HR-MS *m/z* (M+H)⁺: Calcd for C₂₄H₃₈NO₅: 420.2750, Found, 420.2742; [α]_D²⁶ +42.3 (*c*

0.21, EtOH); IR *v*_{max} (KBr) cm⁻¹ 3440, 2930, 2860, 1765, 1695, 1655, 1540, 1460, 1380, 1325, 1205, 1110, 1050, 950; UV λ_{max}^{EtOH} nm (log ε) 232 (4.53).

The ¹H and ¹³C NMR spectra for these compounds (Table 1). suggested that their planar structures were very similar to that of **1**.¹⁾ Their IR and UV spectra were substantially identical to those of **1**. From HMBC and the result of the FAB-MS analysis, **1a~c** were deduced to be

Table 1-2. Continued.

(2) $^{13}\text{C-NMR}^a$

Compound	1 ^b	1a	1b	1c	2	3
Position						
2	168.4 (s)	168.1 (s)	168.1 (s)	168.1 (s)	168.2 (s)	168.0 (s)
3	125.1 (s)	124.8 (s)	124.8 (s)	124.8 (s)	124.9 (s)	124.1 (s)
4	133.9 (d)	133.7 (d)	133.6 (d)	133.6 (d)	133.8 (d)	135.1 (d)
5	87.0 (s)	86.9 (s)	86.9 (s)	86.9 (s)	87.0 (s)	84.5 (s)
6	31.2 (t)	31.02 (t)	31.03 (t)	31.0 (t)	31.16 (t)	25.8 (q) ^h
7	8.0 (q)	7.8 (q)	7.8 (q)	7.8 (q)	7.9 (q)	25.7 (q) ^h
8	24.1 (q)	24.0 (q)	24.0 (q)	24.0 (q)	24.1 (q)	
1'	170.1 (s)	169.7 (s)	169.7 (s)	169.7 (s)	169.9 (s)	169.7 (s)
2'	44.0 (t)	43.8 (t)	43.8 (t)	43.8 (t)	43.9 (t)	43.8 (t)
3'	63.0 (d)	63.6 (d)	63.6 (d)	63.6 (d)	63.7 (d)	63.6 (d)
4'	132.7 (d)	132.4 (d)	132.4 (d)	132.4 (d)	132.07 (d)	132.5 (d)
5'	128.0 (d)	127.9 (d)	127.9 (d)	127.9 (d)	128.3 (d)	127.9 (d)
6'	127.6 (d)	127.3 (d)	127.3 (d)	127.3 (d)	127.3 (d)	127.3 (d)
7'	130.9 (d)	130.6 (d)	130.6 (d)	130.6 (d)	132.14 (d)	130.6 (d)
8'	30.9 (t)	30.8 (t)	30.8 (t)	30.8 (t)	38.1 (t)	30.8 (t)
9'	55.1 (d)	54.9 (d)	54.9 (d)	54.9 (d)	71.9 (d)	54.9 (d)
10'	56.0 (d)	55.8 (d)	55.8 (d)	55.8 (d)	63.9 (d)	55.8 (d)
11'	27.2 (t)	28.4 (t) ^d	28.7 (t) ^e	28.80 (t) ^f	34.5 (t)	28.8 (t) ⁱ
12'	26.1 (t)	27.0 (t) ^d	28.4 (t) ^e	28.75 (t) ^f	27.3 (t)	28.7 (t) ⁱ
13'	28.92 (t) ^c	25.9 (t) ^d	27.0 (t) ^e	28.72 (t) ^f	28.8 (t) ^g	28.4 (t) ⁱ
14'	28.89 (t) ^c	31.04 (t)	26.0 (t) ^e	28.5 (t) ^f	28.5 (t) ^g	27.0 (t) ⁱ
15'	28.6 (t) ^c	21.9 (t)	31.04 (t)	27.0 (t) ^f	28.4 (t) ^g	26.0 (t) ⁱ
16'	31.2 (t)	13.8 (q)	21.9 (t)	26.0 (t) ^f	31.18 (t)	31.1 (t)
17'	22.1 (t)		13.8 (q)	31.1 (t)	22.0 (t)	21.9 (t)
18'	13.9 (q)			21.9 (t)	13.9 (q)	13.8 (q)
19'				13.8 (q)		

^aMultiplicity in parenthesis was determined by DEPT.

