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## Recent Work

### **Title**

Fueling Future with Algal Genomics

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## **Fueling Future with Algal Genomics**

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## Algae for Energy and Environment

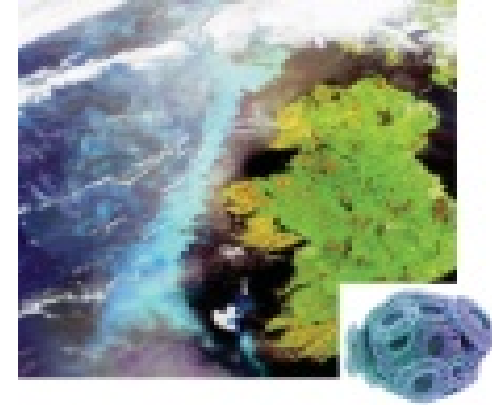
### Energy

50% of global photosynthesis  
Biomass for biofuels  
Model systems for plants



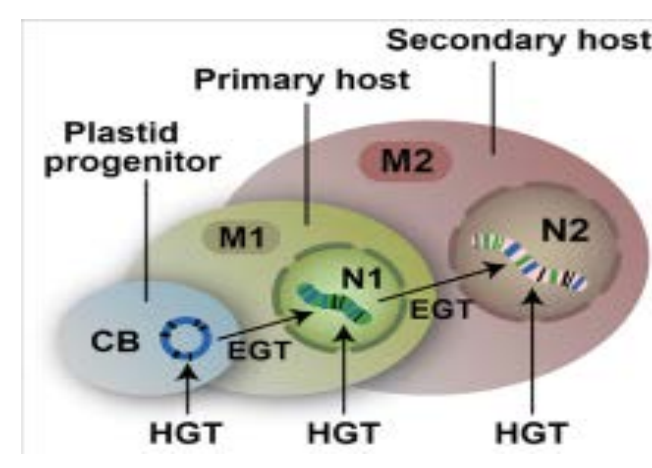
### Environment

Carbon fixation and cycling  
Biomineralization, biogeochemistry  
Blooms can be toxic, blooms can be HUGE



### Evolution

Very diverse, all over eukaryotic tree  
Photosynthesis acquired many times  
Endosymbiosis is a principal driver of evolution

