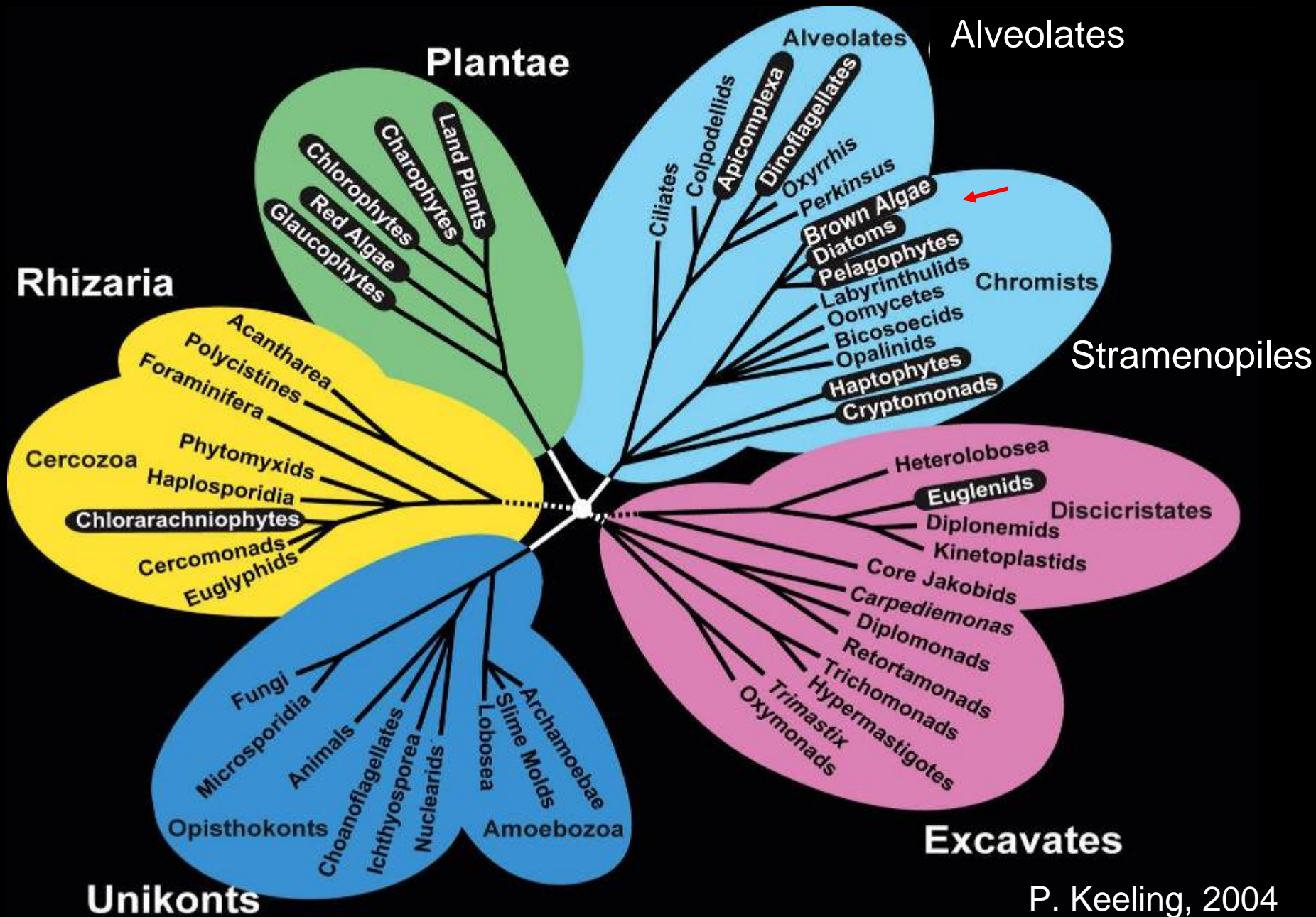


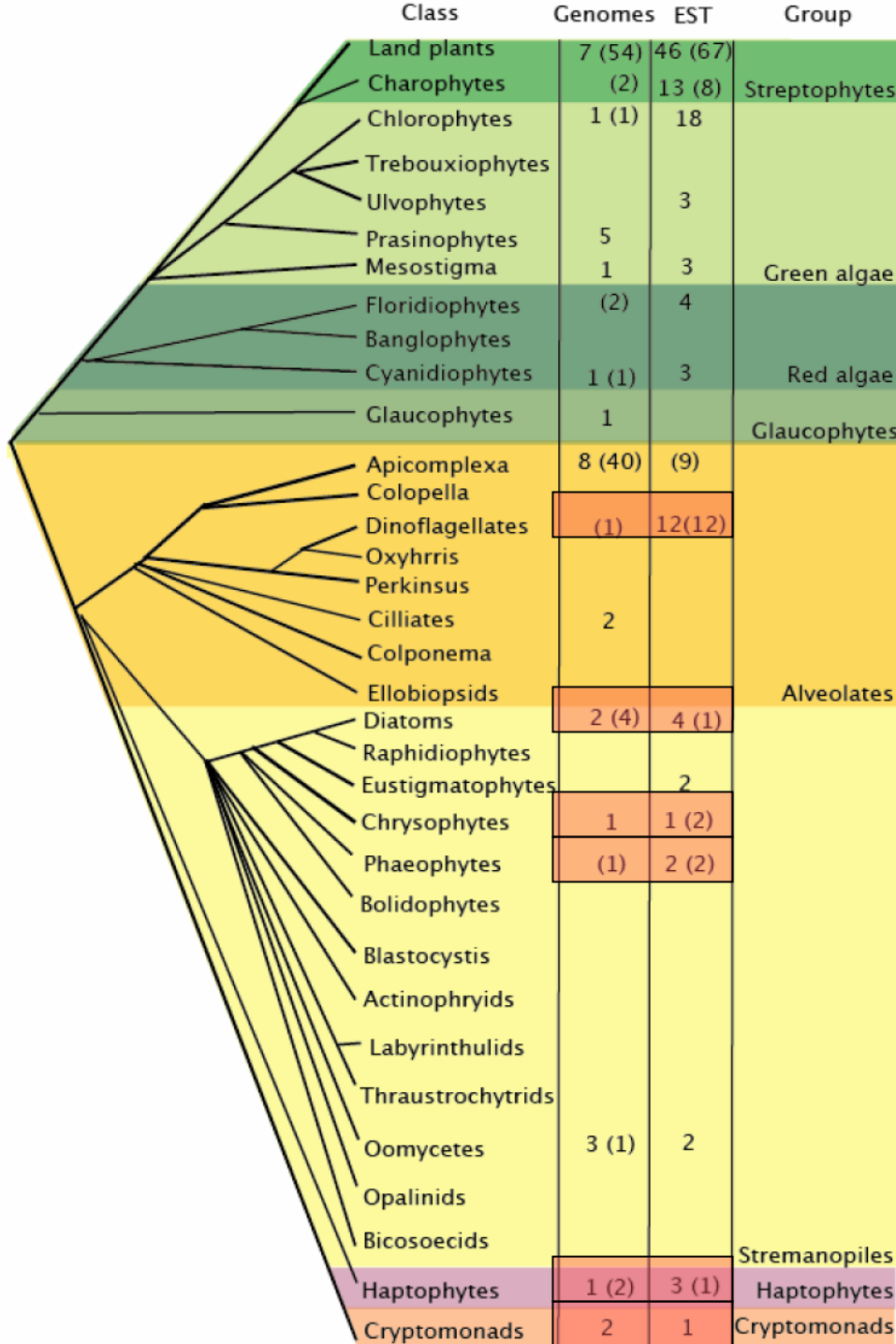


Ginger Armbrust
School of Oceanography
University of Washington

Sequencing Algal Genomes

Major Groups of Eukaryotes



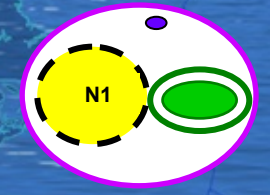


Streptophytes

Green Algae

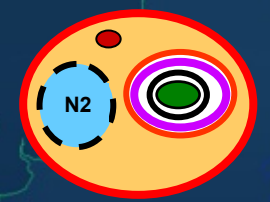
Red Algae

Primary endosymbionts



