

sampling to enable Lagrangian tracking and near-real time analyses of a bloom population's genomic and biochemical signatures.

Bold Talks

T1. SPECIES DELIMITATION IN THE *CAULERPA RACEMOSA/PELTATA* COMPLEX (CHLOROPHYTA, CAULERPACEAE)

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The rampant morphological plasticity displayed by many species of *Caulerpa* has resulted in numerous infraspecific taxa and synonymies. This is most evident in the *C. racemosa/peltata* complex, which currently has more than 30 described varieties and forms. Although recent molecular studies have indicated that many of these infraspecific taxa deserve recognition at the species level, no major taxonomic revisions have been made. The present study investigated molecular and morphological variation within and between taxa currently assigned to the complex, with emphasis on the Indo-pacific region. Molecular variation was assessed by analyses of partial *tufA*, *rbcL* and *rps3-rpl16* gene sequences. Our results revealed that the *C. racemosa/peltata* complex represents at least 10 distinct genetic species, with morphology alone unable to delimit many of these species. *Caulerpa peltata* and *C. racemosa* vars. *laetevirens* and *turbinata* were found to represent environmentally induced forms of a single, earlier-described species, and thus *C. chemnitzia*, currently regarded as a synonym of *C. racemosa* var. *turbinata*, is reinstated. *Caulerpa cylindracea*, *C. lamourouxii*, *C. macrodisca*, *C. nummularia* and *C. oligophylla* are also reinstated and three new species proposed.

T2. WHAT DO CHLOROPLAST GENOMICS TELL US ABOUT EUGLENOID PHYLOGENIES?

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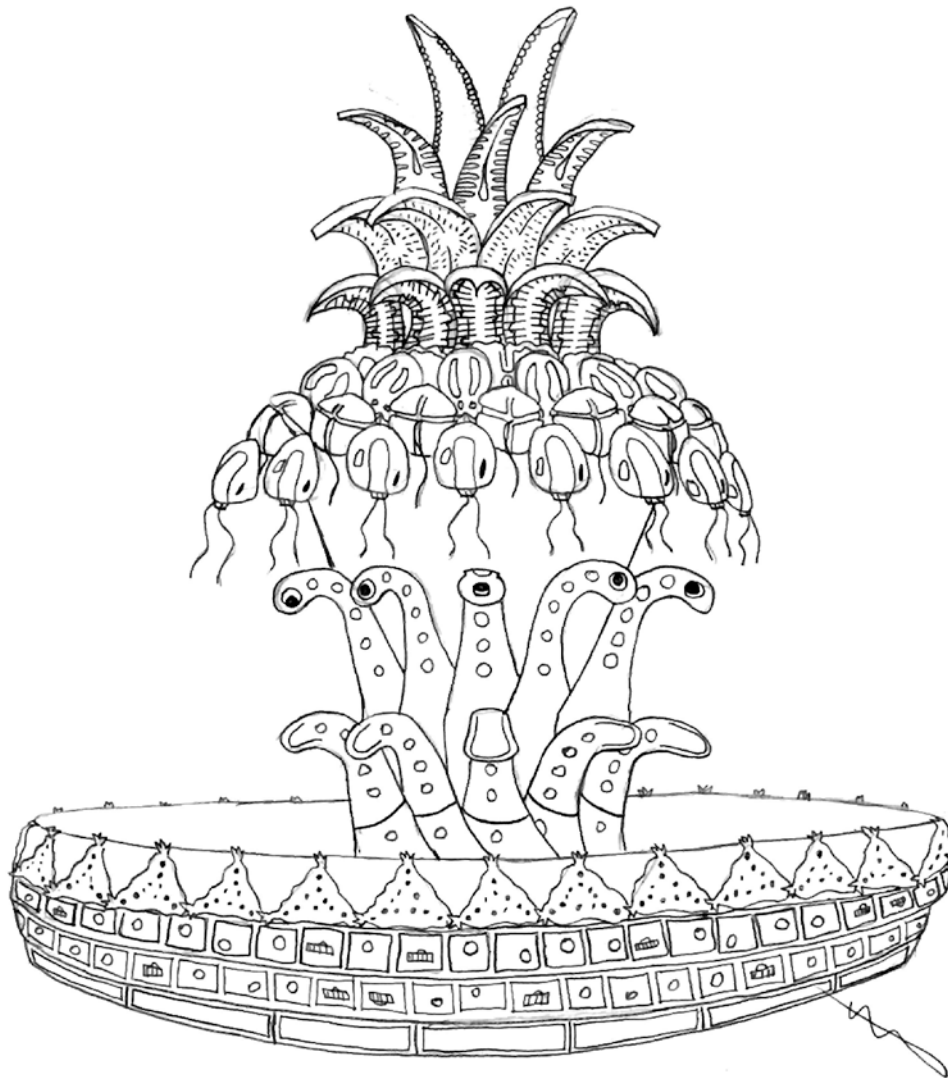
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Current understanding of photosynthetic euglenoid phylogenetics is largely based on 18S, 28S, 16S and 23S rRNA genes. Recent works sequencing the chloroplast genomes of photosynthetic euglenoids have enabled the phylogenetic analysis to be expanded and include a large number of chloroplast-encoded genes. A dataset including 8 photosynthetic euglenoid taxa and 11 representative green algal taxa was created and analyzed for over 60 genes using both ML and Bayesian analyses. The resulting tree topologies were consistent with previous studies of both chloroplast-encoded and nuclear-encoded rRNA genes, placing the Eutreptiales at the base of the euglenoid lineage followed by the divergence of *Discoplastis* prior to *Euglena*, *Colacium*, and *Strombomonas*. However, the new phylogenetic trees demonstrated greater support within the euglenoids than has previously been seen. Additionally, the basal position of *Pyramimonas* relative to the photosynthetic euglenoid taxa strongly supports this taxon as an extant representative of the euglenoid green algal chloroplast donor and implies that acquisition of the chloroplast was the result of a single endosymbiotic event.

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