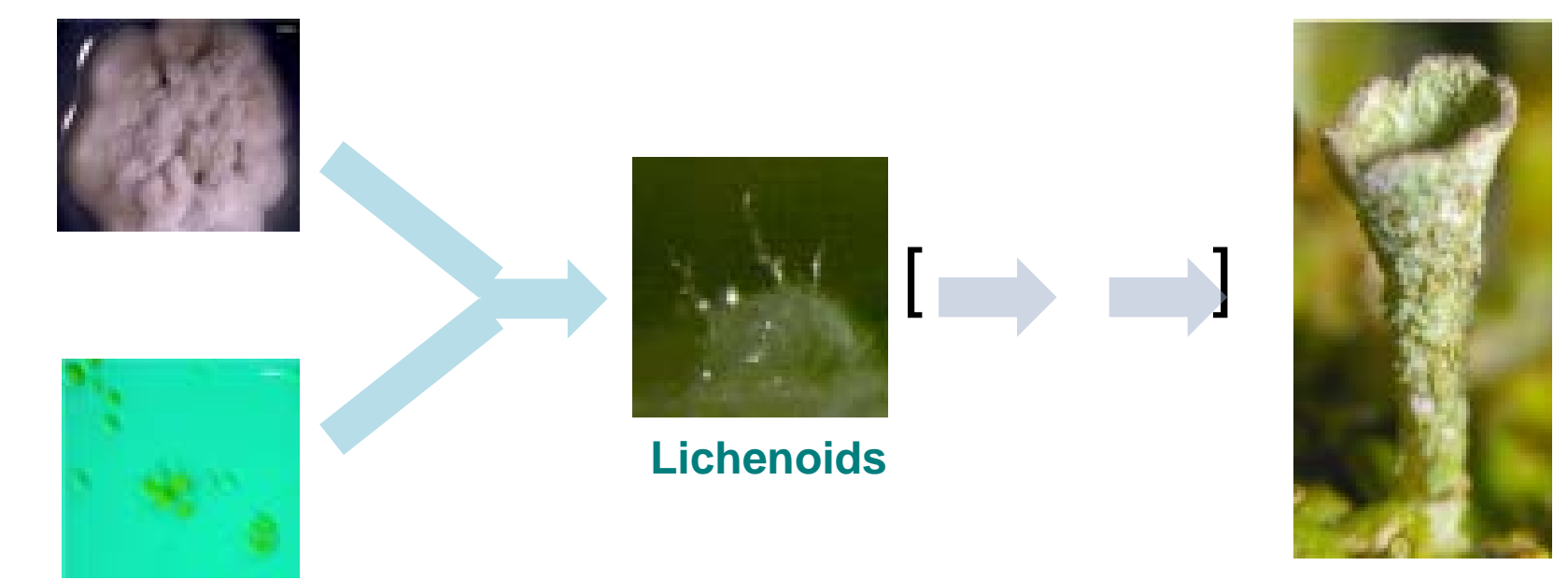


## Abstract

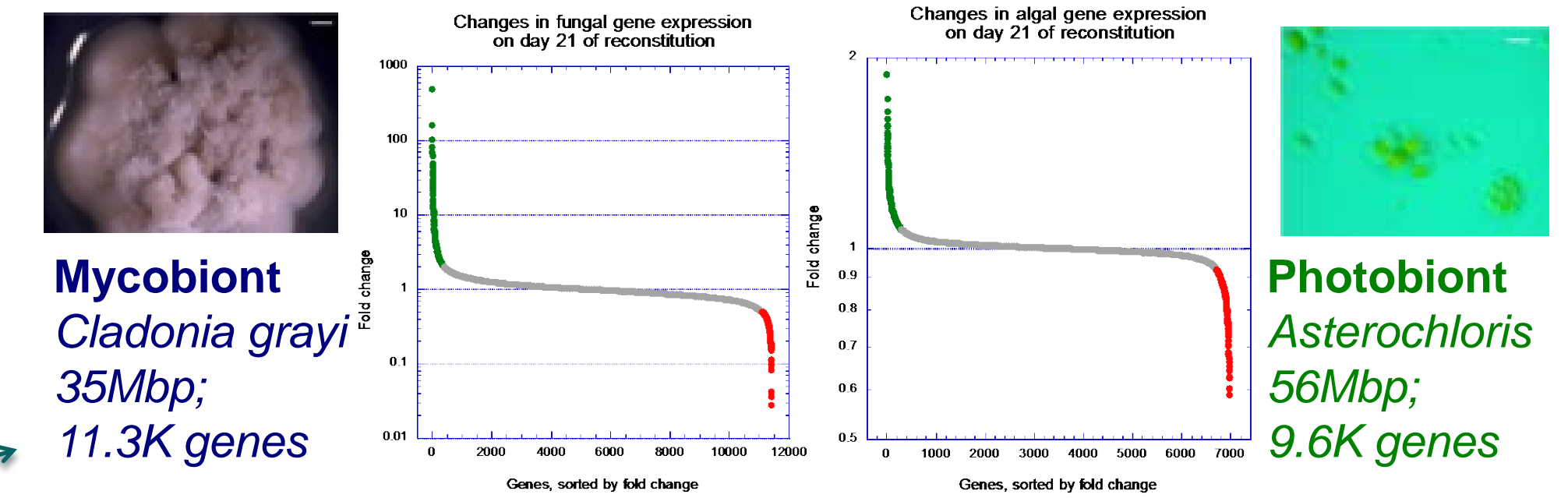
Algae constitute a major component of fundamental eukaryotic diversity, play profound roles in the carbon cycle, and are prominent candidates for biofuel production. The US Department of Energy Joint Genome Institute (JGI) is leading the world in algal genome sequencing (<http://jgi.doe.gov/Algae>) and contributes ¼ of the algal genome projects worldwide (GOLD database, 2012). The sequenced algal genomes offer catalogs of genes, networks, and pathways. The sequenced 'first of its kind' genomes of a haptophyte *E.huxleyi*, chlorarachniophyte *B.natans*, and cryptophyte *G.theta* fill the gaps in the eukaryotic tree of life and carry unique genes and pathways as well as 'molecular fossils' of secondary endosymbiosis. Natural adaptation to conditions critical for industrial production is encoded in algal genomes, for example, growth of *A.anophagefferens* at very high cell densities during the harmful algal blooms or a global distribution across diverse environments of *E.huxleyi*, able to live on sparse nutrients due to its expanded pan-genome. Communications and signaling pathways can be derived from simple symbiotic systems like lichens or complex marine algae metagenomes. Collectively these datasets derived from algal genomics contribute to building a comprehensive parts list essential for algal biofuel development.

## Algal Symbiosis: lichen (fungus+alga)

Genomics of lichen symbiosis, and its *in vitro* reconstitution.



Differences in gene expression in the lichenoids.



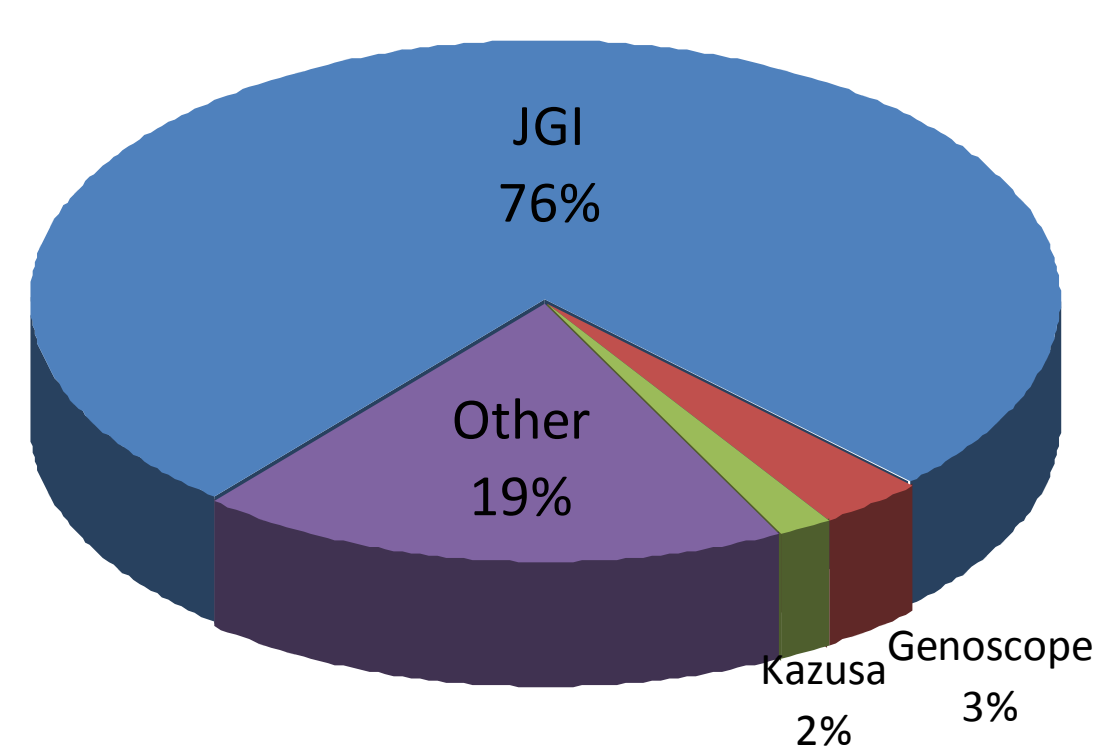
**Mycobiont**  
*Cladonia grayi*  
35Mbp;  
11.3K genes

