SUPPLEMENTARY MATERIAL

Analysis of Biological Diversity between the cyanobacteria Cylindrospermospsis and Sphaerospermopsis

Reno Nooblath
Federal University of Pará (UFPA), reno.bioinfo@gmail.com, +55 (91) 98208-1316, Augusto Corrêa Street, 01 – Bairro Guamá – CEP 66075-110 Belém–Pará – Amazônia, Brasil.

Daniel Gomes

Federal University of Pará (UFPA), daniel.h.gomes18@gmail.com, +55 (91) 98126-7143, Augusto Corrêa Street, 01 – Bairro Guamá – CEP 66075-110 Belém – Pará – Amazônia, Brasil.

Vinícius Abreu

Federal University of Pará (UFPA), vabreuufpa@gmail.com, +55 (91) 99810-7845, Augusto Corrêa Street, 01 – Bairro Guamá – CEP 66075-110 Belém –Pará – Amazônia, Brasil.

Sintia Silva de Almeida

Federal University of Pará (UFPA), sintiaalmeida@gmail.com, +55 (91) 98218-2015, Augusto Corrêa Street, 01 – Bairro Guamá – CEP 66075-110 Belém – Pará – Amazônia, Brasil.

Table S1 . Origin of the *Cylindrospermopsis* and *Sphaerospermopsis* strains used in this study and their taxonomic identification on NCBI, organized in ascending order based on the number of scaffolds..

Organism	Taxonomy ID	Scafolds	Origin of Sample	Size	GC%
C. raciborskii KLL07	683357	1	Israel	3.80818	40.2
C. raciborskii N8	1524929	1	China	3.85717	40.1
C. raciborskii Cr2010	2108055	1	Netherlands	3.75785	40.2
C. curvispora GIHE G1	2666332	2	South Korea	4.05721	40117
C. raciborskii DSH	3117726	2	China	4.0	40
C. raciborskii GIHE 2018	2588993	3	South Korea	3.62982	40.2
C. raciborskii CS-505	533240	6	Australia	3.9	40
R. brookii D9	533247	47	Brazil	3.2	40
C. raciborskii CENA 302	1170768	58	Brazil	3.5	40
C. raciborskii CENA 303	1170769	77	Brazil	3.4	40.5
C. raciborskii MVCC14	940191	99	Uruguay	3.6	40.1
C. raciborskii KL1	2787621	100	USA	3.7	40
C. raciborskii PAMP2012	2969974	134	Brazil	3.2	40
C. sp. CR12	1747196	136	Malaysia	3.7	40
C. raciborskii MVCC 19	940192	155	Uruguay	3.5	40
C. raciborskii CS508	533243	162	Australia	3.6	40
C. raciborskii CYRF	2021698	166	Brazil	4.2	40
C. raciborskii 1523720	77022	173	Índia	3.2	40
C. raciborskii CYLP	2021699	188	Brazil	4.2	40
C. raciborskii CHAB3438	1480071	189	China	3.5	40.5
C. raciborskii ITEPA-A1	1810942	195	Brazil	3.6	40

S. torques-reginae ITEP-024	984208	1	Brazil	5.3	37.5
S. kisseleviana NIES-73	1973480	2	Japan	5.4	37.5
S. sp. SIO1G1	2607814	38	Puerto Rico	5.2	36.5
S. sp. FACHB-1194	2692862	108	China	5.4	37.5
S. sp. LEGE 08334	1828651	119	Mexico	5.5	37
S. sp. LEGE 00249	1380707	177	Portugal	5.3	37.5

Suplementary Table S2. Proposed function of the proteins encoded by the saxitoxin biosynthetic gene cluster from the *Sphaerospermopsis* group.

Protein	Amino acids	Product	Strain	Organism	Identity (%)	Function	Acession number
sxt	266	Phytanoyl-CoA dioxygenase	*S. torques ITEP024*	*S. LEGE 08334*	100	phytanoyl-CoA dioxygenase	WP_194055575.1
sxtJ	747	carbamoyltransferase	*S. torques ITEP024*	*S. LEGE 08334*	100	carbamoyltransferase	MBE9056840.1
sxtK	54	DUF5989	*S. torques ITEP024*	*Nostoc sp. ChiQUE01a*	89	DUF5989	MDZ8239473.1
sxtJ	747	carbamoyltransferase	*S. LEGE 08334*	*S. torques ITEP024*	100	carbamoyltransferase	QYX30560.1
sxtK	54	DUF5989	*S. LEGE 08334*	*Nostoc sp. ChiQUE01a*	89	DUF5989	MDZ8239473.1
sxt	747	Nodulation protein nolO	*S. torques ITEP024*	*S. LEGE 08334*	100	SxtJ family membrane protein	WP_194055576
sxt	108	hypothetical protein	*S. torques ITEP024*	*S. LEGE 08334*	100	macrolide family glycosyltransferase	WP_194055579.1
sxt	385	Carbamoyl-phosphate synthase small chain	*S. torques ITEP024*	*S. LEGE 08334*	99	glutamine-hydrolyzing carbamoyl-phosphate	WP_194055594.1

Supplementary Table S3. Proposed function of the proteins encoded by saxitoxin biosynthetic gene cluster in the genomes of the *C. raciborskii* strains *R. brookii* D9 , MVCC14, MVCC19,CENA302, ITEP-A1, and the CYRF.

Protein	Amino acids	Product	Strains	Organism	Identity(%)	Function	Acession number
SxtA	1245	PKS	*R. brookii D9*	*C. raciborskii T3*	99	Polyketide synthase-related protein	ABI75094.1
	1245		*C. raciborskii CENA302*	*C. raciborskii T3*	100	Polyketide synthase-related protein	ABI75094.1
	1245		*C. raciborskii ITEP-A1*	*C. raciborskii T3*	100	Polyketide synthase-related protein	ABI75094.1
	1245		*C. raciborskii MVCC14*	*C. raciborskii T3*	100	Polyketide synthase-related protein	ABI75094.1
	1245		*C. raciborskii MVCC19*	*C. raciborskii T3*	99	Polyketide synthase-related protein	ABI75094.1
	860		*C. raciborskii CYRF*	*C. raciborskii T3*	99	polyketide synthase-related protein	ABI75094.1
SxtB	318	Cytidine deaminase	*R. brookii D9*	*C. raciborskii T3*	100	Cytidine deaminase	ABI75093.1
	318		*C. raciborskii CENA302*	*R. brookii D9*	100	SxtB	EFA72782.1
	318		*C. raciborskii ITEP-A1*	*C. raciborskii T3*	100	Cytidine deaminase	ABI75093.1
	318		*C. raciborskii MVCC14*	*C. raciborskii T3*	100	Cytidine deaminase	ABI75093.1
	318		*C. raciborskii MVCC19*	*C. raciborskii T3*	89	Cytidine deaminase	WP_254011061.1
	318		*C. raciborskii CYRF*	*Heteroscytonema crispum UCFS10*	92	SxtB	AYN62266.1

SxtC	117	Regulatory	*R. brookii D9*	*C. raciborskii T3*	100	SxtC	ABI75092.1
	94		*C. raciborskii CENA302*	*C. raciborskii T3*	100	SxtC	ABI75092.1
	94		*C. raciborskii ITEP-A1*	*C. raciborskii T3*	100	sxtC	ABI75092.1
	117		*C. raciborskii MVCC14*	*C. raciborskii T3*	100	sxtC	ABI75092.1
	94		*C. raciborskii MVCC19*	*Heteroscytonema crispum UCFS10*	91	sxtC	AYN62265.1
	117		*C. raciborskii CYRF*	*C. raciborskii T3*	100	sxtC	AYN62265.1
SxtD	252	Sterole desaturase-like protein	*R. brookii D9*	*C. raciborskii T3*	99	Sterole desaturase	ABI75089.1
	252		*C. raciborskii CENA302*	*R. brookii D9*	100	SxtD	EFA72785.1
	252		*C. raciborskii ITEP-A1*	*R. brookii D9*	100	SxtD	EFA72785.1
	252		*C. raciborskii MVCC14*	*R. brookii D9*	100	SxtD	EFA72785.1
SxtE	128	Unknown protein	*R. brookii D9*	*C. raciborskii T3*	99	SxtE	ABI75095.1
	45		*C. raciborskii CENA302*	*C. raciborskii T3*	100	SxtE	ABI75095.1
	45		*C. raciborskii ITEP-A1*	*C. raciborskii T3*	100	SxtE	ABI75095.1
	128		*C. raciborskii MVCC14*	*C. raciborskii T3*	100	SxtE	ABI75095.1
	127		*C. raciborskii MVCC19*	*Microseira wollei*	88	SxtE	ACZ26228.1
	120		*C. raciborskii CYRF*	*Microseira wollei*	92	SxtE	ACZ26228.1