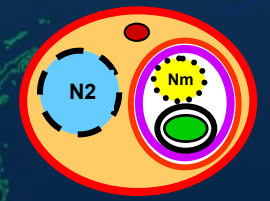
Alveolates

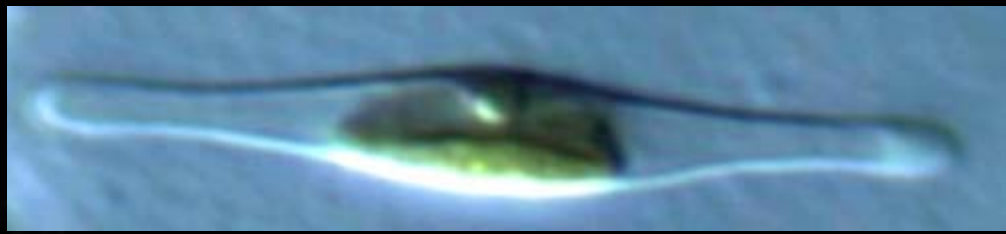
Secondary endosymbionts



Stramenopiles

Cryptomonads



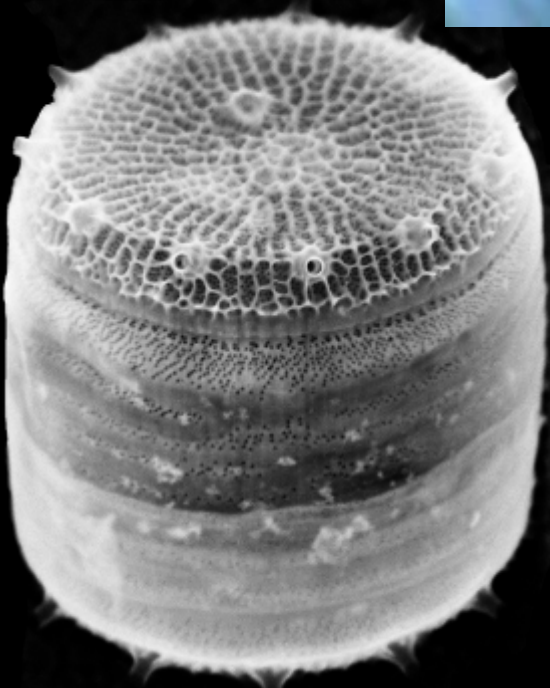


Phaeodactylum tricornutum
27 Mb, ~11,000 genes, finished

Chris Bowler

Diatom

Whole Genome Projects



Thalassiosira pseudonana
(Armbrust et al. 2004)

