frontiers | Frontiers in Microbiology

TYPE Correction
PUBLISHED 10 November 2023
DOI 10.3389/fmicb.2023.1328336

OPEN ACCESS

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RECEIVED 26 October 2023
ACCEPTED 30 October 2023
PUBLISHED 10 November 2023

CITATION
Turk Dermastia T, Vascotto I, Francé J, Stanković D and Mozetič P (2023) Corrigendum: Evaluation of the *rbcL* marker for metabarcoding of marine diatoms and inference of population structure of selected genera. *Front. Microbiol.* 14:1328336. doi: 10.3389/fmicb.2023.1328336

Corrigendum: Evaluation of the *rbcL* marker for metabarcoding of marine diatoms and inference of population structure of selected genera

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KEYWORDS

***rbcL*, metabarcoding, monitoring, diatoms, population genetics, *Pseudo-nitzschia*, Adriatic**

A corrigendum on
Evaluation of the *rbcL* marker for metabarcoding of marine diatoms and inference of population structure of selected genera

by Turk Dermastia, T., Vascotto, I., Francé, J., Stanković, D., and Mozetič, P. (2023). *Front. Microbiol.* 14:1071379. doi: 10.3389/fmicb.2023.1071379

In the published article, there was an error. In section **2. Methods**, *2.3. Amplification and Illumina MiSeq sequencing*, the forward primer 708F-DEG has been incorrectly pasted as the same as the 18S-V9R primer. The paragraph previously stated:

"Two markers were chosen for metabarcoding, namely the 150 base pair (bp) 18S-V9 region and a ~ 312 bp barcode within the *rbcL* chloroplast gene. The primers used to amplify the 18S gene were the universal eukaryotic 18S-V9F (TTGTACACACCGCCCGTCGC) and 18S-V9R (CCTTCYGCAGGTTCACCTAC; Piredda et al., 2017). Libraries for the *rbcL* barcode were built using the diatom-specific primers 708F-DEG (CCTTCYGCAGGTTCACCTAC) and R3-DEG (CCTTCTAATTTACCWACWACWG), both modified from Vasselon et al. (2017a)."

The corrected sentence appears below:

"Two markers were chosen for metabarcoding, namely the 150 base pair (bp) 18S-V9 region and a ~312 bp barcode within the *rbcL* chloroplast gene. The primers used to amplify the 18S gene were the universal eukaryotic 18S-V9F (TTGTACACACCGCCCGTCGC) and 18S-V9R (CCTTCYGCAGGTTCACCTAC; Piredda et al., 2017). Libraries for the *rbcL* barcode were built using the diatom-specific primers 708F-DEG (AGGTGAAGYWAAAGGTTCWTAYTTAAA) and R3-DEG (CCTTCTAATTTACCWACWACWG), both modified from Vasselon et al. (2017a)."

The authors apologize for this error and state that this does not change the scientific conclusions of the article in any way. The original article has been updated.

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