SxtF	471	MATE	*R. brookii D9*	*C. raciborskii T3*	99	Sodium-driven multidrug and toxic compound extrusion protein	ABI75096.1
	471		*C. raciborskii CENA302*	*C. raciborskii T3*	100	Sodium-driven multidrug and toxic compound extrusion protein	ABI75096.1
	471		*C. raciborskii ITEP-A1*	*C. raciborskii T3*	100	Sodium-driven multidrug and toxic compound extrusion protein	ABI75096.1
	471		*C. raciborskii MVCC14*	*C. raciborskii T3*	100	Sodium-driven multidrug and toxic compound extrusion protein	ABI75096.1
	471		*C. raciborskii MVCC19*	*C. raciborskii T3*	100	Sodium-driven multidrug and toxic compound extrusion protein	ABI75096.1
	220		*C. raciborskii CYRF*	*Heteroscytonema crispum UCFS10*	83	SxtM1	AYN62272.1
SxtG	377	Amidinotransferase	*R. brookii D9*	*C. raciborskii T3*	100	Amidinotransferase	ABI75097.1
	377		*C. raciborskii CENA302*	*C. raciborskii T3*	100	Amidinotransferase	ABI75097.1
	377		*C. raciborskii ITEP-A1*	*C. raciborskii T3*	100	Amidinotransferase	ABI75097.1
	377		*C. raciborskii*	*C. raciborskii T3*	100	Amidinotransferase	ABI75097.1

			MVCC14				
	377		*C. raciborskii MVCC19*	*C. raciborskii T3*	100	Amidinotransferase	ABI75097.1
	377		*C. raciborskii CYRF*	*C. raciborskii T3*	100	Amidinotransferase	ABI75097.1
SxtH	334	Phenylpropionate dioxygenase	*R. brookii D9*	*C. raciborskii T3*	100	Phenylpropionate dioxygenase	ABI75098.1
	334		*C. raciborskii CENA302*	*C. raciborskii T3*	100	Phenylpropionate dioxygenase	ABI75098.1
	334		*C. raciborskii ITEP-A1*	*C. raciborskii T3*	100	Phenylpropionate dioxygenase	ABI75098.1
	334		*C. raciborskii MVCC14*	*C. raciborskii T3*	100	Phenylpropionate dioxygenase	ABI75098.1
	334		*C. raciborskii MVCC19*	*C. raciborskii T3*	100	Phenylpropionate dioxygenase	ABI75098.1
	334		*C. raciborskii CYRF*	*C. raciborskii T3*	100	Phenylpropionate dioxygenase	ABI75098.1
SxtI	612	Carbamoyltransferase	*R. brookii D9*	*C. raciborskii T3*	100	NodU/CmcH-related carbamoyltransferase	ABI75099.1
	596		*C. raciborskii CENA302*	*C. raciborskii T3*	99	NodU/CmcH-related carbamoyltransferase	ABI75099.1
	612		*C. raciborskii ITEP-A1*	*C. raciborskii T3*	100	NodU/CmcH-related carbamoyltransferase	ABI75099.1
	612		*C. raciborskii MVCC19*	*C. raciborskii T3*	99	NodU/CmcH-related carbamoyltransferase	ABI75099.1
	612		*C. raciborskii CYRF*	*C. raciborskii T3*	99	NodU/CmcH-related carbamoyltransferase	ABI75099.1

SxtJ	147	Regulatory	*R. brookii D9*	*C. raciborskii T3*	100	SxtJ	ABI75100.1
	134		*C. raciborskii MVCC14*	*C. raciborskii T3*	99	SxtJ	ABI75100.1
	147		*C. raciborskii MVCC19*	*C. raciborskii MVCC14*	100	SxtJ	OHY34958.1
	147		*C. raciborskii CENA302*	*C. raciborskii MVCC14*	100	SxtJ	OHY34958.1
	147		*C. raciborskii CYRF*	*C. raciborskii MVCC14*	100	SxtJ	OHY34958.1
SxtK	54	Unknown protein	*C. raciborskii CENA302*	*C. raciborskii T3*	100	SxtK	ABI75101.1
	54		*C. raciborskii ITEP-A1*	*C. raciborskii T3*	100	SxtK	ABI75101.1
	54		*C. raciborskii MVCC19*	*C. raciborskii T3*	100	SxtK	ABI75101.1
	54		*C. raciborskii CYRF*	*C. raciborskii T3*	100	SxtK	ABI75101.1
	54		*C. raciborskii MVCC14*	*C. raciborskii T3*	100	SxtK	ABI75101.1

SxtL	435	GDSL-lipase	*R. brookii D9*	*C. raciborskii T3*	100	GDSL-lipase	ABI75102.1
	407		*C. raciborskii CENA302*	*C. raciborskii T3*	99	GDSL-lipase	ABI75102.1
	420		*C. raciborskii ITEP-A1*	*C. raciborskii T3*	99	GDSL-lipase	ABI75102.1
	419		*C. raciborskii MVCC14*	*C. raciborskii T3*	99	GDSL-lipase	ABI75102.1
	419		*C. raciborskii MVCC19*	*C. raciborskii T3*	99	GDSL-lipase	ABI75102.1
	432		*C. raciborskiiCYRF*	*C. raciborskii T3*	99	GDSL-lipase	ABI75102.1
SxtM	475	MATE	*R. brookii D9*	*C. raciborskii MVCC14*	99	SxtM, partial	AFQ99040.1
	429		*C. raciborskii CENA302*	*C. raciborskii MVCC14*	99	SxtM, partial	AFQ99040.1
	482		*C. raciborskii ITEP-A1*	*C. raciborskii T3*	99	Sodium-driven multidrug and toxic compound extrusion protein	ABI75103.1
	475		*C. raciborskii MVCC14*	*R. brookii D9*	99	SxtSUL	EFA72771.1
	475		*C. raciborskii MVCC19*	*C. raciborskii MVCC14*	99	SxtM	AFQ99040.1

	182		*C. raciborskii CYRF*	*C. raciborskii T3*	99	Sodium-driven multidrug and toxic compound extrusion protein	ABI75103.1
SxtN	302	Sulfotransferase	*R. brookii D9*	*Microseira wollei*	89	SxtSUL	ACG63834.1
	302		*C. raciborskii CENA302*	*R. brookii D9*	100	SxtSUL	EFA72773.1
	302		*C. raciborskii MVCC14*	*R. brookii D9*	100	SxtSUL	EFA72773.1
	270		*C. raciborskii CYRF*	*C. raciborskii T3*	100	SxtSUL	EFA72773.1
SxtO	200	Adenylylsulfate kinase	*R. brookii D9*	*C. raciborskii T3*	100	Adenylylsulfate kinase	ABI75115.1
	159		*C. raciborskii CENA302*	*R. brookii D9*	100	Adenylylsulfate kinase	EFA72764.1
	200		*C. raciborskii MVCC14*	*R. brookii D9*	100	Adenylylsulfate kinase	EFA72764.1
	200		*C. raciborskii MVCC19*	*C. raciborskii MVCC14*	100	Adenylylsulfate kinase	OHY34903.1
	200		*C. raciborskii MVCC19*	*C. raciborskii CENA302*	100	Adenylylsulfate kinase	OPH09277
	200		*C. raciborskii MVCC19*	*C. raciborskii T3*	100	Adenylylsulfate kinase	ABI75115.1
	200		*C. raciborskii CYRF*	*C. raciborskii T3*	100	Adenylylsulfate kinase	ABI75115.1
SxtP	408	RTX toxin	*R. brookii D9*	*C. raciborskii T3*	99	Putative saxitoxin-binding protein	ABI75114.1
	408		*C. raciborskii CENA302*	*C. raciborskii T3*	100	Putative saxitoxin-binding protein	ABI75114.1

	408		*C. raciborskii MVCC14*	*C. raciborskii T3*	100	Putative saxitoxin-binding protein	ABI75114.1
	408		*C. raciborskii MVCC19*	*C. raciborskii T3*	100	Putative saxitoxin-binding protein	ABI75114.1
	408		*C. raciborskii CYRF*	*C. raciborskii T3*	100	Putative saxitoxin-binding protein	ABI75114.1
SxtQ	258	Unknown protein	*R. brookii D9*	*C. raciborskii T3*	99	SxtQ	ABI75113.1
	239		*C. raciborskii CENA302*	*R. brookii D9*	100	SxtQ	EFA72766.1
	239		*C. raciborskii MVCC14*	*R. brookii D9*	100	SxtQ	EFA72766.1
	239		*C. raciborskii MVCC19*	*C. raciborskii T3*	100	SxtQ	EFA72766.1
	239		*C. raciborskii CYRF*	*C. raciborskii T3*	100	SxtQ	EFA72766.1
SxtR	258	Acyl transferase	*R. brookii D9*	*C. raciborskii T3*	100	Acyl-CoA N-acyltransferase	ABI75112.1
	258		*C. raciborskii CENA302*	*C. raciborskii T3*	100	Acyl-CoA N-acyltransferase	ABI75112.1
	258		*C. raciborskii MVCC14*	*C. raciborskii T3*	100	Acyl-CoA N-acyltransferase	ABI75112.1
	258		*C. raciborskii MVCC19*	*C. raciborskii T3*	100	Acyl-CoA N-acyltransferase	ABI75112.1
	258		*C. raciborskii CYRF*	*C. raciborskii T3*	100	Acyl-CoA N-acyltransferase	ABI75112.1
SxtS	241	Phytanoyl-CoA dioxygenase	*R. brookii D9*	*C. raciborskii T3*	99	Phytanoyl-CoA dioxygenase	ABI75110.1
	241		*C. raciborskii CENA302*	*R. brookii D9*	100	SxtS	EFA72768.1
	241		*C. raciborskii MVCC14*	*R. brookii D9*	100	SxtS	EFA72768.1