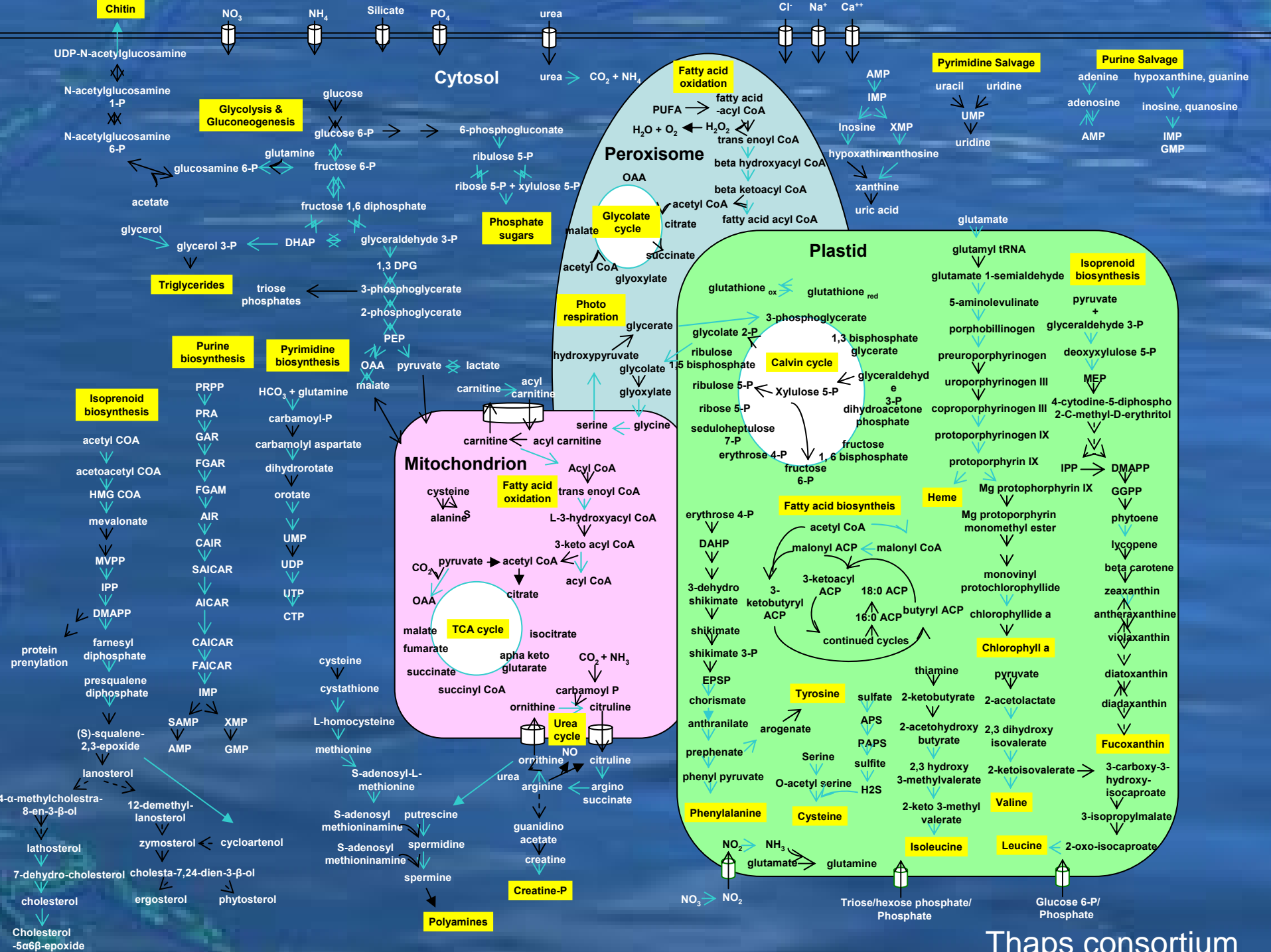
32 Mb, ~11,500 genes, finished



Fragilariopsis cylindrus
~35-45 Mb (1X coverage)



Pseudo-nitzschia multiseriis
~300 Mb (1X)

