CORRECTION Open Access

Correction to: Minnesota peat viromes reveal terrestrial and aquatic niche partitioning for local and global viral populations

Anneliek M. ter Horst¹, Christian Santos-Medellín¹, Jackson W. Sorensen¹, Laura A. Zinke¹, Rachel M. Wilson², Eric R. Johnston³, Gareth Trubl⁴, Jennifer Pett-Ridge⁴, Steven J. Blazewicz⁴, Paul J. Hanson⁵, Jeffrey P. Chanton², Christopher W. Schadt³, Joel E. Kostka^{6,7} and Joanne B. Emerson^{1,8*}

Correction to: Microbiome 9, 233 (2021) https://doi.org/10.1186/s40168-021-01156-0

Following the publication of the original article [1], the co-author reported that Funding section was not included. Below is the Funding section.

Funding for this work was provided by the UC Davis College of Agricultural and Environmental Sciences and Department of Plant Pathology as new lab start-up to JBE (for research expenses and the majority of support for AMH). Additional support for AMH was provided by an award from the U.S. Department of Energy (DOE), Office of Science, Office of Biological and Environmental Research (BER), Genomic Science Program, Number DE-SC0021198 (grant to JBE). Support for CSM was provided by an award from the DOE BER, Genomic Science Program, Number DE-SC0020163 (grant to JBE). Support for PJH and CWS was provided by the U.S. Department of Energy, Office of Science, Office of Biological and Environmental Research. ORNL is managed by UT-Battelle, LLC, for the DOE under contract DE-AC05-1008 00OR22725. Contributions by RMW, JPC, and JEK were supported by the Office of Biological and Environmental Research, Terrestrial Ecosystem Science Program, under United States DOE contracts DE-SC0007144 and DE-SC0012088 (grants to JEK). Data collection for the Alaskan samples was supported by the USGS Mendenhall Postdoctoral Fellowship program and for the Puerto Rico samples by DOE BER Early Career Research Program grant SCW1478 (to JPR). Analyses and data collection conducted by Lawrence Livermore National Laboratory (LLNL) were conducted under the auspices of DOE Contract DE-AC52-07NA27344 and supported by the DOE BER Genomic Science Soil Microbiome SFA SCW1632 and LLNL LDRD 18-ERD-041 (to SJB). Sequencing for the Puerto Rico samples was supported by JGI Community Sequencing Award #2017 (JGI project ID #502924) and several NERSC allocations (to JPR).

The original article has been updated.

Author details

¹Department of Plant Pathology, University of California Davis, Davis, CA, USA. ²Department of Earth, Ocean, and Atmospheric Science, Florida State University, Tallahassee, FL, USA. ³Biosciences Division, Oak Ridge National Laboratory, Oak Ridge, TN, USA. ⁴Physical and Life Sciences Directorate, Lawrence Livermore National Laboratory, Livermore, CA, USA. ⁵Environmental Sciences Division, Oak Ridge National Laboratory, Oak Ridge, TN, USA. ⁶Schools of Biology and Earth & Atmospheric Sciences, Georgia Institute of Technology, Atlanta, GA, USA. ⁷Center for Microbial Dynamics and Infection, Georgia Institute of Technology, Atlanta, GA 30332, USA. ⁸Genome Center, University of California Davis, Davis, CA, USA.

The original article can be found online at https://doi.org/10.1186/s40168-021-01156-0.

*Correspondence: jbemerson@ucdavis.edu

Published online: 25 January 2022



© The Author(s) 2022. **Open Access** This article is licensed under a Creative Commons Attribution 4.0 International License, which permits use, sharing, adaptation, distribution and reproduction in any medium or format, as long as you give appropriate credit to the original author(s) and the source, provide a link to the Creative Commons licence, and indicate if changes were made. The images or other third party material in this article are included in the article's Creative Commons licence, unless indicated otherwise in a credit line to the material. If material is not included in the article's Creative Commons licence and your intended use is not permitted by statutory regulation or exceeds the permitted use, you will need to obtain permission directly from the copyright holder. To view a copy of this licence, wist http://creativecommons.org/licenses/by/4.0/. The Creative Commons Public Domain Dedication waiver (http://creativecommons.org/publicdomain/zero/1.0/) applies to the data made available in this article, unless otherwise stated in a credit line to the data.

⁸ Genome Center, University of California Davis, Davis, CA, USA Full list of author information is available at the end of the article

ter Horst *et al. Microbiome* (2022) 10:17 Page 2 of 2

Reference

 Ter Horst AM, Santos-Medellín C, Sorensen JW, et al. Minnesota peat viromes reveal terrestrial and aquatic niche partitioning for local and global viral populations. Microbiome. 2021;9:233. https://doi.org/10. 1186/s40168-021-01156-0.

Ready to submit your research? Choose BMC and benefit from:

- fast, convenient online submission
- $\bullet\,$ thorough peer review by experienced researchers in your field
- rapid publication on acceptance
- support for research data, including large and complex data types
- gold Open Access which fosters wider collaboration and increased citations
- $\bullet\,\,$ maximum visibility for your research: over 100M website views per year

At BMC, research is always in progress.

Learn more biomedcentral.com/submissions