	241		*C. raciborskii MVCC19*	*C. raciborskii T3*	99	Phytanoyl-CoA dioxygenase	ABI75110
	241		*C. raciborskii CYRF*	*C. raciborskii T3*	100	Phytanoyl-CoA dioxygenase	ABI75110
SxtT	334	Phenylpropionate dioxygenase	*R. brookii D9*	*C. raciborskii T3*	99	Phenylpropionate dioxygenase	ABI75109.1
	334		*C. raciborskii CENA302*	*R. brookii D9*	100	SxtT	EFA72769.1
	334		*C. raciborskii MVCC14*	*R. brookii D9*	100	SxtT	EFA72769.1
	334		*C. raciborskii MVCC19*	*R. brookii D9*	100	SxtT	EFA72769.1
	334		*C. raciborskii CYRF*	*C. raciborskii T3*	100	Phenylpropionate dioxygenase	EFA72769.1
SxtU	248	Alcohol dehydrogenase	*R. brookii D9*	*C. raciborskii T3*	100	Short-chain alcohol dehydrogenase	ABI75108.1
	248		*C. raciborskii CENA302*	*R. brookii D9*	100	SxtU	EFA72770.1
	248		*C. raciborskii MVCC14*	*R. brookii D9*	100	SxtU	EFA72770.1
	248		*C. raciborskii MVCC19*	*R. brookii D9*	93	SxtU	EFA72770.1
	249		*C. raciborskii CYRF*	*C. raciborskii T3*	100	Short-chain alcohol dehydrogenase	ABI75108.1
SxtDIOX	334	(2Fe-2S)-binding protein	*R. brookii D9*	*Microseira wollei*	86	SxtDIOX	ACG63835.1
	334		*C. raciborskii CENA302*	*R. brookii D9*	99	SxtDIOX	EFA72772.1
	334		*C. raciborskii MVCC14*	*R. brookii D9*	99	SxtDIOX	EFA72772.1

Supplementary Table S4. Proposed function of the proteins encoded by cylindrospermopsin biosynthetic gene cluster in the genomes of the *C. raciborskii* strains CS-505, CR12, DSH and CHAB-3438.

Protein	Amino acids	Proposed function	Strain	Organism	Identity(%)	Function	Acession number
CyrA	391	Amidinotransferase	*C. raciborskii CS-505*	*C. raciborskii AWT205*	100	Amidinotransferase	ABX60160.1
	391		*C. raciborskii CR12*	*C. raciborskii AWT205*	99	Amidinotransferase	ABX60160.1
	391		*C. raciborskii CHAB3438*	*C. raciborskii AWT205*	100	Amidinotransferase	ABX60160.1
CyrB	2917	NRPS/PKS	*C. raciborskii CS-505*	*C. raciborskii AWT205*	100	Mixed NRPS/PKS	ABX60161.1
	2917		*C. raciborskii CR12*	*C. raciborskii AWT205*	100	Mixed NRPS/PKS	ABX60161.1
	2917		*C. raciborskii CHAB3438*	*Raphidiopsis curvata HB1*	100	Mixed NRPS/PKS	AHN91606.1
CyrC	1667	PKS	*C. raciborskii CS-505*	*C. raciborskii AWT205*	99	Polyketide synthase	ABX60163.1
	1667		*C. raciborskii CR12*	*C. raciborskii AWT205*	99	Polyketide synthase	ABX60163.1
	1667		*C. raciborskii CHAB3438*	*Raphidiopsis curvata HB1*	100	Polyketide synthase	AHN91608.1

CyrD	1851	PKS	*C. raciborskii CS-505*	*C. raciborskii AWT205*	100	Polyketide synthase	ABX60152.1
	1876		*C. raciborskii CR12*	*C. raciborskii AWT205*	99	Polyketide synthase	ABX60152.1
	1876		*C. raciborskii CHAB3438*	*Raphidiopsis curvata HB1*	100	Polyketide synthase	AHN91609.1
CyrE	1888	PKS	*C. raciborskii CS-505*	*C. raciborskii AWT205*	99	Polyketide synthase	ABX60162.1
	1888		*C. raciborskii CR12*	*C. raciborskii AWT205*	99	Polyketide synthase	ABX60162.1
	1888		*C. raciborskii CHAB3438*	*Raphidiopsis curvata HB1*	100	Polyketide synthase	AHN91607.1
CyrF	1357	PKS	*C. raciborskii CS-505*	*C. raciborskii AWT205*	100	Polyketide synthase	ABX60153.1
	1357		*C. raciborskii CR12*	*C. raciborskii AWT205*	99	Polyketide synthase	ABX60153.1
	1357		*C. raciborskii CHAB3438*	*Raphidiopsis curvata CHAB1150*	100	Polyketide synthase	AFC35246.1
CyrG	478	Uracil ring formation	*C. raciborskii CS-505*	*C. raciborskii AWT205*	100	Putative uracil ring formation	ABX60154.1
	478		*C. raciborskii CR12*	*C. raciborskii AWT205*	99	Putative uracil ring formation	ABX60154.1
	478		*C. raciborskii CHAB3438*	*Raphidiopsis curvata HB1*	99	Putative uracil ring formation	AHN91611.1
CyrI	276	Hydroxylation of C-7	*C. raciborskii CS-505*	*C. raciborskii CHAB3438*	100	Putative 2-oxoglutarate-dependent iron oxygenase	AHN91588.1
	276		*C. raciborskii CS-505*	*C. raciborskii CR12*	99	Putative 2-oxoglutarate-dependent iron oxygenase	WP_057178790
	278		*C. raciborskii*	*C. raciborskii*	99	Putative 2-oxoglutarate-	AHN91588.1

			CR12	*CHAB3438*		dependent iron oxygenase	
	276		*C. raciborskii CHAB3438*	*C. raciborskii CR12*	99	Putative 2-oxoglutarate-dependent iron oxygenase	WP_057178790.1
CyrK	465	Exporter	*C. raciborskii CS-505*	*C. raciborskii AWT205*	99	Multidrug exporter MatE	ABX60156.1
	465		*C. raciborskii CR12*	*C. raciborskii CS-505*	99	MATE family efflux transporter	OBU75962.1
	451		*C. raciborskii CHAB3438*	*Raphidiopsis curvata CHAB1150*	100	Multidrug exporter MatE	AFC35248.1
CyrL	249	Transposase	C. raciborskii CS-505	*C. raciborskii AWT205*	100	Transposase	ABX60157.1
	153		C. raciborskii CHAB3438	*C. raciborskii CR12*	98	Transposase	WP_161808566.1
CyrH	476	Uracil ring formation	*C. raciborskii CS-505*	*C. raciborskii AWT205*	100	Amidohydrolase	ABX60158.1
	476		*C. raciborskii CR12*	*C. raciborskii AWT205*	99	Amidohydrolase	ABX60158.1
	476		*C. raciborskii CHAB3438*	*Raphidiopsis curvata CHAB1150*	100	Amidohydrolase	AHN91614.1
CyrJ	259	Sulfotransferase	C. raciborskii CS-505	*C. raciborskii AWT205*	100	Putative sulfotransferase	ABX60159.1
	259		*C. raciborskii CR12*	*C. raciborskii AWT205*	99	Putative sulfotransferase	ABX60159.1
	261		*C. raciborskii CHAB3438*	*Raphidiopsis curvata HB1*	100	Putative sulfotransferase	AHN91615
CyrM	105	Transposase	*C. raciborskii CS-505*	*C. raciborskii AWT205*	97	Transposase protein	ABX60157.1

CyrN	219	Adenylyl-sulfate kinase	C. raciborskii CS-505	*C. raciborskii AWT205*	100	Adenylylsulfate kinase	ABX60164.1
CyrO	515	Regulator	*C. raciborskii CS-505*	*C. raciborskii AWT205*	99	Hypothetical protein	AHN91599.1

Suplementary Table S5. Proposed function of the proteins encoded by anabaenopeptin biosynthetic gene cluster of the Sphaerospermopsis group.

