



OPEN ACCESS

APPROVED BY
Frontiers Editorial Office,
Frontiers Media SA, Switzerland

*CORRESPONDENCE

Zheng Wang
✉ wang.zheng@yale.edu
Oded Yarden
✉ oded.yarden@mail.huji.ac.il

RECEIVED 09 August 2024
ACCEPTED 12 August 2024
PUBLISHED 20 August 2024

CITATION

Wang Z, Kim W, Wang Y-W, Yakubovich E, Dong C, Trail F, Townsend JP and Yarden O (2024) Corrigendum: The Sordariomycetes: an expanding resource with Big Data for mining in evolutionary genomics and transcriptomics. *Front. Fungal Biol.* 5:1478516. doi: 10.3389/ffunb.2024.1478516

COPYRIGHT

© 2024 Wang, Kim, Wang, Yakubovich, Dong, Trail, Townsend and Yarden. This is an open-access article distributed under the terms of the [Creative Commons Attribution License \(CC BY\)](https://creativecommons.org/licenses/by/4.0/). 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: The Sordariomycetes: an expanding resource with Big Data for mining in evolutionary genomics and transcriptomics

Zheng Wang^{1*}, Wonyong Kim², Yen-Wen Wang¹,
Elizabeta Yakubovich³, Caihong Dong⁴, Frances Trail^{5,6},
Jeffrey P. Townsend^{1,7} and Oded Yarden^{3*}

¹Department of Biostatistics, Yale School of Public Health, New Haven, CT, United States, ²Korean Lichen Research Institute, Suncheon National University, Suncheon, Republic of Korea, ³Department of Plant Pathology and Microbiology, The Robert H. Smith Faculty of Agriculture, Food and Environment, The Hebrew University of Jerusalem, Rehovot, Israel, ⁴Institute of Microbiology, Chinese Academy of Sciences, Beijing, China, ⁵Department of Plant Biology, Michigan State University, East Lansing, MI, United States, ⁶Department of Plant, Soil and Microbial Sciences, Michigan State University, East Lansing, MI, United States, ⁷Department of Ecology and Evolutionary Biology, Program in Microbiology, and Program in Computational Biology and Bioinformatics, Yale University, New Haven, CT, United States

KEYWORDS

Sordariomycetes, evolution, genomics, transcriptomics, Big Data, *Neurospora*, *Fusarium*, *Trichoderma*

A Corrigendum on

The Sordariomycetes: an expanding resource with Big Data for mining in evolutionary genomics and transcriptomics

By Wang Z, Kim W, Wang Y-W, Yakubovich E, Dong C, Trail F, Townsend JP and Yarden O (2023). *Front. Fungal Biol.* 4:1214537. doi: 10.3389/ffunb.2023.1214537

In the published article, there was an error in the **Funding** statement. We omitted mention of one of the grants supporting this study, IOS 1916137. The **Funding** originally read:

“The work of ZW, Y-WW, and JT was supported by funding awarded to JT by the National Institutes of Health R01, grant AI146584, and by the National Science Foundation, grant IOS1457044; the work of EY and OY was supported by funding award BSF-2018712 to OY. The work of CD was supported by the National Natural Science Foundation of China (32272786 and 31872163). FT was supported by the National Institutes of Health, R01 grant AI146584, and the Michigan State University AgBioResearch. The work of WK and FT was supported by the National Science Foundation, IOS 1456482, awarded to FT. WK was partly supported by the Basic Science Research Program through the National Research Foundation of Korea, funded by the Ministry of Education (2019R1I1A1A01057502).”

The correct **Funding** statement appears below.

“The work of ZW, Y-WW, and JT was supported by funding awarded to JT by the National Institutes of Health R01, grant AI146584, and by the National Science Foundation, grants IOS 1457044 and IOS 1916137; the work of EY and OY was supported by funding BSF-2018712 to OY. The work of CD was supported by the National Natural Science Foundation of China (32272786 and 31872163). FT was supported by the National Institutes of Health, R01 grant

AI146584, and the Michigan State University AgBioResearch. The work of WK and FT was supported by the National Science Foundation, IOS 1456482, awarded to FT. WK was partly supported by the Basic Science Research Program through the National Research Foundation of Korea, funded by the Ministry of Education (2019R1I1A1A01057502).”

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.