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Editorial: Ecological and genetic insights into seaweeds' diversity and adaptation

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Editorial on the Research Topic

Ecological and genetic insights into seaweeds' diversity and adaptation

Seaweeds (marine macroalgae) have long been recognized as important primary producers and ecological engineers capable of modifying the surrounding coastal rocky environments and ecosystem services (Harley et al., 2012). However, climate change, anthropogenic pressures and other biotic/abiotic factors in the past decade have imposed unparalleled impacts on the diversity, distribution, reproduction, population structure, biogeography and ecological function of seaweeds globally (Breeman, 1990; Müller et al., 2009; Martínez et al., 2018; Fernández et al., 2019; Song et al., 2021; Bringloe et al., 2022). There are a number of research gaps that still need to be investigated in order to better understand the drivers of diversity and the response of seaweeds under climate change: (a) How do different seaweed species respond to the interactive effects of biotic and abiotic factors? (b) How does genetic variation translate into fitness variation in natural population? (c) How does eco-physiological performance enhance resilience and adaptability to a changing environment? And (d) how do biochemical and metabolic processes affect seaweeds' cellular structure and biological function under different climate change scenarios? Answering these questions is a monumental task that requires unveiling the links between genotypes, phenotypes, and fitness by integrating perspectives from ecology, physiology, to molecular genetics and biochemistry (Nelson et al., 2019).

Uniting eco-physiological, population genetic and genomic methods can help to comprehensively understand mechanisms underlying species' diversity, adaptation and evolution (Hu et al., 2020). Coupling eco-physiology with both observational and experimental approaches provides opportunities to rapidly understand responses to environmental stressors (Sabovijević et al., 2022), whilst use of genetic methods, including comparative transcriptomics and proteomics, create novel discovery tools to provide a mechanistic understanding of adaptive diversification, particularly some genes

and proteins linked to traits with potential adaptability and evolvability (Voelckel et al., 2017).

The Research Topic “*Ecological and Genetic Insights into Seaweeds’ Diversity and Adaptation*” has brought together several articles reporting on new advances in this field.

An understanding of the mechanisms underpinning seaweed tolerance and adaptation to environmental variables is a prerequisite to maintain, conserve, restore, and breed new cultivars of commercial seaweeds. The contribution “*Calcium-Calmodulin-Involved Heat Shock Response of Neoporphyra haitanensis*” by Zheng et al. highlighted the important role of Ca²⁺-CaM signal transduction in the edible seaweed *N. haitanensis* (synonym: *Pyropia haitanensis*) responding to heat stress. In particular, Ca²⁺-CaM interacts with phosphatidylinositol (PI) signaling system to trigger heat shock proteins (HSPs) to maintain protein homeostasis, regulate the transport of substances into and out of mitochondria, and activate glycolysis to provide energy. This case study used multiple research methods, including eco-physiological experiments, transmission electron microscopy, molecular biology (e.g. Quantitative Real-Time PCR and yeast two-hybrid assay) and transcriptome sequencing, providing new mechanistic understanding of whether and how seaweeds respond and adapt to a changing environment.

Another contribution “*The mechanism of maintaining intracellular homeostasis in the red alga Pyropia haitanensis under hyposaline stress*” by Wen et al. identified some key proteins and metabolites in *P. haitanensis* adapting to hyposaline stress using proteomics and targeted metabolomics. The response process involved protein synthesis and processing, fatty acid and energy metabolism, and protein folding and stability. They also found that glycolysis was the main energy supply pathway under hyposaline stress, providing additional insights into metabolic adaptation to eutrophicated coastal waters.

Sexual and asexual reproductions have different effects on selection efficacy in the wild, enabling natural populations to have dissimilar genetic diversity, local adaptability and evolvability (Hu et al., 2020; Simón-Porcar et al., 2021). The publication “*Genomic consequences and selection efficacy in sympatric sexual versus asexual kelps*” by Vranken et al. examined the genomic consequences of sympatric sexual and clonal (asexual) morphs of the kelp *Ecklonia radiata* in western Australia by using genome-wide single nucleotide polymorphisms (SNPs). They not only confirmed significant asexual reproduction in clonal populations, but also found sexual reproduction in the clonal morph as well as interbreeding between sexual and clonal morphs through co-ancestral analysis and crossing experiments. The decreased selection efficacy and the maladaptation of clonal populations to local environment hint at high vulnerability of *E. radiata* to environmental changes.

Intertidal seaweeds are periodically exposed to drastic changes in active solar radiation, implying the potential existence of photosynthetic adaptation. The contribution “*Xanthophyll cycle-related non-photochemical quenching protects Sargassum thunbergii from high light-induced photoinhibition*” by Nan et al. examined the photosynthetic performance and xanthophyll cycle activity of *S. thunbergii* in response to high light using chlorophyll fluorescence and high-performance liquid chromatography (HPLC). They found that the sustained high light induced the down-regulation of

photosystem II (PSII) activity and the increase in non-photochemical quenching (NPQ), and the latter is highly correlated to the xanthophyll cycle. These combined results further indicate that xanthophyll cycle-induced NPQ can protect *S. thunbergii* from high light stress.

The contribution “*Deep genetic divergences and geographic distribution of the red algal genus Caulacanthus (Gigartinales)*” by Yang and Kim applied multi-loci markers based phylogenetic analysis and found at least seven species with deep divergence in the turf-forming red alga *Caulacanthus*, which currently includes three accepted species (*C. okamurae* Yamada, *C. salifugus* A. B. Cribb, and *C. ustulatus* (Turner) Kützing). This previously underestimated intra-specific lineage diversity indicates a strong geographic subdivision, possibly stemming from a long-term geographic discontinuity and limited genetic exchange. The proposed independent evolutionary patterns in the genus *Caulacanthus* imply that allopatric diversification events are likely common in other seaweed species.

The contribution “*A review of reproduction in the seaweed genus Fucus (Ochrophyta, Fucales): Background for renewed consideration as a model organism*” by Hatchett et al. comprehensively summarized reproductive characteristics of the brown genus *Fucus* as a model species for studying reproduction biology. Several other unique characteristics of *Fucus*, such as gamete structure, selfing (self-fertilization) and reproductive strategies, free-living individuals with morphological variability (ecads) formed by hybridization and polyploidy, and evolution of diplontic life cycle, also offer great opportunities for studying adaptation and evolution by combining genetic, molecular, and multi-omics (e.g. transcriptome, metabolome and proteome) and manipulated eco-physiological approaches considering the current ongoing and future predicted climate change.

There is still a huge gap in the link between ecology and genetics, but this Research of Topic reveals the diversity of perspectives required to enable us to understand adaptation and evolution of seaweeds, and provides a good example of the integration of multidisciplinary approaches that may help to uncover the underpinning mechanism associated with changing climate.

Author contributions

Z-MH: Funding acquisition, Supervision, Validation, Writing – original draft, Writing – review & editing, Conceptualization. MS: Funding acquisition, Validation, Writing – review & editing, Conceptualization. CX: Validation, Writing – review & editing, Conceptualization. YM: Validation, Writing – review & editing, Conceptualization. GW: Validation, Writing – review & editing, Conceptualization. TB: Validation, Writing – review & editing, Conceptualization.

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Conflict of interest

The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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