Protein	Amino acids	Product	Strain	Organism	Identity (%)	Function	Acession number
aptA1	4161	Siderophore biosynthesis non-ribosomal peptide synthetase modules	*S. torques ITEP024*	*Aphanizomenon flos-aquae*	90	non-ribosomal peptide synthetase	WP_190382984.1
	4109		*S. Kisseleviana NIES 73*	*Dolichospermum sp. LEGE 00246*	83		WP_1939621
aptA2	2208	Polyketide synthase	*S. torques ITEP024*	*S. LEGE 08334*	97	Polyketide synthase	WP_194056036.1
	2226		*S. Kisseleviana NIES 73*	*S. FACHB 1194*	95		WP_190346674.1
	2186		*S. sp SIO1G1*	*S. LEGE 08334*	74		WP_194056036.1
	2224		*S. FACHB 1194*	*S. Kisseleviana NIES 73*	96		WP_096571779.1
	2212		*S. LEGE 08334*	*S. torques reginae ITEP024*	97		WP_220609901.1

aptB	1069	Siderophore biosynthesis non-ribosomal peptide	*S. torques ITEP024*	*S. LEGE 08334*	95	non-ribosomal peptide synthetase	WP_194056038.1
	1087		*S. Kisseleviana NIES 73*	*S. FACHB 1194*	95	amino acid adenylation	WP_242052557.1
	1074		*S. sp SIO1G1*	*S. torques ITEP024*	72	non-ribosomal peptide synthetase	WP_220609902.1
	1088		*S. FACHB 1194*	*S. Kisseleviana NIES 73*	95	non-ribosomal peptide synthetase	WP_096571778.1
	1073		*S. LEGE 08334*	*S. torques reginae ITEP024*	95	non-ribosomal peptide synthetase	WP_220609902.1
aptC	2576	Siderophore biosynthesis non-ribosomal peptide synthetase modules	*S. torques ITEP024*	*Nodularia spumigena*	90	non-ribosomal peptide synthetase	WP_063874470.1
	2587		*S. Kisseleviana NIES 73*	*Dolichospermum sp. LEGE 00246*	97	non-ribosomal peptide synthetase	WP_193962698.1
	2562		*S. sp SIO1G1*	*Aphanizomenonaceae cyanobacterium TIOX110*	74	amino acid adenylation	WZB86541.1
	2570		*S. FACHB 1194*	*S. Kisseleviana NIES*	81	non-ribosomal	WP_096571777.1

				73			
	2200		*S. LEGE 08334*	*S. FACHB 1194*	78	peptide synthetase	WP_190346675.1
aptD	1415	Siderophore biosynthesis non-ribosomal peptide	*S. torques ITEP024*	*S. LEGE 08334*	88		WP_194056042.1
	1363		*S. Kisseleviana NIES 73*	*Dolichospermum*	93		WP_193962697.1
	1397		*S. sp SIO1G1*	*Aphanizomenonaceae cyanobacterium TIOX110*	74	amino acid adenylation	WZB86542.1
	1419		*S. FACHB 1194*	*S. Kisseleviana NIES 73*	84		WP_272110476.1
	1420		*S. LEGE 08334*	*S. torques reginae ITEP024*	88	non-ribosomal peptide synthetase	WP_220609905.1
aptE	392	2-isopropylmalate synthase	*S. torques ITEP024*	*S. FACHB 1194*	98	2-isopropylmalate synthase	WP_190346677.1
	392		*S. LEGE 08334*	*S. Kisseleviana NIES 73*	93		WP_272110474.1
	253		*S. Kisseleviana NIES 73*	*S. FACHB 1194*	100		MBD2144629.1
	392		*S. LEGE 08334*	*S. Kisseleviana NIES 73*	93		WP_272110474.1
aptF	813	ATP-binding cassette	*S. FACHB 1194*	*Sphaerospermopsis reniformis*	95	ATP-binding cassette	GCL35044.1
	761		*S. sp SIO1G1*	*Okeanomitos*	73		WZB86544.1

				corallinicola			
	803		*S. torques ITEP024*	*S. FACHB 1194*	86		WP_190346678
	761		*S. Kisseleviana NIES 73*	*S. LEGE 08334*	94		MBE9057071.1
	769		*S. LEGE 08334*	*S. Kisseleviana NIES 73*	94		BAZ82708.1

Suplementary Table S6. Proposed function of the proteins encoded by Sphaerociclamida biosynthetic gene cluster

Protein	Amino acids	Product	Strain	Organism	Identity (%)	Function	Acession number
sphG	710	cyanobactin maturation protease	*S. sp. LEGE 00249*	*Aphanizomenon gracile PMC638.10*	95	cyanobactin maturation protease	MDM3844803.1
sphF	290	LynF/TruF/PatF family peptide O-prenyltransferase	*S. sp. LEGE 00249*	*Chrysosporum ovalisporum Ak1311*	99	LynF/TruF/PatF family peptide O-prenyltransferase	MDH6088854.1
sphE	47	anacyclamide/piricyclamide	*S. sp. LEGE 00249*	*Dolichospermum sp. JUN01*	97	anacyclamide/piricyclamide	MBO1057685.1
sphA	667	cyanobactin maturation protease	*S. sp. LEGE 00249*	*Sphaerospermopsis aphanizomenoides*	95	cyanobactin maturation protease	MBE9236410.1

Suplementary Table S7. Proposed function of the proteins encoded by Nocuolin biosynthetic gene cluster

Protein	Aminoacids	Product	Strain	Organism	Identity (%)	Function	Acession number
nocT	597	AarF/ABC1/UbiB kinase family protein	*S. sp. LEGE 00249*	*S. Aphanizomenoids*	99	AarF/ABC1/UbiB kinase family protein	MBE9236862.1
nocS	2101	tectonin domain-containing protein	*S. sp. LEGE 00249*	*S. FACHB 1194*	96	tectonin domain-containing protein	WP_242052555.1
nocR	426	NocR	*S. sp. LEGE 00249*	*Nostoc sp. CCAP 1453/38*	82	NocR	AKL71651.1
nocQ	2325	Oxidoreductase	*S. sp. LEGE 00249*	*S. Aphanizomenoids*	99	oxidoreductase	MBE9235326.1
nocP	1286	Polyketide synthase	*S. sp. LEGE 00249*	*S. Aphanizomenoids*	99	polyketide synthase	MBE9235325.1
nocO	452	hypothetical protein	*S. sp. LEGE 00249*	*S. Aphanizomenoids*	87	Hypothetical protein	MBE9235324.1
nocM	92	acyl carrier protein	*S. sp. LEGE 00249*	*S. Aphanizomenoids*	92	*acyl carrier protein*	MBE9235322.1
nocN	471	hypothetical protein	*S. sp. LEGE 00249*	*Anabaena sp. PCC 7108*	87	Hypothetical protein	WP_016949101.1
nocK	397	DUF3419 family protein	*S. sp. LEGE 00249*	*S. Aphanizomenoids*	99	DUF3419 family protein	MBE9235319
nocJ	349	NocJ	*S. sp. LEGE 00249*	*Nostoc sp. CCAP 1453/38*	89	NocJ	AKL71643.1
nocI	372	acyl-CoA dehydrogenase	*S. sp. LEGE 00249*	*S. Aphanizomenoids*	100	acyl-CoA dehydrogenase	MBE9235317.1
nocH	698	AMP-binding protein	*S. sp. LEGE 00249*	*S. Aphanizomenoids*	100	AMP-binding protein	MBE9235316.1

nocG	347	3-oxoacyl-[acyl-carrier-protein] synthase	*S. sp. LEGE 00249*	*S. Aphanizomenoids*	99	3-oxoacyl-[acyl-carrier-protein] synthase III	MBE9235315.1
nocF	872	aminotransferase	*S. sp. LEGE 00249*	*S. aphanizomenoides BCCUSP55*	89	aminotransferase	MBK1987674
nocE	486	NAD(P)-binding	*S. sp. LEGE 00249*	*S. Aphanizomenoids*	100	NAD(P)-binding	MBE9235313.1
nocD	231	Isoprenylcysteine carboxylmethyltransferase	*S. sp. LEGE 00249*	*S. Aphanizomenoids*	100	Isoprenylcysteine carboxylmethyltransferase	MBE9235312.1
nocB	184	NocB	*S. sp. LEGE 00249*	*Nostoc sp. CCAP 1453/38*	89	NocB	AKL71634.1
nocA	214	NocA	*S. sp. LEGE 00249*	*Nostoc sp. CCAP 1453/38*	90	NocA	AKL71633.1

Supplementary Table S8. Proposed function of proteins encoded by hassallidin gene cluster identified in the genomes of the C. raciborskii strains CENA303, PAMP 2012, KL1, KLL07, CR 2010, CS-505, CS-508, GIHE-2018, GIHE-G1, DSH, N8, CR12, 1523720, CYRF and S. torques reginae ITEP-024 como a única do gênero Sphaerospermopsis.

Protein	Aminoacids	Proposed function	Strain	Organism	Identity (%)	Function	Acession number
HasA	555	*ABC-transporter*	*C. raciborskii CS-505*	*C. raciborskii CR12*	99	ABC transporter ATP-binding protein	KRH96585.1
	555		*C. raciborskii CS-508*	*C. raciborskii CS-505*	99	ABC transporter-like protein	EFA70507.1
	555		*C. raciborskii CR12*	*C. raciborskii CS-505*	99	ABC transporter-like protein	EFA70507.1
	555		*C. raciborskii CENA303*	*C. raciborskii CR12*	88	ABC transporter ATP-binding protein	KRH96585.1
	555		*C. raciborskii CR12*	*C. raciborskii CR2010*	99	ABC transporter ATP-binding protein	UJL33519.1
	555		*C. raciborskii CR12*	*C. raciborskii KLL07*	99	ABC transporter ATP-binding protein	UJS03222.1
HasB	670	Alpha amylase	*C. raciborskii CS-505*	*C. raciborskii CR12*	97	Alpha amylase	KRH96572.1
	670		*C. raciborskii CS-508*	*C. raciborskii CS-505*	99	Alpha-amylase	EFA70488.1
	670		*C. raciborskii CR12*	*C. raciborskii CS-505*	97	Alpha amylase	EFA70488.1

