

## Editorial

Macroalgae with their simple morphologies, rampant evolutionary convergence, extensive phenotypic plasticity in response to environmental factors, and incompletely understood life histories owing in part to alternation of heteromorphic generations have long frustrated biologists tasked with providing meaningful identification. Even for the specialist confronted with exclusively vegetative material (reproduction typically betraying ordinal and familial affinities), or even with reproductive material when considering species within a genus, this can be a challenging and at times intractable task. The microalgae share all of the previous problems with the macroalgae, but have the added complexity of being small such that the diagnostic features are observable only through microscopy. For many lineages and geographic regions dichotomous keys are not even available for microalgae and where they do exist may only take the researcher to the level of species complex or genus.

Among others, it is because of the previous challenges that algal taxonomists have become increasingly reliant on molecular tools in the last 25 years for routine identifications, species discovery and other taxonomic research. Although a step in the right direction, Saunders (2005), in championing the barcode vision (minimalist approach to marker use; Hebert *et al.*, 2003a) to the algal community considered that the tendency for different laboratories to focus on their preferred markers was generating an unsatisfactory shortcoming in ongoing efforts, i.e., the lack of universally applied markers was limiting the development of a global system for algal identification, which would facilitate comparisons among research groups. This was not an argument against the obvious need to develop and compare multiple and divergent molecular markers for phylogenetic and taxonomic studies, but a plea to colleagues that consensus on a standard marker among all researchers, for the purposes of quick and accurate species identification, would be a powerful tool for the rapid assignment of specimens to known species, as well as generate collateral data on the ecological and biogeographical limits of species.

The new field of DNA barcoding has explicitly recognized the previous shortcomings and championed the use of ~670 bp of the mitochondrial marker cytochrome c oxidase subunit 1 (COI-5P) to establish a global comparative genetic database. In a pair of foundation publications Hebert *et al.* (2003a, 2003b) established the utility of COI-5P as a "core of a global bio-identification system for animals" reporting that this gene could be used to assign unknown species to higher-level taxa, and where comprehensive databases exist species level assignments were possible. Rather serendipitously for the red (e.g., Saunders, 2005, 2008; Robba *et al.*, 2006; Clarkston & Saunders, 2010; Le Gall & Saunders, 2010) and brown (e.g., Kucera & Saunders, 2008; McDevit & Saunders, 2009, 2010) macroalgae, the COI-5P marker was very quickly established as a suitable region for the purposes of DNA barcoding and work in these organisms has blossomed. This fortuitous start to DNA barcoding in the algae was not, however, to carry over into the other lineages, or indeed other major groups of life (notably the fungi and land plants). And thus the dream of a single universal barcode has, not surprisingly, given way to the new reality that a single barcode marker will not meet the needs of the entire biodiversity community. This is especially true for the algae, which fall out on most of the major lineages on the eukaryote tree of life (Hampel *et al.*, 2009). Regardless, the mandate to use as few molecular markers as is feasible to generate a global identification system for eukaryotic species

remains a worthy pursuit and the primary objective of the global barcode community (<http://www.barcodeoflife.org/> and <http://ibol.org/>).

In this special volume we have papers that both use DNA barcoding to resolve issues of taxonomic concern, as well as others dedicated to the ongoing task of identifying the best markers to include the various algal lineages in the global barcoding initiative. This volume starts with three manuscripts in which DNA-barcoding is used to explore diversity within selected florideophycean taxa on restricted geographical scales. Rueness (this issue) presents barcode data for a hand full of species mainly from Europe and takes advantage of available data from North American samples to uncover cryptic diversity in *Batrachospermum helminthosum*, report a range extension of *Ptilota gunneri*, highlight geographic separation between populations of *Plumaria plumosa*, and present sequences of three invasives species (*Antithamnion hubbsii*, *Gracilaria vermiculophylla* and *Heterosiphonia japonica*). Kim *et al.* (this issue) built a barcode library for the Korean Gracilariaceae – a taxon of economic interest. They used the DNA barcode to recognize five species that are difficult to distinguish based on morphological data including *Gracilaria incurvata*, *Gracilaria parvispora*, *Gracilaria textorii*, *Gracilaria vermiculophylla*, and *Gracilariopsis chorda*. These commercial species can now be identified based on their DNA barcode. Le Gall and Saunders (this issue) conducted a biodiversity survey of the Canadian and French floras and present their results for the Nemaliales. They uncovered cryptic diversity in the supposedly cosmopolitan species *Nemalion helminthoides* restricting its distribution and resurrecting *Nemalion lubricum* and *Nemalion multifidum* for the Mediterranean and boreal species, respectively. Manghisi *et al.* (this issue) highlighted the introduction of an invasive species, *Agardhiella subulata*, within a coastal lagoon in Sicilia. They used the DNA barcode to track the origin of this introduction and demonstrated that young plantlets of *Agardhiella* were growing on oyster shells that were imported from the Netherlands to Sicilia.

A few papers in this issue focus on comparing the efficiency of COI, a relatively new marker in algal molecular systematics, with more classical markers. Freshwater *et al.* (this issue) compare the utility of COI and *rbcL* to delineate species of the Gelidiales. The COI gene, which displays more variable sequence and a wider barcode gap, outperformed the *rbcL* in delimiting closely related species and the study revealed cryptic species within the genus *Pterocliadiella*. Sherwood *et al.* (this issue) compared COI with LSU and UPA for 290 specimens of Florideophyceae collected during the Hawaiian Rhodophyta Biodiversity Survey. Their analyses confirmed that COI is the most variable marker and showed that barcode data, combined with other genes acquired in the context of a floristic survey, have some phylogenetic signal that can be used to improve resolution at deeper nodes. Mattio and Payri (this issue) explored the utility of nuclear ITS-2, a portion of the chloroplastic *RubisCO* operon, a mitochondrial spacer (mtsp), COI and *cox3* to delineate 13 closely related species of the highly plastic brown algal genus *Sargassum* and showed that the mitochondrial markers (COI and *cox3*) were the most useful for this purpose.

The previous papers establish that COI is an efficient DNA-barcode marker for red and brown algae; however, this marker is not suitable for green algae. This issue includes two papers which explore potential markers (*rbcL*, *tufA*, UPA, LSU, SSU, ITS) for marine (Saunders & Kucera, this issue) and freshwater (Hall *et al.*, this issue) green algae. Both studies stress the need for developing a barcode marker for green algae and indicate that none of the tested markers were ideal, however, *rbcL*, ITS2 and *tufA* were the most promising (Hall *et al.*, this

issue) and Saunders & Kucera (this issue) recommended the use of *tufA* to standardize barcode initiatives in the Chlorophyceae.

Finally, Mann *et al.* (this issue) present an extensive review of the state of DNA-barcoding in diatoms thoroughly exploring the advantages, limitations and challenges in developing barcoding for these organisms. Reaching beyond the scope of their target organisms, many of the issues that they discuss can be extended to all algae if not all protists.

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