Sequencing the Algal Tree of Life

Alan Kuo¹, Igor Grigoriev¹

¹Lawrence Berkeley National Laboratory

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
DISCLAIMER

This document was prepared as an account of work sponsored by the United States Government. While this document is believed to contain correct information, neither the United States Government nor any agency thereof, nor The Regents of the University of California, nor any of their employees, makes any warranty, express or implied, or assumes any legal responsibility for the accuracy, completeness, or usefulness of any information, apparatus, product, or process disclosed, or represents that its use would not infringe privately owned rights. Reference herein to any specific commercial product, process, or service by its trade name, trademark, manufacturer, or otherwise, does not necessarily constitute or imply its endorsement, recommendation, or favoring by the United States Government or any agency thereof, or The Regents of the University of California. The views and opinions of authors expressed herein do not necessarily state or reflect those of the United States Government or any agency thereof or The Regents of the University of California.
Algae, defined as photosynthetic eukaryotes other than plants, constitute a major component of the Earth's biodiversity. They play profound roles in the carbon cycle, can impose health and economic costs through toxic blooms, and are candidate sources for biofuels. 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.

Phylogenomic analysis of Bigelowiella supports a Stramenopile-Alveolate-Rhizarian clade. - John Archibald, personal communication.

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

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

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

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

Strain-specific genes suggest an Emiliania pan-genome.