Phylogeny and species delineation in the marine diatom Pseudo-nitzschia (Bacillariophyta) using cox1, LSU, and ITS2 rRNA genes: A perspective in character evolution

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Abstract

Analyses of the mitochondrial cox1, the nuclear-encoded large subunit (LSU), and the internal transcribed spacer 2 (ITS2) RNA coding region of Pseudo-nitzschia revealed that the P. pseudodelicatissima complex can be phylogenetically grouped into three distinct clades (Groups I-III), while the P. delicatissima complex forms another distinct clade (Group IV) in both the LSU and ITS2 phylogenetic trees. It was elucidated that comprehensive taxon sampling (sampling of sequences), selection of appropriate target genes and outgroup, and alignment strategies influenced the phylogenetic accuracy. Based on the genetic divergence, ITS2 resulted in the most resolved trees, followed by cox1 and LSU. The morphological characters available for Pseudo-nitzschia, although limited in number, were overall in agreement with the phylogenies when mapped onto the ITS2 tree. Information on the presence/absence of a central nodule, number of rows of poroids in each stria, and of sectors dividing the poroids mapped onto the ITS2 tree revealed the evolution of the recently diverged species. The morphologically based species complexes showed evolutionary relevance in agreement with molecular phylogeny inferred from ITS2 sequence-structure data. The data set of the hypervariable region of ITS2 improved the phylogenetic inference compared to the cox1 and LSU data sets. The taxonomic status of P. cuspidata and P. pseudodelicatissima requires further elucidation.

Keywords: Pseudo-nitzschia; cox1; character evolution; molecular markers; phylogeny.