Shornephine A: Structure, chemical stability and P-glycoprotein inhibitory properties of a rare diketomorpholine from an Australian marine-derived *Aspergillus* sp.

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1 DNA Taxonomic Analysis of CMB-M081F

1.1 ITS Gene Sequence of CMB-M081F

BLAST search (closest match):

Aspergillus terreus strain CO1 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence Sequence ID: <u>gb|KC582297.1</u>| Length: 583 Number of Matches: 1

Related Information

-				_			Related Information
Range 1	l: 2 to	239 GenBank Graphics			Next Match	Previous Match	
Score		Expect	Identities	Gaps	Strand		
407 bit	ts(220) 2e-110	233/238(98%)	5/238(2%)	Plus/Minu	IS	
Query	5	GAT-CATTGTTGAG	ITTT-ACTGATTGCAAAGA	ATCACACTCAGACTG	CAAGCTTTCA	60	
Sbjct	239	GATCCATTGTTGAAAG	TTTAACTGATTGCAAAGA	ATCACACTCAGACTG	CAAGCTTTCA	180	
Query	61	GAACAGGGTTCATGTT	GGGGTCTCCGGCGGGCACG	GGCCCGGGGGGGGGAGT	Ceccccccee	120	
Sbjct	179	GAACAGGGTTCATGTT	GGGGTCTCCGGCGGGGCACG	GGCCCGGGGGGGGGAGT	GCCCCCCGG	120	
Query	121	CGGCCAGCAACGCTGG	CGGGCCCGCCGAAGCAACA	AGGTACAATAGTCAC	GGGTGGGAGG	180	
Sbjct	119	CGGCCAGCAACGCTGG	CGGGCCCGCCGAAGCAACA	AGGTACAATAGTCAC	GGGTGGGAGG	60	
Query	181	TTGGGCCATAAAGACCO	CGCACTCGGTAATGATCCT	TCCGCAG-TTCACCC	TACGGAAG 2	37	
Sbjct	59	TTGGGCCATAAAGACCO	CGCACTCGGTAATGATCCT	TCCGCAGGTTCACCC	PACGGAAG 2	2	

Aspergillus terreus strain CO1 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence

GenBank: KC582297.1 FASTA Graphics

Go to: 🖂

LOCUS	KC582297 583 bp DNA linear PLN 19-MAY-2013								
DEFINITION	Aspergillus terreus strain CO1 18S ribosomal RNA gene, partial								
	sequence; internal transcribed spacer 1, 5.85 ribosomal RNA gene,								
and internal transcribed spacer 2, complete sequence; and 28									
who some low and space 2, complete sequence, and 205									
ACCESSION	Kosolar								
MCCESSION									
VERSION	KC582297.1 G1:499109366								
KEYWORDS									
SOURCE	Aspergillus terreus								
ORGANISM	Aspergillus terreus								
	Eukaryota; Fungi; Dikarya; Ascomycota; Pezizomycotina;								
	Eurotiomycetes; Eurotiomycetidae; Eurotiales; Trichocomaceae;								
	mitosporic Trichocomaceae; Aspergillus.								
REFERENCE	1 (bases 1 to 583)								
AUTHORS	Suja,M., Vasuki,S. and Sajitha,N.								
TITLE	Isolation of endophytic fungi from Seaweeds								
JOURNAL	Unpublished								
REFERENCE	2 (bases 1 to 583)								
AUTHORS	Suja, M., Vasuki, S. and Sajitha, N.								
TITLE	Direct Submission								
JOURNAL	Submitted (06-FEB-2013) CAS in Marine Biology, Faculty of Marine								
	Sciences, Annamalai University, Parangipettai, Cuddalore, Tamilnadu								
	608502, India								