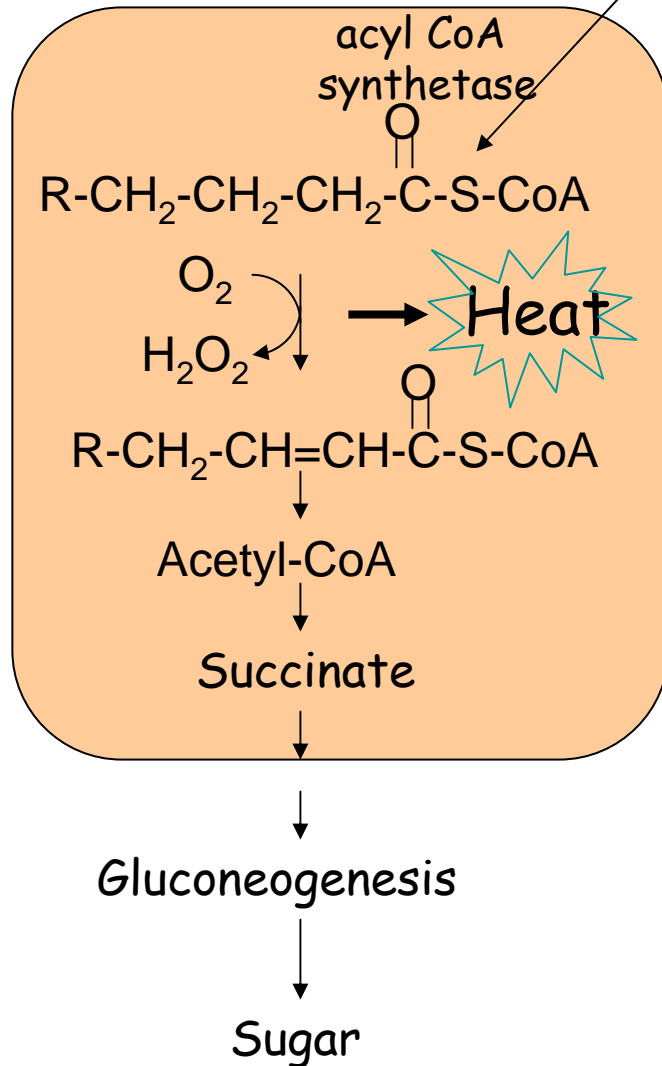


Plant Fatty Acid Oxidation

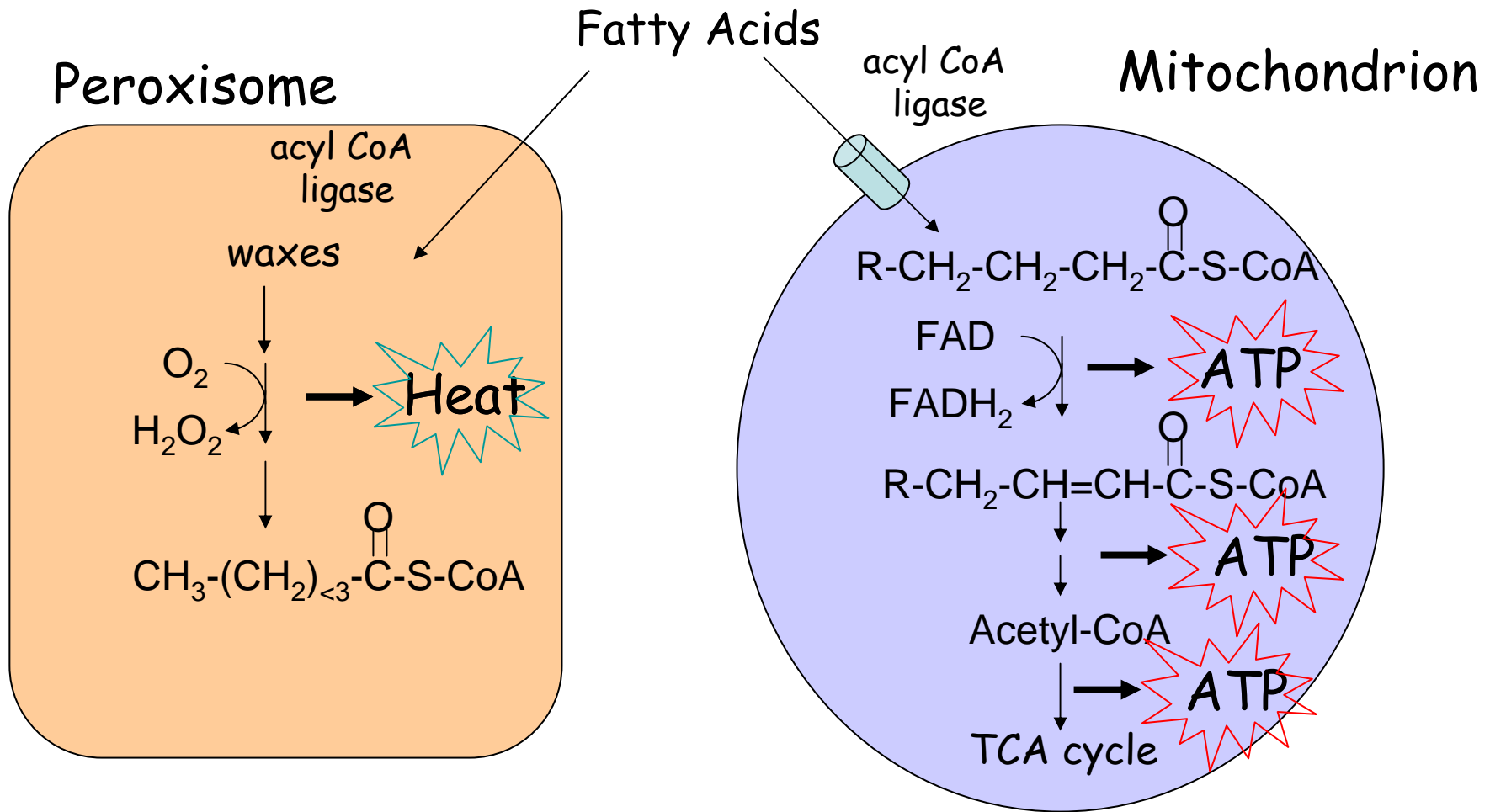
(used primarily during seed germination)