	571		*R. brookii D9*	*C. raciborskii CR12*	79	Alpha amylase	KRH96572.1
	670		*C. raciborskii CENA303*	*R. brookii D9*	99	Alpha amylase	EFA73364.1
	329		*C. raciborskii CENA302*	*C. raciborskii CR12*	79	Alpha-amylase	KRH96572.1
	670		*C. raciborskii CR12*	*C. curvispora GIHE G1*	98	Alpha-amylase	WP_187706034.1
	210		*C.raciboskii PAMP2012*	*C. raciborskii CR12*	73	Alpha-amylase	KRH96572.1
	571		*R. brookii D9*	*C.raciboskii PAMP2012*	98	Alpha-amylase	MCZ2202904.1
	670		*C. raciborskii GIHE 2018*	*C. curvispora GIHE G1*	99	Alpha-amylase	WP_187706034.1
	670		*C. raciborskii GIHE 2018*	*C. raciborskii CR12*	98	Alpha-amylase	WP_057178215.1
	670		*C. curvispora GIHEG1*	*C. raciborskii CR12*	99	Alpha-amylase	WP_057178215.1
	670		*C. raciborskii KLL07*	*C. raciborskii CR12*	98	Alpha-amylase	WP_057178215.1
	670		*C. raciborskii KLL07*	*C. curvispora GIHEG1*	98	Alpha-amylase	WP_187706034.1
	670		*C. raciborskii N8*	*C. raciborskii CR12*	100	Alpha-amylase	WP_057178215.1
	670		*C. raciborskii N8*	*C. curvispora GIHEG1*	99	Alpha-amylase	WP_187706034.1
	502		*C. raciborskii PAMP2012*	*C. curvispora GIHEG1*	81	Alpha-amylase	WP_187706034.1
	502		*C. raciborskii PAMP2012*	*C. raciborskii CR12*	81	Alpha-amylase	WP_057178215.1

	523		*C. raciborskii 1523720*	*C. raciborskii CR12*	98	Alpha-amylase	WP_057178215.1
	523		*C. raciborskii 1523720*	*C. curvispora GIHEG1*	98	Alpha-amylase	WP_187706034.1
HasC	342	Methyltransferase	*C. raciborskii CS-505*	*C. raciborskii CR12*	95	Methyltransferase domain-containing protein	KRH96618.1
	342		*C. raciborskii CS-508*	*C. raciborskii CS-505*	98	Hypothetical protein	EFA70501.1
	361		*C. raciborskii CR12*	*C. raciborskii CS-505*	95	Hypothetical protein	EFA70501.1
	342		*R. brookii D9*	*C. raciborskii CS-505*	83	Methyltransferase domain-containing protein	OBU78171.1
	357		*C. raciborskii CENA303*	*C. raciborskii CR12*	95	Methyltransferase domain-containing protein	KRH96618.1
	344		*C. raciborskii CENA302*	*R. brookii D9*	93	Hypothetical protein	EFA73367.1
	342		*C. raciborskii CR12*	*C. raciborskii CHAB 3438*	99	Methyltransferase domain-containing protein	MCH4903615.1
	342		*C. raciborskii CS-508*	*C. raciborskii CHAB 3438*	97	Methyltransferase domain-containing protein	MCH4903615.2
	71		*C.raciboskii PAMP2012*	*C. raciborskii CHAB 3438*	100	Methyltransferase domain-containing protein	MCH4903615.1
	372	acetylglucosamine	*C. raciborskii CR2010*	*C. curvispora GIHEG1*	97	acetylglucosamine	WP_187706020.1
	372		*C. raciborskii GIHE 2018*	*C. raciborskii CR12*	100	acetylglucosamine	WP_057178233.1
	372		*C. raciborskii GIHE 2018*	*C. curvispora GIHE G1*	97	acetylglucosamine	WP_187706020.1

	372		*C. curvispora GIHEG1*	*C. raciborskii CR12*	97	acetylglucosamine	WP_057178233.1
	372		*C. raciborskii N8*	*C. raciborskii CR12*	99	undecaprenyldiphospho-muramoylpentapeptide	WP_057178233
	372		*C. raciborskii N8*	*C. curvispora GIHEG1*	97	undecaprenyldiphospho-muramoylpentapeptide	WP_187706020.1
HasD	265	Glycosyl transferase family	*C. raciborskii CS-505*	*C. raciborskii CR12*	99	Glycosyl transferase family 2	KRH96581.1
	265		*C. raciborskii CS-508*	*C. raciborskii CS-505*	99	Glycosyl transferase family 2	EFA70500.1
	275		*C. raciborskii CR12*	*C. raciborskii CS-505*	99	Glycosyl transferase family 2	EFA70500.1
	267		*C. raciborskii ITEP-A1*	*Anabaena sp. 90*	83	Glycosyl transferase family 2	AFW95739.1
	266		*C. raciborskii CR12*	*C. curvispora GIHE G1*	100	Glycosyl transferase family 2	QNP29407.1
	266		*C. raciborskii CR12*	*C. raciborskii GIHE 2018*	100	Glycosyl transferase family 2	TPX27091.1
	266	Dolichol-phosphate mannosyltransferase	*C. raciborskii GIHE 2018*	*C. raciborskii CENA303*	76	polyprenol monophosphomannose synthase	OSO97128.1
	266		*C. raciborskii GIHE 2018*	*C. raciborskii KL1*	76	polyprenol monophosphomannose synthase	MBG0742668.1
	266		*C. raciborskii GIHE 2018*	*C. raciborskii KL1*	76	polyprenol monophosphomannose synthase	MBG0742668.1
	266		*C. raciborskii GIHE 2018*	*C. raciborskii CENA303*	76	polyprenol monophosphomannose synthase	OSO97128.1
	266		*C. curvispora GIHEG1*	*C. raciborskii CENA303*	76	polyprenol monophosphomannose	WP_141303791.1

						synthase	
	266	Dolichol-phosphate mannosyltransferase	*C. curvispora GIHEG1*	*C. raciborskii KL1*	76	polyprenol monophosphomannose synthase	MBG0742668.1
	265	Dolichol-phosphate mannosyltransferase	*C. raciborskii KLL07*	*C. raciborskii KL1*	77	polyprenol monophosphomannose synthase	MBG0742668.1
	265	Dolichol-phosphate mannosyltransferase	*C. raciborskii KLL07*	*C. raciborskii CENA303*	77	polyprenol monophosphomannose synthase	OSO97128.1
	266	Dolichol-phosphate mannosyltransferase	*C. raciborskii N8*	*C. raciborskii KL1*	76	polyprenol monophosphomannose synthase	MBG0742668.1
	266	Dolichol-phosphate mannosyltransferase	*C. raciborskii N8*	*C. raciborskii CENA303*	76	polyprenol monophosphomannose synthase	OSO97128.1
HasE	154	GtrA family protein	*C. raciborskii CS-505*	*C. raciborskii CR12*	100	Hypothetical protein	KRH96580.1
	151		*C. raciborskii CS-508*	*C. raciborskii CR12*	99	Hypothetical protein	KRH96580.1
	151		*C. raciborskii CR12*	*C. raciborskii CS-505*	100	Hypothetical protein	OBU77708.1
	184		*C. raciborskii CENA303*	*Scytonema hofmanni UTEX B 1581*	70	Hypothetical protein	WP_051502819.1
	184		*C. raciborskii ITEP-A1*	*Anabaena sp. 90*	68	GtrA-like protein	AFW95740.1
	197	Polyketide synthase	*C. raciborskii 1523720*	*C. raciborskii CR12*	96	non-ribosomal peptide synthetase	WP_057178252.1
	197	Polyketide synthase	*C. raciborskii 1523720*	*C. curvispora GIHEG1*	96	non-ribosomal peptide synthetase	WP_187706030.1

HasF	547	Putative membrane protein	*C. raciborskii CS-505*	*C. raciborskii CR12*	99	Dolichyl-phosphate-mannose-protein mannosyltransferase	KRH96579.1
	547		*C. raciborskii CS-508*	*C. raciborskii CS-505*	99	Dolichyl-phosphate-mannose-protein mannosyltransferase	OBU77709.1
	547		*C. raciborskii CR12*	*C. curvispora GIHEG1*	99	Dolichyl-phosphate-mannose-protein mannosyltransferase	WP_187706028.1
	547		*C. raciborskii CR12*	*C. raciborskii CS-505*	99	Conserved hypothetical protein	EFA70498.1
	545		*C. raciborskii CENA303*	*Anabaena sp. 90*	68	Putative membrane protein	AFW95741.1
	62		*C. raciborskii CENA302*	*Anabaena sp. Syke748*	75	Putative membrane protein	AHZ20765.1
	547		*C. curvispora GIHEG1*	*C. raciborskii CR12*	99	Dolichyl-phosphate-mannose-protein mannosyltransferase	KRH96579.1
HasG	312	AMP-dependent synthetase/ligase	*C. raciborskii CENA303*	*Anabaena sp. 90*	87	AMP-dependent synthase/ligase	AFW95742.1
HasK	452	Major facilitator transporter	*C. raciborskii CS-505*	*C. raciborskii CR12*	98	MFS transporter	KRH96587.1
	456		*C. raciborskii CR12*	*C. raciborskii CR2010*	98	MFS transporter	UJL33521.1
	456		*C. raciborskii CR12*	*C. raciborskii CS- 508*	97	MFS transporter	OHY34101.1
	456		*C. raciborskii CR12*	*C. raciborskii CHAB 3438*	97	MFS transporter	MCH4903619.1
	456		*C. raciborskii CR12*	*C. curvispora GIHEG1*	96	MFS transporter	TPX27098.1
	456		*C. raciborskii CS-508*	*C. raciborskii CS-505*	99	Hypothetical protein	EFA70509.1
	452		*C. raciborskii CR12*	*C. raciborskii CS-505*	98	MFS transporter	OBU77700.1
	449		*R. brookii D9*	*C. raciborskii CS-505*	66	MFS transporter	OBU77700.1
	449		*C. raciborskii CENA303*	*C. raciborskii CS-505*	66	MFS transporter	OBU77700.1
	449		*C. raciborskii ITEP-*	*R. brookii D9*	96	Major facilitator	EFA73366.1