2 Cytotoxicity (MTT) Assays

The MTT 3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide assay was modified from that previously described¹ using adherent cell lines SW620 and KB-3-1, and their respective P-gp over-expressing daughter cell lines SW620 Ad300 and KB-V1. Briefly, cells were harvested with trypsin and dispensed into 96-well microtiter assay plates at 2,000 cells/well for SW620, SW620 Ad300 and KB-3-1, and 5,000 cells/well for KB-V1, then incubated for 18 h at 37 °C with 5% CO₂ (to allow cells to attach). Test compounds were dissolved in 5% DMSO in PBS (v/v) and aliquots (20 μ L) tested over a series of final concentrations ranging from 10 nM to 30 μ M. Control wells were treated with 5% aqueous DMSO. After 68 h incubation at 37 °C with 5% CO₂, an aliquot (20 μ L) of MTT in PBS (4 mg/mL) was added to each well (final concentration of 0.4 mg/mL), and the microtiter plates incubated for a further 4 h at 37 °C with 5% CO₂. After this final incubation the medium was aspirated and precipitated formazan crystals dissolved in DMSO (100 μ L/well). The absorbance of each well was measured at 580 nm and IC₅₀ values were calculated as the concentration of analyte required for 50% inhibition of cancer cell growth (compared to negative controls). All experiments were performed in duplicate.

3 Chromatograms

3.1 HPLC-DAD chromatogram of CMB-M081F M1 agar plate extract



Figure S1. Expansion of HPLC-DAD (254 nm) chromatogram of the crude extract CMB-M81F highlighting the DKM **1** and DKPs **2**–**4**.



3.2 HPLC-DAD-ESIMS chromatograms of Mosher esters

Figure S2. Analytical HPLC (Zorbax SB-C₈ 5 μ m 150 × 4.6 mm column, 1.0 mL/min, gradient elution from 90% H₂O:MeCN to 100% MeCN over 15 min followed by a 5 min hold at 100% MeCN, with isocratic 0.05% HCO₂H in MeCN modifier), monitoring single ion extractions at *m*/*z* 383 [M+H]⁺ for the Mosher ester of phenyllactic acid). (a) Co-injection of *R*- and *S*-MTPA esters of authentic (*S*)-phenyllactic acid, (b) Co-injection of *R*-MTPA ester of authentic (*S*)-phenyllactic acid recovered from hydrolysis of shornephine A (1), (c) *R*-MTPA ester of phenyllactic acid recovered from hydrolysis of shornephine A (1) (d) *S*-MTPA ester of authentic (*S*)-phenyllactic acid and (e) *R*-MTPA ester of authentic (*S*)-phenyllactic acid.

3.3 Methanolysis of shornephine A (1)



Figure S3. HPLC-DAD (254 nm) chromatogram of shornephine A (1) after incubation in MeOH for (a) 30 min, (b) 8 h and (c) 24 h (100% conversion to **1a**)

3.4 Methanolysis of cyclo-(L-phenylalanine-L-mandelic acid) (17)



Figure S4. HPLC-DAD (254 nm) chromatogram of *cyclo*-(L-phenylalanine-L-mandelic acid) (17) after incubation in MeOH for (a) 30 min and (b) 1 h (100% conversion to **17a**)

3.5 Methanolysis of *cyclo*-(*N*-methyl-L-tyrosine-L-phenyllactic acid) (26)



Figure S5. HPLC-DAD (254 nm) chromatogram of *cyclo*-(*N*-methyl-L-tyrosine-L-phenyllactic acid) (26) after incubation in MeOH for (a) 3 h and (b) 24 h.



