HETEROCYCLES, Vol. 59, No. 2, 2003, pp. 497 - 500, Received, 15th October, 2002 STRUCTURE DETERMINATION OF LUSTROMYCIN, AN ANTIBIOTIC AGAINST ANAEROBIC BACTERIA

Masaki Handa, Hideaki Ui, Daisuke Yamamoto, Soichi Monma, Yuzuru Iwai, Toshiaki Sunazuka, and Satoshi Omura*

Kitasato Institute for Life Sciences, Kitasato University, and The Kitasato Institute, 5-9-1 Minato-ku, Tokyo 108-8641, Japan

Abstract – Extensive homo and heteronuclear two-dimensional NMR studies revealed lustromycin, an anti-anaerobic antibiotic. Its structure consists of a decaline ring system fused to a 10-membered macrolactone and a 14-membered macrolactone having an enol ether moiety conjugated with a maleic anhydride functionality.

In the course of screening of anti-anaerobic antibiotics from actinomycetes, we have found novel antibiotics, thiotetromycin, ¹ clostomicin, ² lustromycin (1), ³ and luminamicin (2). ⁴ Luminamicin (2) was identical with coloradocin whose structure was determined by McAlpine.⁵ The biological properties of **1** were found to be similar to those of 2^{3} . This paper deals with the structure elucidation of lustromycin (1). Structure determination of 1 ($C_{32}H_{38}O_{13}$) was performed based on the NMR spectral analyses. As described in the preceding paper,³ the structure of **1** was expected to resemble **2** ($C_{32}H_{38}O_{12}$) closely. ¹H and ¹³C NMR spectral signals of both compounds observed in CDCl₃ were assigned by various 1D- and 2D-NMR spectral experiments (Table 1).⁶ Comparison of MS and NMR spectral data of 1 and 2 revealed that **1** contained another O-methyl group instead of a C-methyl group present in **2**. ¹H- and ¹³C-NMR spectral analyses of 1 indicated the presence of a 14-membered lactone ring (C-16-C-29) containing an enol ether moiety conjugated with an unsaturated cyclic anhydride, and also the presence of an isopentenyl unit (C-13~C-16, CH₃-14). The spectral NMR data of these parts shown by 1 are in fair agreement with those of 2 as shown in Table 1. Connectivity of the remaining part (C-1~C-12) was further analyzed using ¹H-¹H COSY and HMBC experiments (Figure 1). The partial structures including C-4~C-6, C-7~C-8 and C-9~C-11 were assigned by interpretation of the COSY cross-peaks. HMBC experiments revealed the partial structure C-4 to C-8 by correlations between H-8/C-6, H-5/C-7 and H-6/C-7, and confirmed the direct linkage of C-7 to C-12 by correlations H-6 to C-12 and H-12 to C-8. The

