

The Power of Diversity I: *Prochlorococcus* enters the genomic era

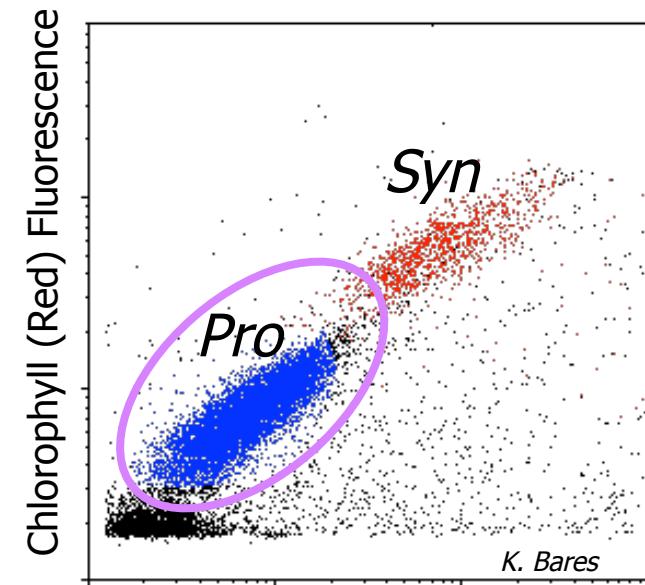
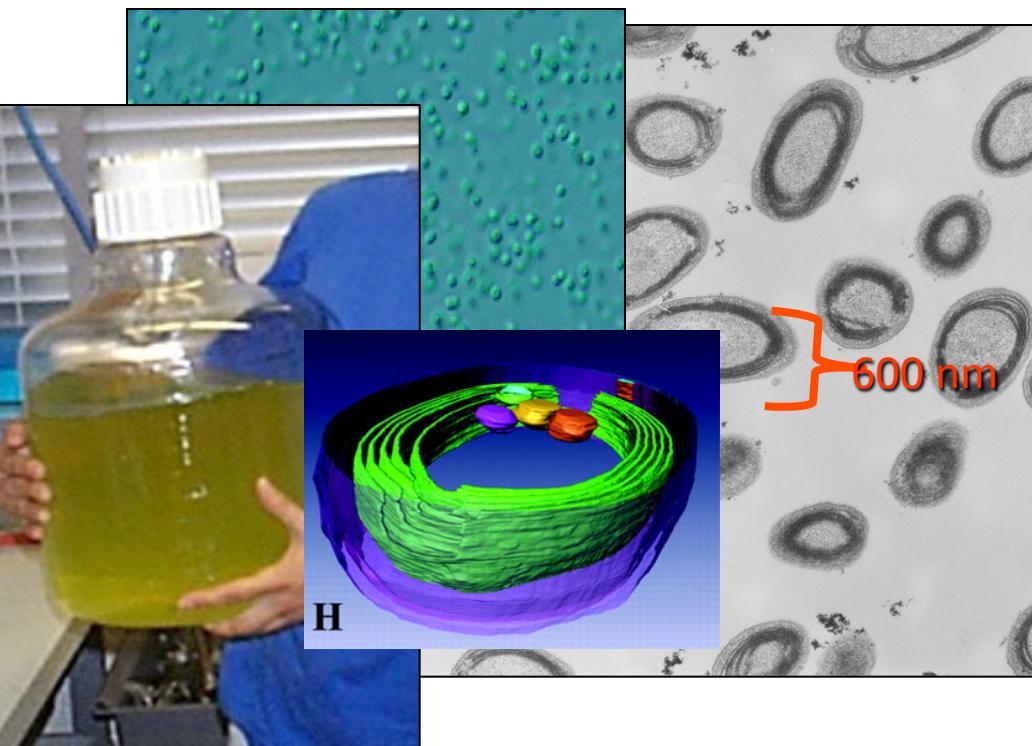
Chisholm

C-MORE Summer Course

June 6, 2012

What is *Prochlorococcus*?

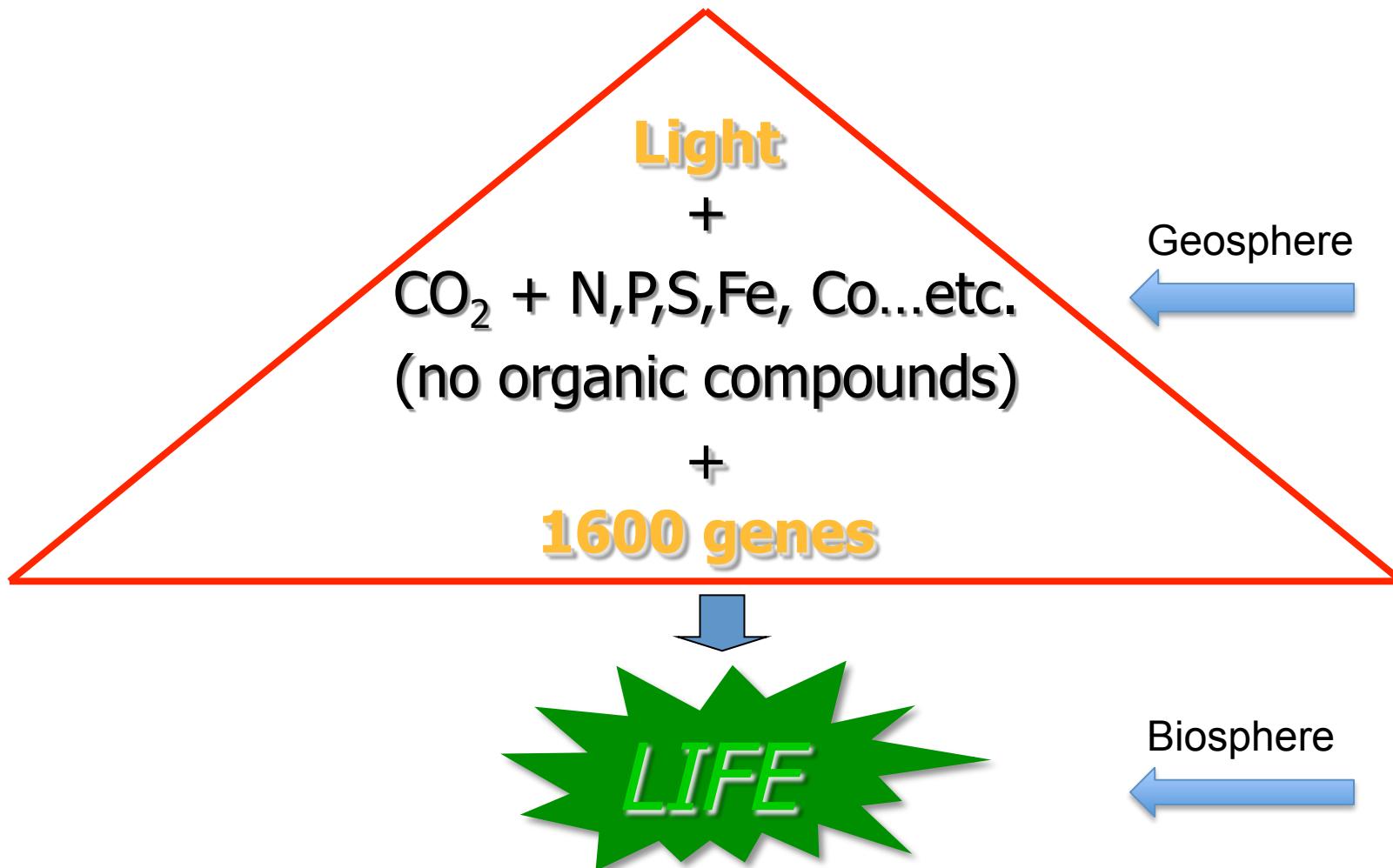
- Smallest cell in the oceans that fluoresces red
- Contains Divinyl Chl a and Chl b
- Oceanic cyanobacterium, 0.6 - 0.8 μm diameter
- Smallest (size and genome), and most abundant photosynthetic cell on Earth



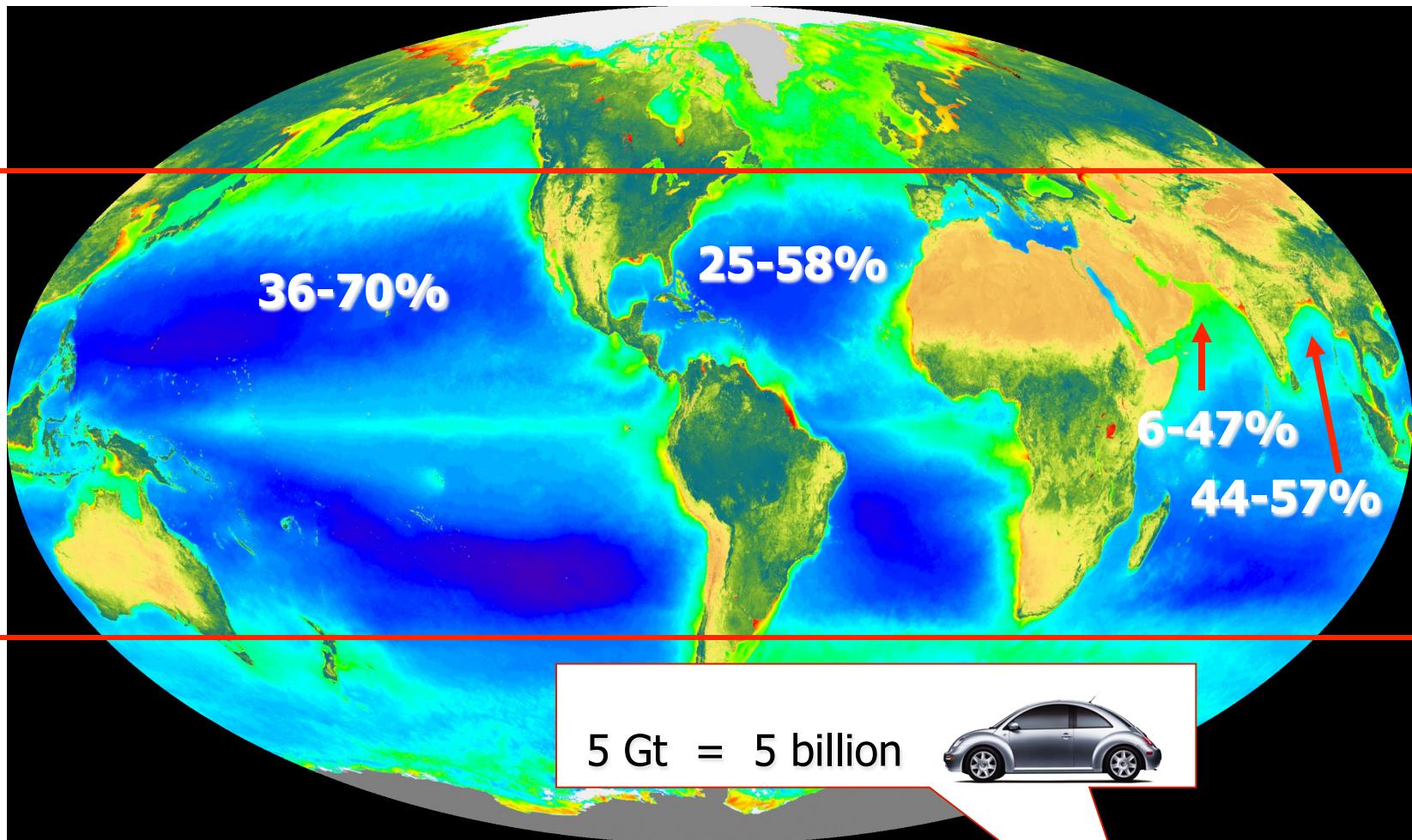
Forward Angle Light Scatter
(Size)

Prochlorococcus is the ‘minimal life’ form:

Smallest amount of information that can make life from scratch



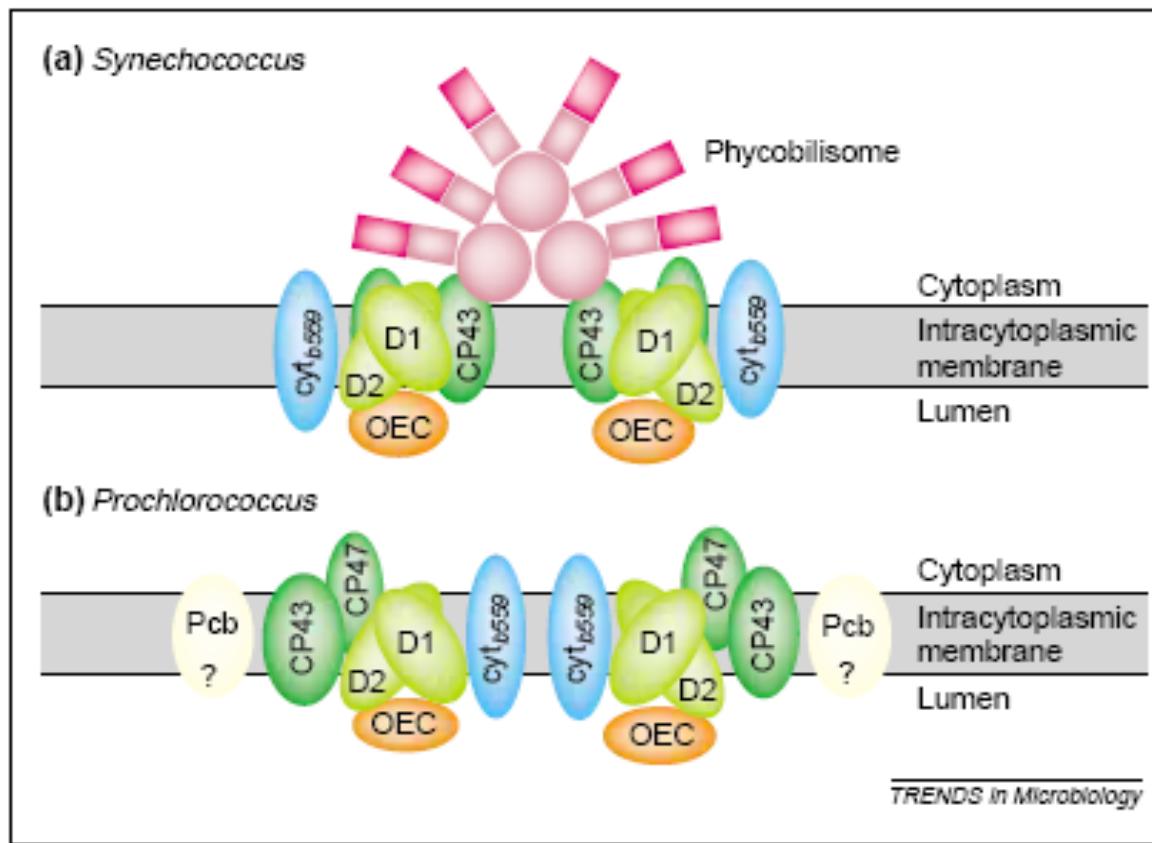
A significant fraction of global chlorophyll



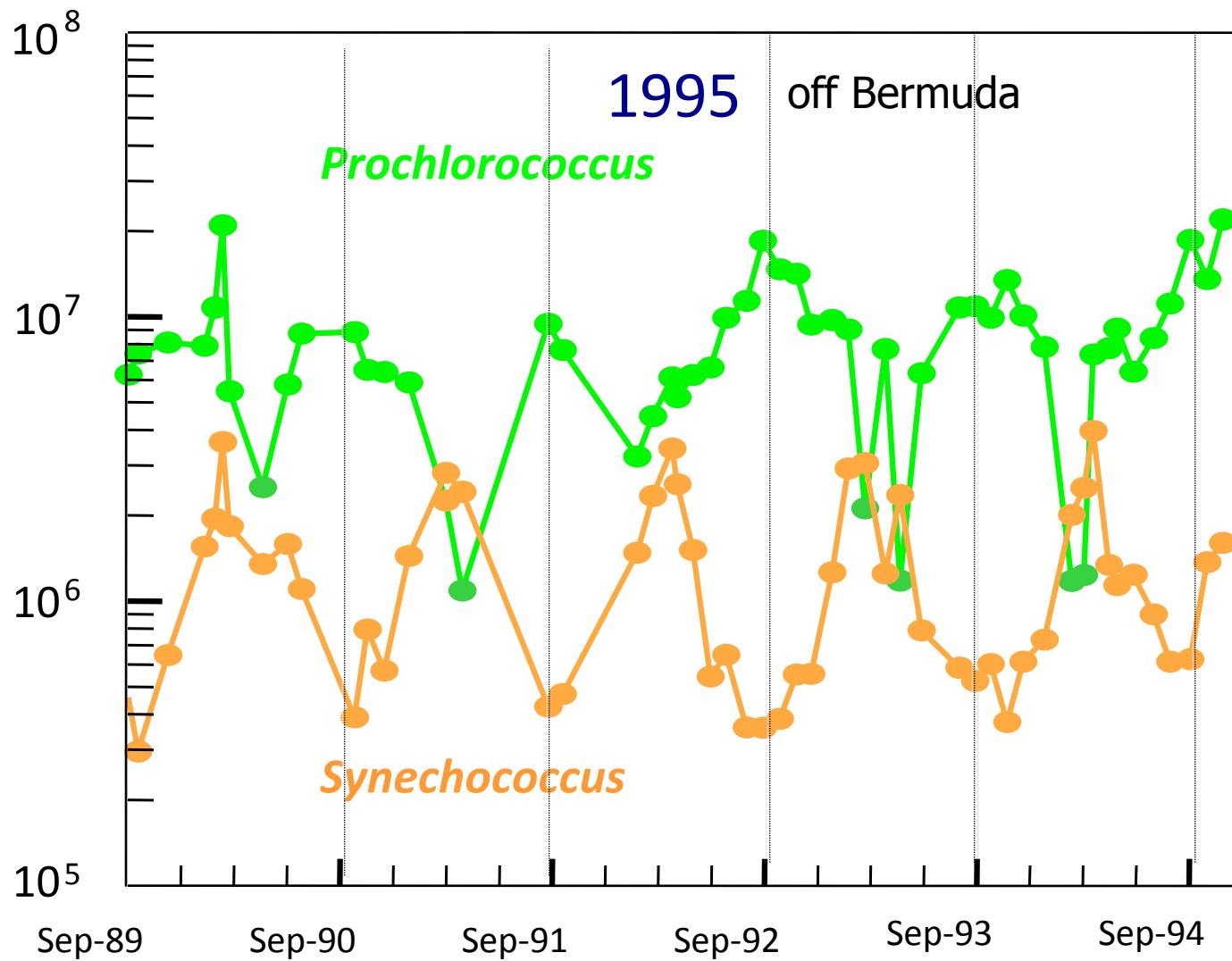
Record concentration:
700,000 cells ml⁻¹

Global
photosynthesis ≈ 5 Gt C yr⁻¹

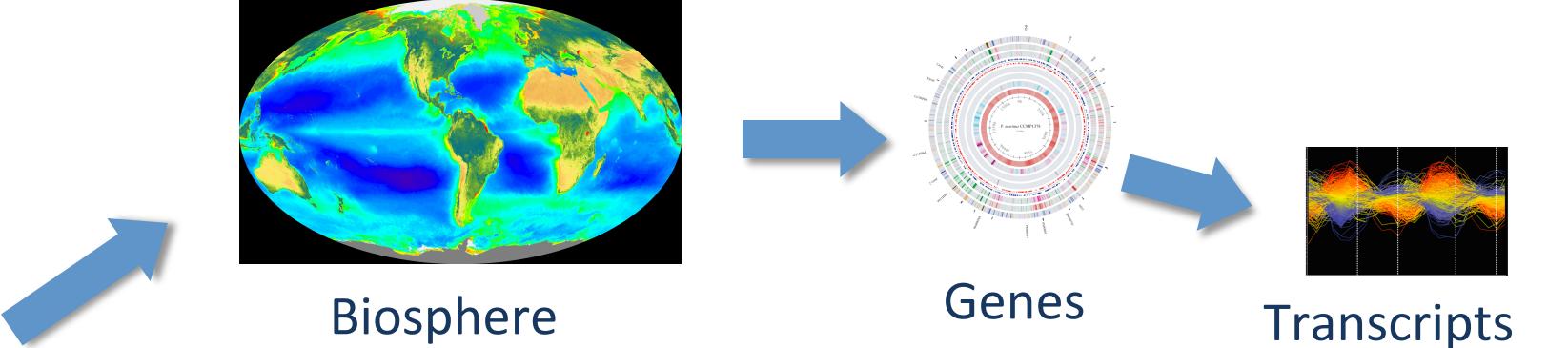
Prochlorococcus is basically a slightly smaller *Synechococcus*, with a different light harvesting system



They share (and partition) the “small size bin”

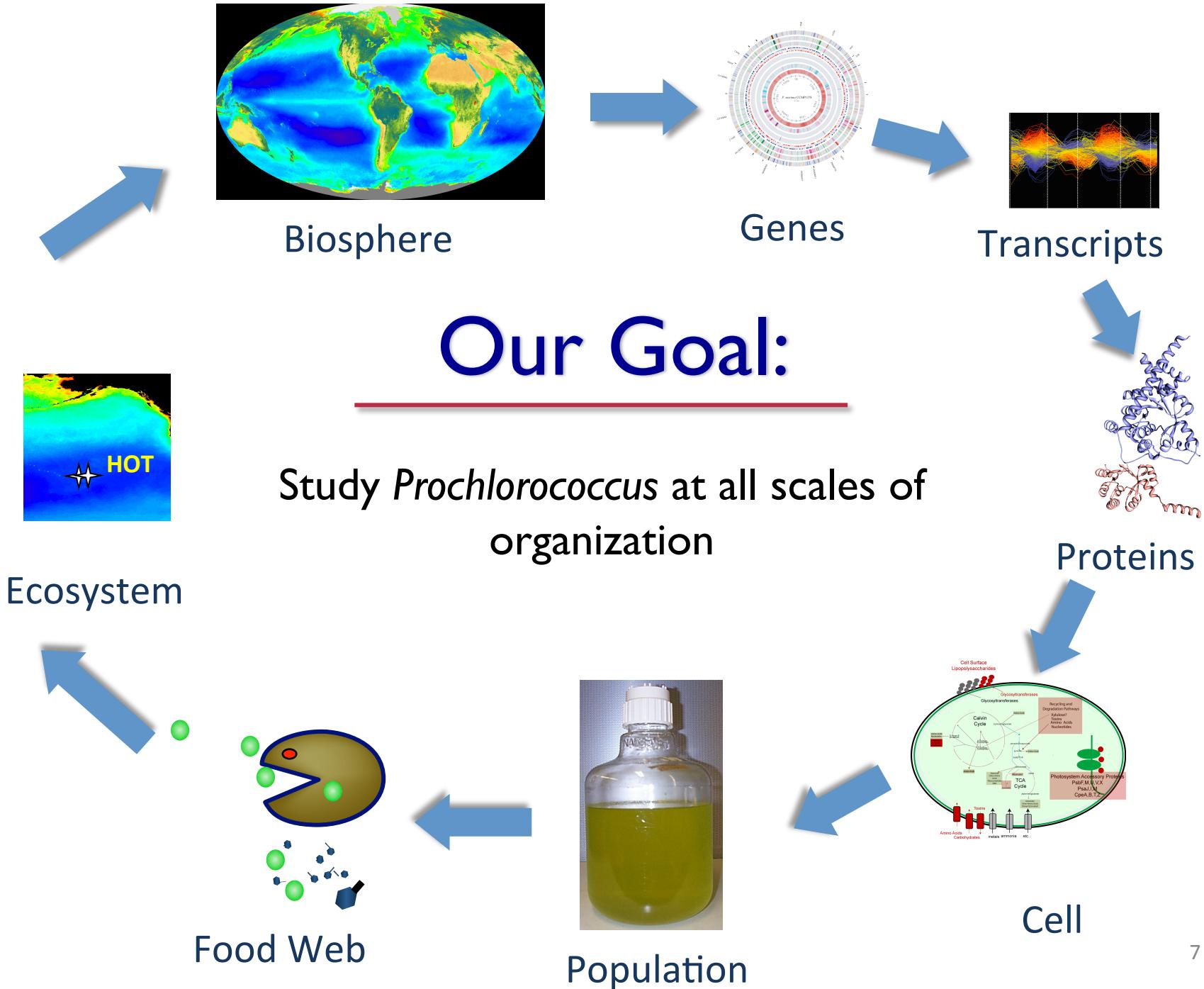


DuRand et al 2001



Our Goal:

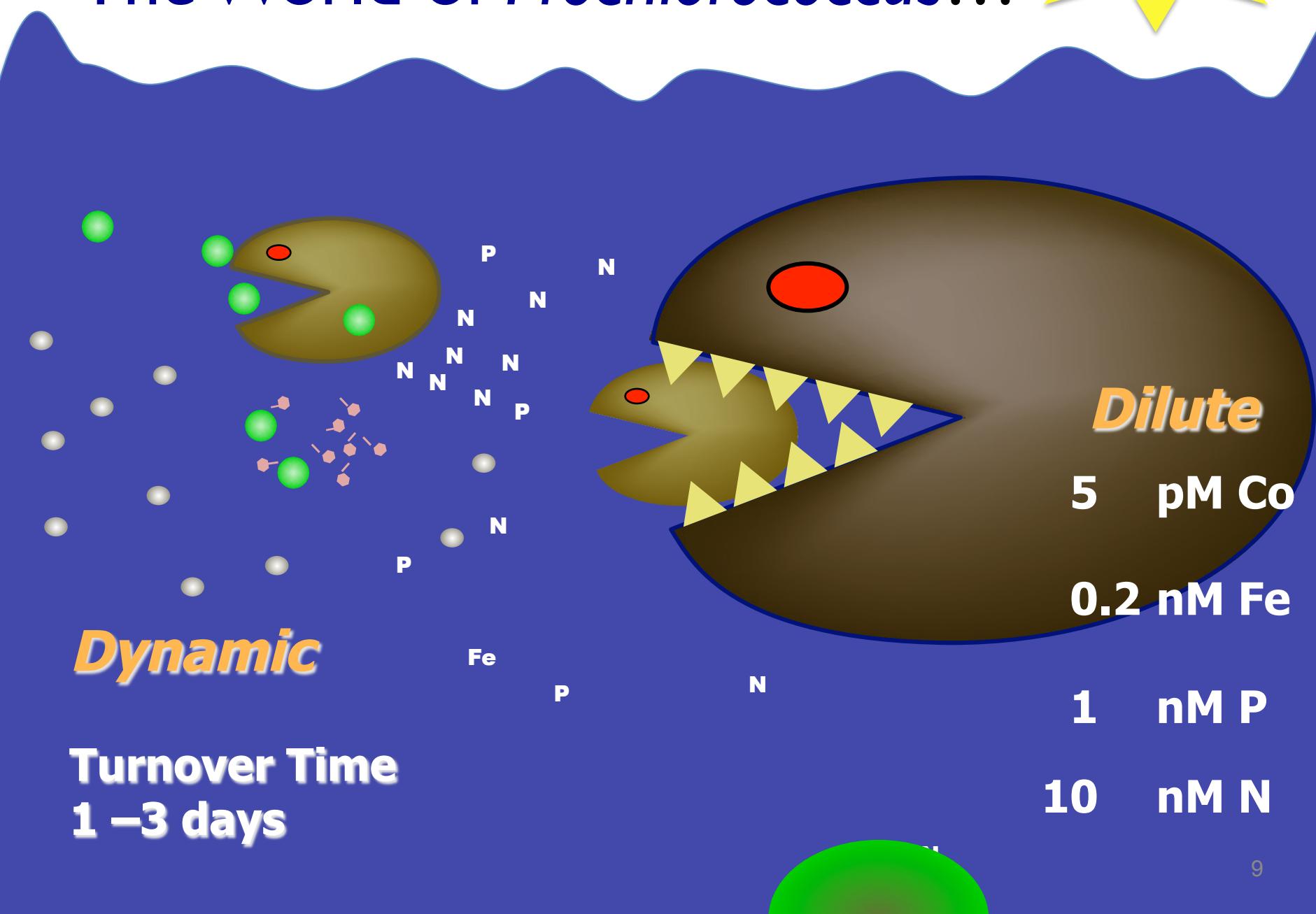
Study *Prochlorococcus* at all scales of organization



Components of two lectures

- ◆ The Cell
- ◆ Niche Dimensions of *Prochlorococcus*
- ◆ Single Cell Genomics
- ◆ Phage
- ◆ Interactions (and signaling?)

The World of Prochlorococcus...

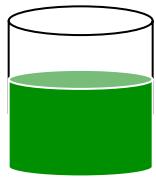


Dynamic

**Turnover Time
1 –3 days**

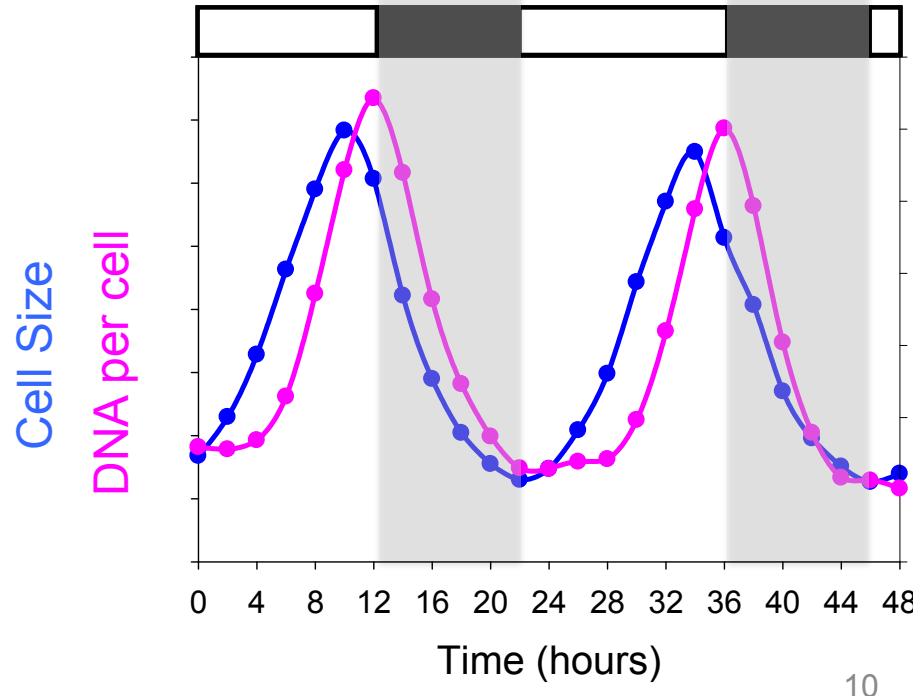
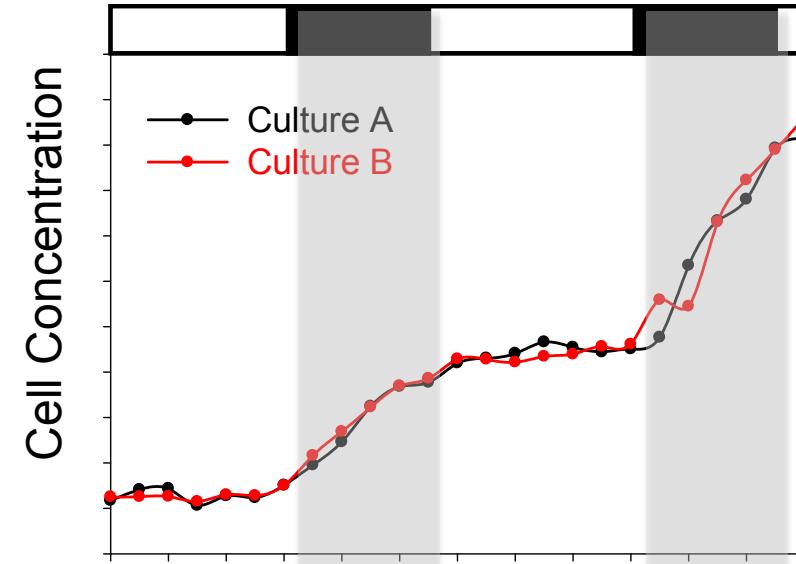
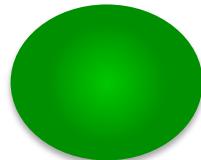
Tight Cell Cycle Synchrony