Table S1. 1D and 2D NMR (600 MHz, CDCl₃) data of shornephine A (1)

r	mult, (J in HZ)	δ_{C}	COSY	ROESY	$^{1}\text{H} - ^{13}\text{C} \text{HMBC}$
1		167.7			
2 4.32	2, d (11.1)	57.3	3a/b	2', 16/17	1, 3, 4
3 a 3.	26, d (13.7)	36.9	2, 3b		1, 2, 4, 5, 12
b 2.	.81, dd (13.7, 11.1)		2, 3a		1, 2, 4, 5
4		88.5			
4-OH 2.07	7, br s			3b	3, 4
5		131.5			
6 6.91	1, d (7.7)	117.1	7	3a	4, 7, 10
7 6.69	9 ^b , m	117.3 ^e	8		5, 9
8 6.67	7 ^b , m	121.2 ^e	6, 7		7, 10
6 6.91	1, d (7.7)	117.1	7	3a	4, 7, 10
9		141.4			
9-OH ^d					
10		135.9			
11-NH 6.34	4, s			16, 17	4, 5
12		94.9			
13		44.9			
14 6.39	9, dd (17.3, 10.6)	144.1	15a/b	3b, 16/17	13, 16/17
15 a 5.	18, d (17.3)	113.1	14, 15b	16/17	13, 14
b 5.	.11, d <i>(10.6)</i>		14, 15a		13, 14
16 1.38	8, s	22.9		2, 14	12, 13, 14
17 1.38	8, s	25.8		2, 14	12, 13, 14
1'		165.9			
2' 4.76	6, dd (8.8, 1.6)	78.5	3′a/b	2, 3'a	3', 4'
3' a 3.	32, d (15.1)	34.4	2′, 3′b	2'	4', 5'/9'
b 2.	.92, dd (15.1, 8.8)		2′, 3′a		1', 2', 4', 5'/9'
4'		136.2			
5'/9' 7.20	0 ^b	126.7 ^f			
6'/8' 7.20	0 ^b	129.3 ^f			
7' 7.20	0 ^b	128.5			

^{a 13}C NMR assignments supported by gHSQC and gHMBC data.
 ^{b,c} overlapping signals.
 ^d not observed.
 ^{e,f} assignments are interchangeable



Table S2. 1D and 2D NMR (600 MHz, DMSO-*d*₆) data of *seco*-shornephine A methyl ester (1a)

pos	$\delta_{\rm H}$, mult, (<i>J</i> in Hz)	δ_{C}^{a}	COSY	ROESY	$^{1}H - ^{13}C HMBC$
1		172.5			
1-OMe	3.38, s	52.1			1
2	3.79, ddd, (9.7, 8.0, 5.4)	49.8	3a/b, 2-NH	2-NH, 6	1, 1', 3
2-NH	7.35, d, (8.0)		2	2, 2′, 3b	1', 2
3	a 2.32, dd, (14.2, 5.4)	32.8	3b, 2	6	1, 2, 4, 5, 12, 13
	b 2.24, dd, (14.2, 9.7)		3a, 2	2-NH	1, 2, 4, 5, 12, 13
4		55.8			
5		130.0			
6	6.56, d, (7.4)	117.0	7	2, 3a, 14, 16, 17	4, 8, 10
7	6.78, dd, (8.0, 7.4)	121.4	6, 8		5, 9
8	6.70, d, (8. <i>0</i>)	115.6	7		6, 9, 10
9		141.5			
9-OH	9.50, br s				
10		131.0			
11-NH	10.20, br s				
12		179.7			
13		42.3			
14	6.04, dd, (<i>17.4</i> , <i>10.8</i>)	143.5	15a/b	6, 16, 17	13, 17
15	a 5.07, dd, (10.8, 0.6)	113.8	14		13
	b 4.99, dd, (17.4, 0.6)		14		13, 14
16	1.01, s	22.1		6, 14	4, 13, 14, 17
17	0.93, s	21.8		6, 14	4, 13, 14, 16
1'		173.5			
2'	3.90, dd, (9.6, 3.3)	72.5	3'a/b	2-NH	1'
2'-OH	5.53, br s		2'		
3'	a 2.79, dd, (<i>13.8</i> , <i>3.3</i>)	40.4	2′, 3′b		2', 4', 5'/9'
	b 2.61, dd, (<i>13.8</i> , <i>9.6</i>)		2′, 3′a		2', 4', 5'/9'
4′		138.8			
5′/9′	7.22, d, (7.2)	129.7	6'/8'		5'/9', 7'
6'/8'	7.26, ddd, (7.2, 7.2, 0.6)	128.2	5'/9', 7'		6'/8', 4'
7′	7.18, td, (7.2, 0.6)	126.3	6'/8'		5'/9'