**Photobiont**  
*Asterochloris*  
56Mbp;  
9.6K genes

PI: Danielle Armaleo, Duke University

## Algal Genomes Sequenced by JGI

### ALGAL GENOMES BY SEQUENCING CENTER



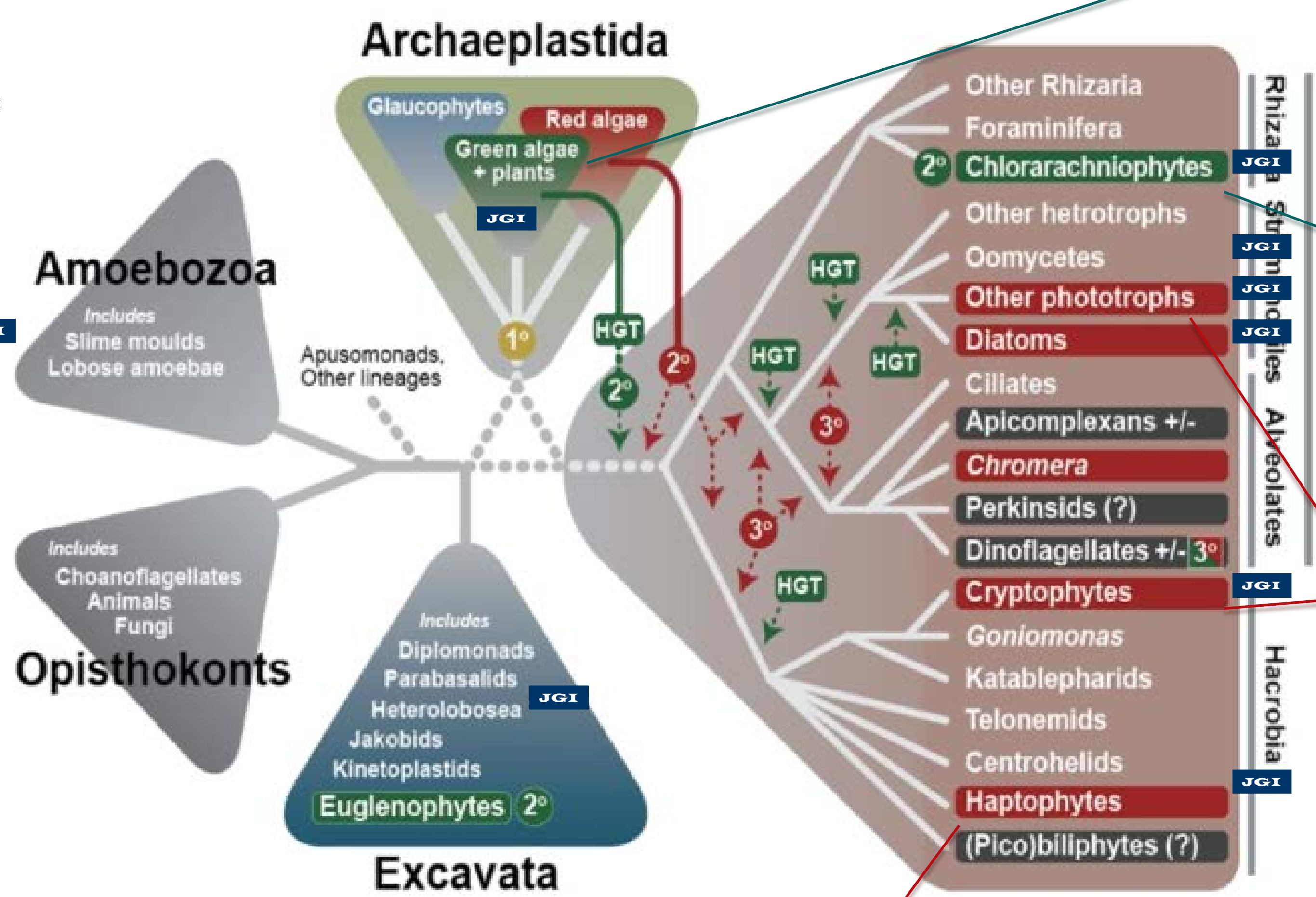
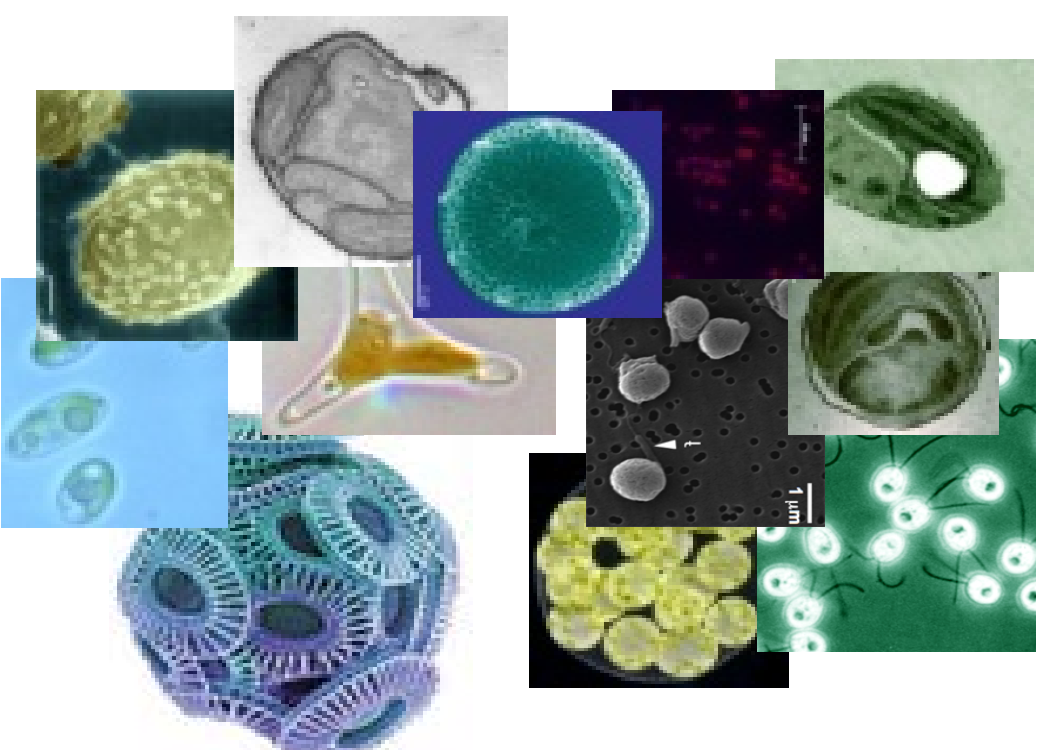
11 genomes published by JGI:

- Thalassiosira* (2004)
- Ostreococcus*, 2 sp. (2007)
- Chlamydomonas* (2007)
- Phaeodactylum* (2008)
- Micromonas*, 2 sp. (2009)
- Volvox* (2010)
- Chlorella* (2011)
- Aureococcus* (2011)
- Coccomyxa* (2012)

7 more genomes released:

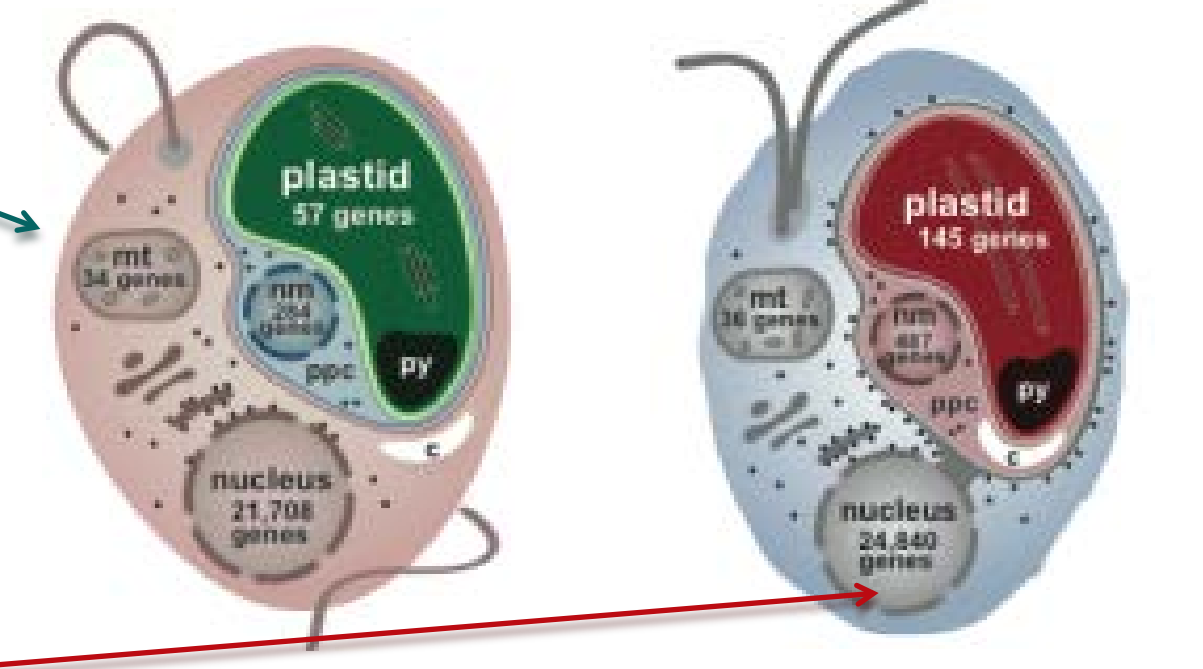
- Emiliania*
- Ostreococcus* (a 3rd sp)
- Fragilariopsis*
- Bigelowiella*
- Asterochloris*
- Guillardia*
- Pseudo-nitzschia*