Fatty Acids

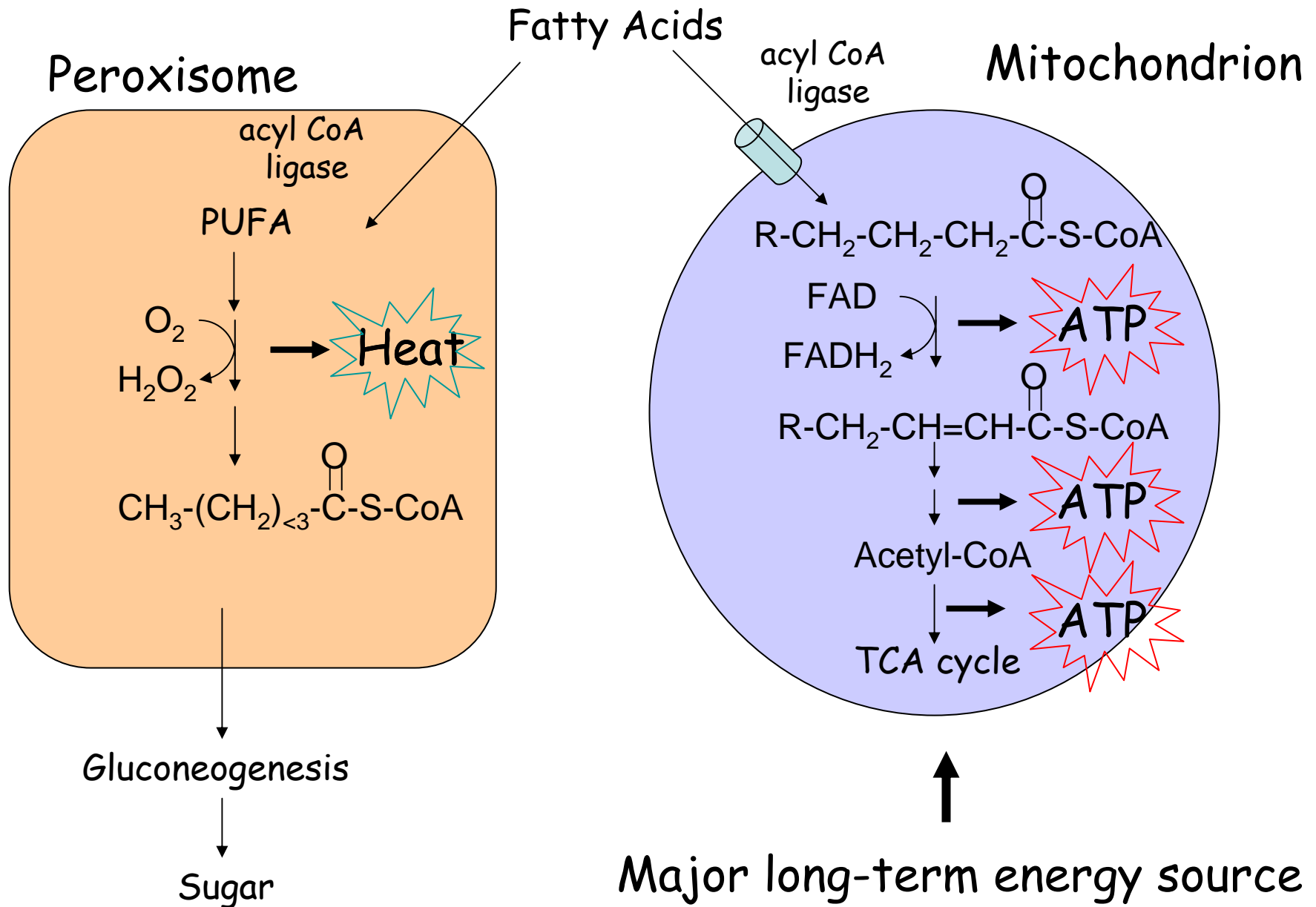
Peroxisome



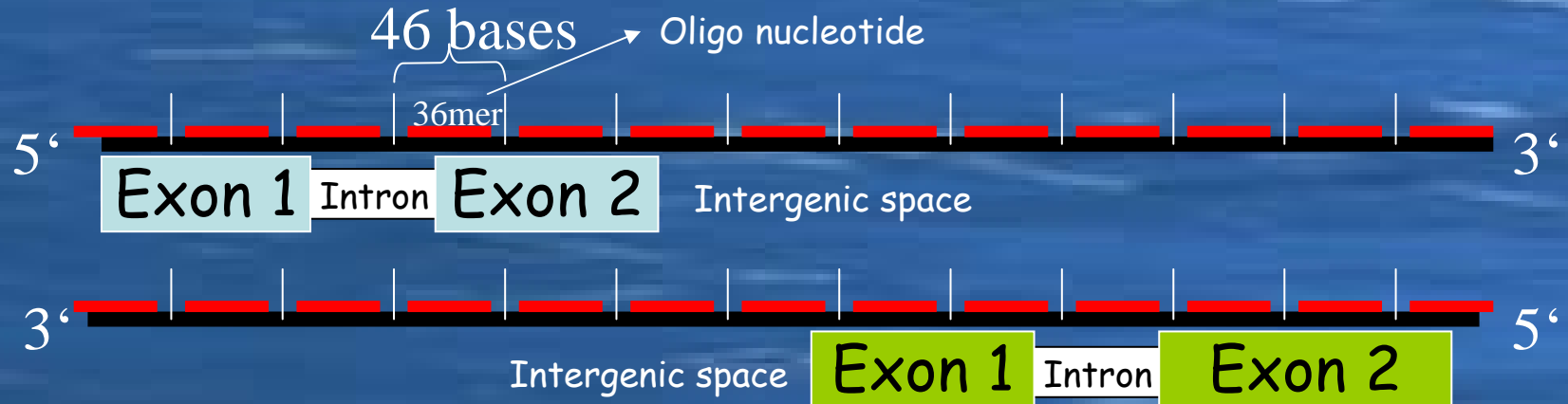
Animal Fatty Acid Oxidation



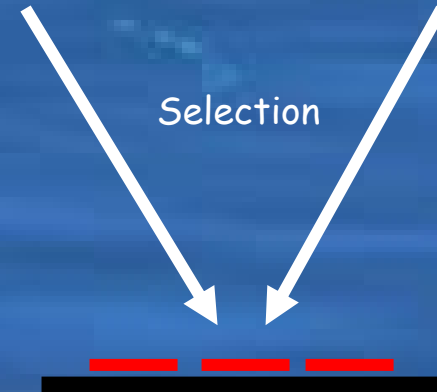
Diatom Fatty Acid Oxidation



1. Tiling Microarrays (1.8 million probes)



2. Gene-Only Microarrays (180,000 probes)



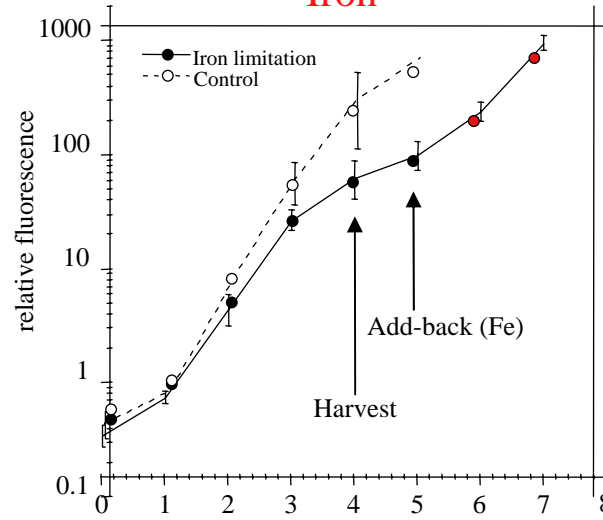
3. Proteomics 4000 peptides

Thomas Mock, Vaughn Iverson, Chris Berthiaume, Karie Holtermann, Colleen Durkin, Tiffany Truong, Audrey Djunaedi (UW); Mike Sussman, Matt Rodesch, Kathryn Richman, Matt Robinson, Toivo Kallas, Edward Hutlin, Sandra BonDurant (U. Wisconsin); Manoj Samanta (Systemix Inst.);

