



Microbiomes of aquatic animals

Isa Schön · Diego Fontaneto ·
Elena L. Peredo

Published online: 3 August 2023

© The Author(s), under exclusive licence to Springer Nature Switzerland AG 2023

The holobiont approach (Bosch & Miller, 2017) in the study of animal ecology places strong emphasis on the strict association between the animals and their microbes, which are beneficial for the host's survival and fitness (Cornwallis et al., 2023). Such a strict association, called phyllosymbiosis, is known to hold true at different spatial scales (Härer & Rennison, 2023) and explanations for such a pattern have

been suggested to be related to evolutionary and/or ecological mechanisms. The host and the associated microbiota may co-evolve, with similarities in the composition of the microbiota between hosts that reflect the phylogenetic relatedness of the hosts (Lim & Bordenstein, 2020). Yet, the similarity between the differences in microbiota compositions and the host phylogenetic relationships could also be the effect of host filtering: phylogenetically related hosts may have similar ecologies, indirectly filtering for similar microbes regardless of any evolutionary association between the host and the microbiota (Mazel et al., 2018).

The general rules governing the relationship between the host and its associated microbiota are currently not clearly defined. Inferences regarding the potential processes that control these systems are biased by our skewed knowledge of the observed patterns, dominated by data on microbiota mostly from model vertebrate species (Legrand et al., 2020; Kuziel & Rakoff-Nahoum, 2022). In addition, early studies focused on animals with a strong association with their microbiota, for example, corals (e.g. Pollock et al., 2018) even if new data on a broad spectrum of taxa are becoming available (Boscaro et al., 2022).

The phyllosymbiosis pattern of host-microbiota associations seems to be indeed much looser than what is seen in corals, sponges, vertebrates and in several terrestrial and aquatic invertebrates (e.g. Hammer et al., 2017, 2019; Eckert et al., 2021; Boscaro et al., 2022). The aim of the current special issue is

Guest editors: Isa Schön, Diego Fontaneto & Elena L. Peredo / Aquatic Microbiomes

Handling editor: Sidinei M. Thomaz

I. Schön (✉)
Freshwater Biology, Royal Belgian Institute of Natural Sciences, 1000 Brussels, Belgium
e-mail: ischoen@naturalsciences.be

I. Schön
Centre of Environmental Sciences (CMK), University of Hasselt, 3590 Diepenbeek, Belgium

D. Fontaneto
National Research Council of Italy (CNR), Water Research Institute (IRSA), Molecular Ecology Group (MEG), 28922 Verbania Pallanza, Italy

E. L. Peredo
Thomas H Gosnell School of Life Sciences, Rochester Institute of Technology, Rochester, NY, USA

E. L. Peredo
The Ecosystems Center, Marine Biological Laboratory, Woods Hole, MA 02543, USA

to provide additional evidence on the strength of phylosymbiosis as a pattern and to explore additional mechanisms that may explain the observed patterns of association between animals and their microbiota, with a special emphasis on aquatic environments, and using genetic/genomic approaches for the description of the microbiome composition.

The ten papers included in this special issue explore patterns and processes involved in the association with their microbiomes in animals belonging to six different phyla: Arthropoda, Chordata, Cnidaria, Mollusca, Platyhelminthes, and Rotifera. They cover different approaches, from those obtaining data from one single species to those comparing species across the whole phylum; they gather data from different parts of the world, including marine and freshwater habitats. We here provide a summary of their content, without citing the papers in the references, because according to Clarivate, journals can be suppressed for too many self-citations, even in prefaces of special issues.

The first five papers analyzed the potential environmental drivers of the differences in microbiomes in a single species: the first one focused on the effect of cultivation conditions on the microbiome of a flatworm (Platyhelminthes, Catenulida) species. The second one explored the effects of thermal stress on the microbiome of endosymbiotic dinoflagellates from a coral (Cnidaria, Scleractinia) species. The third one combined field collections and common garden experiments to assess the effects of changes in salinity on the microbiome of a species of water strider (Arthropoda, Hexapoda, Hemiptera). The fourth one focused on the microbiome of an ostracod (Arthropoda, Crustacea) species, reporting that it was different from the known microbiomes of other freshwater ostracods, but had large variability even among ostracod individuals from the same population. The fifth compared the microbiomes of the juveniles of a species of freshwater fish (Chordata, Actinopterygii) through time and under different diet treatments indicating a strong influence of initial diet on the gut microbiome.

Two papers compared microbiomes between pairs of closely related species. One paper studied the microbiomes of two clam (Mollusca, Bivalvia) species in different seasons, highlighting that the same bacterial genera were dominant regardless of differences between host species and seasons. The other

paper compared the hindgut microbiome of two fish (Chordata, Actinopterygii) species in an African lake showing that the two fish species had different diets, but not different microbiomes.