			A1			superfamily MFS_1	
	445	Long-chain-fatty-acid--CoA ligase	*C. raciborskii KLL07*	*Nostocaceae cyanobacterium*	92	MAG TPA: fatty acid-CoA ligase family protein	HLO88498
	444	hypothetical protein	*C. raciborskii KLL07*	*Nostocaceae cyanobacterium*	80	alpha/beta hydrolase-fold protein	HLO88501.1
HasL	254	3-oxoacyl-acyl-carrier-protein reductase	*C. raciborskii CS-505*	*C. raciborskii CR12*	99	3-oxoacyl-ACP reductase	KRH96575.1
	254		*C. raciborskii CS-508*	*C. raciborskii CS-505*	100	3-oxoacyl-ACP reductase	EFA70493.1
	254		*C. raciborskii CR12*	*C. raciborskii CS-505*	99	3-oxoacyl-ACP reductase	EFA70493.1
	254		*C. raciborskii CENA303*	*C. raciborskii CS-505*	87	3-oxoacyl-ACP reductase	EFA70493.1
	254		*C. raciborskii CR12*	*S. torques reginae ITEP024*	87	3-oxoacyl-ACP reductase	WP_220609295.1
	254		*C. raciborskii CS-505*	*S. torques reginae ITEP024*	87	3-oxoacyl-ACP reductase	WP_220609295.1
	254		*C. raciborskii CR2010*	*S. torques ITEP024*	87	3-oxoacyl-ACP reductase	WP_220609295.1
	254		*C. raciborskii GIHE 2018*	*S. torques ITEP024*	87	3-oxoacyl-ACP reductase	WP_220609295.1
	254		*C. raciborskii KLL07*	*S. torques ITEP024*	87	3-oxoacyl-ACP reductase	WP_220609295.1
	254		*C. raciborskii N8*	*S. torques ITEP024*	87	3-oxoacyl-ACP reductase	WP_220609295.1
	254		*C. raciborskii PAMP2012*	*S. torques ITEP024*	89	3-oxoacyl-ACP reductase	WP_220609295.1
	254		*C. raciborskii 1523720*	*S. torques ITEP024*	87	oxidoreductase	WP_220609295.1
	254		*S. torques ITEP024*	*Cronbergia sp. UHCC*	95	oxidoreductase	WP_323283647

				0137]			
HasM	192	Aspartyl/asparaginyl beta-hydroxylase	*C. raciborskii CS-505*	*C. raciborskii CR12*	99	Hydroxylase	KRH96574.1
	192		*C. raciborskii CS-508*	*C. raciborskii CS-505*	99	Aspartyl/asparaginyl beta-hydroxylase	EFA70492.1
	192		*C. raciborskii CR12*	*C. raciborskii CS-505*	99	Hydroxylase	OBU77714.1
	204		*C. raciborskii CENA303*	*Anabaena sp. 90*	73	Aspartyl/asparaginyl beta-hydroxylase	AFW95748.1
	192		*C. raciborskii CR12*	*S. torques reginae ITEP024*	70	Aspartyl/asparaginyl beta-hydroxylase	WP_220609294.1
	197	Polyketide synthase	*C. raciborskii 1523720*	*C. raciborskii CR12*	96	Non-ribosomal peptide synthetase	WP_057178252.1
	197	Polyketide synthase	*C. raciborskii 1523720*	*C. curvispora GIHEG1*	96	Non-ribosomal peptide synthetase	WP_187706030.1
	3051	NRPS	*C. raciborskii CS-505*	*C. raciborskii CR12*	98	Non-ribosomal peptide synthetase	KRH96616.1
	2824		*C. raciborskii CS-508*	*C. raciborskii CR12*	96	Non-ribosomal peptide synthetase	KRH96616.1
	3049		*C. raciborskii CR12*	*C. raciborskii CS-505*	98	Non-ribosomal peptide synthetase	OBU77715.1
	3050		*C. raciborskii CENA303*	*C. raciborskii CS-505*	71	Non-ribosomal peptide synthetase	OBU77715.1
	3049		*C. raciborskii*	*C. raciborskii CR12*	99	Non-ribosomal peptide	WP_072149121.

			CR2010			synthetase	1
	3049		*C. raciborskii CR2010*	*C. raciborskii CS505*	97	Non-ribosomal peptide synthetase	EFA70490.1
	3049		*C. raciborskii CR2010*	*S. torques ITEP024*	70	Non-ribosomal peptide synthetase	WP_220609293.1
	3049		*C. raciborskii GIHE 2018*	*C. curvispora GIHE G1*	99	Non-ribosomal peptide synthetase	WP_187706032.1
	3049		*C. raciborskii GIHE 2018*	*C. raciborskii CR12*	99	Non-ribosomal peptide synthetase	WP_072149121.1
	3049		*C. curvispora GIHEG1*	*C. raciborskii CR12*	99	Non-ribosomal peptide synthetase	WP_072149121.1
HasN	3049	NRPS	*C. curvispora GIHEG1*	*C. raciborskii CS505*	97	Non-ribosomal peptide synthetase	EFA70490.1
	3050		*C. raciborskii KLL07*	*C. curvispora GIHEG1*	99	Non-ribosomal peptide synthetase	WP_187706032.1
	3050		*C. raciborskii KLL07*	*C. raciborskii CR12*	98	Non-ribosomal peptide synthetase	WP_072149121.1
	3050		*C. raciborskii KLL07*	*C. raciborskii CS505*	96	Non-ribosomal peptide synthetase	EFA70490
	3050		*C. raciborskii KLL07*	*S. torques ITEP024*	71	Non-ribosomal peptide synthetase	WP_220609293.1
	3049		*C. raciborskii N8*	*C. curvispora GIHEG1*	99	Non-ribosomal peptide synthetase	WP_187706032.1
	3049		*C. raciborskii N8*	*C. raciborskii CR12*	100	Non-ribosomal peptide synthetase	WP_072149121.1
	3049		*C. raciborskii N8*	*C. raciborskii CS505*	98	Non-ribosomal peptide synthetase	EFA70490.1
	3050		*C. raciborskii PAMP2012*	*C. curvispora GIHEG1*	*71*	Non-ribosomal peptide synthetase	WP_187706032.1
	3050		*C. raciborskii*	*C. raciborskii CR12*	*71*	Non-ribosomal peptide	*WP_072149121.*

			PAMP2012			synthetase	*1*
	3055		*C. raciborskii 1523720*	*C. raciborskii CR12*	*94*	Non-ribosomal peptide synthetase	*WP_072149121.1*
	3055		*C. raciborskii 1523720*	*C. raciborskii CS505*	*95*	Non-ribosomal peptide synthetase	*EFA70490.1*
	3056		*S. torques ITEP024*	*Cronbergia sp. UHCC 0137]*	*85*	Non-ribosomal peptide synthetase	WP_323283649.1
HasO	3661	NRPS	*C. raciborskii CR12*	*C. raciborskii CS-505*	100	Non-ribosomal peptide synthase	EFA70489.1
	3670		*C. raciborskii CENA303*	*C. raciborskii CR12*	72	Non-ribosomal peptide synthase	KRH96573.1
	3049		*C. raciborskii CR12*	*C. curvispora GIHEG1*	97	Non-ribosomal peptide synthase	WP_187706032.1
	3049		*C. raciborskii CR12*	*C. raciborskii CS-505*	100	Non-ribosomal peptide synthase	EFA70490.1
	3049		*C. raciborskii CR12*	*S. torques reginae ITEP024*	71	Non-ribosomal peptide synthase	WP_220609293.1
	3662		*C. raciborskii CR2010*	*C. raciborskii CR12*	97	Non-ribosomal peptide synthase	WP_057178216.1
	3659		*C. raciborskii GIHE 2018*	*C. raciborskii CR12*	97	Non-ribosomal peptide synthase	WP_057178216.1
	3659		*C. curvispora GIHEG1*	*C. raciborskii CR12*	97	Non-ribosomal peptide synthase	WP_057178216.1
	3662		*C. raciborskii KLL07*	*C. curvispora GIHEG1*	99	Non-ribosomal peptide synthase	WP_187706033.1
	3662		*C. raciborskii KLL07*	*C. raciborskii CR12*	97	Non-ribosomal peptide synthase	WP_057178216.1
	3661		*C. raciborskii N8*	*C. raciborskii CR12*	100	Non-ribosomal peptide synthase	WP_057178216.1
	3661		*C. raciborskii N8*	*C. curvispora GIHEG1*	97	Non-ribosomal peptide synthase	WP_057178216.1
	3670		*C. raciborskii*	C. raciborskii CR12	72	Non-ribosomal peptide	*WP_057178216.*