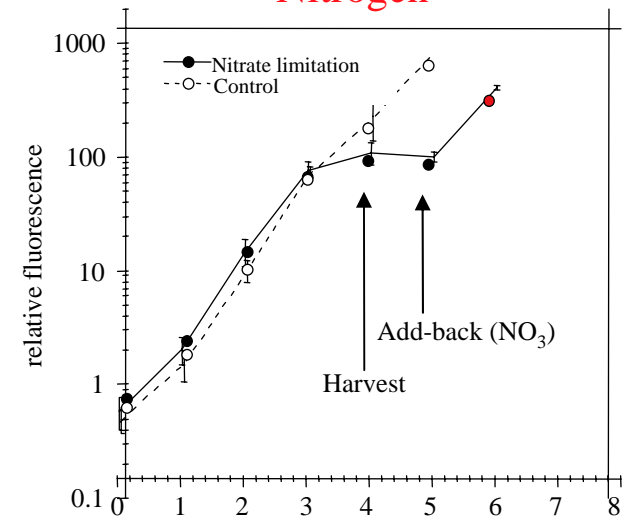
Growth experiments



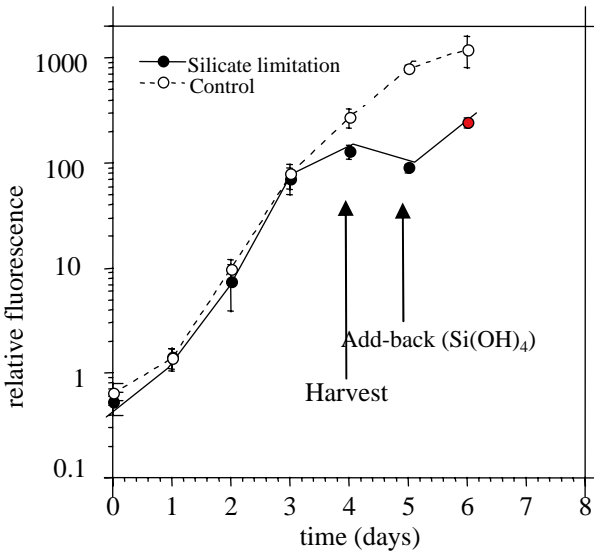
Iron



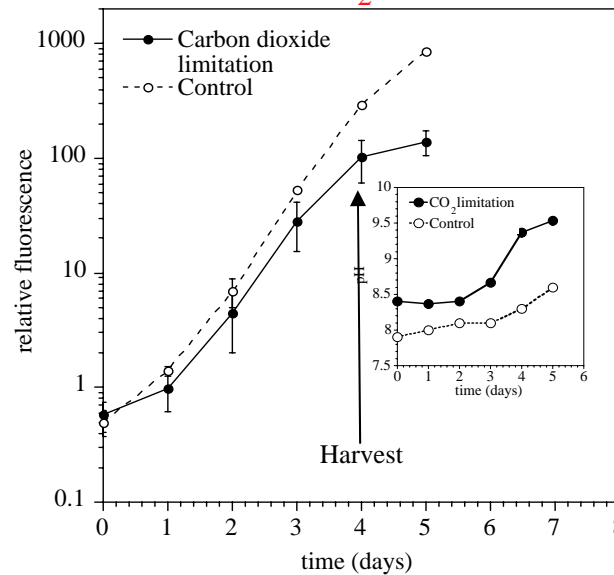
Nitrogen



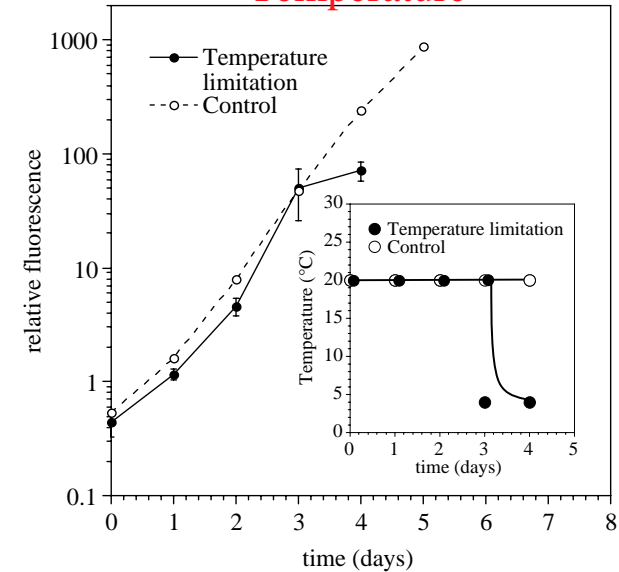
Silicon



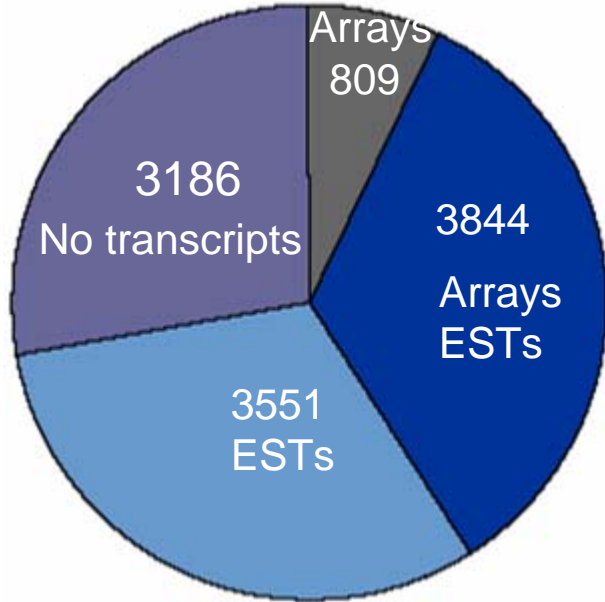
CO₂



