

DNA Taxonomy: Bar Coding and Species Delineation

3.A1

DNA-BASED SPECIES DELIMITATION IN ALGAE

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Species are basic units in studies of biodiversity, systematics, biogeography and ecology but their delimitation has been relatively neglected methodologically. Despite the wide acceptance of the idea that species represent fundamental units of biological organization, there has been a great deal of disagreement with regard to the criteria used to delimit species, which has led to a proliferation of different species concepts. More recently important conceptual progress has been made in thinking about species concepts. By treating species as separately evolving metapopulation lineages and with recent advances in methods for DNA-based species delimitation, formal analyses of species boundaries have become possible. DNA-based taxonomy provides a convenient and reliable tool for species circumscription and delineation, especially in organisms in which morphological discrimination is difficult or impossible, such as many algal taxa. Here we discuss recent advances in DNA-taxonomy of marine macro-algae. We present a number of case studies in green (*Boodlea*, *Bryopsis*), brown (*Dictyota*) and red (*Portieria*) algae and show how DNA-taxonomy can provide new insights into morphological evolution, biogeography and speciation of seaweeds.

3.A2

ADVANTAGES, LIMITATIONS AND CHALLENGES IN DEVELOPING DNA-BARCODING FOR ALGAE

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Identification of algae is a challenging task, which requires experience, skills, access to the literature and, in some cases, to culture facilities. In the last 25 years, phycologists have relied increasingly on molecular tools for accurate identification and species delineation. Since 2003, the DNA-barcode approach standardized and scaled up the practices of molecular taxonomy. The standard barcode marker for animals, the mitochondrial cytochrome c oxidase subunit 1 (CO1-5P), has proven useful for both red and brown algae. However this marker is not universal for all algae and novel markers still have to be tested in many photosynthetic lineages of the tree of life. In addition to the challenge of developing markers, it is mandatory to achieve a comprehensive library of barcode data for algae.

3.A3

THE ITS2 DATABASE: SEQUENCE-STRUCTURE PHYLOGENETICS AND DISTINGUISHING SPECIES

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Ten years ago two hypotheses initiated the ITS2 Database: (1) Compensatory base changes in the internal transcribed spacer 2 (ITS2) secondary structure correlate with the biological species concept. (2) ITS2 secondary structure information enlarges the taxonomic applicability for the ITS2 from subspecies to orders and beyond – and improves accuracy and robustness when reconstructing ITS2 phylogenies. A pipeline consisting of the ITS2 Database, the software tools 4SALE and ProfDistS enabling one to test those hypotheses on a large scale basis is presented – evaluations, phycological case studies and further aspects concerning ITS2 and/or RNA sequence-structure phylogenetics (phylochips, barcoding, 3D structures) are discussed. Exploring the phycocosmos, this talk associates sequence-analysis