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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

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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 (CCTTCYGCAGGTTACCTAC; Piredda et al., 2017). Libraries for the *rbcL* barcode were built using the diatom-specific primers 708F-DEG (CCTTCYGCAGGTTACCTAC) 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 (CCTTCYGCAGGTTACCTAC; Piredda et al., 2017). Libraries for the *rbcL* barcode were built using the diatom-specific primers 708F-DEG (AGGTGAAGYWAAAGGTTCTWATYTTAAA) 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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