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Editorial: Holobiont interactions

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Editorial on the Research Topic

Holobiont interactions

The holobiont concept has emerged as a theoretical and experimental framework to study the interactions between hosts and their associated microbial communities in all types of ecosystems and organisms, providing a paradigm shift from bipartite interactions to a community-based integration of factors that determine the resilience of organisms. The spread of this concept across biological sciences, including aspects of mathematics (bioinformatics, statistics, and modelling), results from a recent realisation of the ubiquitous nature of host-associated microbes and their central role in host biology, ecology, and evolution, particularly regarding adaptation to environmental change. Yet, several challenges in holobiont research remain, including the theoretical and experimental approaches to elucidate the role of microbiota in host adaptation and evolution, and inherent bioinformatics challenges of complex multicomponent datasets. Consequently, the application of holobiont manipulation to enhance host health and ecosystem restoration is extremely limited.

Understanding the intricate role of microbial communities in influencing a host's capacity to adapt to environmental shifts and evolve is a pivotal aspect of holobiont research. But defining the boundaries of the holobiont, determining which organisms are integral parts and which are not, and elucidating the stability and flexibility of these associations over time and space all pose experimental challenges. These challenges include manipulating or isolating intricate microbial communities to establish causative links in holobiont studies, which is not always possible with obligate symbionts. Metabolic or genetic comparisons between symbiotic and artificially acquired aposymbiotic host counterparts can help unravel organism interactions. For example, [Vallier et al.](#) employed high throughput transcriptomics at various developmental and symbiotic states to enhance our comprehension of the insect endosymbiotic model involving the cereal weevil *Sitophilus oryzae* and its intracellular bacterium *Sodalis pierantonius*. Nevertheless, numerous methodological hurdles remain, especially for non-model organisms. To address these challenges, microscale technologies can play a crucial role. [Lyndby et al.](#), for instance, employed optical and electro-chemical microsensors to investigate how light is modulated at the water-tissue interface of the upside-down jellyfish, *Cassiopeia*. This technological approach represents a significant advancement, shedding light on microscale interactions within holobionts. In the case of the jellyfish, it unveiled the mesoglea's role in buffering the physio-chemical microenvironment, effectively regulating oxygen and pH dynamics in the dark, while also providing light attenuation in tissues containing symbionts.

The intricacies of host-microbe metabolic interactions are further compounded when considering the influence of neighbouring biotic environments on microbiomes, as expounded by [Clements and Hay](#) in the context of corals. The authors underscore the prevalent transition of coral reefs from coral to macroalgal dominance, yet the precise role of macroalgae in coral decline remains insufficiently understood. This challenge echoes across holobiont research, necessitating the development of effective theoretical and experimental approaches. Designing experiments to explore the nuanced dynamics of host-microbe interactions and their impact on holobiont health becomes complex due to the intricate relationships with local and associated microbial communities. [Bergman et al.](#), in their examination of environmental generalism and holobiont interactions in high-latitude corals, caution against oversimplification, emphasizing the context-dependent nature of host-microbe interactions across diverse environmental conditions, locations, and temporal changes. Despite these complexities, progress is being made in accessing and unravelling these intricacies, offering rewarding insights. [Jacquiod et al.](#), for instance, employed bacterial and fungal amplicon sequencing alongside multifactorial host genotype and environment information, providing an initial assessment of individual (genotype and environment) effects as well as their interactions on holobiont relationships in the field. However, the vast and intricate datasets generated in multifaceted holobiont research present bioinformatics challenges. Analysing and interpreting these complex, interdisciplinary datasets demand advanced computational tools, statistical methods, and bioinformatics expertise. While demanding, this analytical process is crucial, as successful application to one organism can lay the foundation for further methodological advancements in subsequent studies.

Once armed with an expanded knowledge base, technological advances, and ability to control associations, there is potential to craft practical strategies for manipulating the holobiont towards positive outcomes, such as identifying key pathways for integrative pest management strategies (e.g. [Vallier et al.](#)). However, delving into the applications of holobiont manipulation for enhancing host health and contributing to ecosystem restoration remains an area of limited exploration. [Heric et al.](#) showcase a promising example of this potential for corals, where bacterial probiotics can play a mitigating role in coral bleaching by diminishing reactive oxygen species (ROS) levels within the microalgal partner of corals, Symbiodiniaceae, through the production of bacterial antioxidants. While this intervention has shown efficacy in cultured environments, its applicability to Symbiodiniaceae within the coral holobiont, especially in the context of natural bleaching events, is yet to be tested. This becomes increasingly crucial considering the escalating prevalence of coral diseases during bleaching events, as revealed by [Moriarty et al.](#), and the potential protective role of the holobiont microbiome, or alternatively, its role as a source for opportunistically pathogenic bacteria.

Holobiont research, particularly in understanding microbiome interactions, presents a potential, albeit hotly debated, paradigm shift in our comprehension of evolution and ecology. An influential contribution to this discourse within our Research Topic is [Rosenberg's](#) article, "*Rapid acquisition of microorganisms and microbial genes can help explain punctuated evolution*," delving into

the role of microorganisms in the evolutionary processes of animals and plants. The proposition suggests that the swift incorporation of microorganisms from the environment into host microbiomes, coupled with the subsequent integration of microbial genes into host genomes through horizontal gene transfer, can elucidate instances of punctuated evolution. This hypothesis finds support in evidence from significant evolutionary events driven by microorganisms. However, it's crucial to emphasise that this perspective doesn't diminish the importance of host genetics in steering evolutionary trajectories and determining adaptive capacities. In a case study on oysters, [Hemraj et al.](#) illuminate how microbiomes respond to acidic and low oxygen environments, potentially affecting the nutritional status of oysters. Nevertheless, the study underscores that oysters exhibit the ability to regulate their physiological processes, maintaining homeostasis in the short term despite environmental challenges. This dual consideration of microbial influences and host genetics contributes to a more nuanced understanding of the intricate interplay in shaping evolutionary dynamics.

The generalisability of the holobiont concept across diverse organisms and ecosystems remains a challenge. Nevertheless, amidst the aspects requiring refinement, this Research Topic underscores the active efforts of researchers to address gaps by conducting additional studies, applying innovative methodologies, reviewing current status, refining research approaches, and integrating findings from various biological systems. These collective endeavours aim to unravel the intricate dynamics of holobiont interactions and enhance our understanding of this emerging field.

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