^{a 13}C NMR assignments supported by gHSQC and gHMBC data.



pos	$\delta_{\rm H}$, mult, (<i>J</i> in Hz)	$\delta_{C}{}^{a}$	COSY	ROESY	$^{1}\text{H} - ^{13}\text{C} \text{HMBC}$
1	7.42, d (7.5)	124.4	2		3, 16b
2	7.21, dd (7.5, 7.5)	124.9	1, 3		1, 3, 4, 4a, 16b
3	7.45, dd (7.5, 7.5)	130.2	2,4		1, 16b
4	8.07, br s	b	3		
4a		142.5			
5a	6.04, br s	80.2		21, 22, 24	
7		168.4			
8	5.34, q (7.1)	53.5	17		7, 10, 15a, 17
10		160.1			
10a		120.7			
11	8.27, d (7.5)	127.1	12		10, 12, 14a
12	7.77, dd <i>(</i> 7. <i>5, 7</i> . <i>5)</i>	128.3	11, 13		10a, 11
13	7.51, dd <i>(8.1, 7.5)</i>	134.9	12, 14		11, 14a
14	7.72, d <i>(8.1)</i>	127.8	13		10, 10a, 13
15a		150.6			
15b		89.2			
16	α 3.15, d (14.8)	43.8		21, 22	15a, 15b, 18
	β 3.06, d <i>(14.8)</i>			21, 22	5a, 15b
16a		59.4			
16b		133.3			
17	1.64, d (7. <i>1</i>)	18.3	8		7, 8
18		40.5			
19	5.78, dd (17.0, 10.9)	143.4	20α,β	16α, 21, 22	18, 22
20	α 5.13, d (10.9)	115.9	19	21, 22	18, 19
	β 5.11, d (17.0)		19	21, 22	18, 19
21	0.98, s	22.6	22	5a, 19	18, 19, 22
22	1.17, s	22.8	21	5a, 19	18, 19, 21
23		170.8		-	· · · · ·
24	2.65, br s	23.6		21, 22	23
15b-OH	2.21, br s				15a

 $^{a\ 13}C$ NMR assignments supported by gHSQC and gHMBC data b not observed



Table S4. 1D and 2D NMR (600 MHz, $CDCl_3$) data of 5-N-acetyladreemin (3)²

pos	$\delta_{\rm H}$, mult, (J in Hz)	δ_{C}^{a}	COSY	ROESY	$^{1}\text{H} - ^{13}\text{C} \text{HMBC}$
1	7.39, d (7.8)	124.7	2		4, 16
2	7.18, dd (7.8, 7.8)	124.5	1, 3		4
3	7.36, dd (7.8, 7.2)	130.1	2,4		1, 4a
4	8.03, br s	121.2	3		2
4a		142.2			
5a	6.04, br s	81.2		16β, 21, 22	16, 18
7		169.1			
8	5.41, q (7.2)	53.6	17		7
10		160.1			
10a		121.2			
11	8.27, dd (7.8, 1.2)	127.8	12		
12	7.50, dd (7.8, 7.2)	127.5	11, 13		10a
13	7.72, ddd (8.4, 7.2, 1.2)	135.2	12, 14		14a
14	7.66, d (<i>8</i> . <i>4</i>)	126.3	13		
14a		149.4			
15a		151.1			
15b	4.41, dd (<i>10.3</i> , <i>5.5</i>)	90.2	16α,β	16α,β, 17	15a
16a		60.1			
16b		132.3			
16	α 3.02, dd (12.8, 5.5)	59.2	15b, 16β		18
	β 2.69 ^b		15b, 16a		18
17	1.44, d (7.2)	19.1	8	15b	
18		41.2			
19	5.85, dd (17.4, 11.0)	145.3	20α, β	16β, 21, 22	
20	α 5.12 d (17.4)	115.1	19, 20β		21, 22
	β 5.11, d (<i>11.0</i>)		19, 20α	21, 22	21, 22
21	1.21, s	22.1	22		4a, 18, 20
22	1.03, s	22.3	21		4a, 18, 20
23		171.4			
24	2.67, s	23.6			

