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# Editorial: Aiptasia: a model system in coral symbiosis research

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## Editorial on the Research Topic

[Aiptasia: a model system in coral symbiosis research](#)

Tropical coral reefs are among the most diverse and productive ecosystems in the world and support a range of ecosystem goods and services that contribute to the well-being of millions of people. However, coral reef cover is declining globally because of local and global anthropogenic impacts (Wilkinson, 1999). In particular, the frequency and severity of mass bleaching events caused by global climate change are expected to further increase in the future and threaten the long-term survival of coral reefs (Hughes et al., 2017).

The trophic and structural foundations of this marine ecosystem rely on the mutualistic relationships that exist between scleractinians and their associated microbial symbionts (photosynthetic dinoflagellates, bacteria, archaea etc.), forming a meta-organism called the coral holobiont (Stévenne et al., 2021). Despite an increasing understanding about the molecular underpinnings of coral holobiont function, there are still significant gaps in our knowledge. Uncovering the underlying fundamental processes involved in the establishment and maintenance of the interaction between the coral host and its microbial symbionts is essential if we are to fully understand the mechanisms by which they are impacted by stress and whether or how corals might adapt to environmental perturbations and survive.

The use of model organisms has a successful track record, leading to significant progress in molecular, cellular, and developmental biology (Jacobovitz et al., 2023). The model organism Aiptasia, i.e. *Exaiptasia diaphana*, is a small sea anemone found globally in sub-tropical and tropical marine waters, and intracellularly hosts symbiotic dinoflagellates (family: Symbiodiniaceae) (LaJeunesse et al., 2018). Unlike corals, Aiptasia lacks a calcium carbonate skeleton, can be easily manipulated and cultivated under laboratory conditions, and can survive in a facultative symbiotic state, which allows conducting experiments on aposymbiotic control animals (Matthews et al., 2016). Since its formal proposal as a model system to study cnidarian symbiosis in 2008 (Weis et al., 2008). Aiptasia has been adopted by a growing number of laboratories to explore research questions on: development and

cellular regeneration (Fransolet et al., 2012; Fransolet et al., 2013; Bucher et al., 2016); the onset, maintenance, and disruption of symbiosis (Bieri et al., 2016; Bucher et al., 2016; Wolfowicz et al., 2016; Tivey et al., 2022; Rådecker et al., 2023); and metabolic interactions (Rådecker et al., 2018) among others. To date, this community of researchers has made available a genome (Baumgarten et al., 2015), developed omics tools (Lehnert et al., 2014; Baumgarten et al., 2018; Matthews et al., 2018; Simona et al., 2019; Sproles et al., 2019), closed the life cycle (Maegele et al., 2023), and openly shared their research protocols through initiatives such as the “Aiptasia Symbiosis Resource” portal (aiptasia-resource.org). But to make this sea anemone a practical and reliable model system in coral reef research and the symbiosis field more widely, the Aiptasia community still needs to overcome a few hurdles such as developing gene-editing tools, new imaging techniques, etc. This Research Topic showcases the state-of-the-art of the Aiptasia model system and how it can contribute to our comprehension of the cnidarian-Symbiodiniaceae symbiosis, and coral reef conservation.

Accurate quantification of algal density in host tissue is an essential step in studies examining the mechanisms of establishment, maintenance, breakdown, and recovery of cnidarian-Symbiodiniaceae symbioses. Bolzan and Roark compared and evaluated the precision of commonly used methods for determining *in vitro* and *in situ* algal density in the maintenance phase of host colonization in *Exaiptasia diaphana*. They demonstrated that a method using a hemocytometer and requiring terminal sampling (*i.e.*, *in vitro*) yields estimates of algal density with comparable precision to non-terminal sampling methods using confocal microscopy (*i.e.*, *in vivo*). This last method is however more suitable when algal densities are relatively low, as in anemones in the early stages of colonization or re-colonization after symbiont loss. Overall, this study offers valuable methodological guidance for researchers exploring cnidarian-dinoflagellate symbiosis, as well as for educators looking to incorporate the Aiptasia model into their teaching laboratories.

The development of genetic tools for studying gene function and unraveling the molecular mechanisms governing symbiosis is probably the last hurdle to be overcome to make the Aiptasia model indispensable for the study of coral-dinoflagellate symbiosis. In recent years, enormous progress has been made in this field at the host compartment level, with the development of protocols for microinjecting proteins, mRNA, and DNA into Aiptasia zygotes (Jones et al., 2018) and gene-editing via CRISPR-Cas9 in the coral *Acropora millepora* (Cleves et al., 2018). However, our understanding of the mechanisms that orchestrate this symbiosis will remain incomplete until the same methodological advances are available for the associated algal endosymbionts. After three decades of research aimed at developing a robust and reproducible method for genetically transforming Symbiodiniaceae, the goal seems to have finally been achieved with the study of Gornik et al.

