

THE DIATOM PHYLOGENY AS INFERRED FROM NSSU AND 6 CHLOROPLAST GENES

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We have sequenced the nuclear SSU and 6 chloroplast genes for over 200 diatoms and *Bolidomonas*, yielding an aligned dataset of about 10,000 nucleotides. Here we report on our preliminary analyses of this dataset, and give an overview of the diatom phylogeny. We specifically test the placement of several diatoms of interest, including species used as models in genomic studies (*Cyclotella nana* and *Phaeodactylum tricornutum*), and diatoms whose placement in the diatom phylogeny has been particularly problematic or controversial (e.g., *Attheya*, *Striatella*). We find increasing support that the so-called radial centrics are not monophyletic, but rather are a grade. Monophyly of the so-called polar diatoms remains equivocal. We discuss the implications of this tree for the diatom classification and diatom origin. Previous inferences about the Ur-diatom as a small, perhaps siliceous flagellate, have assumed that the outgroup represented the ancestral morphology. Making that same inference by optimizing characters on our phylogeny (and on other molecular phylogenies), yields a very different view, suggesting that the Ur-diatom may have been highly elongate and perhaps even filamentous.