^{a 13}C NMR assignments supported by gHSQC and gHMBC data.
 ^b Overlapping signal



Table S5. 1D and 2D NMR (600 MHz, CDCl₃) of 15b-β-methoxy-5-N-acetylardeemin (4)

pos	$\delta_{\rm H}$, mult, (<i>J</i> in Hz)	δ_{C}^{a}	COSY	ROESY	$^{1}\text{H} - ^{13}\text{C} \text{HMBC}$
1	7.35, d (7.8)	123.8	2	16β	3, 4a
2	7.13, dd (7.8, 0.6)	123.9	1, 3		4
3	7.31, dd (7.8, 0.6)	128.5	2, 4		1, 4a
4	7.98, br d (7.8)	119.5	3		
4a		143.0			
5a	6.10, br s	80.5		24	
7		168.0			
8	5.29, q, (<i>6</i> . <i>6</i>)	54.9	17		7, 15a, 17
10		160.0			
10a		120.8			
11	8.29, d (7.8)	126.9	12		10, 13, 14a
12	7.54, dd (7.8, 1.8)	127.9	11, 13		10a, 14
13	7.80, dd (7.8, 1.8)	134.8	12, 14		11, 14a
14	7.75, d (7.8)	127.9	13		10a, 12
14a		146.3			
15a		148.1			
15b		92.7			
15b-OMe	2.70, s	52.1		16α, 17	15b
16	α 3.15, d (<i>14.4</i>)	37.4	16β	1, 21, 22	5a, 15b
	β 2.79, d (14.4)		16α	19	15a, 18
16a	•	59.1			
16b		134.2			
17	1.64, d (<i>6</i> . <i>6</i>)	18.9	8	15b-OMe	7, 8
18		40.9			
19	5.85, dd (17.5, 10.8)	143.3	20α, β	16b	
20	α 5.12, d (17.5)	114.9	19		18
	β 5.11. d (<i>10.8</i>)		19		18
21	1.20, s	22.6		16α	18, 19, 22
22	1.01. s	23.3		16a	18, 19, 21
23	··· , ~			1000	-,,
24	2.66, br s	23.9		5a	

^{a 13}C NMR assignments supported by gHSQC and gHMBC data



Figure S7. HMBC NMR (600 MHz, CDCl₃) spectrum of shornephine A (1)



Figure S8. ¹H NMR (600 MHz, DMSO- d_6) and UV-vis spectra of *seco*-shornephine A methyl ester (1a)



Figure S9. HMBC NMR (600 MHz, DMSO-*d*₆) spectrum of *seco*-shornephine A methyl ester (1a)





Figure S13. ¹³C NMR (150 MHz, CDCl₃) spectrum of 5-*N*-acetylardeemin (3)



Figure S15. ¹³C NMR (150 MHz, CDCl₃) spectrum of 15b-β-methoxy-5-*N*-acetylardeemin (4)



Figure S17. ¹³C NMR (150 MHz, CDCl₃) spectrum of *cyclo*-(L-phenylalanine-L-mandelic acid) (17)



Figure S18. ¹H NMR (600 MHz, CDCl₃) spectrum of *cyclo*-(L-phenylalanine-L-phenyllactic acid) (18)



Figure S19. ¹³C NMR (150 MHz, CDCl₃) spectrum of *cyclo*-(L-phenylalanine-L-phenyllactic acid) (18)



