

DNA-BASED SPECIES DELIMITATION IN DIATOMS

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Species are basic units in studies of biodiversity, systematics, biogeography and ecology. We all accept the idea that species represent fundamental units of biology. Because there has been a great deal of disagreement with regards to the criteria used to delimit species this has led to a proliferation of different species concepts. Among the diatoms the morphological species concept is that most commonly used. However, more and more cryptic species have been revealed and many of these cryptic species are supported by a biological species concept through breeding experiments. The phylogenetic species concept has revealed many paraphyletic taxa, which some workers are reluctant to accept. However in nearly every case where paraphyletic taxa have been discovered, good morphological genera and species would have to be disregarded to accept that the phylogenetic species must be monophyletic. By treating species as separately evolving metapopulation lineages formal analyses of species boundaries become possible. Using metapopulations as the evolving unit, it is possible to demonstrate that evolution proceeds from polyphyly to paraphyly to monophyly. I present a number of case studies in diatoms at the class and generic level to show how DNA-taxonomy can provide new insights into morphological evolution, biogeography and speciation of diatoms and how the recognition of paraphyletic taxa is unavoidable because evolution is not a static process.