^bData from reference 1).

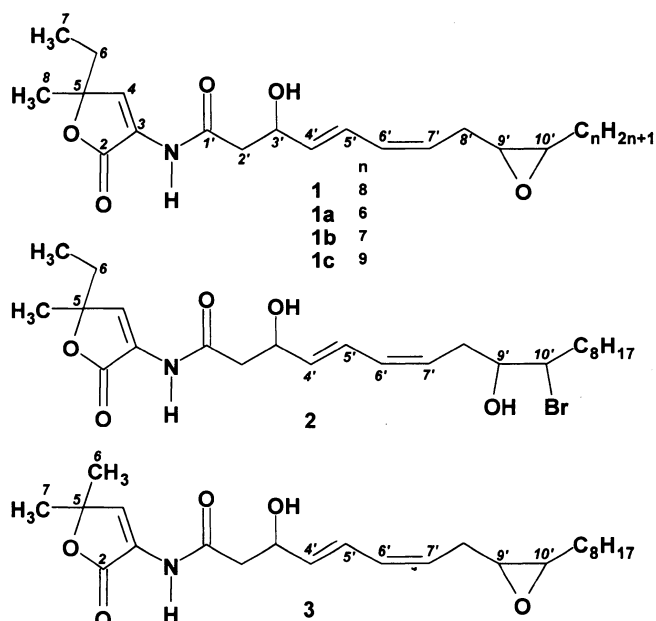
c-i, interchangeable.

derivatives of **1**, with different alkyl chain lengths at their amide moiety (Fig. 1).

Compound **2** had the molecular formula of $\text{C}_{25}\text{H}_{40}\text{BrNO}_5$. The chemical shifts of H-9' (δ_{H} 3.50) and H-10' (δ_{H} 4.05) on **2** were lower than those on **1** (δ_{H} 2.90 and

2.87, respectively). This suggests the absence of the epoxide ring in compound **2**. COSY indicated that a hydroxyl group was correlated with H-9', but not with H-10'. The chemical shift of C-10' on **2** (δ_{C} 63.9) was lower than the corresponding carbon on **1** (δ_{C} 56.0), suggesting

Fig. 1. Planar structures of korormicin (**1**) and the derivatives.



the binding of bromine at this carbon. Fig. 1 shows the planar structure of **2** that was established.

Compound **3** had the molecular formula of $C_{24}H_{37}NO_5$, one methylene unit difference from **1**. HSQC data were shown to be almost identical to each other in the amide part of **1** and **3**. However, the lactone moiety lacked a secondary carbon (δ_C 31.2; C-6 in **1**). A methyl group with a higher chemical shift (δ_C 8.0 and δ_H 0.74 in **1**) also disappeared. Instead, two methyl groups were observed: δ_C 25.7 and 25.8 in ^{13}C NMR, and δ_H 1.420 and 1.423 in 1H NMR, respectively. Fig. 1 shows the planar structure of **3** that was established.

The regiochemistry at the double bonds and the epoxide in compounds **1a**~**c**, **2**, and **3** was found from their coupling constants, $J_{4',5'}$, $J_{6',7'}$, and $J_{9',10'}$, respectively, recorded on 1H NMR charts. All derivatives shared conformation with **1**: C-4'/C-5', Z; C-6'/C-7', E; C-9'/C-10' (except **2**), *cis* (Table 2). The complete configuration for these new compounds is unknown now.

The strength of the antibacterial activity of these derivatives was compared by using the paper disk method.¹⁾ The result (Table 3) indicates that all derivatives have

Table 2. Coupling constant $^3J_{H-H}$ of selected bondings (Hz) for compounds **1**, **1a**~**c**, **2**, and **3**.