Culture



==

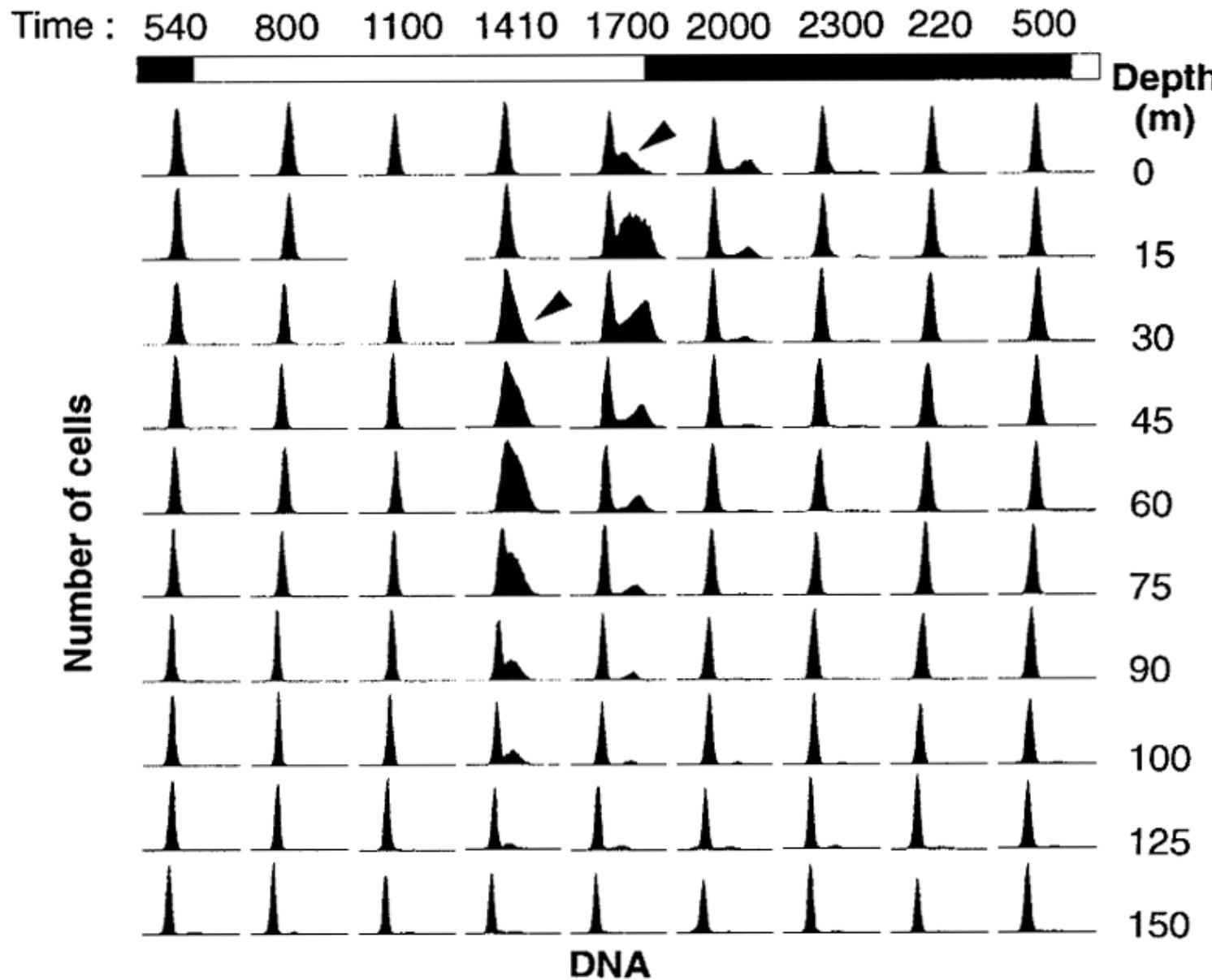
Cell



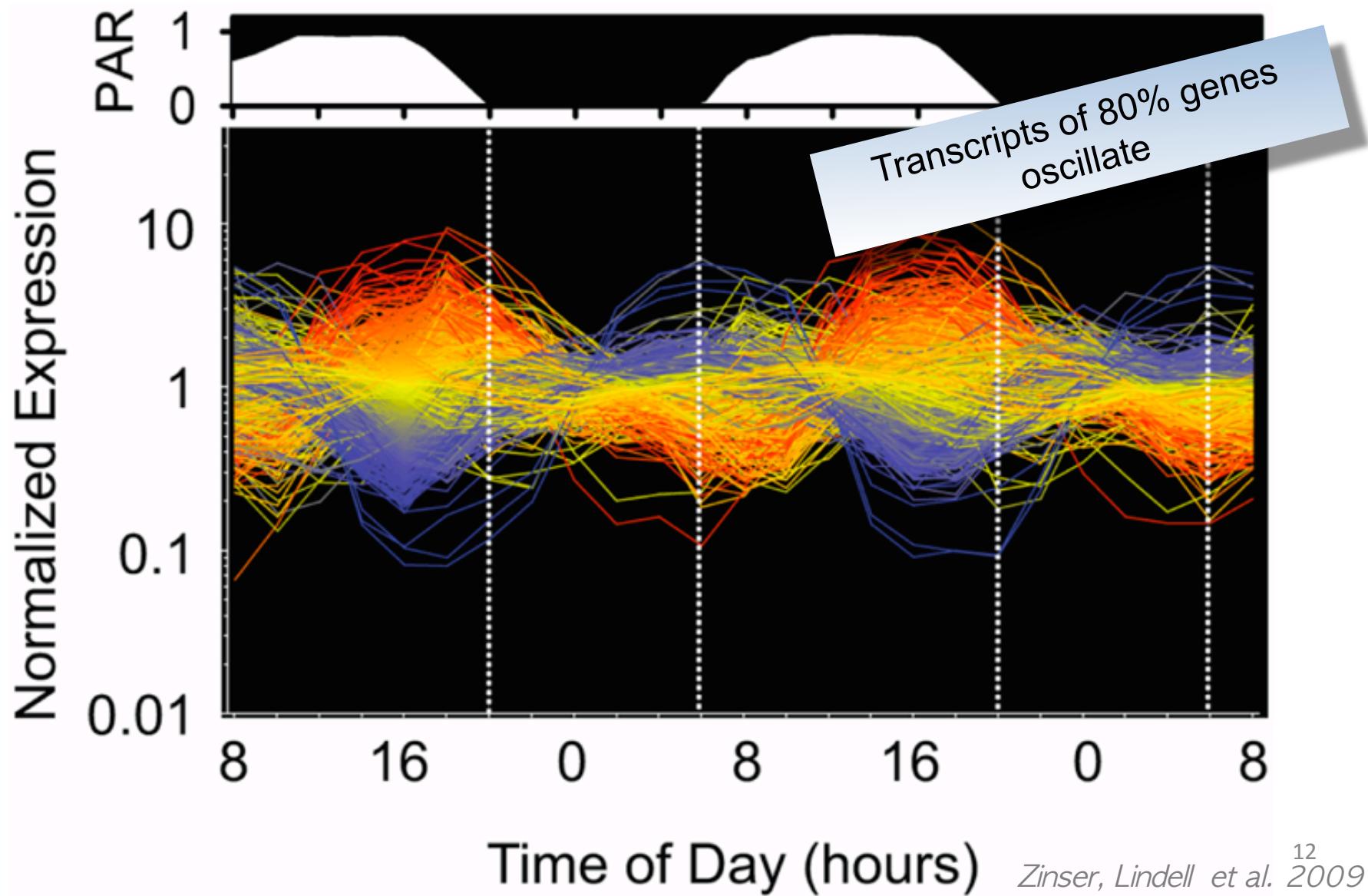
Can see it growing in the wild

1 April 1992

Equatorial
Pacific



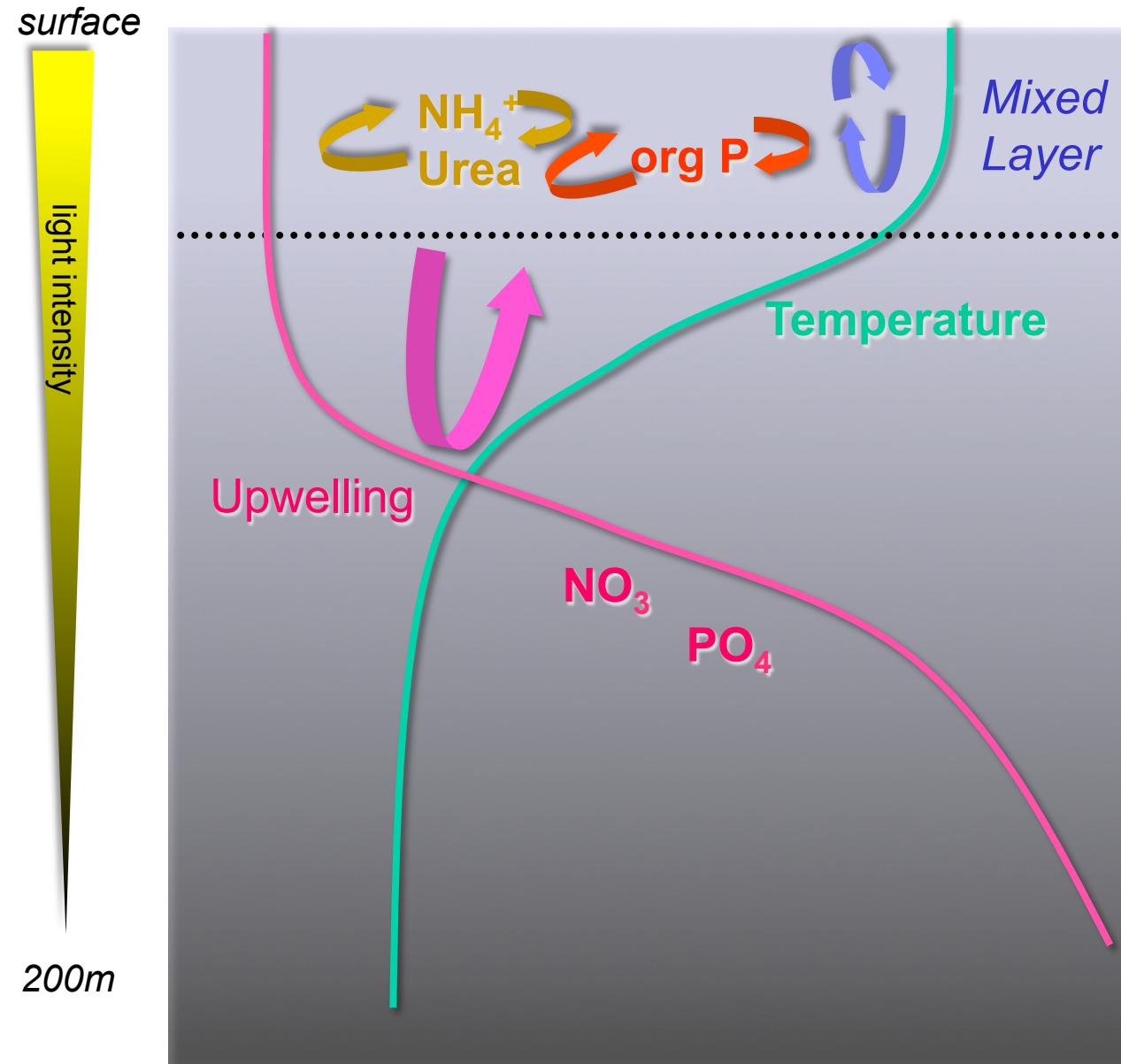
Gene expression highly choreographed



Components of two lectures

- ◆ The Cell
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- ◆ Single Cell Genomics
- ◆ Phage
- ◆ Interactions (and signaling?)

Structure of the ocean habitat

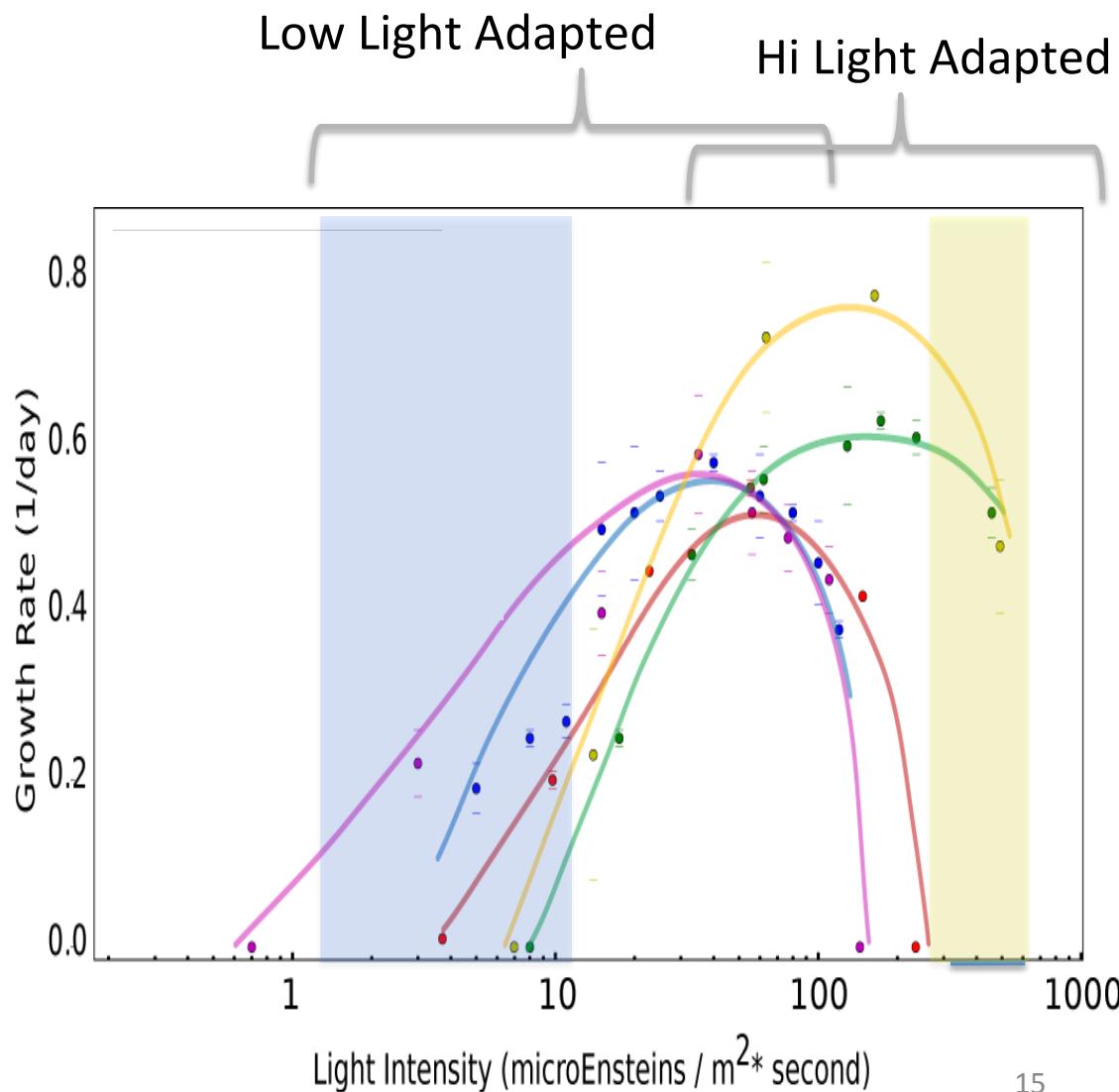
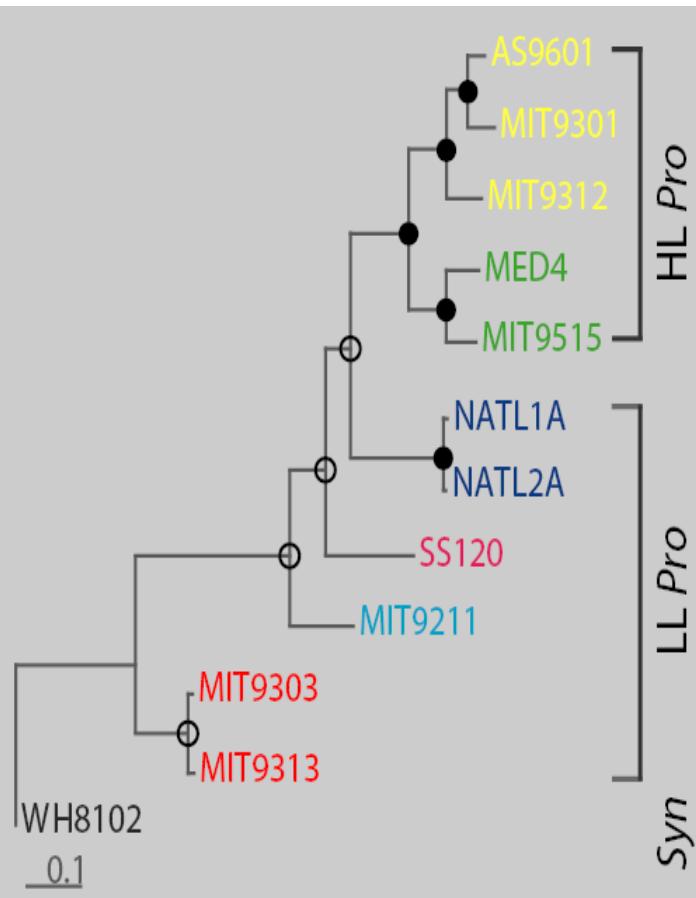


...physical and
chemical
gradients...