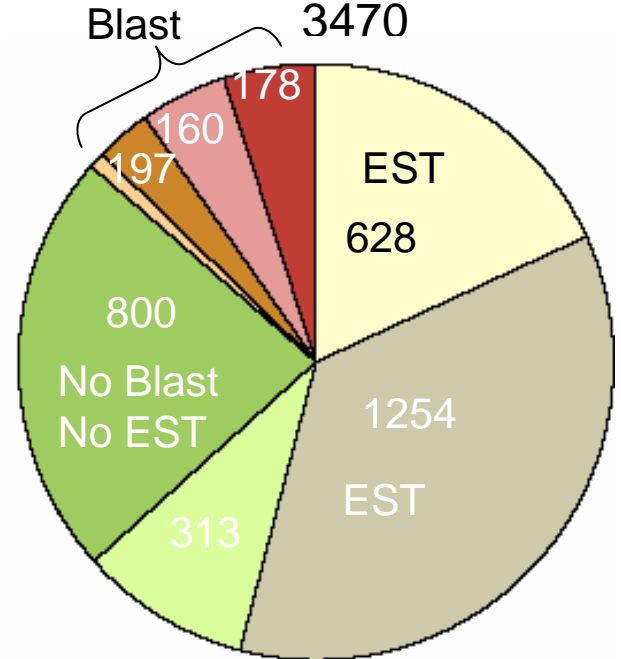
Temperature



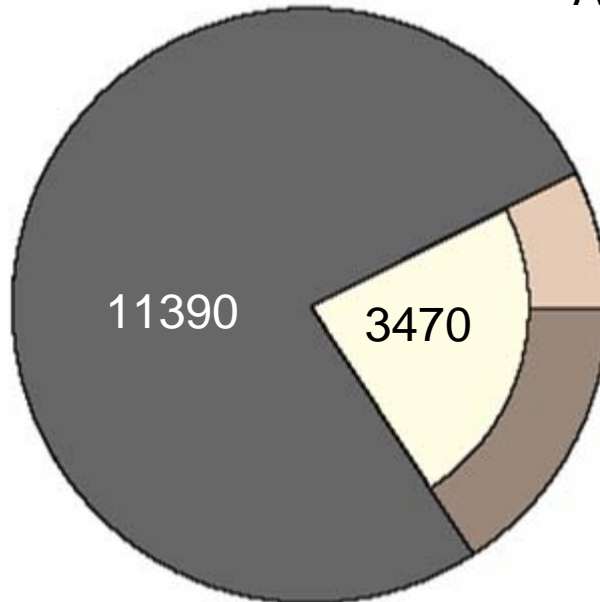
Modeled genes
11390



Discovered genes
3470



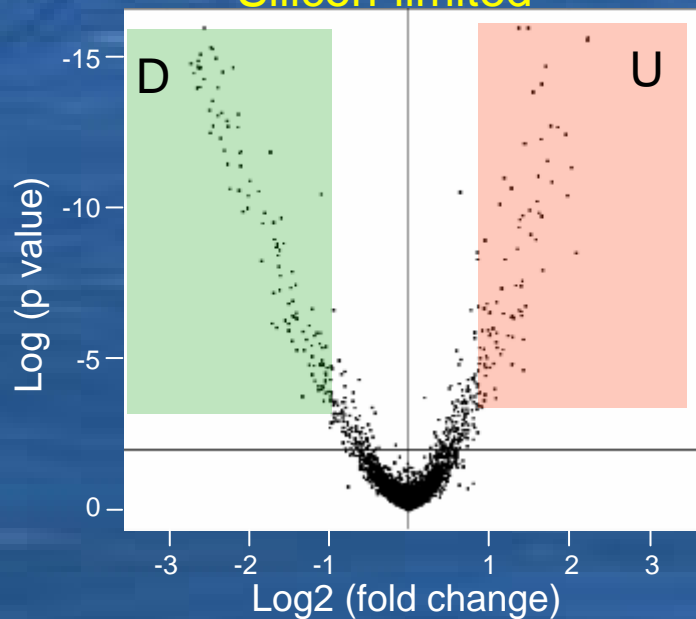
All genes
14860



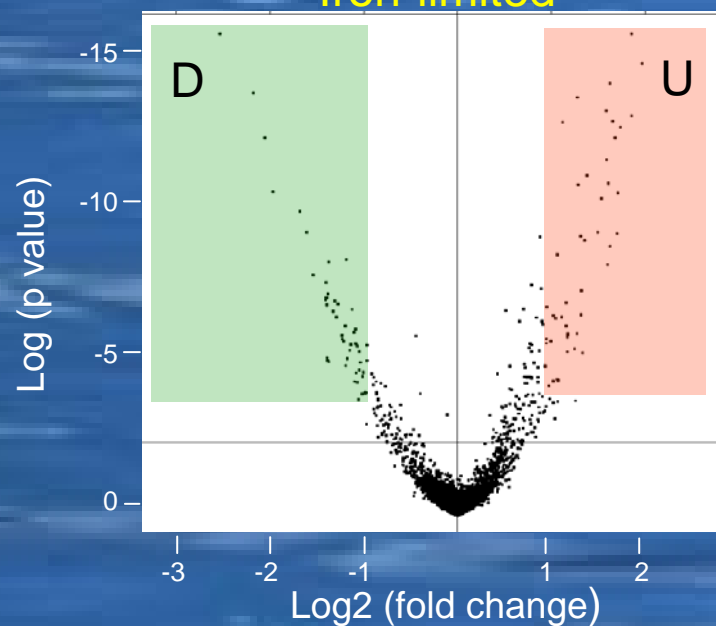
About 3470 new genes!

