

# **Sequencing the Algal Tree of Life**

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July 2011

The work conducted by the U.S. Department of Energy Joint Genome Institute is supported by the Office of Science of the U.S. Department of Energy under Contract No. DE-AC02-05CH11231

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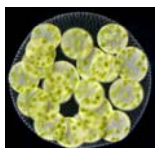
## SEQUENCING THE ALGAL TREE OF LIFE

Algae, defined as photosynthetic eukaryotes other than plants, constitute a major component of fundamental eukaryotic diversity. Acquisition of the ability to conduct oxygenic photosynthesis through endosymbiotic events has been a principal driver of eukaryotic evolution, and today algae continue to underpin aquatic food chains as primary producers. Algae play profound roles in the carbon cycle, can impose health and economic costs through toxic blooms, and are candidate sources for bio-fuels; all of these research areas are part of the mission of DOE's Joint Genome Institute (JGI). To date JGI has sequenced, assembled, annotated, and released to the public the genomes of 15 species and strains of algae, sampling most of the major clades of photosynthetic eukaryotes. With more algal genomes currently undergoing analysis, JGI continues its commitment to driving forward basic and applied algal science.

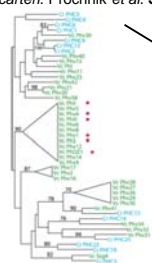
### Chlorophyceae

**Chlamydomonas** - The *Chlamydomonas* genome reveals the evolution of key animal and plant functions. Merchant *et al.* *Science* 2007.

**Volvox** - Genomic analysis of organismal complexity in the multicellular green alga *Volvox carteri*. Prochnik *et al.* *Science* 2010.



Comparative genomics between *Volvox* and *Chlamydomonas* associates multicellularity with expansion of perophorin extracellular matrix gene family.

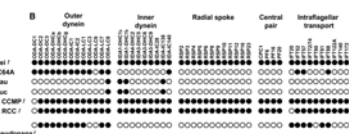


### Trebouxiophyceae

**Chlorella** - The *Chlorella variabilis* NC64A genome reveals adaptation to photosymbiosis, coevolution with viruses, and cryptic sex. Blanc *et al.* *Plant Cell* 2010.

**Coccomyxa** - Annotation released, manuscript under preparation.

**Asterochloris** - Undergoing annotation.

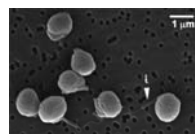


Conservation of meiotic and flagellar genes suggests cryptic sex in *Chlorella variabilis*.

### Prasinophyceae

**Ostreococcus** - The tiny eukaryote *Ostreococcus* provides genomic insights into the paradox of plankton speciation. Palenik *et al.* *PNAS* 2007.

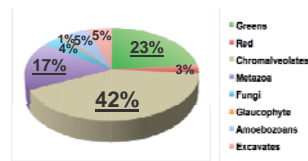
**Micromonas** - Green evolution and dynamic adaptations revealed by genomes of the marine picoeukaryotes *Micromonas*. Worden *et al.* *Science* 2009.



Intronic repeat elements exemplify divergence between two strains of *Micromonas*.

### Chlorarchniophyta

**Bigelowiella** - Annotation released, manuscript under preparation.

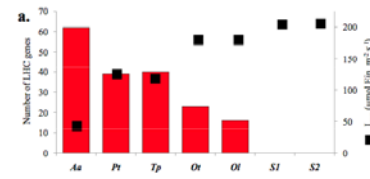
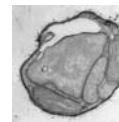


Phylogenomic analysis of *Bigelowiella* supports a Stramenopile-Alveolate-Rhizarian clade.

- John Archibald, personal communication.

### Pelagophyta

**Aureococcus** - Niche of harmful alga *Aureococcus anophagefferens* revealed through ecogenomics. Gobler *et al.* *PNAS* 2011.



Ecogenomics of *Aureococcus* correlates light-harvesting complex genomic expansion with adaptation to low-light environments.

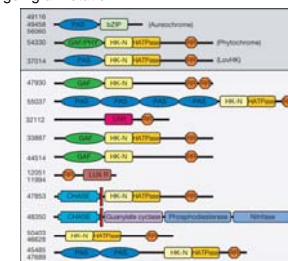
### Bacillariophyta

**Thalassiosira** - The genome of the diatom *Thalassiosira pseudonana*: ecology, evolution, and metabolism. Armbrust *et al.* *Science* 2004.

**Phaeodactylum** - The *Phaeodactylum* genome reveals the evolutionary history of diatom genomes. Bowler *et al.* *Nature* 2008.

**Fragilariopsis** - Annotation released, manuscript under preparation.

**Pseudo-nitzschia** - Undergoing annotation.

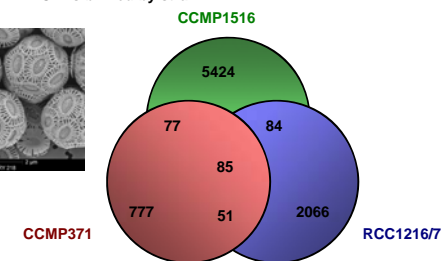
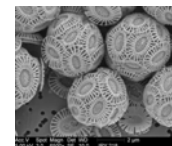


The *Phaeodactylum* genome includes many genes horizontally transferred from bacteria, including 2-component signaling systems.

### Haptophyta

**Emiliania** - Annotation released, manuscript under preparation.

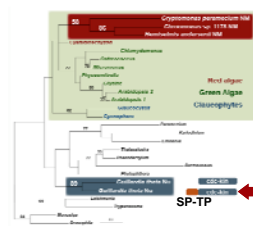
#### IV. ORFs binned by strain



Strain-specific genes suggest an *Emiliania* pan-genome.

### Cryptophyta

**Guillardia** - Annotation released, manuscript under preparation.



Some *Guillardia* nucleomorph functions are fulfilled by genes derived from the host, not transferred from the endosymbiont. - John Archibald, personal communication.