### Algal projects worldwide



## Snapshot of Algal Evolution: Nucleomorph-retaining algae

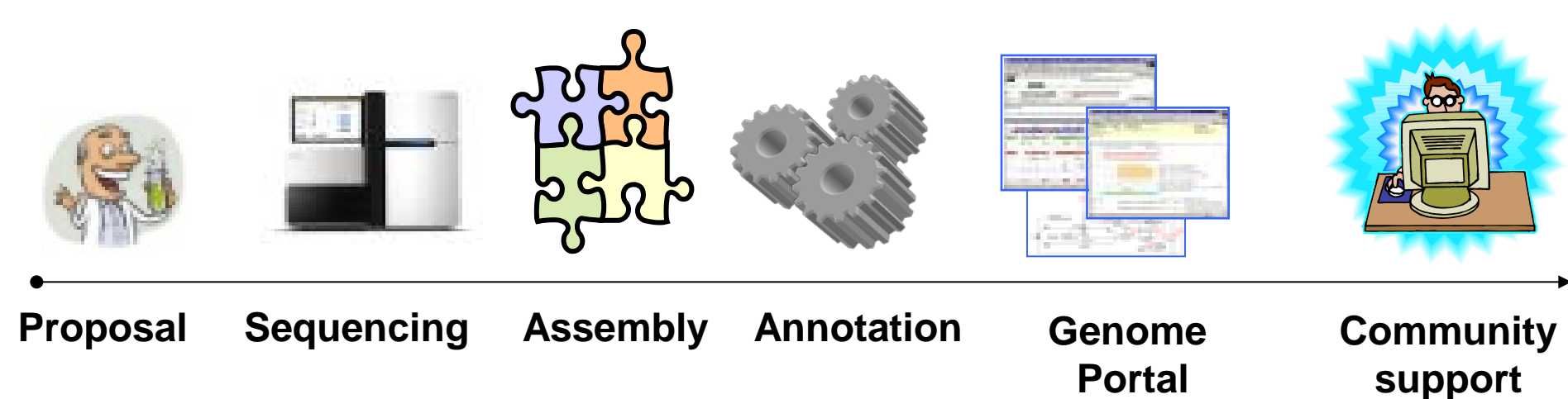
*Bigelowiella natans* and *Guillardia theta*



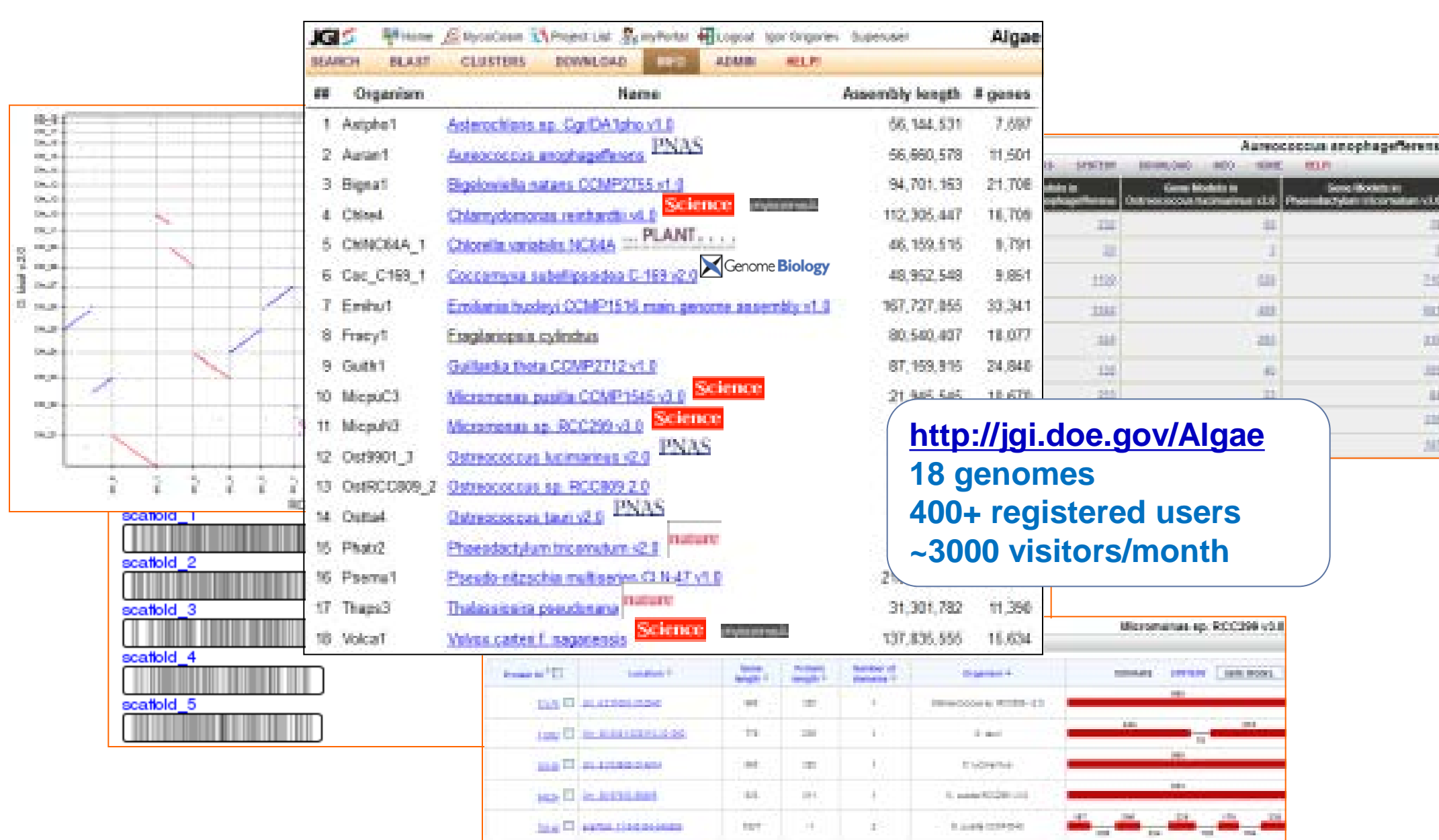
genome	size	# genes	size	# genes
nucleomorph	373 kbp	283	551 kbp	485
chloroplast	69 kbp	61	122 kbp	147
mitochondrion	95 Mbp	21380	N/A	N/A
nucleus	95 Mbp	21380	87 Mbp	24525

