MS/MS-Based Molecular Networking Approach for the Detection of Aplysiatoxin-Related Compounds in Environmental Marine Cyanobacteria

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SUPPLEMENTARY DATA

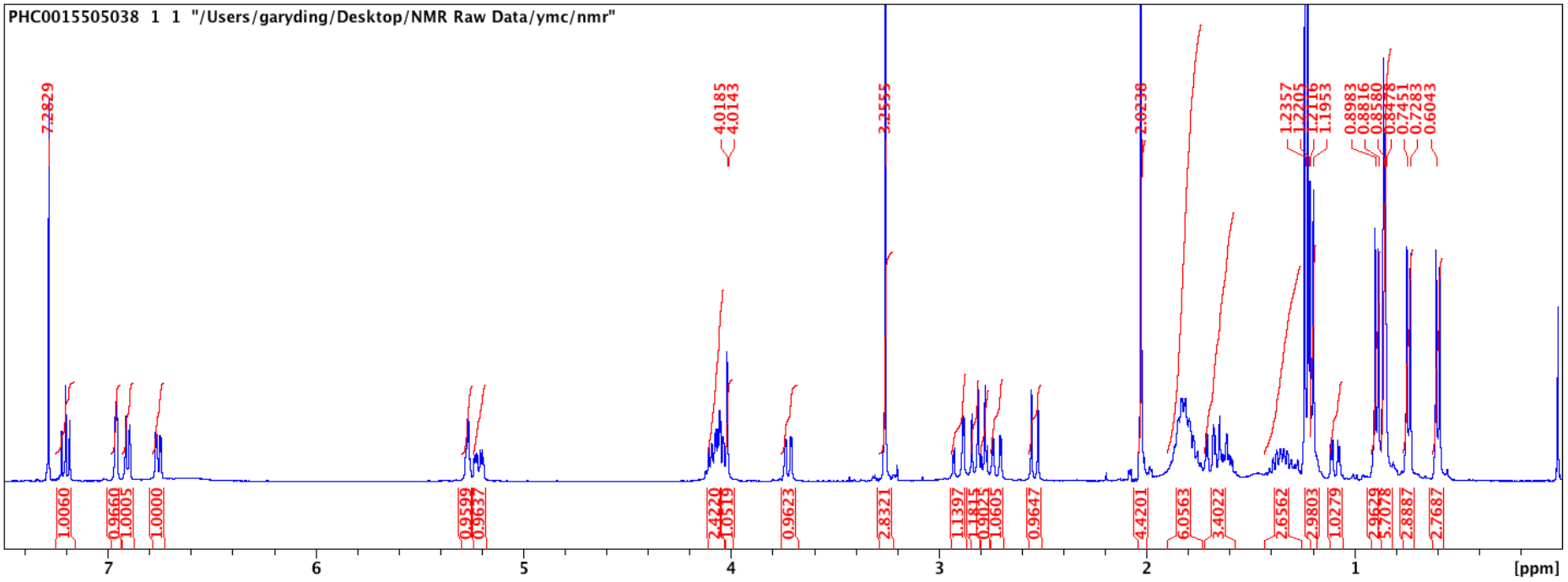

Figure S1. ^{1}H spectrum of debromoaplysiatoxin (**1**) recorded in $CDCl_3$ at 400 MHz

Table S1: Cyanobacterial strains partial 16s-ITS rRNA gene and its closet homologues in the nucleotide collection database

Strain	No. of bp	BLASTn closest homolog (accession#) organism	Score	Coverage/ Identity [%]
TLT/PHB/001	1465	*Trichodesmium erythraeum* IMS101	2529	1433/1465 [97.8%]
		Trichodesmium sp.	2508	1425/1460 [97.6%]
		Okeania sp. PNG05-4	2503	1386/1401 [98.9%]
		Oscillatoria sp. PAB-21	2471	1356/1365 [99.3%]
TLT/PHC/001	1399	*Okeania* sp. PNG05-4	2490	1383/1400 [98.8%]
		Oscillatoria sp. PAB-21	2471	1356/1365 [99.3%]
		Oscillatoria nigroviridis 3LOSC	2471	1356/1365 [99.3%]
		Okeania sp. NAC8-18	2412	1335/1349 [99.0%]
TLT/PHC/002	1363	*Oscillatoria* sp. PAB-21	2451	1352/1364 [99.1%]
		Oscillatoria nigroviridis 3LOSC	2451	1352/1364 [99.1%]
		Okeania sp. PNG05-4	2423	1347/1364 [98.8%]
		Hydrocoleum glutinosum M34	2399	1331/1347 [98.8%]

Table S2. Complete 16s rRNA sequence of cyanobacterial samples

TLT/PHB/001

CTCAGGATGAACGCTGGCGGTCTGCTTAACACATGCAAGTCGAACGGACCCTTCGGGGTTAGTGGCGGACGGGTGAGTAA
CGCGTGAGAATCTGCCTTCAGGTCTGGGACAACAGAAGGAAACTTCTGCTAATCCCGGATGAGCCTTTGGGTAAAAGATA
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TCAAGTCAGCATGCCCCTTACGTCCTGGGCTACACACGTACTACAATGGTCTGGACAGAGGGTAGCCAACCCGCGAGGGC
GAGCCAATCTCAAAAACCAGGCCTCAGTTCAGATTGCAGGCTGCAACTCGCCTGCATGAAGGAGGAATCGCTAGTAATCG
CAGGTCAGCATACTGCGGTGAATCCGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGAAGTTGGCCACGCCCGA
AGTCATTACTCTAACTCGTAAGAGAGGGGGATGCCGAAGGCAGGGCTGATGACTGGGGTGAAGTCGTAACAAGGTAGCC
GTACCGGAAGGTGTGGCTGGATCACCTCCTT

TLT/PHC/001

GGACGGGTGAGTAACGCGTGAGAATCTGCCTTCAGGTCTGGGACAACAGAAGGAAACTTCTGCTAATCCCGGATGAGCCT
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CTCTGGTCAGGCAGTGGAAACTACAAAGCTAGAGTCTGGTAGGGGCAAAGGGAATTCCCGGCGTAGCGGTGAAATGCGT
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TLT/PHC/002

TCTGGGACAACAGAAGGAAACTTCTGCTAATCCCGGATGAGCCGTGAGGTAAAAGAGAAATTGCCTGGAG
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GTGTGGCTGGATCACCTCCTT