	1			2				2 ^{Ref. 5}		
No.	δ_{C}	(m)	$\delta_{\rm H}$	δ_{C}	(m)	$\delta_{\rm H}$	δ_{C}	(m)	$\delta_{\rm H}$	$\delta_{\rm H}$
1	171.0	(s)	-	173.1	(s)	-	172.8	(s)	-	
2	87.4	(d)	3.73	82.8	(d)	3.75	81.8	(d)	3.79	3.75
3	78.2	(d)	3.93	32.9	(t)	2.46	32.9	(t)	2.43	3.90
						1.41			1.22	
4	45.1	(d)	2.00	38.3	(d)	2.20	37.7	(d)	2.16	1.98
5	123.8	(d)	5.53	128.3	(d)	5.47	128.3	(d)	5.51	5.54
6	130.7	(d)	6.05	130.2	(d)	5.88	129.9	(d)	5.82	6.03
7	28.7	(d)	2.28	29.6	(d)	2.21	29.2	(d)	2.14	2.40
8	32.5	(t)	1.61	27.9	(t)	1.69	27.5	(t)	1.66	1.65
0	(1.0		1.02	7 0 7	(1)	1.43	(0.(1.21	1.02
9	64.8	(d)	4.03	70.5	(d)	3.65	69.6	(d)	3.52	4.03
10	38.2	(t)	2.10	40.9	(d)	1.93	38.8	(d)	1.85	2.06
11	(0.2	(1)	1.69	77 4	(1)	2.25	75.0	(1)	2.10	1.74
11	69.3	(d)	3.97	//.4	(d)	3.35	/5.3	(d)	3.18	4.86
12	37.9	(d)	2.24	38.0	(d)	1.82	37.9	(d)	1.97	2.27
13	/5.3	(s)	-	/6.5	(s)	-	/5.9	(s)	-	-
14	143.1	(s)	-	142.0	(s)	-	141.5	(s)	-	-
15	122.7	(d)	6.04	123.4	(d)	6.04	121.6	(d)	5.85	5.87
16	36.8	(d)	3.19	37.2	(d)	3.20	36.4	(d)	3.05	2.94
17	64.3	(t)	4.88	64.3	(t)	4.8/	63.7	(t)	4.79	4.58
10	171 7		4.09	172.0		4.05	171.0		3.97	4.27
18	1/1./	(s)	-	172.0	(s)	-	1/1.0	(s)	- 12	2 92
19	33.6	(t)	2.81	33.5	(t)	2.86	32.9	(t)	2.43	2.83
20	10 ((1)	2.52	10 (2.49	17.0		1.22	2.03
20	18.0	(t)	3.46	18.0	(t)	3.29	17.8	(t)	3.37	3.48
21	122 5	(-)	2.72	122 5	(-)	2.67	122 7	(-)	2.61	2.71
21	133.3	(s)	-	155.5	(s)	-	155.7	(s)	-	-
22	164.2	(s)	-	164.2	(s)	-	103.3	(s)	-	-
23	104.2	(s)	-	104.3	(s)	-	104.1	(s)	-	-
24	130.3	(S) (d)	- 5 66	136.3	(S) (d)	- 5.62	137.3	(S) (d)	5.60	- 5 0 1
23	90.0	(d)	J.00 7.86	90.7	(d)	J.05	90.3	(b) (b)	5.02	J.01 7.80
20	72.0	(u)	7.80	130.8	(u) (t)	/.04	133.0	(u)	/./1	1.09
27	12.0	(I) (4)	4.19	12.1	(l) (d)	4.19	/1.0	(l) (d)	4.09	4.24
20	72.4	(d)	4.31	72.2	(d)	4.49	05.0	(b) (b)	4.20	5.64
29	72.4	(a)	5.50	12.2	(u)	5.42	12.3	(u)	5.20	5.52
$2-OCH_3$	59.1	(q)	3.35	57.9	(q)	3.24	57.2	(q)	3.18	3.38
3-OCH ₃	60.3	(q)	3.43	-		-	-		-	3.41
10-CH ₃	-		-	16.0	(q)	0.97	15.6	(q)	0.85	-
11-OCOCH₃	-		-	-		-	-		-	2.03
14-CH ₃	15.0	(q)	1.68	15.1	(q)	1.72	14.7	(q)	1.64	1.55
28-0C0CH	_		_	_		_	_		_	2 15

Table 1 ¹H- and ¹³C-NMR Spectral Data of **1** and **2**, and ¹H-NMR Spectral Data of **3**

1 and 2 were measured in $CDCl_3$ at 600 MHz (¹H) and 150 MHz (¹³C).

3 was measured in CDCl₃ at 400 MHz (1 H).

Ref. 5 was measured in DMSO-d 6.

six-membered ring consisting of the C-7 to C-12 chain was proved by correlations between H-8/C-10, H-10/C-8, H-10/C-12 and H-12/C-8. The direct linkages between C-12 to C-13, C-4 to C-13 and C-4 to C-3 were indicated by correlations of H-11 to C-13, H-5 to C-13, and H-3 to C-4, 5 and 13, respectively. An ester bond between C-29 and C-1 was deduced by correlation of H-29 to C-1 as well as from the chemical shift values of C-29 ($\delta_{\rm C}$ 72.4) and H-29 ($\delta_{\rm H}$ 5.36). Additional HMBC experiments also proved the partial



Figure 1 Connection of partial structure of 1

structure of C-1~C-3. The presence of 2- and 3-OCH₃ in **1** was verified by observation of HMBC crosspeaks between H-2/C-2-OCH, H-2-OCH/C-2, H-3/C-3-OCH and H-3-OCH/C-3, respectively. Substitution of the free hydroxyl groups at C-11 and C-28 was deduced from the lower-field shifts of the respective ¹H signals due to their acetylation. From the molecular formula and the degree of unsaturation of **1**, remaining two oxygen-baring carbons (C-13 and C-19) seemed to form ether ring, although the ether bond linkage between C-9 and C-13 in **1** could not be verified by its NMR spectral analyses. Therefore we present the skeletal structure of lustromycin (**1**) as shown in Figure 2 based on the spectral analogies with those of luminamicin (**2**).

Lustromycin (1) is related to a class of 10-membered macrolide antibiotics including nodusmicin, ⁷ nargenicin, ⁸ and luminamicin (coloradocin) (Figure 2).



Figure 2 Structures of lustromycin, luminamicin, nodusmicin, and nargenicin

Lustromycin (1) could be a new lead compound for the medication to compete with vancomycin which is used clinically in pseudomembranous colitis therapy.

Further efforts to determine its stereochemistry and synthetic studies are in progress.

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