



Corrigendum: Genomic and Genotypic Characterization of *Cylindrospermopsis raciborskii*: Toward an Intraspecific Phylogenetic Evaluation by Comparative Genomics

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Keywords: cyanobacteria, genome assembly, pan-genome, bioinformatics, natural products, cyanotoxins, nitrogen fixation

A corrigendum on

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by Abreu, V. A. C., Popin, R. V., Alvarenga, D. O., Schaker, P. D. C., Hoff-Risseti, C., Varani, A. M., et al. (2018). *Front. Microbiol.* 9:306. doi: 10.3389/fmicb.2018.00306

There was an error in the placement of some of the decimal points and the thousands separators of **Table 1** as published. The correct version of **Table 1** appears below. The authors apologize for the mistake. This error does not change scientific conclusions of the article in any way.

The original article has been updated.

OPEN ACCESS

Edited and reviewed by:

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Specialty section:

This article was submitted to
Aquatic Microbiology,
a section of the journal
Frontiers in Microbiology

Received: 06 March 2018

Accepted: 25 April 2018

Published: 15 May 2018

Citation:

Abreu VAC, Popin RV, Alvarenga DO,
Schaker PDC, Hoff-Risseti C,
Varani AM and Fiore MF (2018)
Corrigendum: Genomic and
Genotypic Characterization of
Cylindrospermopsis raciborskii:
Toward an Intraspecific Phylogenetic
Evaluation by Comparative Genomics.
Front. Microbiol. 9:979.
doi: 10.3389/fmicb.2018.00979

TABLE 1 | Comparison of the genomic features and subsystem annotation of the studied strains.

	CENA302	CENA303	D9	ITEP-A1	MVCC-14	CS-508	CS-505	CR12
Genomic Statistics								
No. of contigs	58	77	47	195	99	162	6	136
Total size (bp)	3,476,418	3,398,605	3,186,511	3,605,836	3,594,524	3,556,598	4,159,260	3,723,955
Longest contig length (bp)	324,204	403,228	526,794	266,816	299,478	193,915	4,011,384	279,631
Shortest contig length (bp)	580	511	3,501	1,008	1,035	1,027	2,519	1,058
Mean contigs size (bp)	59,938	43,581	67,798	18,491	36,308	21,954	693,210	27,383
Median contigs size (bp)	18,631	7,321	29,593	2,823	4,917	5,661	14,642	6,201
GC content (%)	40.08	40.26	40.06	40.15	40.08	40.15	40.28	40.03
N50	162,402	135,818	127,752	91,008	150,437	62,252	4,011,384	79,912
Subsystem Statistics-SEED								
No. of Subsystems	350	354	347	349	351	346	360	356
No. of coding sequences	3,392	3,360	3,120	3,391	3,533	3,346	4,073	3,475
Coding sequences in	1,363	1,342	1,307	1,364	1,384	1,355	1,590	1,366
Subsystems	or 41%	or 40%	or 42%	or 41%	or 40%	or 41%	or 40%	or 40%
Coding sequences not in	2,029	2,018	1,813	2,027	2,149	1,991	2,483	2,109
Subsystems	or 59%	or 60%	or 58%	or 59%	or 60%	or 59%	or 60%	or 60%

Conflict of Interest Statement: The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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