ORAL PRESENTATION

THE DIATOM PHYLOGENY: STATUS AND PROSPECTS

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Nuclear SSU gene data have predominately returned a result in which radially organized centric diatoms graded into bipolar or multipolar organized centrics which themselves graded into pennate diatoms. Recent hypotheses, however, have proposed that each of these groups was monophyletic. In fact, SSU does not robustly resolve any of these competing ideas. Organellar and developmental anatomy of the diatoms remains unknown for the vast majority of diatoms, but seems to align taxa in much the same way as the SSU data. The greatest amount of existing molecular data besides SSU has been gathered from the *rbc*L gene. Most *rbc*L data has been gathered in studies of ordinal and lower taxa. Our lab has added *rbc*L and *psb*C data (chloroplast genes), seeking to fill in obvious gaps. Results are promising, although the trees returned to date do not reflect either traditional classifications or the SSU trees, possibly simply due to low signal to noise in the chloroplast data rather than some fundamental bias. This low signal to noise may be overcome by the addition of genes and taxa. There is broad congruence between biostratigraphic distributions of diatoms and molecular phylogenies, but long ghost lineagaes are implied both by molecular phylogenies and traditional classifications. Some of the gaps may reflect large gaps in taxon sampling. The next century will see the use of entire genomes in phylogenetic inference. There are already examples in higher animals of the use of these data to infer large scale phylogenies, and already cautionary tales that such data are themselves not a panacea. In particular, taxon sampling remains an issue. A major challenge to diatomists of the 21st century will be to integrate these new technologies with traditional explorations of diatom diversity, and to formally integrate the apparent high number of extinct taxa that would appear to occupy the basal and middle of the diatom tree.