PI: John Archibald, Dalhousie University

## JGI Genome Project Pipeline



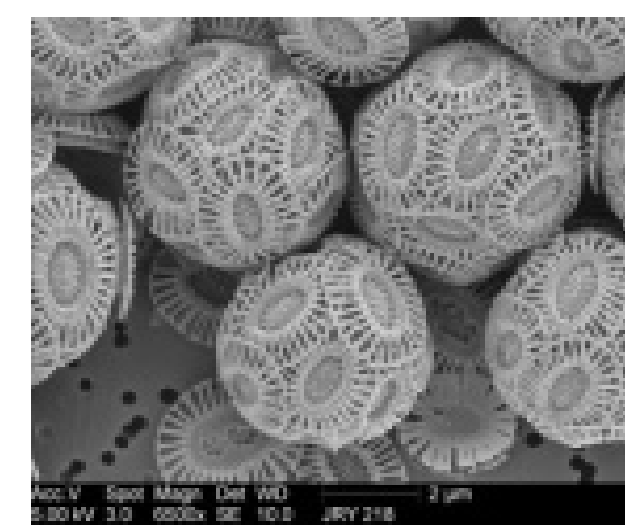
## JGI Algal Genome Portal (<http://jgi.doe.gov/Algae/>): Comparative genomics tools



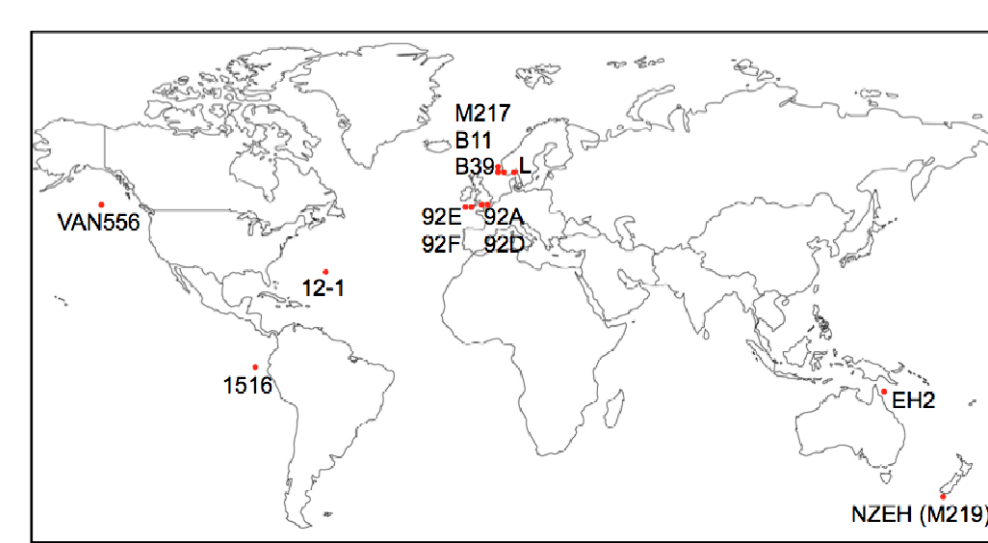
<http://jgi.doe.gov/Algae>  
18 genomes  
400+ registered users  
~3000 visitors/month

