






Correction: A phylogenomic and ecological analysis of the globally abundant Marine Group II archaea (Ca. Poseidoniales ord. nov.)

Christian Rinke  · Francesco Rubino  · Lauren F. Messer · Noha Youssef · Donovan H. Parks · Maria Chuvochina · Mark Brown · Thomas Jeffries · Gene W. Tyson · Justin R. Seymour · Philip Hugenholtz 

Published online: 21 November 2019
© The Author(s) 2019

Correction to: The ISME Journal

<https://doi.org/10.1038/s41396-018-0282-y>

In the abstract of the article, the family ‘Candidatus Poseidonaceae’ is misspelled. The proper spelling is ‘Candidatus Poseidoniaceae’.

In the introduction, the citations for the original discovery of marine planktonic Archaea were presented in the incorrect order. We have now corrected the first sentence in the abstract to:

“Following the original discovery of marine planktonic Archaea [1, 2], members of this domain are now known to be ubiquitous and abundant in the marine environment [3].”

The corrected order of the citations is:

1. Fuhrman JA, McCallum K, Davis AA. Novel major archaeobacterial group from marine plankton. *Nature*. 1992;356:148–9. (March 1992)
2. DeLong EF. Archaea in coastal marine environments. *Proc Natl Acad Sci USA*. 1992;89:5685–9. (June 1992)

We have now also added a note about a preprint of a separate analysis of MGII that became available while this manuscript was in review:

“Note: while this paper was under review, a preprint of a separate analysis of MGII became available [65], which has since been published [66].”

65. Tully BJ. Metabolic diversity within the globally abundant marine group II euryarchaea drives. *Ecol Patterns*. bioRxiv 349548. 2018. <https://doi.org/10.1101/349548>.

66. Tully BJ. Metabolic diversity within the globally abundant Marine Group II Euryarchaea offers insight into ecological patterns. *Nat Commun*. 2019;10:271. <https://doi.org/10.1038/s41467-018-07840-4>.

The funding sources have been omitted from the acknowledgements section of the manuscript. The corrected acknowledgements are as follows:

Acknowledgements We thank Alyson Santoro and William Orsi for access to marine size-fractionated metagenomes, Meng Li and Gregory Dick for access to deep-sea MGII genomes, Fauzi Haroon for access to Red Sea MAGs, and T. Ingleton for assistance with the Port Hacking sample collection. This study was financially supported by an Australian Research Council (ARC) Future Fellow Award (FT170100213) awarded to CR and by an ARC Laureate Fellowship (FL150100038) awarded to PH.