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Editorial: Symbiotic interactions of algae and microorganisms: physiology and industrial applications

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Editorial on the Research Topic

[Symbiotic interactions of algae and microorganisms: physiology and industrial applications](#)

Algae (micro- and macro) are one of the most diverse groups of species, representing a considerable part of terrestrial and aquatic ecosystems. The diversity of algae enables tailoring of the biomass for a spectrum of bioproducts, including pigments, biofertilizers, ink, nutraceuticals, fish feed, lubricating oils, food supplements, and cosmetics (Arora and Philippidis, 2023). Macroalgae, or seaweeds, are a vital part of aquaculture in addition to being a sustainable source of several marketed bioactive compounds. Interactions of seaweeds with microorganisms in natural ecosystems significantly impact their composition, metabolic activities, response to climate change, pollution, and anthropogenic activities, ultimately determining the suitability of their usage. The surface of seaweeds is a highly active interface, perfect for harboring a consortium of microorganisms, including bacteria, fungi, protozoa, and diatoms. Elucidation and understanding of interactions between algae and microorganisms are crucial from both an ecological and industrial standpoint (Ren et al., 2022). Moreover, a fundamental understanding of the changes in the microbial community in response to biotic and abiotic stress is necessary for optimizing the yield of the target bioactive compounds and controlling detrimental invaders.

Another important aspect of algae-microbial symbiosis is harnessing algae-based technologies for developing sustainable and cost-effective strategies for waste water remediation, biofuels, and bioproducts. One of the critical barriers to the successful translation of technology from research to market is the high cost of cultivating and harvesting algal biomass. Symbiotic interactions of algae with other microorganisms such as bacteria, yeast, and fungi could potentially enhance biomass productivity and quality, in addition to easing harvesting and reducing culture crashes by outcompeting invaders (Arora et al., 2019). Moreover, co-cultures of algae with other beneficial

microorganisms alter the metabolism of the algae, which can be leveraged for improving or augmenting the yield of the desired bioproduct (Caudal et al., 2022). The added advantage of using mixed cultures is that they may enhance nutrient availability, reduce the consumption of nutrients, and prevent the accumulation of auto-inhibitors in the culture, thus enabling the recycling of the culture medium.

In this Research Topic, “*Symbiotic Interactions of Algae and Microorganisms: Physiology and Industrial Applications*,” the published research articles focus on underpinning the complex interplay between the algae and microbes to aid a better understanding of the interactions. For instance, Nguyen et al. characterized the succession of microbial communities associated with *Ulva fasciata*, a green macroalga playing a pivotal role in brackish and marine ecosystems, significantly affecting the growth of the alga. The authors utilized an integrated multi-trophic aquaculture (IMTA) system to monitor the temporal dynamics of the microbial communities cultivated in seawater effluents of fish (grey mullet) ponds to identify key biomarker. Co-culturing fish with seaweeds using IMTA systems is reported to reduce the load of pollutants in the effluents as the nutrients are taken up by algae for their growth. Notably, the microbial community present on the surface of the alga was comprised of 11 different bacterial phyla, with *Proteobacteria*, *Bacteroidetes*, *Planctomycetes*, and *Deinococcus-Thermus* accounting for >95% of the total population. Interestingly, *Deinococcus-Thermus* was first detected in this study, indicating its role in enhancing resilience to extreme environments. Overall, four families—*Saprospiraceae*, *Thiohalorhabdaceae*, *Sphingomonadaceae*, and *Rhodobacteraceae*—were identified as prominent biomarkers whose relative abundance significantly differed over time, contributing to the knowledge about microbial communities associated with *Ulva fasciata*.

In another study, Xu et al. explored the seasonal diversity of microbial (eukaryotic and bacterial) communities of economically important seaweeds: *Neoporphyra haitanensis* (monoculture, zone P), mixed cultures of *Gracilaria lemaneiformis*, and *Saccharina japonica* (zone G) as compared to seaweeds collected from Fujian Province’s largest mariculture bases in south China. For the eukaryotic community, the enriched phyla were *Bacillariophyta*, *Chlorophyta*, and *Cnidaria*; but their proportions differed among the three study zones, with the highest diversity occurring in December (highest salinity levels) and the lowest in May (lowest salinity levels). For the bacterial community, *Proteobacteria* was the most dominant phylum among all the zones. The study evidenced that zone P resulted in maximum release of dissolved organic carbon, resulting in the dominance of *Flavobacteriaceae*, which can degrade fucoidan (sulfated fucose-containing polysaccharides), in addition to utilizing sugars such as lactose, sucrose, and inositol and reducing nitrates to nitrites.

In addition, the study by Steinrücken et al. analyzed the bacterial community composition in three *Phaeodactylum* (Diatom) strains during batch cultivations (start, linear phase, and stationary phase) to optimize algal biomass and quality. The most dominant bacterial genera present in the microalgal cultures (>97%) belonged to the classes *Alphaproteobacteria*, *Gammaproteobacteria* (phylum *Proteobacteria*), and *Bacteroidia*

(phylum *Bacteroidetes*), indicating that the microalgae to some degree have an influence on the development of the bacterial communities in different settings.

On another aspect, Ma et al. research provided molecular insights into the nutritional adaptation mechanism of mixotrophic flagellate *Poterioochromonas malhamensis* feeding on microalgal prey. The flagellate is widely distributed in aquatic ecosystems, and is considered a potential biocontrol for cyanobacterial blooms due to its unique capacity to degrade microcystin. However, this characteristic also makes it a potential invader in microalgal cultivation systems, especially *Chlorella*. The predator, *P. malhamensis*, cultivated in autotrophy fed with digestible (GT-1) green microalgae, *Chlorella sorokiniana*, showed upregulation of pigment and photosynthesis biosynthesis genes but downregulation of light harvesting complex genes, reducing the overall photosynthesis efficiency. On the contrary, mixotrophic cultures showed upregulation of carbon and nitrogen metabolism, indicating switching of the metabolism towards β -1,3-glucan. Moreover, feeding *P. malhamensis* with indigestible (CMBB-146) algae revealed downregulation of lysosome enzymes and upregulation of apoptosis and necrosis genes, resulting in the death of the flagellate.

In conclusion, the published research articles provided a fundamental understanding of the different aspects of algal-microbiome interactions and how these can be exploited for the restoration of ecosystems in response to global changes as well as for the development of sustainable bioproducts.

Author contributions

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Conflict of interest

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