Two other papers studied multiple species within a taxonomic group. One paper compared the microbiome of seven leaf beetle species (Arthropoda, Hexapoda, Coleoptera) demonstrating that the most relevant drivers of the differences were firstly the host species identity and only secondarily the type of habitat. The other paper demonstrated that a combination of effects of host ecology and host habitat was stronger in driving differences in microbiomes associated with rotifers (Rotifera) than host phylogenetic distances.

The last paper of the special issue reviewed the literature on the effect of gender-based differences in the microbiota of aquatic animals, a poorly studied factor of differences. They also provided evidence for the importance of gender on microbiome composition from the peculiar example of a freshwater snail (Mollusca, Gastropoda) with sexual and asexual populations.

Our hope is that the breadth of host organisms, habitat, approaches, questions, and hypotheses of the papers included in this special issue will provide solid and convincing arguments towards more comprehensive broad-ranging studies on host-microbiome relationships, not only in aquatic habitats.

Funding There was no specific funding related to this publication.

Data availability No data are linked to this publication.

Declarations

Competing interests The authors declare to have no competing interests.

References

- Boscaro, V., C. C. Holt, N. W. Van Steenkiste, M. Herranz, N. A. Irwin, P. Álvarez-Campos, et al., 2022. Microbiomes of microscopic marine invertebrates do not reveal signatures of phylosymbiosis. *Nature Microbiology* 7(6): 810–819. <https://doi.org/10.1038/s41564-022-01125-9>.
- Bosch, C. G. & D. J. Miller, 2017. *The Holobiont Imperative: Perspectives from Early Emerging Animals*, Springer, Vienna.
- Cornwallis, C. K., A. van'tPadje, L. Ellers, M. Klein, R. Jackson, E. T. Kiers, S. A. West & L. M. Henry, 2023.

- Symbioses shape feeding niches and diversification across insects. *Nature Ecology & Evolution*. <https://doi.org/10.1038/s41559-023-02058-0>.
- Eckert, E. M., N. Anicic & D. Fontaneto, 2021. Freshwater zooplankton microbiome composition is highly flexible and strongly influenced by the environment. *Molecular Ecology* 30: 1545–1558. <https://doi.org/10.1111/mec.15815>.
- Hammer, T. J., D. H. Janzen, W. Hallwachs, S. P. Jaffe & N. Fierer, 2017. Caterpillars lack a resident gut microbiome. *Proceedings of the National Academy of Sciences USA* 114: 9641–9646. <https://doi.org/10.1073/pnas.1707186114>.
- Hammer, T. J., J. G. Sanders & N. Fierer, 2019. Not all animals need a microbiome. *FEMS Microbiology Letters* 366: fnz117. <https://doi.org/10.1093/femsle/fnz117>.
- Härer, A. & D. J. Rennison, 2023. The biogeography of host-associated bacterial microbiomes: revisiting classic biodiversity patterns. *Global Ecology & Biogeography* 32: 931–944. <https://doi.org/10.1111/geb.13675>.
- Kuziel, G. A. & S. Rakoff-Nahoum, 2022. The gut microbiome. *Current Biology* 32: 257–264. <https://doi.org/10.1016/j.cub.2022.02.023>.
- Legrand, T. P., J. W. Wynne, L. S. Weyrich & A. P. Oxley, 2020. A microbial sea of possibilities: current knowledge and prospects for an improved understanding of the fish microbiome. *Reviews in Aquaculture* 12(2): 1101–1134. <https://doi.org/10.1111/raq.12375>.
- Lim, S. J. & S. R. Bordenstein, 2020. An introduction to phyllosymbiosis. *Proceedings of the Royal Society B* 287: 20192900. <https://doi.org/10.1098/rspb.2019.2900>.
- Mazel, F., K. M. Davis, A. Loudon, W. K. Kwong, M. Groussin & L. W. Parfrey, 2018. Is host filtering the main driver of phyllosymbiosis across the tree of life? *mSystems* 3: 97–18. <https://doi.org/10.1128/mSystems.00097-18>.
- Pollock, F. J., R. McMinds, S. Smith, D. G. Bourne, B. L. Willis, M. Medina, et al., 2018. Coral-associated bacteria demonstrate phyllosymbiosis and cophylogeny. *Nature Communications* 9: 4921. <https://doi.org/10.1038/s41467-018-07275-x>.

Publisher's Note Springer Nature remains neutral with regard to jurisdictional claims in published maps and institutional affiliations.