## The dominant phytoplankter *Emiliania huxleyi*

**Haptophyte**  
*E.huxleyi*  
168Mbp;  
33.3K genes

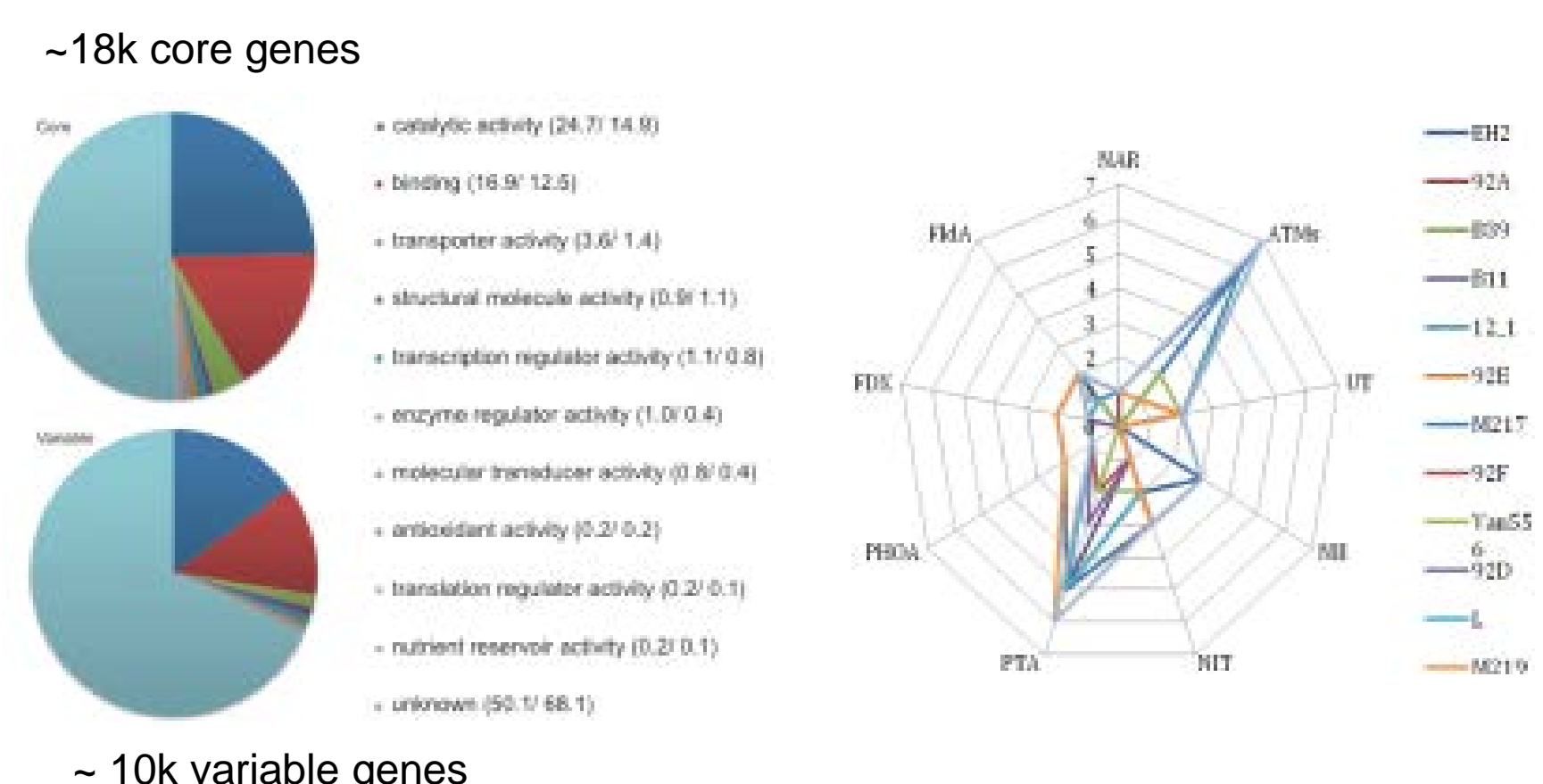


*Ehux* is globally distributed, locally abundant, and well adapted to a wide range of environments.



Geography and phylogeny of 14 strains of *Ehux*.

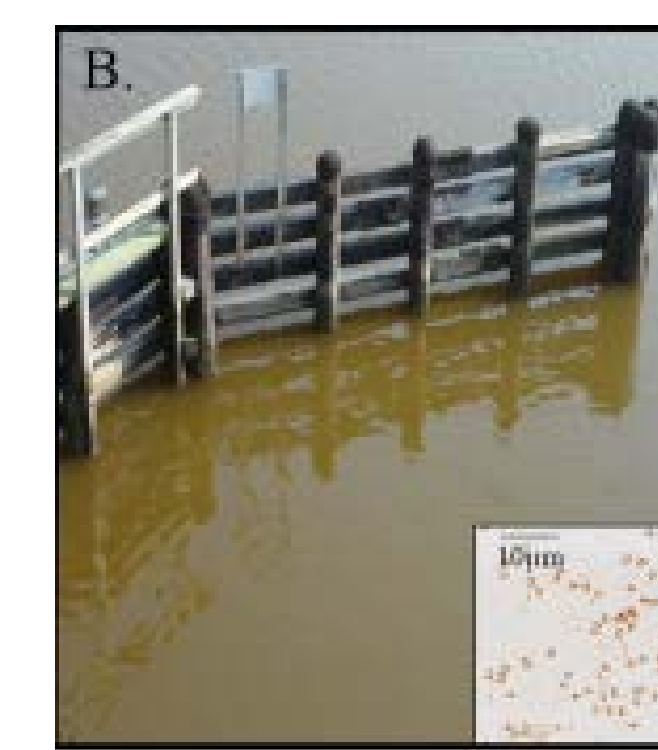
*Ehux* has core and variable genomes.



