



Corrigendum: Assessing the Diversity and Distribution of Apicomplexans in Host and Free-Living Environments Using High-Throughput Amplicon Data and a Phylogenetically Informed Reference Framework

OPEN ACCESS

Edited by:

Ludmila Chistoserdova,
University of Washington,
United States

Reviewed by:

Isabelle Florent,
Muséum National d'Histoire
Naturelle, France

*Correspondence:

Javier del Campo
jdelcampo@rsmas.miami.edu;
fonamental@gmail.com
Patrick J. Keeling
pkeeling@mail.ubc.ca

Specialty section:

This article was submitted to
Evolutionary and Genomic
Microbiology,
a section of the journal
Frontiers in Microbiology

Received: 25 June 2020

Accepted: 31 August 2020

Published: 08 October 2020

Citation:

del Campo J, Heger TJ,
Rodríguez-Martínez R, Worden AZ,
Richards TA, Massana R and
Keeling PJ (2020) Corrigendum:
Assessing the Diversity and
Distribution of Apicomplexans in Host
and Free-Living Environments Using
High-Throughput Amplicon Data and
a Phylogenetically Informed Reference
Framework.
Front. Microbiol. 11:576322.
doi: 10.3389/fmicb.2020.576322

Javier del Campo^{1,2*}, Thierry J. Heger^{1,3}, Raquel Rodríguez-Martínez⁴,
Alexandra Z. Worden⁵, Thomas A. Richards⁴, Ramon Massana⁶ and Patrick J. Keeling^{1*}

¹ Department of Botany, University of British Columbia, Vancouver, BC, Canada, ² Department of Marine Biology and Ecology, Rosenstiel School of Marine and Atmospheric Science, University of Miami, Miami, FL, United States, ³ Soil Science Group, CHANGINS, University of Applied Sciences and Arts Western Switzerland, Nyon, Switzerland, ⁴ Department of Biosciences, Living Systems Institute, College of Life and Environmental Sciences, University of Exeter, Exeter, United Kingdom,

⁵ GEOMAR – Helmholtz Centre for Ocean Research Kiel, Kiel, Germany, ⁶ Department of Marine Biology and Oceanography, Institut de Ciències del Mar (CSIC), Barcelona, Spain

Keywords: apicomplexans, diversity, distribution, phylogeny, classification, metabarcoding, environmental sequencing, reference database

A Corrigendum on

Assessing the Diversity and Distribution of Apicomplexans in Host and Free-Living Environments Using High-Throughput Amplicon Data and a Phylogenetically Informed Reference Framework

by del Campo, J., Heger, T. J., Rodríguez-Martínez, R., Worden, A. Z., Richards, T. A., Massana, R., et al. (2019). *Front. Microbiol.* 10:2373. doi: 10.3389/fmicb.2019.02373

In the original article, the reference for Kotabová et al., 2012 was incorrectly written as Kotabová, E., Vancová, M., Lukeš, J., Oborník, M., Modri, D., Lukeš, M., et al. (2012). Morphology, ultrastructure and life cycle of *Vitrella brassicaformis* n. sp., n. gen., a novel chromerid from the great barrier reef. *Protist* 163, 306–323. doi: 10.1016/j.protis.2011.09.001. It should be Oborník, M., Modrý, D., Lukeš, M., Cernotíková-Stríbrná, E., Cihlár, J., Tesarová, M., et al. (2012). Morphology, ultrastructure and life cycle of *Vitrella brassicaformis* n. sp., n. gen., a novel chromerid from the great barrier reef. *Protist* 163, 306–323. doi: 10.1016/j.protis.2011.09.001 Furthermore, the reference should be cited as Oborník et al. 2012.

In the original article Moore, R. B., Oborník, M., Janouškovec, J., Chrudimský, T., Vancová, M., Green, D. H., et al. (2008). A photosynthetic alveolate closely related to apicomplexan parasites. *Nature* 451, 959–963. doi: 10.1038/nature06635 was not cited in the article. The citation has now been inserted in INTRODUCTION, Paragraph 3 and should read:

Understanding what this diversity and distribution means requires a more detailed dissection of which apicomplexans appear in which environments. This is currently not possible because we lack a robust phylogenetic framework (e.g., a reference tree) upon which to base such inferences.

Moreover, it has recently been shown that the apicomplexans are the sister group to another odd collection of microbial predators (colpodellids) and putatively symbiotic algae (chromerids), collectively known as chrompodellids or “Apicomplexan-related lineages” (ARLs) (Leander et al., 2003; Moore et al., 2008; Oborník et al., 2012; Woo et al.,

2015). These lineages have aided in understanding of how apicomplexans evolved to become parasites and the ecological conditions that might have led to this transition.

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

REFERENCES

- Leander, B. S., Harper, J. T., and Keeling, P. J. (2003). Molecular Phylogeny and Surface Morphology of Marine Aseptate Gregarines (Apicomplexa): *Selenidium* spp. and *Lecudina* spp. *J. Parasitol.* 89, 1191–1205. doi: 10.1645/GE-3155
- Moore, R. B., Oborník, M., Janouškovec, J., Chrudimský, T., Vancová, M., Green, D. H., et al. (2008). A photosynthetic alveolate closely related to apicomplexan parasites. *Nature* 451, 959–963. doi: 10.1038/nature06635
- Oborník, M., Modrý, D., Lukeš, M., Cernotíková-Stribrná, E., Cihlár, J., Tesarová, M., et al. (2012). Morphology, ultrastructure and life cycle of *Vitrella brassicaformis* n. sp., n. gen., a novel chromerid from the great barrier reef. *Protist* 163, 306–323. doi: 10.1016/j.protis.2011.09.001
- Woo, Y. H., Ansari, H., Otto, T. D., Klinger, C. M., Kolisko, M., Michálek, J., et al. (2015). Chromerid genomes reveal the evolutionary path from photosynthetic algae to obligate intracellular parasites. *Elife* 4, 1–41. doi: 10.7554/eLife.06974

Copyright © 2020 del Campo, Heger, Rodríguez-Martínez, Worden, Richards, Massana and Keeling. 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.