*impurities present in the spectra due to relative instability of the compounds





Figure S24. ¹H NMR (600 MHz, CDCl₃) spectrum of *cyclo*-(L-alanine-L-mandelic acid) (21)





Figure S26. ¹H NMR (600 MHz, CDCl₃) spectrum of *cyclo*-(L-alanine-L-phenyllactic acid) (22)



Figure S27. ¹³C NMR (150 MHz, CDCl₃) spectrum of *cyclo*-(L-alanine-L-phenyllactic acid) (22)





Figure S29. ¹³C NMR (150 MHz, DMSO-*d*₆) spectrum of *cyclo*-(L-tyrosine-L-mandelic acid) (**23**) *impurities present in the spectra due to relative instability of the compounds



Figure S30. ¹H NMR (600 MHz, CDCl₃) spectrum of *cyclo*-(L-tyrosine-L-phenyllactic acid) (24)



Figure S31. ¹³C NMR (150 MHz, CDCl₃) spectrum of *cyclo*-(L-tyrosine-L-phenyllactic acid) (24)



Figure S32. ¹H NMR (600 MHz, DMSO-*d*₆) spectrum of *cyclo*-(*N*-methyl-L-tyrosine-L-mandelic acid) (**25**)



Figure S33. HMBC NMR (600 MHz, DMSO-*d*₆) NMR spectrum of *cyclo*-(*N*-methyl-L-tyrosine-L-mandelic acid) (25)



Figure S35. HMBC NMR (150 MHz, CDCl₃) spectrum of *cyclo*-(*N*-methyl-L-tyrosine-L-phenyllactic acid) (26)

4 Biological Data

4.1 Antibiotic Screening Data for 1–4 and 1a



Bacillus subtilis ATCC 6051







Staphylococcus aureus ATCC 9144



Figure S36. Antibiotic screening of compounds 1–4 and 1a (continued overleaf)



Escherichia coli ATCC 11775





(%) (100)

Pseudomonas aeruginosa ATCC 10145

Figure S36. Continued... Antibiotic screening of compounds 1-4 and 1a

4.2 Cytotoxicity and Calcein AM Screening Data for 1-4 and synthetic DKMs 17-24 and 19-22

Table S6. Cytotoxicity of compounds and their effects on accumulation of calcein AM in P-gp overexpressing SW620 Ad300 cells using flow cytometry

#	$IC_{50} (\mu M)^a$						
	SW620	SW620 Ad300	KB-3-1	KB-V1			
19	> 30	> 30	> 30	> 30	55.5		
24	> 30	> 30	> 30	> 30	42.7		
23	> 30	> 30	> 30	> 30	41.3		
1	> 30	> 30	> 30	> 30	38.9		
2	> 30	> 30	> 30	> 30	30.8		
4	> 30	> 30	> 30	> 30	30.5		
20					10.4		
3					2.4		
18					1.8		
17					1.3		
22					1.2		
21					1.0		

^a Cell survival was determined by MTT assay.

^b FAR (fluorescence arbitrary ratio) = calcein fluorescence intensity (geometric mean) in the presence of compounds 1– 4 and 17-24, 19-22 at 20 μ M / calcein fluorescence intensity (geometric mean) in the presence of PBS, expressed as a ratio. Positive control is verapamil at 20 μ M which FAR = 71.4



Figure S37. Effect of compounds on accumulation of calcein AM in P-gp-overexpressing SW620 Ad300 cells using flow cytometry



Figure S38. Cytotoxicity of compounds 1, 2, 4, 19, 23 and 24 against SW620, SW620 Ad300, KB-3-1 and KB-V1

5 References

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- (2) Hochlowski, J. E.; Mullally, M. M.; Spanton, S. G.; Whittern, D. N.; Hill, P.; McAlpine, J. B. *J. Antibiot.* **1993**, *46*, 380-386.