			PAMP2012			synthase	*1*
	3670		*C. raciborskii PAMP2012*	C. curvispora GIHEG1	72	Non-ribosomal peptide synthase	*WP_187706033.1*
	3660		*C. raciborskii 1523720*	C. raciborskii CR12	95	non-ribosomal peptide synthetase	*WP_057178216.1*
	3660		*C. raciborskii 1523720*	C. curvispora GIHEG1	94	non-ribosomal peptide synthetase	*WP_187706033*
HasP	354	NAD-dependent epimerase dTDP-glucose 4,6-dehydratase	*C. raciborskii CS-505*	*C. raciborskii CR12*	99	NAD-dependent epimerase	KRH96583.1
	354		*C. raciborskii CR12*	*C. curvispora GIHEG1*	100	NAD-dependent epimerase/dehydratase	WP_187706027.1
	354		*C. raciborskii CS-505*	*C. curvispora GIHEG1*	99	NAD-dependent epimerase/dehydratase	WP_187706027.1
	354		*C. raciborskii CR12*	*C. raciborskii CS-505*	99	NAD-dependent epimerase/dehydratase	EFA70505.1
	352		*C. raciborskii CENA303*	*Anabaena sp. 90*	84	NAD dependent epimerase/dehydratase	AFW95751.1
	370		*C. raciborskii CR2010*	*C. raciborskii CR12*	99	NAD-dependent epimerase/dehydratase	WP_057178224.1
	370		*C. raciborskii GIHE 2018*	*C. raciborskii CR12*	99	NAD-dependent epimerase/dehydratase	WP_057178224.1
	370		*C. raciborskii GIHE 2018*	*C. curvispora GIHE G1*	99	NAD-dependent epimerase/dehydratase	WP_187706027.1
	370		*C. curvispora GIHEG1*	*C. raciborskii CR12*	94	NAD-dependent epimerase/dehydratase	WP_057178224.1
	370		*C. raciborskii KLL07*	*C. curvispora GIHEG1*	100	NAD-dependent epimerase/dehydratase	WP_187706027
	370		*C. raciborskii KLL07*	*C. raciborskii CR12*	100	NAD-dependent epimerase/dehydratase	WP_057178224.1
	354		*C. raciborskii N8*	*C. raciborskii CR12*	100	NAD dependent epimerase/dehydratase	WP_057178224.1
	354		*C. raciborskii N8*	*C. curvispora*	99	NAD dependent	WP_187

				GIHEG1		epimerase/dehydratase	706027.1
	352		*C. raciborskii PAMP2012*	*Anabaena cylindrica*	82	NAD-dependent epimerase/dehydratase	WP_323309738.1
HasQ	402	Glycosyltransferase	*C. raciborskii CS-505*	*C. raciborskii CR12*	99	MGT family glycosyltransferase	KRH96584.1
	402		*C. raciborskii CR12*	*C. raciborskii CS-505*	99	Hypothetical protein	EFA70506.1
	73		*C. raciborskii CENA303*	*C. raciborskii CS-505*	90	MGT family glycosyltransferase	OBU77703.1
	402		*C. raciborskii CS-505*	*S. torques reginae ITEP024*	83	MGT family glycosyltransferase	WP_220609292.1
	402		*C. raciborskii CR2010*	*S. torques ITEP024*	82	Glycosyl transferase	WP_220609292.1
	402		*C. raciborskii GIHE 2018*	*S. torques ITEP024*	72	Glycosyl transferase	WP_220609292.1
	402		*C. curvispora GIHEG1*	*S. torques ITEP024*	83	Glycosyl transferase	WP_220609292.1
	402		*C. raciborskii KLL07*	*S. torques ITEP024*	83	Glycosyl transferase	WP_220609292.1
	402		*C. raciborskii CR12*	*S. torques reginae ITEP024*	83	Glycosyl transferase	WP_220609292.1
	402		*C. raciborskii N8*	*S. torques ITEP024*	82	Glycosyl transferase	WP_220609292.1
	408		*S. torques ITEP024*	*Dolichospermum sp. UHCC 0352*	91	Glycosyl transferase	WP_168652019.1
HasR	206	Putative acyltransferase	*C. raciborskii CENA303*	*Anabaena sp. 90*	68	Hypothetical protein	WP_015080900.1

HasT	245	Glycosyl transferase	*C. raciborskii CS-505*	*C. raciborskii CR12*	99	Glycosyl transferase	KRH96578.1
	245		*C. raciborskii CS-508*	*C. raciborskii CS-505*	100	Glycosyl transferase	EFA70497.1
	245		*C. raciborskii CR12*	*C. raciborskii CS-505*	99	Putative glycosyltransferase	EFA70497.1
	245		*C. raciborskii CR12*	*C. curvispora GIHEG1*	99	Glycosyl transferase	WP_187706029.1
	258		*C. raciborskii CENA303*	*C. raciborskii CR12*	79	Glycosyl transferase	KRH96578.1
	258		*C. raciborskii CR12*	*C. raciborskii PAMP2012*	79	Glycosyl transferase	MCZ2202044.1
	315		*S. torques ITEP024*	*C. raciborskii*	88	Glycosyl transferase	WP_324140027.1
HasU	72	Putative MbtH-like protein	*C. raciborskii CS-505*	*C. raciborskii CR12*	100	Antibiotic synthesis protein MbtH	KRH96576.1
	72		*Cylindrospermopsis CR12*	*S. torques reginae ITEP024*	84	Antibiotic synthesis protein MbtH	WP_220609290.1
	72		*C. raciborskii CS-508*	*C. raciborskii CS-505*	98	Putative MbtH-like protein	EFA70494.1
	72		*C. raciborskii CS-505*	*C. raciborskii DSH*	100	Putative MbtH-like protein	MEE6162471
	72		*C. raciborskii CS-505*	*C. raciborskii CR12*	100	Putative MbtH-like protein	KRH96576.1
	72		*C. raciborskii CS-505*	*C. raciborskii CS-508*	100	Antibiotic synthesis protein MbtH	OHY35853.1
	72		*C. raciborskii CS-505*	*C. curvispora GIHEG1*	100	Putative MbtH-like protein	TPX27085.1
	72		*C. raciborskii CS-505*	*C. raciborskii CR2010*	100	MbtH family NRPS accessory protein	UJL33506.1
	72		*C. raciborskii CS-505*	*C. raciborskii KLL07*	100	MbtH family NRPS accessory protein	UJS03236.1
	72		*C. raciborskii CR12*	*C. raciborskii CS-505*	100	Putative MbtH-like protein	EFA70494.1

	73		*C. raciborskii CENA303*	*Anabaena sp. 90*	87	MbtH-like protein	AFW95756.1
	72		*C. raciborskii CR2010*	*S. torques ITEP024*	84	MbtH family protein	WP_220609290.1
	72		*C. raciborskii GIHE 2018*	*S. torques ITEP024*	72	MbtH family protein	WP_220609290.1
	72		*C. curvispora GIHEG1*	*S. torques ITEP024*	84	MbtH family protein	WP_220609290.1
	72		*C. raciborskii KLL07*	*S. torques ITEP024*	84	MbtH family protein	WP_220609290.1
	72		*C. raciborskii N8*	*S. torques ITEP024*	84	MbtH family protein	WP_220609290.1
	73		*C. raciborskii PAMP2012*	*S. torques ITEP024*	94	MbtH family protein	WP_220609290
	72		*C. raciborskii 1523720*	*S. torques ITEP024*	84	MbtH family protein	WP_220609290.1
	71		*S. torques ITEP024*	*Cronbergia sp. UHCC 0137]*	96	MbtH-like NRPS chaperone	WP_323283663.1
HasV	2153	NRPS	*C. raciborskii CS-505*	*C. raciborskii CR12*	97	Non-ribosomal peptide synthase	KRH96577.1
	2127		*C. raciborskii CS-508*	*C. raciborskii CR12*	99	Non-ribosomal peptide synthase	KRH96577.1
	2153		*C. raciborskii CR12*	*C. curvispora GIHEG1*	99	Non-ribosomal peptide synthase	WP_187706031.1
	2153		*C. raciborskii CR12*	*C. raciborskii CR2010*	99	amino acid adenylation domain-containing protein	UJL33507.1
	2153		*C. raciborskii CR12*	*C. raciborskii KLL07*	99	amino acid adenylation domain-containing protein	UJS06337.1
	2153		*C. raciborskii CR12*	*S. torques reginae ITEP024*	74	Non-ribosomal peptide synthase	WP_220609291.1