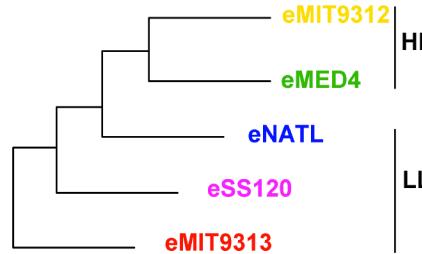
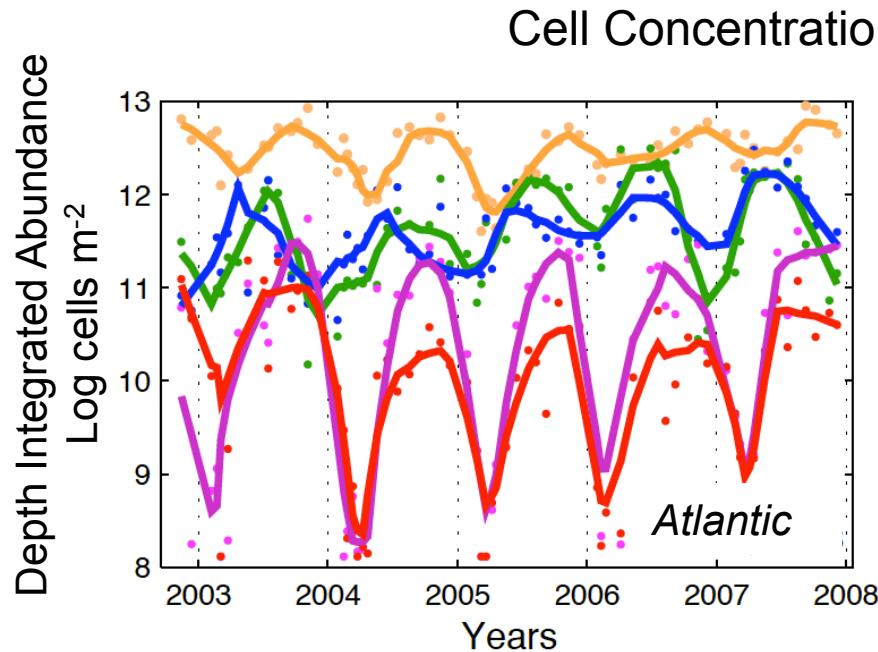
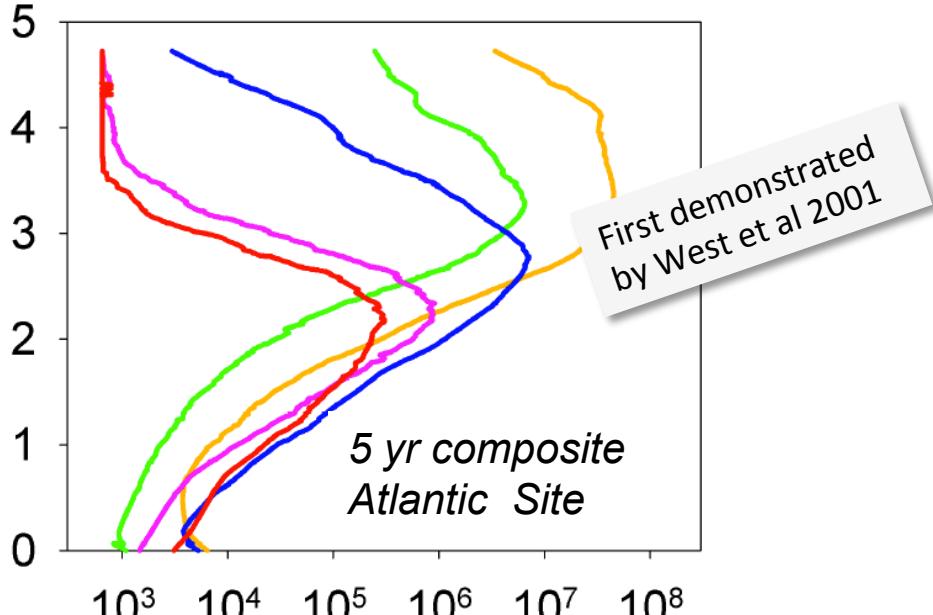
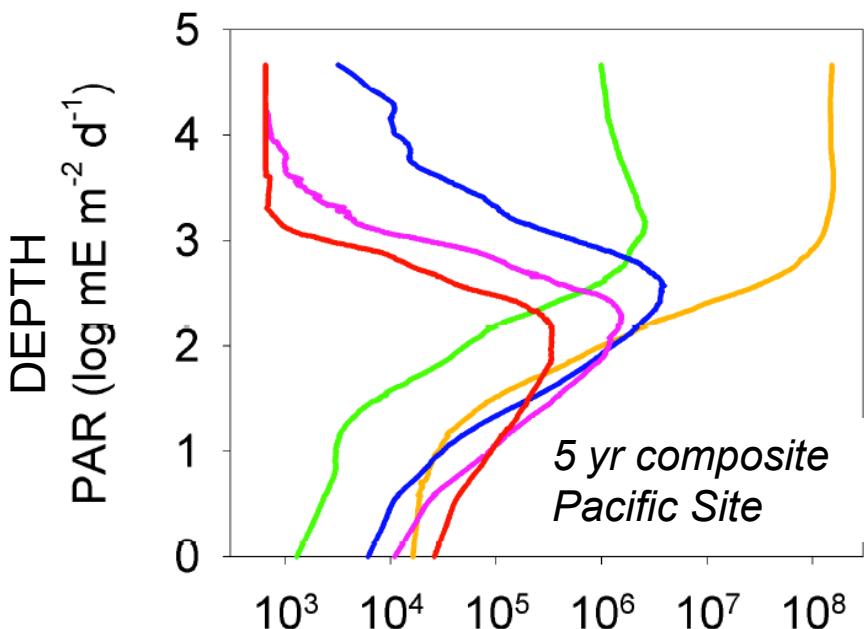
Niche
dimensions!

Light adaptation defines ecotypes...

Whole Genome Phylogeny
(matches rRNA ITS phylogeny)

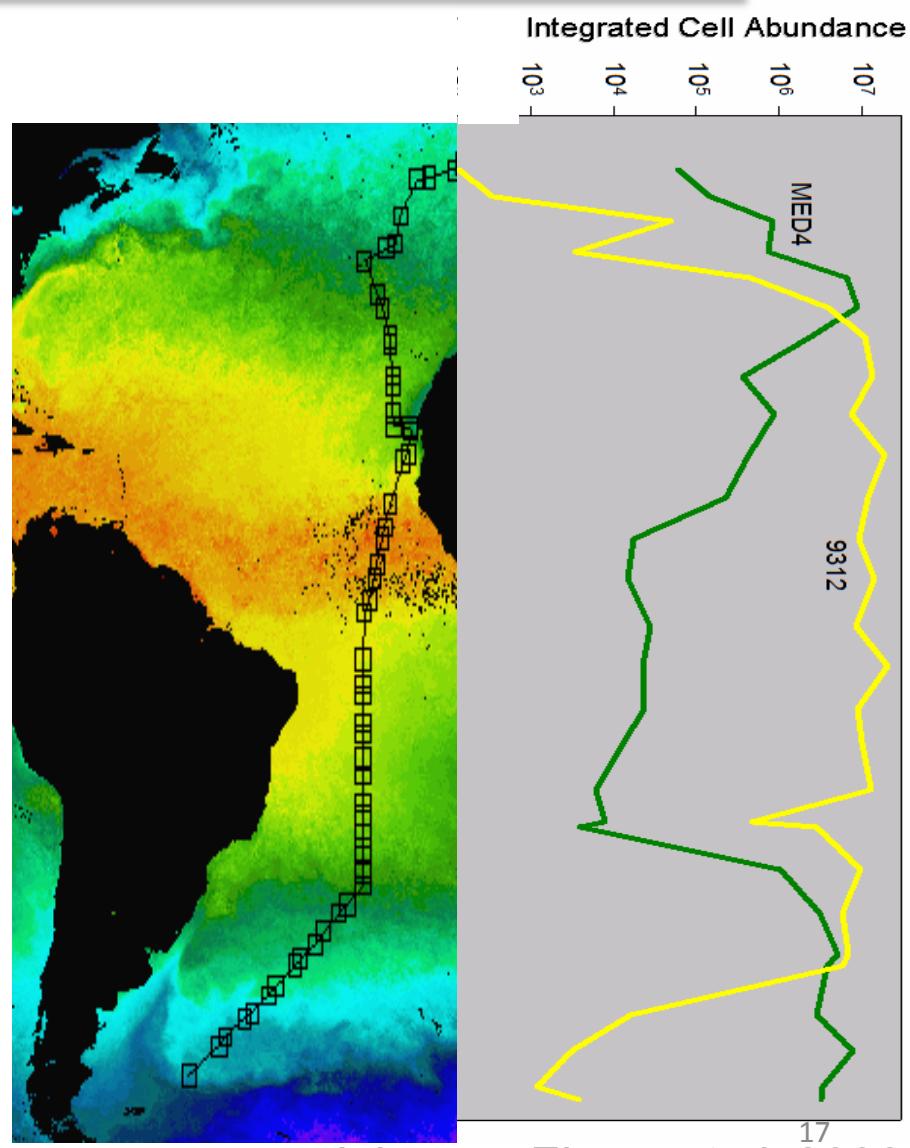
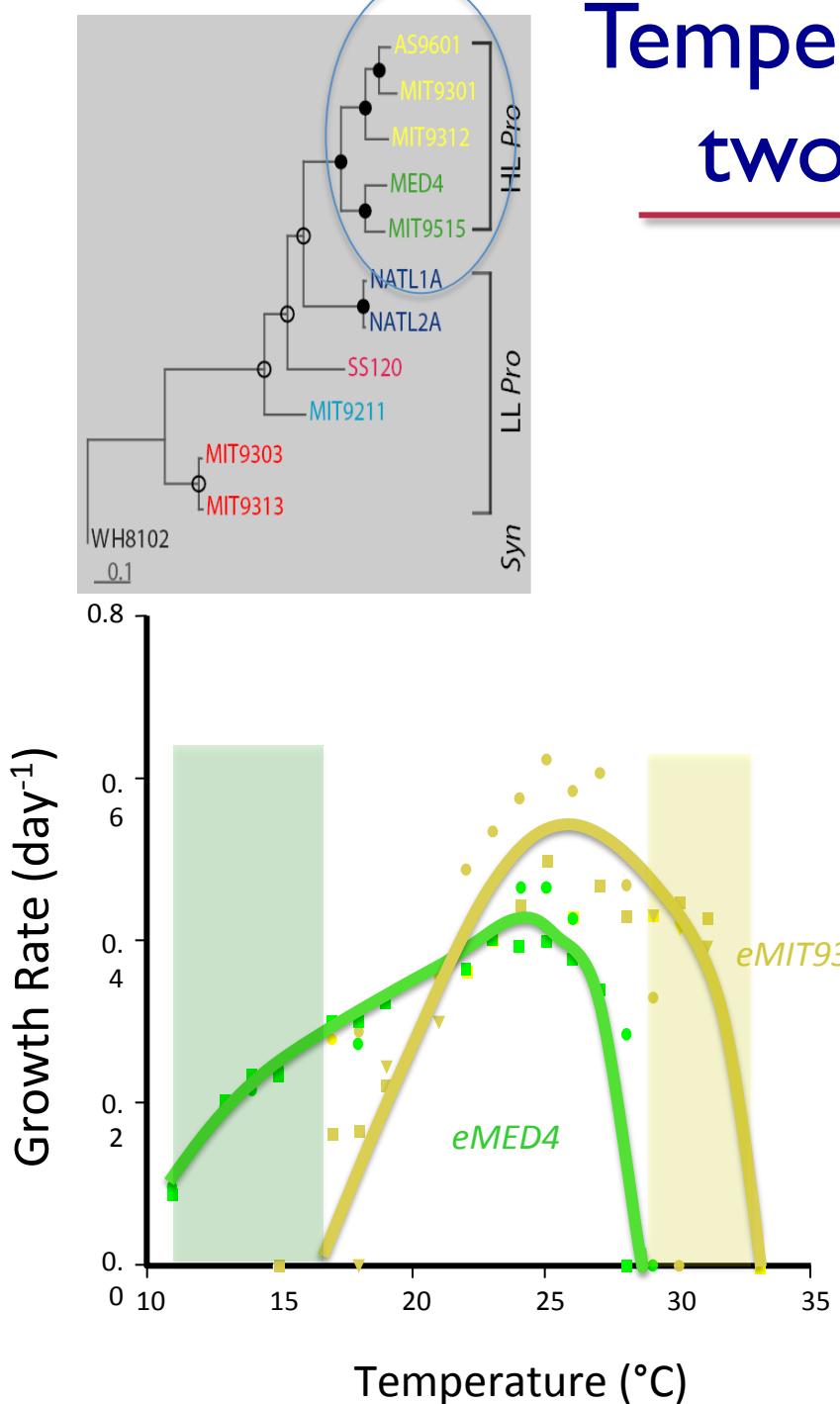


