



ALGAL MODEL SPECIES FOR ADVANCING BIOLOGICAL SCIENCES

Algae are not only responsible for a significant proportion of global annual primary productivity, but they also represent a polyphyletic group of tremendously diverse photosynthetic organisms occupying most habitats on Earth which benefit from sunlight (e.g., Brodie et al. 2017, Strassert et al. 2021). As some species have lost their ability to photosynthesize, they extend their global distribution even further to environments that are secluded from solar irradiance (Kamikawa et al. 2022). The adaptive radiation of algal species is accompanied by an almost infinite number of morphotypes from microbial species to giant kelp forming underwater forests (Brodie et al. 2017). However, the unifying concept shared by all algae is a series of endosymbiotic events, which are responsible for the evolution of diverse lineages shaped by the nature of the endosymbionts and their hosts (e.g., Yoon et al. 2002, Archibald 2015, Burki et al. 2016). This ‘unit of selection’ holobiont concept extends to algal microbiomes and multicellular host-algal systems of which reef-building corals likely being the most prominent associations including an algal partner (e.g., Cirri and Pohnert 2019, Osman et al. 2020).

Thus, algae are tailored to answer some of the most fundamental questions in biology such as the cellular biological mechanisms underpinning morphotypes, the transition to multicellularity, symbiosis, aquatic photosynthesis, genetic recombination and reproduction, and the evolution of evolvability creating adaptive genetic diversity (e.g., Cock and Coelho 2011, Brodie et al. 2017). To address these questions, it makes sense to employ a model organism that grows well in the laboratory, is amenable to experimental work and genetically tractable due to the availability of molecular tools. Further essential characteristics include the availability of a genome sequence and comprehensive data banks as resources for providing insights into the basic biology of the organism (e.g., Falciatore et al. 2020). Thus, the choice of a model organism is not arbitrary but based on convenience and investment into tools and resources for studying a particular area of biology.

In the past, the above-mentioned attributes required for establishing model organisms in biology barely existed for algae. Hence, algae were under-represented and therefore most of the fundamental questions in biology were addressed using classical models such as yeast, *Escherichia coli*, and *Caenorhabditis elegans* despite their shortcomings (e.g., Hunter 2008). Those standard models only very sparsely covered the global biodiversity, and they therefore were likely not most suitable for addressing questions related to evolution and biodiversity and especially photosynthetic life in aquatic systems (e.g., Russell et al. 2017, Falciatore et al. 2020).

The advent of “omics” technologies at the beginning of this century provided a step change for developing algal species into model organisms (Fig. 1). Unicellular algae with small genomes for which a wealth of biological information was already available prior to their genomes and transcriptomes spearheaded the establishment of algal model organisms (e.g., Armbrust et al. 2004, Derelle et al. 2006, Merchant et al. 2007, Bhattacharya et al. 2013). Genomes of multicellular algae followed suit but with initial focus on smaller, more tractable species for the reasons mentioned above (e.g., Cock et al. 2010, Ye et al. 2015, Brawley et al. 2017). The availability of the first algal genomes laid the foundation for developing novel molecular tools with CRISPR/Cas-based genome editing likely being the most impactful tool (e.g., Jiang et al. 2014, Hopes et al. 2016, Nymark et al. 2016, Badis et al. 2021). Further developments of these CRISPR/Cas tools in recent years have made some algal species as genetically tractable as well-established models in biology (e.g., Moosburner et al. 2020, Sizova et al. 2021, Belshaw et al. 2022). Although significant progress has also been made concerning the development of biological resources and data banks for algae (e.g., Maheswari et al. 2008, Vandepoele et al. 2013, Grigoriev et al. 2021), they are not yet matching those of well-established model organisms in terms of their

