PHYLOGENY AND SPECIES DELINEATION IN THE MARINE DIATOM *PSEUDO-NITZSCHIA* (BACILLARIOPHYTA) USING *COX1*, LSU, AND ITS2 RRNA GENES: A PERSPECTIVE IN CHARACTER EVOLUTION[1]

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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