...leading to niche differentiation



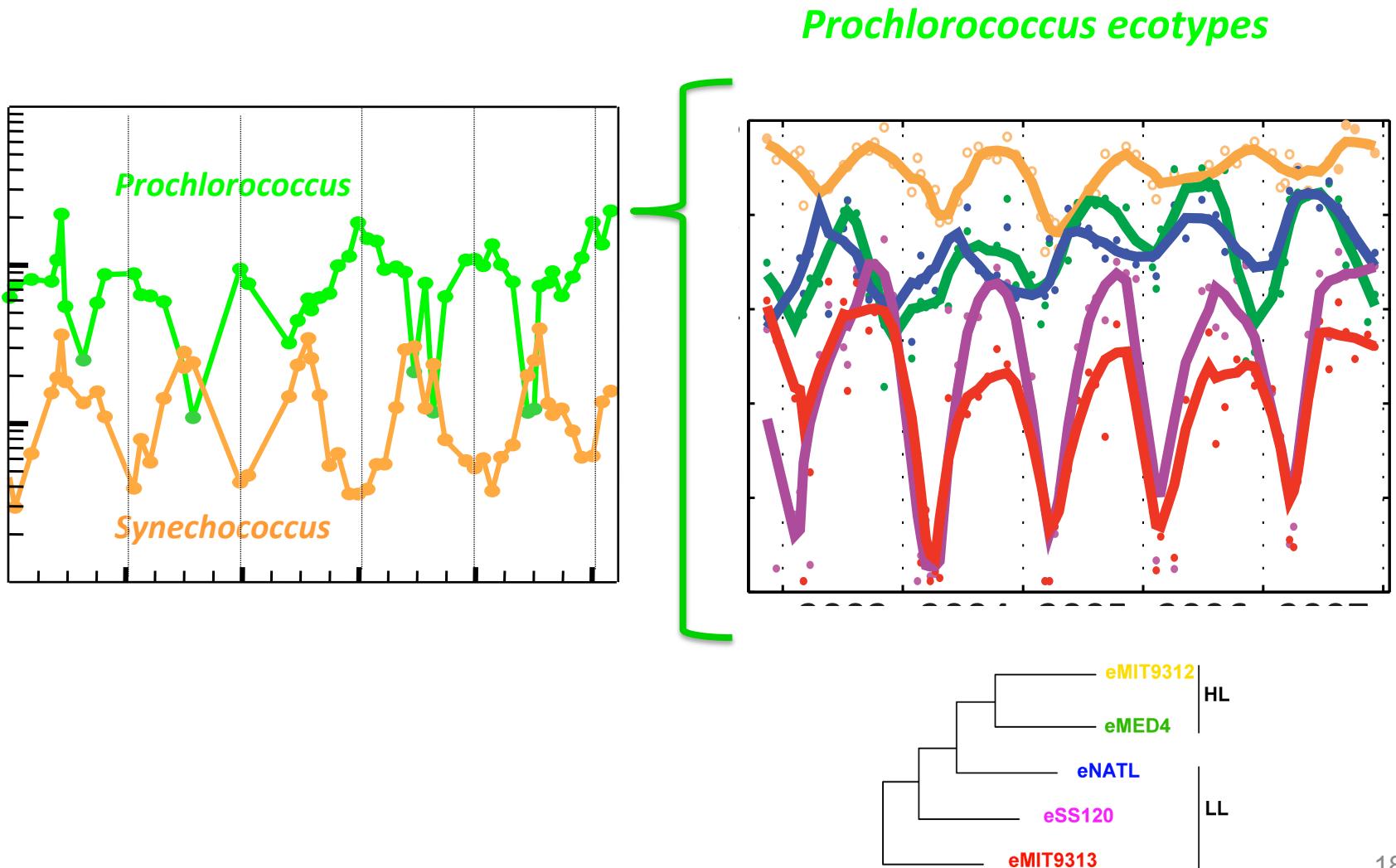
Malmstrom et al 2010

Temperature differentiates the two High Light ecotypes



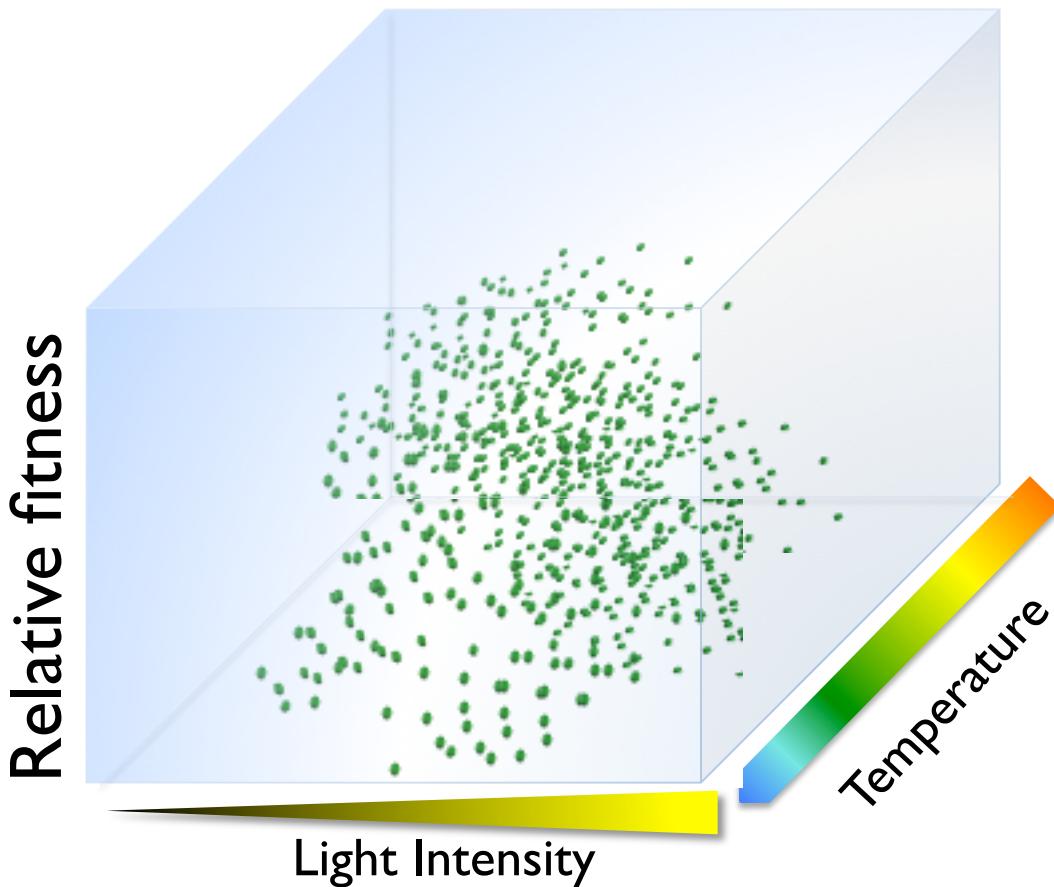
Johnson, Zinser et al, 2006

So there are meaningful layers, within layers, of diversity
(leads to stability)



Beginning to understand *Prochlorococcus* niche differentiation in two dimensions

BUT Remember...



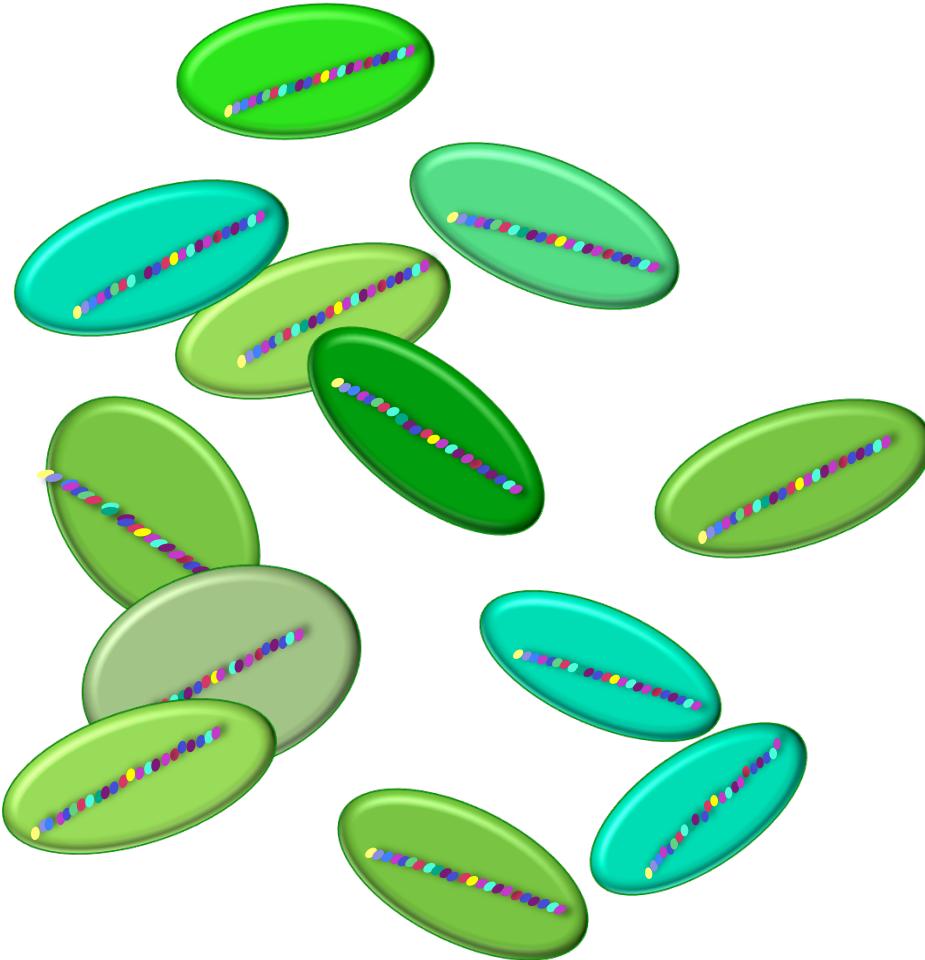
Ecological Niche:

n-dimensional hypervolume

n-2 dimensions to go!

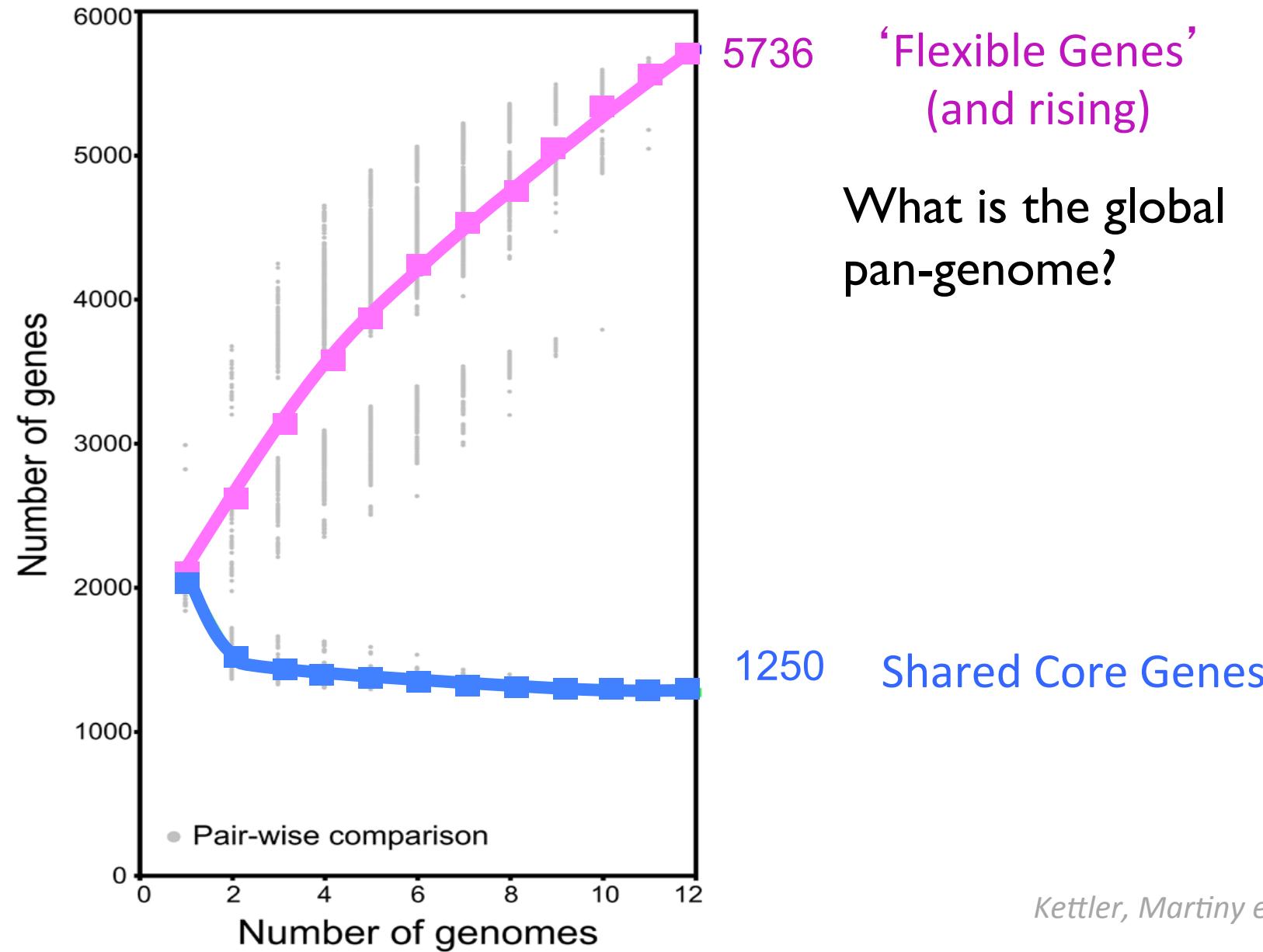
Enter Genomics:

Genomes of 13 strains (now 43)

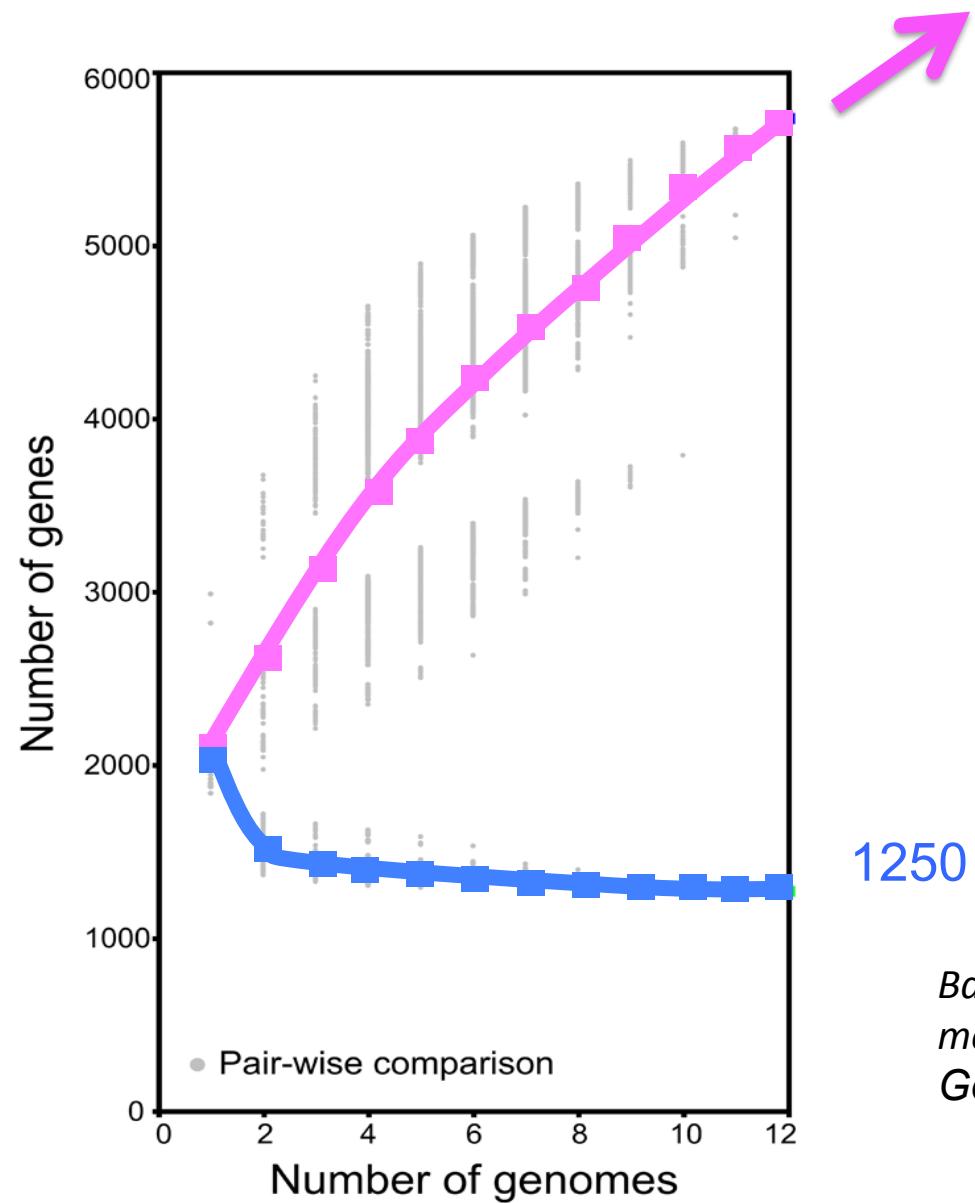


- What genes are “core” i.e. shared by all?
- How many unique genes in the gene pool of ALL *Prochlorococcus*?
- Their functions?

The core and flexible genomes



Global Pan-genome is huge



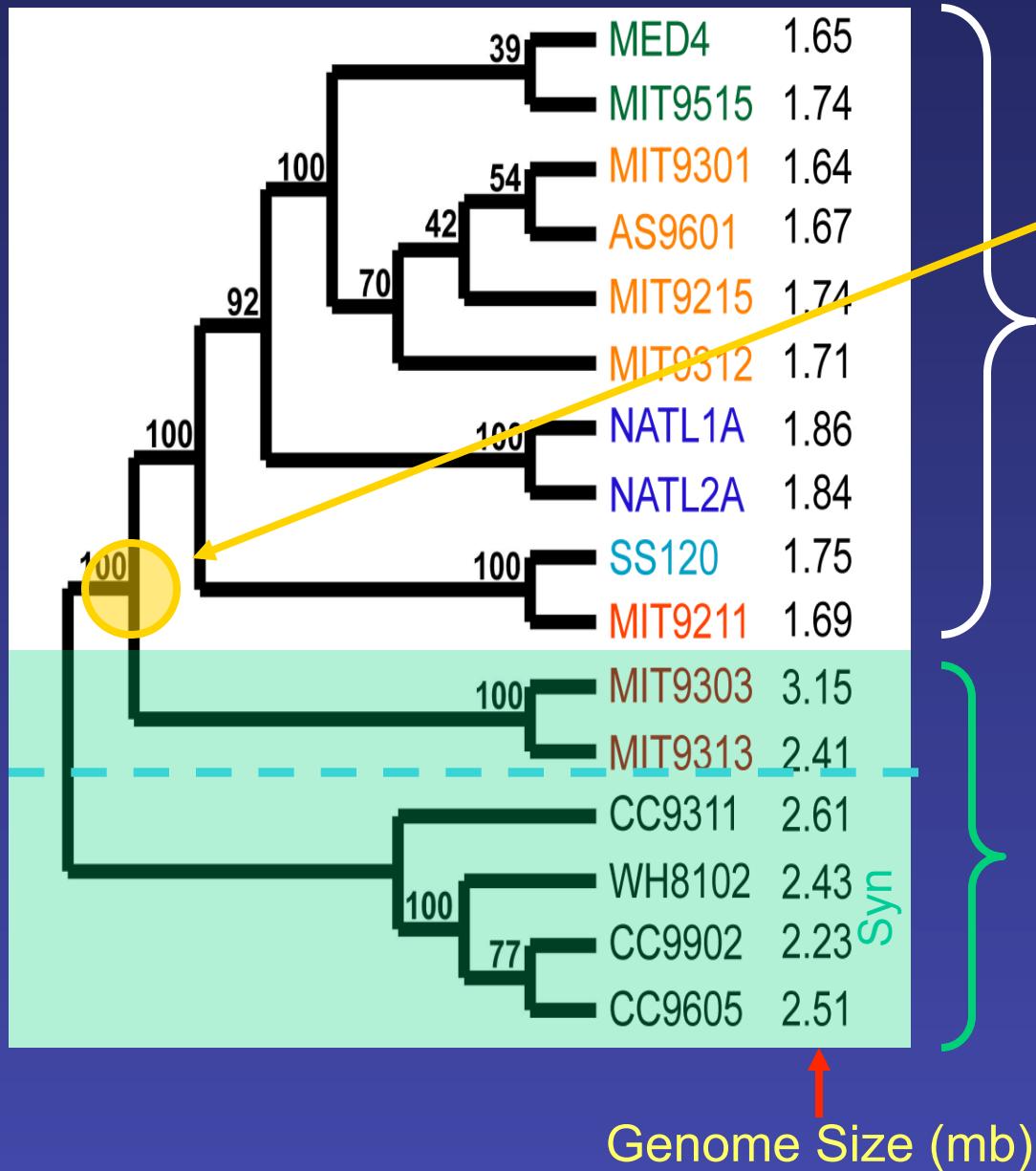
Total of 57,792 genes
distributed among an effective
population size of 10^{11} cells

(Total number of cells in
oceans is estimated at 10^{27})

1250 Core Genes

Baumdicker et al 2012. *The infinitely many genes model for the distributed genome of bacteria.*
Genome Biol Evol. doi: 10.1093/gbe/evs016

Genome size in *Prochlorococcus* is variable



Systematic Genome Reduction? NO

small genomes

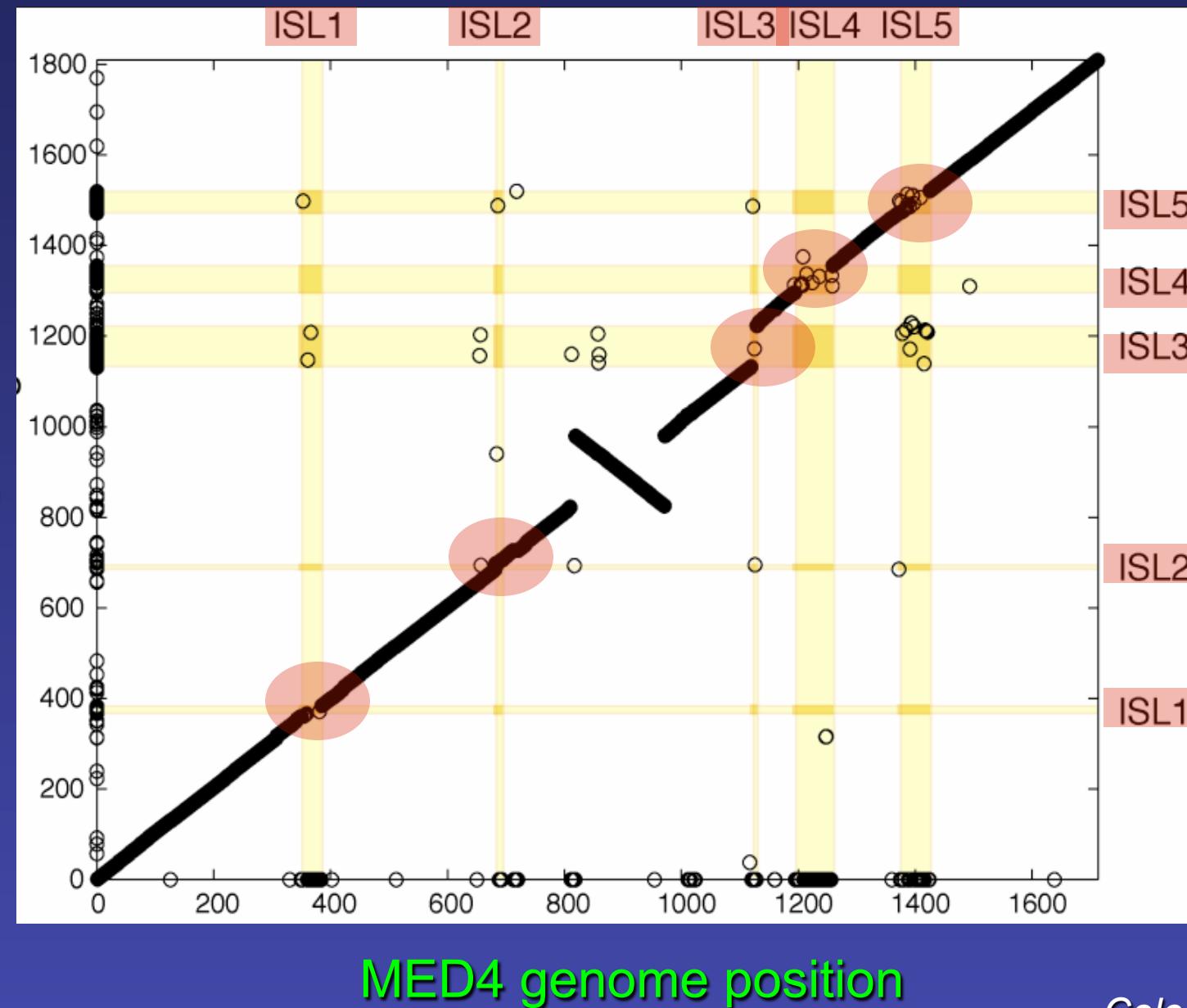
Genes are gained and lost – with most of the action in the “leaves of the tree”