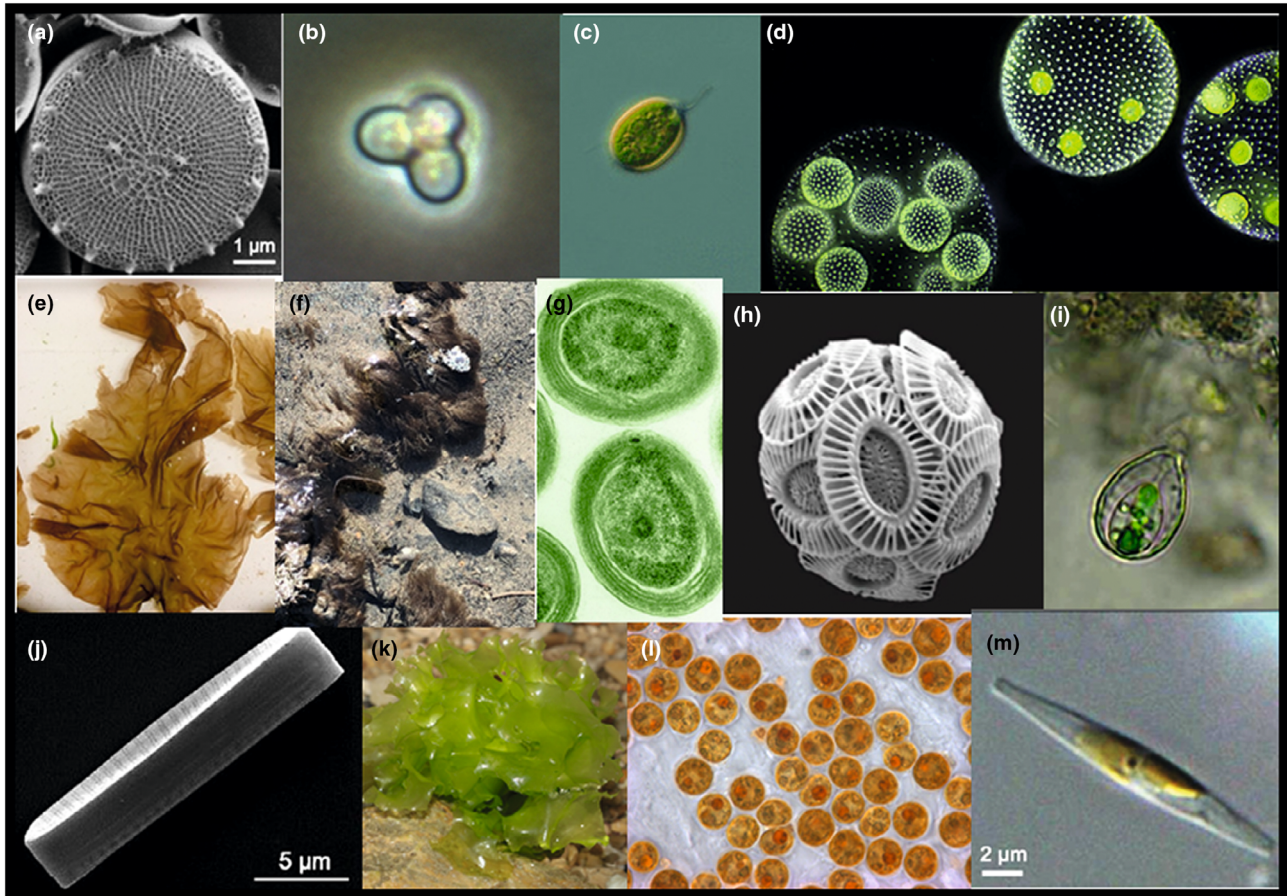


Fig. 1. Selected model species in phycology. (a) *Thalassiosira pseudonana* (Bacillariophyta; Falcitore et al. 2020); (b) *Cyanidioschyzon merolae* (Rhodophyta; User:NEON_ja, CC BY-SA 3.0); (c) *Chlamydomonas reinhardtii* (Chlorophyta; PROYECTO AGUA**/** WATER PROJECT, CC BY-NC-SA 2.0); (d) *Volvox* (Chlorophyta; Frank Fox, CC BY-SA 3.0 DE); (e) *Porphyra umbilicalis* (Rhodophyta; akinisbet, some rights reserved (CC BY-NC)); (f) *Ectocarpus siliculosus* (Phaeophyta; Susan J. Hewitt, some rights reserved (CC BY-NC)); (g) *Prochlorococcus marinus* (Cyanophyta; Luke Thompson from Chisholm Lab and Nikki Watson from Whitehead, MIT, CC0); (h) *Emiliana huxleyi* (Haptophyta; Gerecht, Andrea; Supraha, Luka; Langer, Gerald; Henderiks, Jorijntje, CC BY 3.0); (i) *Paulinella chromatophora* (Cercozoa; J. Van Etten and D. Bhattacharya); (j) *Fragilariopsis cylindrus* (Bacillariophyta; Falcitore et al. 2020); (k) *Ulva lactuca* (Chlorophyta; Holger Krisp, CC BY 3.0); (l) *Symbiodinium microadriaticum* (Dinophyta; Todd C. LaJeunesse, CC BY-SA 2.0); (m) *Phaeodactylum tricorutum* (Bacillariophyta; Falcitore et al. 2020).

diversity and comprehension (e.g., Rhee et al. 2003, Chen et al. 2005, Keseler et al. 2011).

The Journal of Phycology is publishing a series of special articles to provide insights into the latest developments of algal models, genomes, and their use to address fundamental questions in biology. Each article will introduce an algal model species, links to key resources, the latest developments, and future areas of research.

I acknowledge the School of Environmental Sciences at the University of East Anglia for support and all authors who have agreed to contribute to this new series of special articles.

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