Compound	1 ^a	1a	1b	1c	2	3
Position						
C-4'/C-5'	10.9	10.8	10.7	10.9	10.9	10.9
C-5'/C-6'	11.2	11.0	11.2	11.3	11.3	11.2
C-6'/C-7'	15.1	14.8	14.9	14.8	15.0	14.8
C-9'/C-10'	4.2	4.2	4.2	4.2	-	4.2

^a Data from reference 1).

Table 3. Antibacterial Activity of compounds **1**, **1a**~**c**, **2**, and **3**^a.

Compound	1	1a	1b	1c	2	3	B
Strain ^b	Halophilicity ^c						
<i>S. costicola</i>	(+)	27	38	34	22	21	26
<i>P. haloplanktis</i>	(+)	26	27	24	19	18	21
<i>E. coli</i>	(-)	-	-	-	-	-	16

^aTen μ g of each compound was used for a paper disk 8 mm in diameter, except the control inhibitor polymixin B (B, 5 μ g was used). Values are diameters in mm of inhibition zone on the agar plate.

^bBacterial strains used were *Salinivibrio costicola* ATCC33508, *Pseudoalteromonas haloplanktis* ATCC14393, and *E. coli* IFO3301.

^c*S. costicola* and *P. haloplanktis* are marine bacteria characterized by their halophilicity (designated as (+)).

antibacterial activity against *Salinivibrio costicola* and *Pseudoalteromonas haloplanktis*, but not against *Escherichia coli*. Specificity against Nqr in the Gram-negative marine bacteria for these derivatives is highly possible from their structural similarity to **1**, but a demonstrative study needs to be done.

Acknowledgments

We would like to thank Dr. SANG-JIN KIM, Korea Ocean Research and Development Institute, for advice on the

fermentation condition, and Mrs. MIEKO KURIHARA at MBI for her technical assistance. This work was performed as a part of The Industrial Science and Technology Project, Technological Development of Biological Resources in Bioconsortia supported by New Energy and Industrial Technology Development Organization (NEDO).

References

- 1) YOSHIKAWA, K.; T. TAKADERA, K. ADACHI, M. NISHIJIMA & H. SANO: Korormicin, a novel antibiotic specifically active against marine Gram-negative bacteria, produced by a marine bacterium. *J. Antibiotics* 50: 949~953, 1997
- 2) UEHARA, H.; T. OISHI, K. YOSHIKAWA, K. MOCHIDA & M. HIRAMA: The absolute configuration and total synthesis of korormicin. *Tetrahedron Lett.* 40: 8641~8645, 1999
- 3) KOBAYASHI, Y.; S. YOSHIDA & Y. NAKAYAMA: Total synthesis of korormicin. *Eur. J. Org. Chem.* 2001: 1873~1881, 2001
- 4) YOSHIKAWA, K.; Y. NAKAYAMA, M. HAYASHI, T. UNEMOTO & K. MOCHIDA: Korormicin, an antibiotic specific for Gram-negative marine bacteria, strongly inhibits the respiratory chain-linked Na⁺-translocating NADH:quinone reductase from the marine *Vibrio alginolyticus*. *J. Antibiotics* 52: 182~185, 1999
- 5) NAKAYAMA, Y.; M. HAYASHI, K. YOSHIKAWA, K. MOCHIDA & T. UNEMOTO: Inhibitor studies of a new antibiotic, korormicin, 2-*n*-heptyl-4-hydroxyquinoline *N*-oxide and Ag⁺ toward the Na⁺-translocating NADH-quinone reductase from the marine *Vibrio alginolyticus*. *Biol. Pharm. Bull.* 22: 1064~1067, 1999
- 6) HAYASHI, M.; Y. NAKAYAMA & T. UNEMOTO: Recent progress in the Na⁺-translocating NADH-quinone reductase from the marine *Vibrio alginolyticus*. *Biochim. Biophys. Acta* 1505: 37~44, 2001
- 7) HAYASHI, M.; N. SHIBATA, Y. NAKAYAMA, K. YOSHIKAWA & T. UNEMOTO: Korormicin insensitivity in *Vibrio alginolyticus* is correlated with a single point mutation of Gly-140 in the NqrB subunit of the Na⁺-translocating NADH-quinone reductase. *Arch. Biochem. Biophys.* 401: 173~177, 2002