Whole Genome Expression Profiling

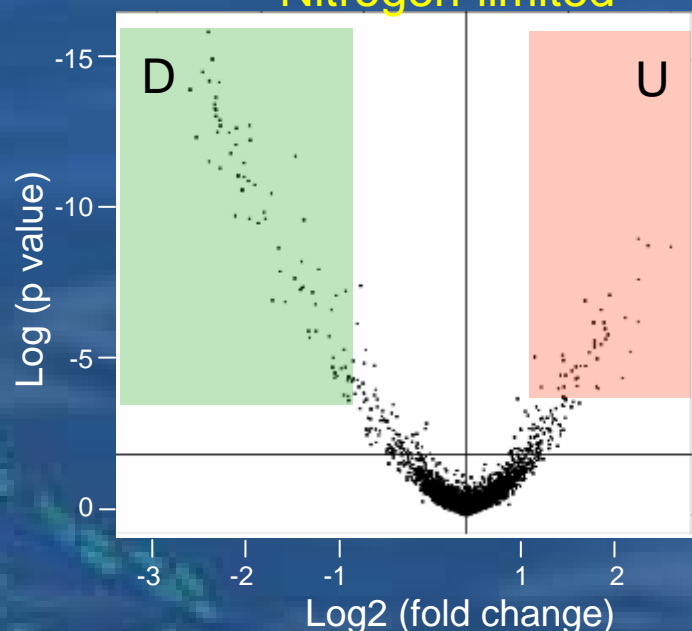
Silicon-limited



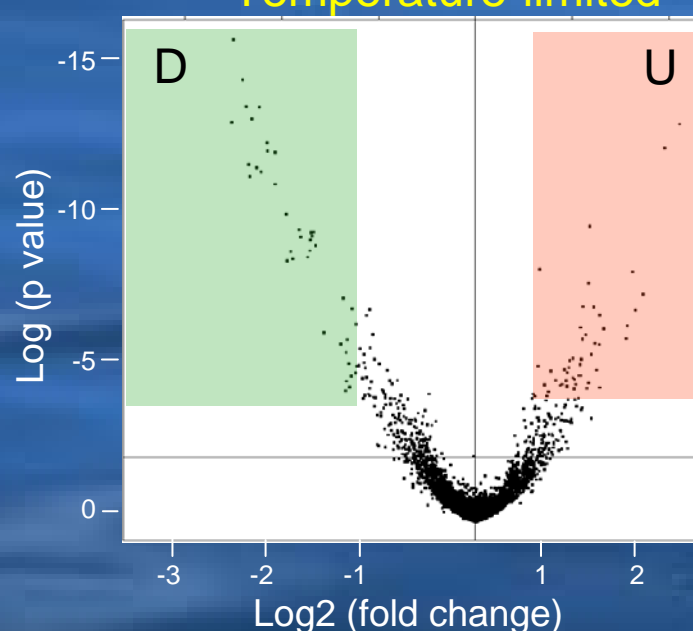
Iron-limited

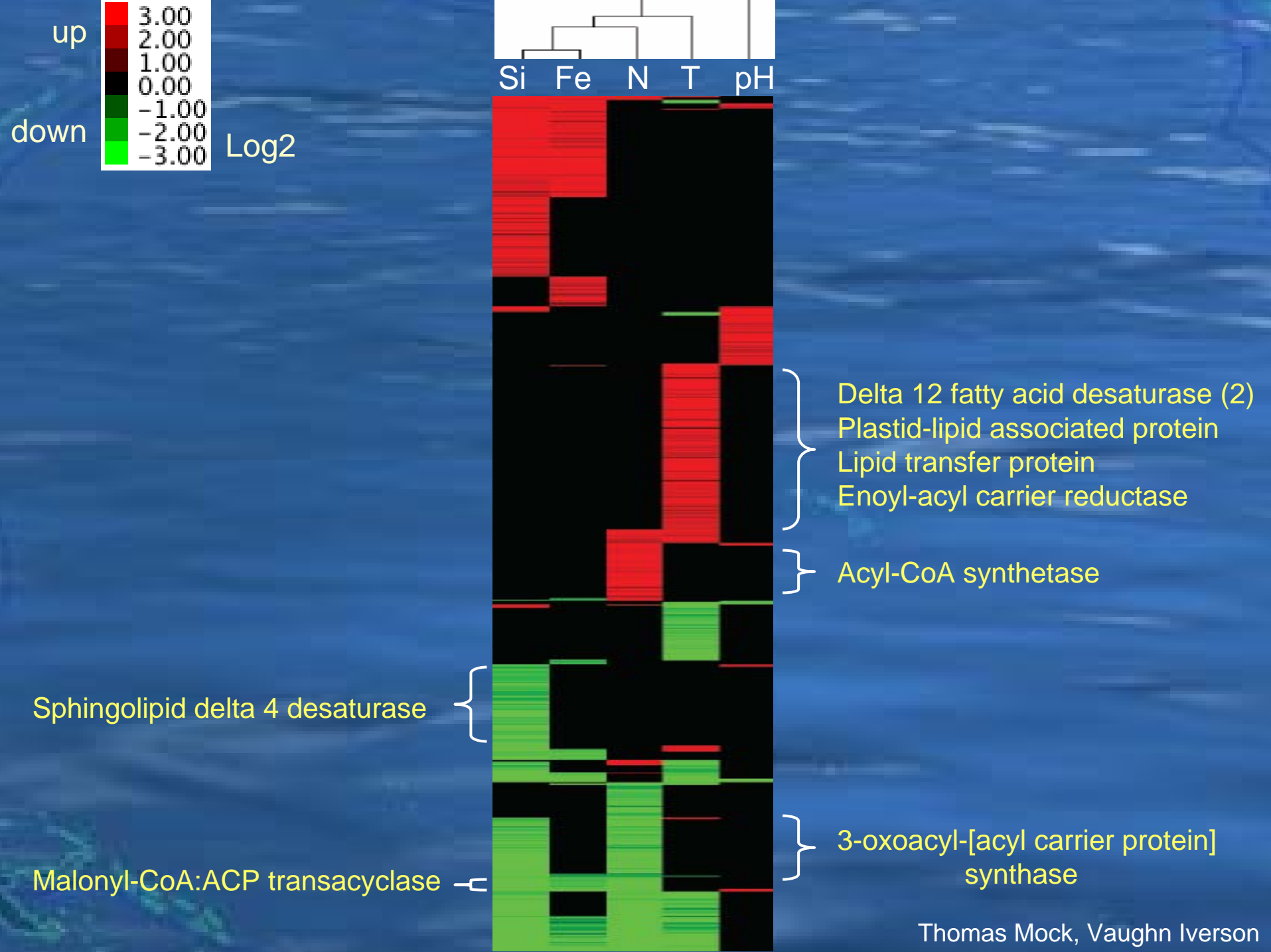


Nitrogen-limited



Temperature-limited





Differentially Expressed Genes

Reduced Temperature

<u>Predicted function</u>	<u>Fold-change</u>
Delta 12 fatty acid desaturase	40
Plastid lipid associated protein	12
Lipid transfer protein	11
Enoyl acyl carrier reductase	10
Delta 12 fatty acid desaturase	7

Minus Nitrogen

<u>Predicted function</u>	<u>Fold-change</u>
Acyl CoA synthase	7

Minus Silicon

<u>Predicted function</u>	<u>Fold-change</u>
3-oxoacyl [acyl carrier protein] synthase	-8
Sphingolipid delta 4 desaturase	-7
Malonyl-CoA:ACP transacylase	-6

Unknown	124
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Unknown	20
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Some Future Directions

- Next generation sequencing (ABI SOLiD)
 - resequence species isolates from different oceans
 - transcriptomics of “non-model” diatoms
 - metatranscriptomics of laboratory consortia
 - metatranscriptomics of field samples
- Data visualization

12 ft

7.5 ft



16 X 30 inch monitors, 1 is management console
9-node cluster, 1 is head node
Runs Rocks 4.3 Linux distribution, based on CentOS 4.5
Resolution: 12800 X 4800 = 61 million pixels
Located with 21 sq foot room with glass doors and windows
In collaboration with Larry Smarr, Cal IT2

Summary

- Whole genome sequence information can be used to predict metabolic pathways
- Identified ~3000 new genes with tiling microarrays; includes most highly upregulated genes
- Next generation sequencing permits analysis of “non-model” algae
- New visualization tools on the horizon

Lab Members

April Bailey	Undergraduate
Sara Bender	Graduate Student
Chris Berthiaume	Systems Administrator
Audrey Djunaedi	Undergraduate
Colleen Durkin	Graduate Student
Claire Ellis	Undergraduate
Ken Hammel	Undergraduate
Kate Hubbard	Graduate Student
Vaughn Iverson	Graduate Student
Julie Koester	Graduate Student
Rachelle Lambert	Undergraduate
Ellen Lin	Technician
Adrian Marchetti	Post-doctoral Researcher
Rhonda Marohl	Technician
Thomas Mock	Post-doctoral Researcher
Mikelle Nuwer	Graduate Student
Irina Oleinikova	Technician
Micaela Parker	Research Scientist
Rita Peterson	Administrator
Francois Ribalet	Post-doctoral Researcher
Tiffany Truong	Undergraduate
Andy Wong	Undergraduate