	2153		*C. raciborskii CR12*	*C. raciborskii KL1*	98	amino acid adenylation domain-containing protein	MBG0742686.1
	2153		*C. raciborskii CR12*	*C. raciborskii CS-505*	97	Non-ribosomal peptide synthase	EFA70495.1
	2147		*C. raciborskii CENA303*	*Anabaena sp. 90*	73	Non-ribosomal peptide synthase	AFW95757.1
	2153		*C. raciborskii GIHE 2018*	*C. raciborskii CR2010*	100	amino acid adenylation	UJL33507.1
	2153		*C. raciborskii GIHE 2018*	*C. raciborskii CR12*	99	Non-ribosomal peptide synthase	WP_057178219
	2153		*C. raciborskii GIHE 2018*	*C. curvispora GIHE G1*	99	Non-ribosomal peptide synthase	WP_187706031.1
	2153		*C. raciborskii GIHE 2018*	*C. raciborskii KLL07*	100	Non-ribosomal peptide synthase	UJS06337.1
	2153		*C. raciborskii GIHE 2018*	*S. torques ITEP024*	74	Non-ribosomal peptide synthase	WP_220609291.1
	2153		*C. curvispora GIHEG1*	*C. raciborskii CR12*	100	Non-ribosomal peptide synthase	WP_057178219.1
	2153		*C. curvispora GIHEG1*	*C. raciborskii CR2010*	100	Non-ribosomal peptide synthase	UJL33507.1
	2153		*C. curvispora GIHEG1*	*C. raciborskii KLL07*	99	Non-ribosomal peptide synthase	UJS06337.1
	2153		*C. curvispora GIHEG1*	*S. torques ITEP024*	74	Non-ribosomal peptide synthase	WP_220609291.1
	2153		*C. raciborskii KLL07*	*C. raciborskii CR2010*	100	Non-ribosomal peptide synthase	UJL33507.1
	2153		*C. raciborskii KLL07*	*C. raciborskii CR12*	99	Non-ribosomal peptide synthase	WP_057178219.1
	2153		*C. raciborskii KLL07*	*C. curvispora GIHEG1*	99	Non-ribosomal peptide synthase	WP_187706031.1

	2153		*C. raciborskii KLL07*	*S. torques ITEP024*	74	Non-ribosomal peptide synthase	WP_220609291.1
	2153		*C. raciborskii N8*	*C. raciborskii CR12*	100	Non-ribosomal peptide synthase	WP_057178219.1
	2153		*C. raciborskii N8*	*C. curvispora GIHEG1*	99	Non-ribosomal peptide synthase	WP_187706031.1
	2153		*C. raciborskii N8*	*C. raciborskii CR2010*	99	amino acid adenylation domain-containing protein	UJL33507.1
	2153		*C. raciborskii N8*	*C. raciborskii KLL07*	99	amino acid adenylation domain-containing protein	UJS06337.1
	2153		*C. raciborskii N8*	*S. torques ITEP024*	74	Non-ribosomal peptide synthase	WP_220609291.1
	2147		*C. raciborskii PAMP2012*	*C. raciborskii KL1*	98	amino acid adenylation	MBG0742686.1
	2147		*C. raciborskii PAMP2012*	*S. torques ITEP024*	77	Non-ribosomal peptide synthase	WP_220609291.1
	2153		*C. raciborskii 1523720*	*C. curvispora GIHEG1*	96	Non-ribosomal peptide synthase	WP_187706031.1
	2153		*C. raciborskii 1523720*	*C. raciborskii CR12*	95	Non-ribosomal peptide synthase	WP_057178219.1
	2153		*C. raciborskii 1523720*	*C. raciborskii CR2010*	95	amino acid adenylation	UJL33507.1
	2153		*C. raciborskii 1523720*	*C. raciborskii KLL07*	95	amino acid adenylation	UJS06337.1
	2142		*S. torques ITEP024*	*C. raciborskii KL1*	76	Non-ribosomal peptide synthase	WP_220609288.1
	1961		*S. torques ITEP024*	*C. curvispora GIHEG1*	74	Non-ribosomal peptide synthase	WP_187706033.1
	1961		*S. torques ITEP024*	*C. raciborskii CR12*	74	Non-ribosomal peptide synthase	WP_057178216.1

HasX	310	Glycosyltransferase	*C. raciborskii CR12*	*Anabaena sp. 90*	73	Glycosyl transferase family 2	AFW95759.1
	310		*C. raciborskii N8*	*S. torques ITEP024*	88	Glycosyltransferase	WP_220609289.1
	267		*C. raciborskii CENA303*	*Anabaena sp. 90*	83	Family 2 glycosyl transferase	AFW95739.1
	82	Hypothetical protein	*C. raciborskii CENA302*	*Scytonema hofmanni UTEX B 1581*	74	Hypothetical protein	WP_051502821.1
	82	Glycosyltransferase	*C. raciborskii PAMP2012*	*S. torques ITEP024*	83	Glycosyltransferase	WP_220609289.1
HasY	2874	NRPS	*C. raciborskii CS-505*	*C. raciborskii CR12*	90	Non-ribosomal peptide synthase	KRH96617.1
	2870		*C. raciborskii CS-508*	*C. raciborskii CR12*	96	Non-ribosomal peptide synthase	KRH96617.1
	2864		*C. raciborskii CR12*	*C. raciborskii CS-505*	90	Non-ribosomal peptide synthase	EFA70496.1
	2864		*C. raciborskii CR12*	*S. torques reginae ITEP024*	76	Non-ribosomal peptide synthase	WP_220609288.1
	2864		*C. raciborskii CR12*	*C. raciborskii KL1*	72	Non-ribosomal peptide synthase	MBG0742682.1
	2864		*C. raciborskii CR12*	*C. raciborskii CENA303*	72	Non-ribosomal peptide synthase	OSO88008.1
	2863		*C. raciborskii CENA303*	*C. curvispora GIHEG1*	72	Non-ribosomal peptide synthase	WP_187706030.1
	2864		*C. raciborskii GIHE 2018*	*C. curvispora GIHEG1*	100	Non-ribosomal peptide synthase	WP_187706030.1
	2864		*C. raciborskii GIHE*	*C. raciborskii CR12*	97	Non-ribosomal peptide	WP_057178252.

			2018			synthase	1
	2864		*C. raciborskii GIHE 2018*	*C. raciborskii KL1*	72	Non-ribosomal peptide synthase	MBG0742682.1
	2864		*C. raciborskii GIHE 2018*	*S. torques ITEP024*	76	Non-ribosomal peptide synthase	WP_220609288.1
	2864		*C. raciborskii GIHE 2018*	*C. raciborskii CENA303*	72	Non-ribosomal peptide synthase	OSO88008.1
	2864		*C. curvispora GIHEG1*	*C. raciborskii CR12*	97	Non-ribosomal peptide synthase	WP_057178252.1
	2864		*C. curvispora GIHEG1*	*S. torques ITEP024*	76	Non-ribosomal peptide synthase	WP_220609288.1
	2864		*C. raciborskii KLL07*	*C. curvispora GIHEG1*	100	Non-ribosomal peptide synthase	WP_220609288.1
	2864		*C. raciborskii KLL07*	*C. raciborskii CR12*	98	Non-ribosomal peptide synthase	WP_220609288.1
	2864		*C. raciborskii KLL07*	*S. torques ITEP024*	76	Non-ribosomal peptide synthase	WP_220609288.1
	2864		*C. raciborskii N8*	*C. curvispora GIHEG1*	99	Non-ribosomal peptide synthase	WP_220609288.1
	2864		*C. raciborskii N8*	*C. raciborskii CR12*	97	Non-ribosomal peptide synthase	WP_220609288.1
	2864		*C. raciborskii N8*	*S. torques ITEP024*	76	Non-ribosomal peptide synthase	WP_220609288.1
	2864		*C. raciborskii N8*	*C. raciborskii KL1*	72	amino acid adenylation domain-containing protein	MBG0742682.1
	2864		*C. raciborskii N8*	*C. raciborskii CENA303*	72	Non-ribosomal peptide synthase	OSO88008.1
	2862		*C. raciborskii PAMP2012*	*S. torques ITEP024*	84	Non-ribosomal peptide synthase	WP_220609288.1
	2862		*C. raciborskii PAMP2012*	*C. raciborskii KL1*	98	Non-ribosomal peptide synthase	MBG0742682.1

	2862		*C. raciborskii PAMP2012*	*C. raciborskii CENA303*	99	Non-ribosomal peptide synthase	OSO88008.1
	2855		*S. torques ITEP024*	*C. raciborskii KL1*	84	Non-ribosomal peptide synthase	MBG074 2686.1
	2855		*S. torques ITEP024*	*C. raciborskii CENA303*	84	Non-ribosomal peptide synthase	OSO88008.1
	2855		*S. torques ITEP024*	*C. curvispora GIHEG1*	76	Non-ribosomal peptide synthase	WP_187706030. 1
	2855		*S. torques ITEP024*	*C. raciborskii CR12*	76	Non-ribosomal peptide synthase	WP_057178252. 1
HasZ	431	Transporter	*C. raciborskii CS-505*	*Cylindrospermopsis CR12*	97	MFS transporter	KRH96586.1
	431		*C. raciborskii CS-505*	*C. curvispora GIHE G1*	97	MFS transporter	QNP29400.1
	431		*C. raciborskii CS-505*	*C. curvispora GIHE G1*	97	MFS transporter	QNP29400.1
	431		*C. raciborskii CS-505*	*C. curvispora GIHE G1*	97	Major facilitator superfamily MFS_0	QNP29400.1
	427		*C. raciborskii CS-508*	*C. raciborskii CS-505*	96	Major facilitator superfamily MFS_1	EFA70508.1
	431		*C. raciborskii CR12*	*C. raciborskii CS-505*	97	Major facilitator superfamily MFS_1	EFA70508.1
	431		*C. raciborskii CS-505*	*C. raciborskii CR12*	97	MFS transporter	WP_057178227. 1
	429		C. raciborskii CENA303	*C. raciborskii CS-505*	68	MFS transporter	OBU77701.1