Check for updates

OPEN ACCESS

APPROVED BY Frontiers Editorial Office, Frontiers Media SA, Switzerland

*CORRESPONDENCE Hua Li ⊠ lih@ihb.ac.cn

RECEIVED 22 January 2024 ACCEPTED 23 January 2024 PUBLISHED 01 February 2024

CITATION

Li Y, Wang F, Yang H, Li H and Hu C (2024) Corrigendum: Balanced biogeographic and local environmental effects determine the patterns of microbial diversity in biocrusts at multi-scales. *Front. Microbiol.* 15:1374406. doi: 10.3389/fmicb.2024.1374406

COPYRIGHT

© 2024 Li, Wang, Yang, Li and Hu. This is an open-access article distributed under the terms of the Creative Commons Attribution License (CC BY). The use, distribution or reproduction in other forums is permitted, provided the original author(s) and the copyright owner(s) are credited and that the original publication in this journal is cited, in accordance with accepted academic practice. No use, distribution or reproduction is permitted which does not comply with these terms.

Corrigendum: Balanced biogeographic and local environmental effects determine the patterns of microbial diversity in biocrusts at multi-scales

Yuanlong Li^{1,2}, Fengdi Wang³, Haijian Yang², Hua Li^{2*} and Chunxiang Hu²

¹Hunan Provincial Key Laboratory of Carbon Neutrality and Intelligent Energy, School of Resource and Environment, Hunan University of Technology and Business, Changsha, China, ²Key Laboratory of Algal Biology, Institute of Hydrobiology, Chinese Academy of Sciences, Wuhan, China, ³Institute of Hematology, Union Hospital, Tongji Medical College, Huazhong University of Science and Technology, Wuhan, China

KEYWORDS

biogeography, biological soil crusts, cyanobacteria, microbial diversity, multiple spatial scales, primary succession, species turnover

A corrigendum on

Balanced biogeographic and local environmental effects determine the patterns of microbial diversity in biocrusts at multi-scales

by Li, Y., Wang, F., Yang, H., Li, H., and Hu, C. (2023). *Front. Microbiol.* 14:1284864. doi: 10.3389/fmicb.2023.1284864

In the published article, there were two spelling mistakes in the abstract and introduction. The term MiSeq was displayed as "MeSeq". The correct statement is "MiSeq".

A correction has been made to the method section of the Abstract. The sentence previously stated:

"(Based on the Illumina MeSeq 16S/18S rRNA sequencing technology, we...)"

The corrected sentence appears below:

"(Based on the Illumina MiSeq 16S/18S rRNA sequencing technology, we...)"

A correction has been made to paragraph 4 of the Introduction. The sentence previously stated:

"(Illumina MeSeq 16S/18S rRNA sequencing was used to examine the...)"

The corrected sentence appears below:

"(Illumina MiSeq 16S/18S rRNA sequencing was used to examine the...)"

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.

Publisher's note

All claims expressed in this article are solely those of the authors and do not necessarily represent those of their affiliated organizations, or those of the publisher, the editors and the reviewers. Any product that may be evaluated in this article, or claim that may be made by its manufacturer, is not guaranteed or endorsed by the publisher.