TOWARD RESOLUTION OF THE "FUZZY NODES"
IN GREEN PLANT PHYLOGENY


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The tree of life is inherently fractal. Look closely at one lineage of a phylogeny and it dissolves into many separate lineages, and so on down to a very fine scale. There is now a great body of phylogenetic research that has provided numerous tools applicable at particular, usually fairly constrained, scales. These tools have left many phylogenetic questions unanswered. We think these questions will remain unanswered until it is possible to do analyses across multiple scales.

The green plant lineage represents the most suitable system for this research because it is one of the oldest and most diverse branches of the tree of life and it contains good examples of the known phylogenetic problems. Investigations on it may draw on a tradition of interdisciplinary collaborative research, facilitated by the Green Plant Phylogeny Research Coordination Group (GPPRCG, "Deep Green").

Our overall objective is to resolve the primary pattern of evolutionary diversification among green plants, and establish a model for doing so that will be applicable to other groups of organisms with long evolutionary histories. We believe that a solid backbone based on genomic and ultrastructural data for selected exemplar taxa will enable the integration of previous and ongoing studies of many more taxa into a comprehensive picture of green plant phylogeny.

To achieve this objective, we will:

* complete a matrix of whole genome sequences for chloroplasts and mitochondria, and develop Bacterial Artificial Chromosome (BAC) nuclear genome libraries (when 1Cs ≤ 100Mb) for ~50 representatives of the critical deep-branching lineages of green plants (Fig. 1);
* produce a comprehensive set of comparable morphological and ultrastructural data for these same taxa;
* incorporate inferences from across the phylogenetic hierarchy in green plants using methods designed to permit scaling across studies.

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Figure 1. Outline phylogeny of the green plants, indicating the currently understood phylogenetic position for 51 candidate exemplar organisms (represented by generic names; see Table 1) and the higher-level taxa to which they are thought to belong. All branches are subject to further testing, but the best-supported branches with current data are indicated with a thick line, branches with some support are indicated with a thin line, and areas of the tree that remain controversial are indicated by labelled ovals. 1. Base of the land plants. 2. Base of the Chlorophyta. 3. Relationships among the siphonous algae and their placement in the Chlorophyta. 4. Base of the land plants. 5. Base of the ferns (moniliforms).

SPECIES
Nephrolepis ovaliscea
Pterosperma sp.
Chlorella sp.
Prototheca wickerhamii
Tetraselmis striata
Volvox carteri
Chlamydomonas reinhardii
Oltmannsellopsis viridis
Ignatius tetrasparsus
Halochlorococcus moorei
Ulothrix sp.
Acrochaete endoxaica
Bolbocellean proliiferum
Ulvula lactuca
Trentepohlia sp.
Blasia pusilla
Sphagnum palustre
Acetabularia acetabulum
Bornetella sphaerica
Mesostigma viride
Coleochaete orbicularis
Chara aspera
Klebsormidium flaccidum
Entransia sp.
Chlorokybus asbestos
Spirogyra sp.
Anthoceros sp.
Notothylas orbicularis
Sphaerocapsa sp.
Marchantia polymorpha
Blastia pusilla
Bazzania tricholata
Haplomitrium sp.
Sphagnum palustre
Takakia ceratophylla
Physcomitrella patens
Andreaea sp.
Tortula ruralis
Selaginella kraussiana
Isoetes engelmannii
Lycopodium lucidum
Equisetum hyemale
Psilotum nudum
Botrychium sp.
Angiopteris everta
Osmunda cinnamomea
Ceratopteris richardii
Marsilea quadrifolia