Using an adapted modular Golden Gate vector system and electroporation, Gornik et al. introduced plasmid DNAs into *Breviolum* sp. (strain SSB01) cells and successfully expressed GFP in the cell nucleus using an intrinsic endogenous dinoflagellate virus nuclear protein promoter with a derived nuclear localisation signal. This algal strain is derived from the H2 clonal line of Aiptasia but

members of this genus also readily form symbioses with other anemones and reef-building corals. The authors of this study were also able to confer puromycin resistance to *Breviolum* sp. via the expression of the puromycin N-acetyltransferase resistance gene, and this transformation was stable for at least one year. Although GFP fluorescence decreased with long-term culture maintenance, implying that further development is needed to optimize this method, this work represents a breakthrough in coral research and paves the way for a deeper understanding of dinoflagellate symbiont biology.

The interactions between the coral host and its microbial symbionts (e.g., photosynthetic dinoflagellates, bacteria, archaea, viruses) are crucial for maintaining a healthy and resilient holobiont in changing and nutrient-poor environments. Over the last fifteen years, the development of DNA sequencing techniques and their increased accessibility have made it possible to explore the cnidarian microbiome and better understand its functions and the role it plays in nutrient recycling, stress response processes, and holobiont health (Bourne et al., 2016; Peixoto et al., 2017; Santoro et al., 2021; Stévenne et al., 2021). Aiptasia is also a powerful tool for studying symbiotic and metabolic interactions between the animal host and its microbial partners, and microbiome research in this model system has only recently gained momentum. For instance, studies have reported the existence of a core microbiome (Röthig et al., 2016), although notable discrepancies in the bacterial community have also been noted across laboratory clonal lines and with wild Aiptasia (Herrera et al., 2017; Hartman et al., 2020), or between aposymbiotic and symbiotic anemones (Röthig et al., 2016). Studies have also started exploring how particular bacteria or consortia can impact the holobiont thermal performance (Dungan et al., 2022; Dörr et al., 2023).

To contribute to the growing knowledge of the bacterial community associated with Aiptasia, Curtis et al. used 16S rRNA gene amplicon sequencing to compare the microbiota associated with different polyp regions and symbiotic states of anemones belonging to four different clonal lines reared under identical environmental conditions. They did not observe major differences in the composition of the microbiome between the tentacles and the column-peduncle region of anemones. In contrast, substantial variations were found between clonal lines and different symbiotic states, which is consistent with previous studies (Röthig et al., 2016; Herrera et al., 2017; Hartman et al., 2020; Wuerz et al., 2023) and the study by Sydnor et al. in this Research Topic. Interestingly, Curtis et al. did not highlight a core microbiome between anemone genotypes reared under identical conditions for several years, but did note that the microbiome of aposymbiotic anemones showed higher structural consistency compared to symbiotic anemones, which possibly hosted different Symbiodiniaceae species that may associate with discrete bacterial taxa (Röthig et al., 2016; Xiang et al., 2022; Wuerz et al., 2023). These results suggest the existence of genetic factors associated with the host and its symbionts that influence the composition of the bacterial community associated with Aiptasia. This study not only highlights the importance of further investigating the environmental and molecular factors that shape bacterial communities in symbiotic cnidarians, but also of evaluating the

amount of variation that can be expected between clonal lines in the Aiptasia model system.

On the same Research Topic, [Sydnor et al.](#) investigated the response of the bacterial communities associated with symbiotic and aposymbiotic Aiptasia of the CC7 laboratory clonal line to short-term thermal elevation. Consistent with previous studies (e.g., [Röthig et al. \(2016\)](#)), they observed a core microbiome composed primarily of bacteria from the families Alteromonadaceae and Rhodobacteraceae, but also found that the symbiotic status had a significant effect on the microbiome composition, suggesting that the presence of Symbiodiniaceae may influence the composition of the bacterial community ([Xiang et al., 2022](#)). Heat stress had a variable effect on microbiome composition. In aposymbiotic anemones; it led to a large increase in rare bacterial taxa, including potential pathogens such as members of the genus *Vibrio*, whereas in symbiotic anemones the family Pelobacteraceae, which contains potential nitrogen fixers, responded dramatically to heat stress. Following these observations, the authors of this study investigated the nitrogen-fixation capacity of the Aiptasia microbiome. Contrary to what is observed in autotrophic coral species, [Sydnor et al.](#) found little evidence of actual expression of the *nifH* gene encoding for the iron protein of nitrogenase, or nitrogen-fixation (measured with the acetylene reduction assay), in both symbiotic states. These observations suggest that Aiptasia, because of its more heterotrophic lifestyle, may perhaps not be an ideal model for all coral species. However, other studies found a large difference between symbiotic and aposymbiotic states in terms of diazotroph communities and nitrogen assimilation, thus arguing that more research is warranted ([Xiang et al., 2022](#)).

This Research Topic presents new advances in coral symbiosis research using Aiptasia, which could inspire and guide the next generation of biologists interested in symbiotic interactions. Although significant progress has been made to date, and this model system is reaching maturity, we need to keep working hard to develop a more comprehensive toolbox to fully understand the molecular dialogue that governs the interactions between the host

animal and its microbial symbionts, under ambient or stress conditions.

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