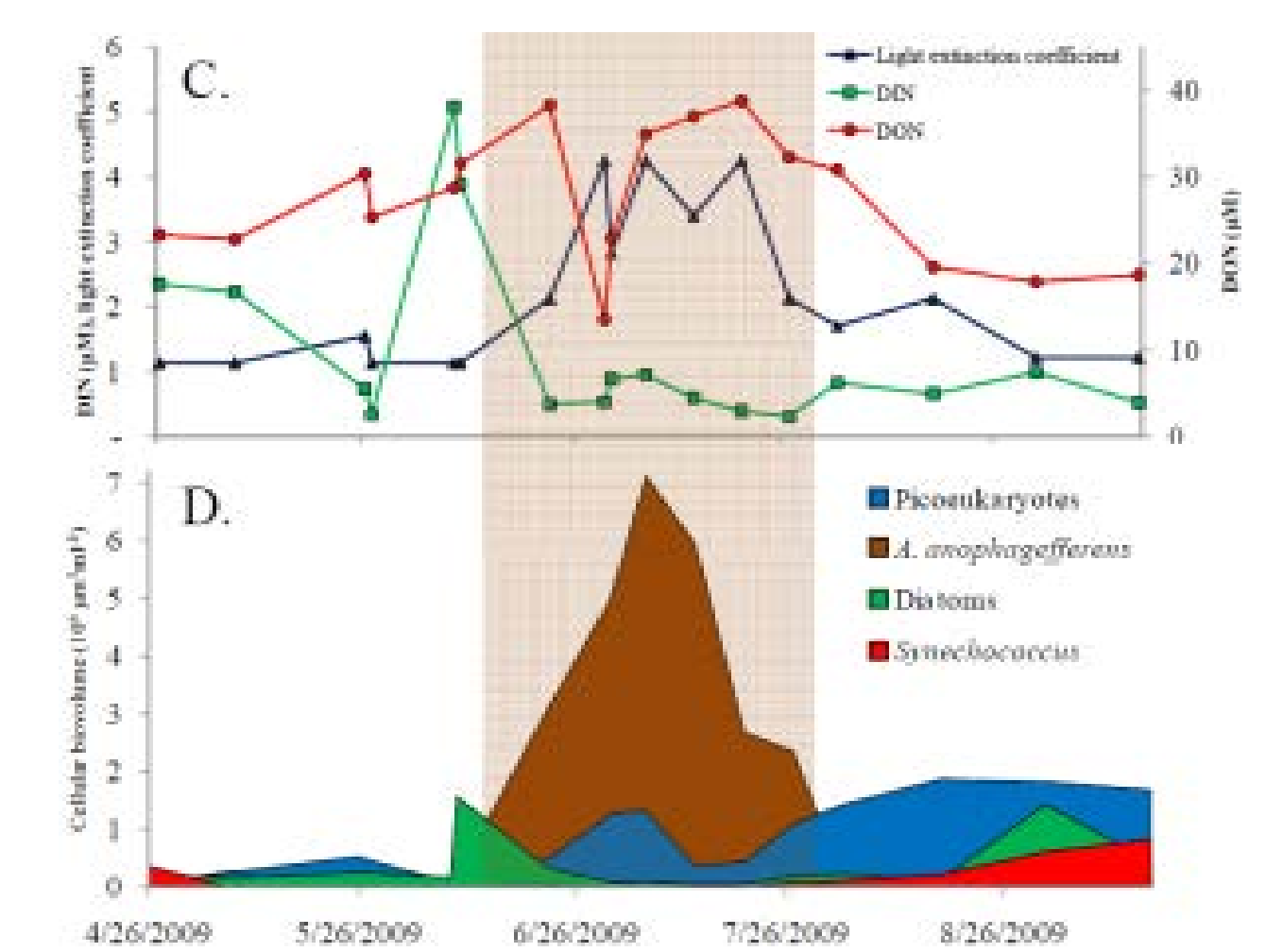
PI: Betsy Read, Cal State University

## The Harmful Algal Bloom Explained

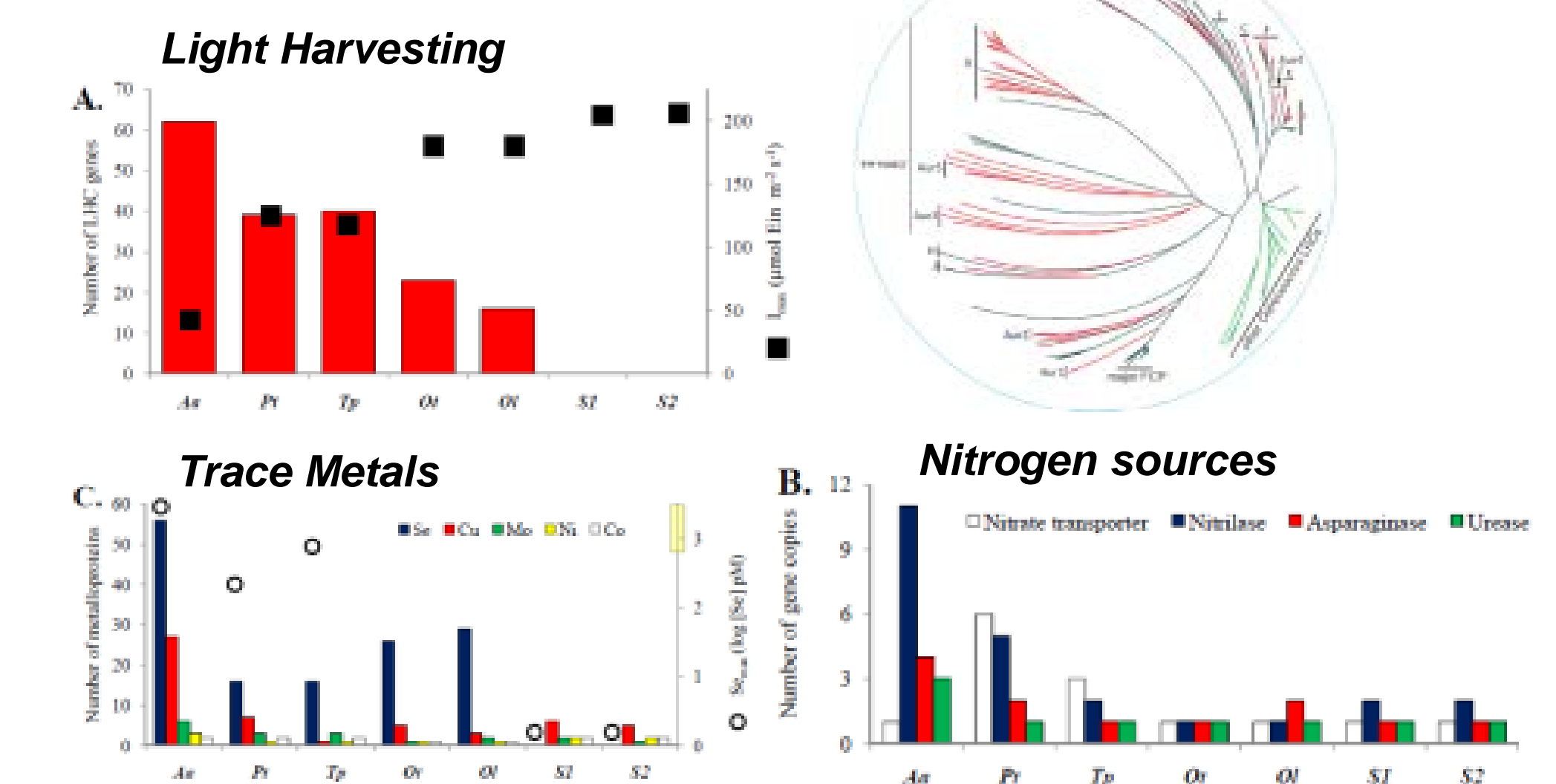
**Pelagophyte**  
*Aureococcus anophagefferens*  
57 Mbp;  
11.5K genes



Estuary niche: low light, high organics, trace metals



## Comparative genomics: gene family expansions to fit the niche



PI: Chris Gobler, Stony-Brooks (PNAS 2011)

Propose your genome projects for the next JGI Community Sequencing Program Call (Spring 2013) at <http://www.jgi.doe.gov/CSP/>