large genomes

1810
genes

1574 Shared genes

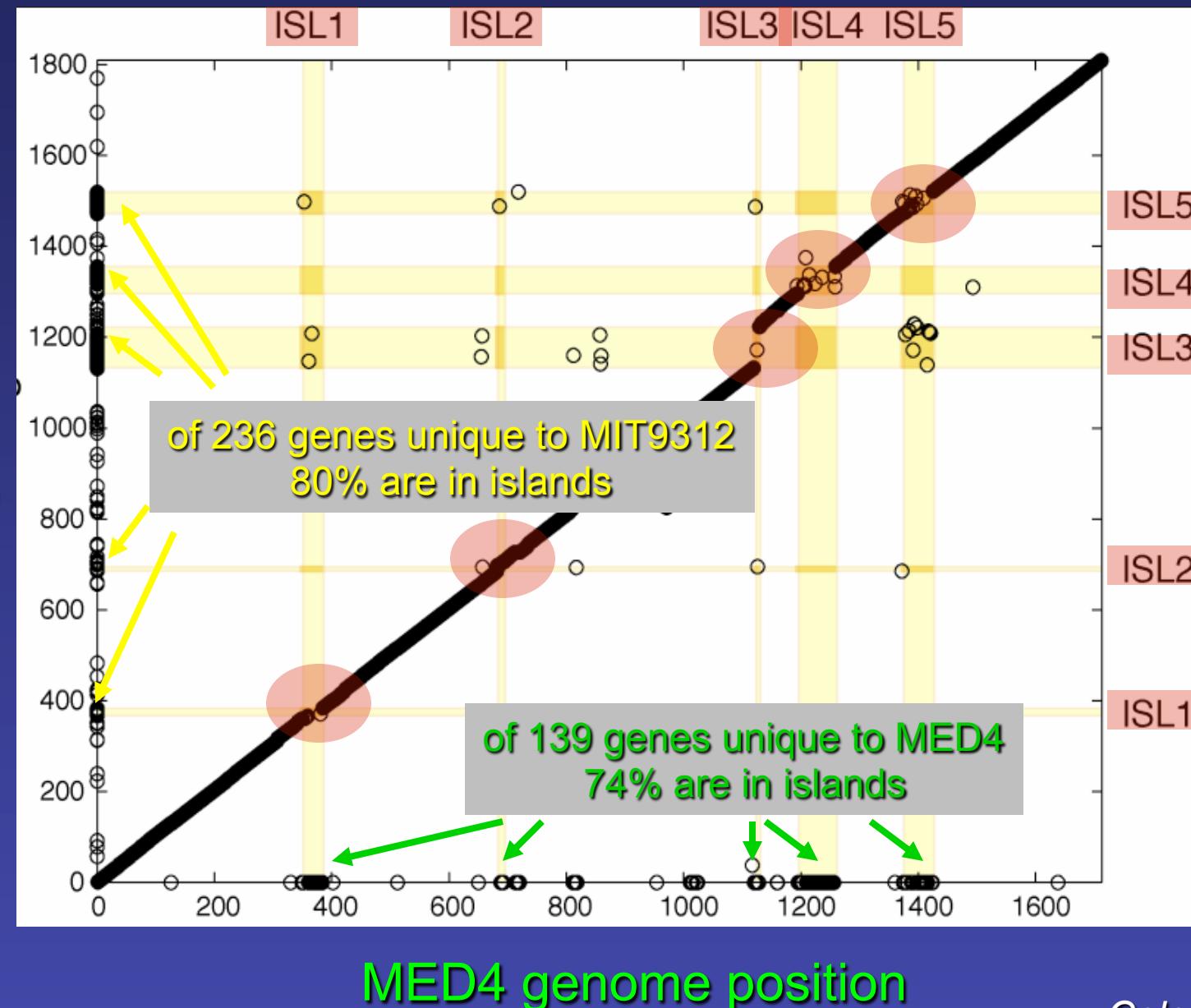
1713
genes



1810
genes

1574 Shared genes

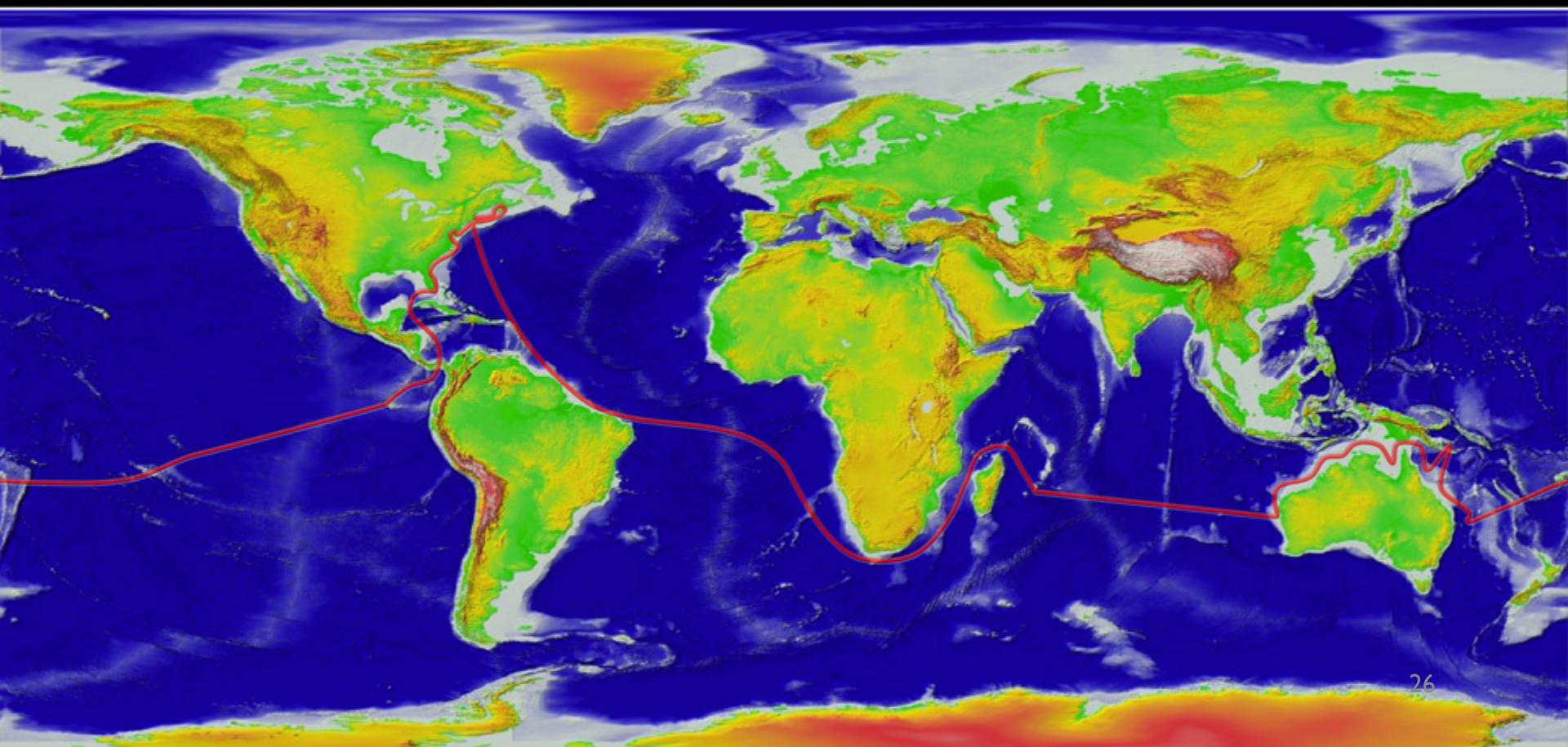
1713
genes



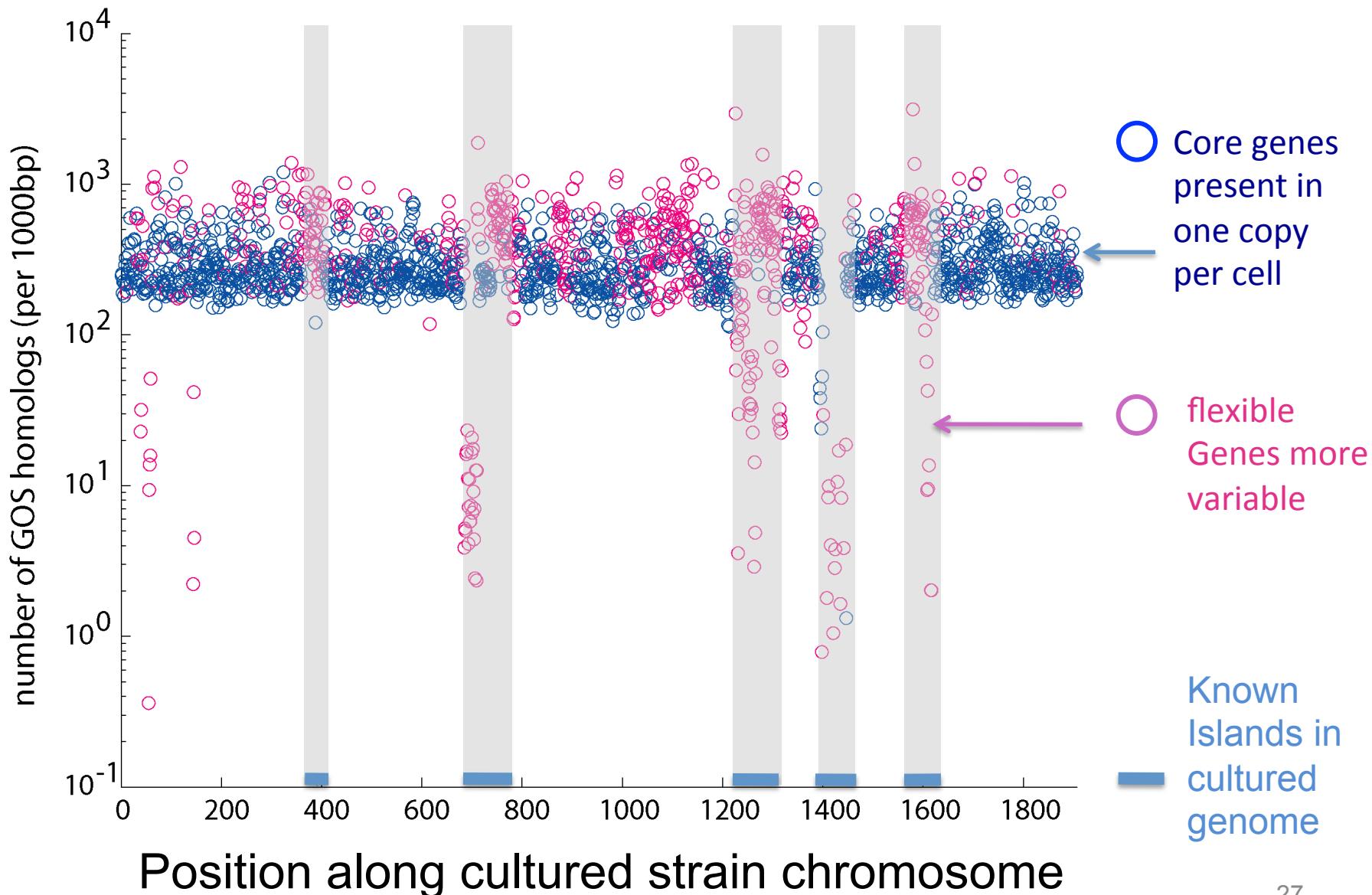
Phage are implicated as playing a role in island gene dynamics

Prochlorococcus genes are abundant in the Global Ocean Survey (GOS)

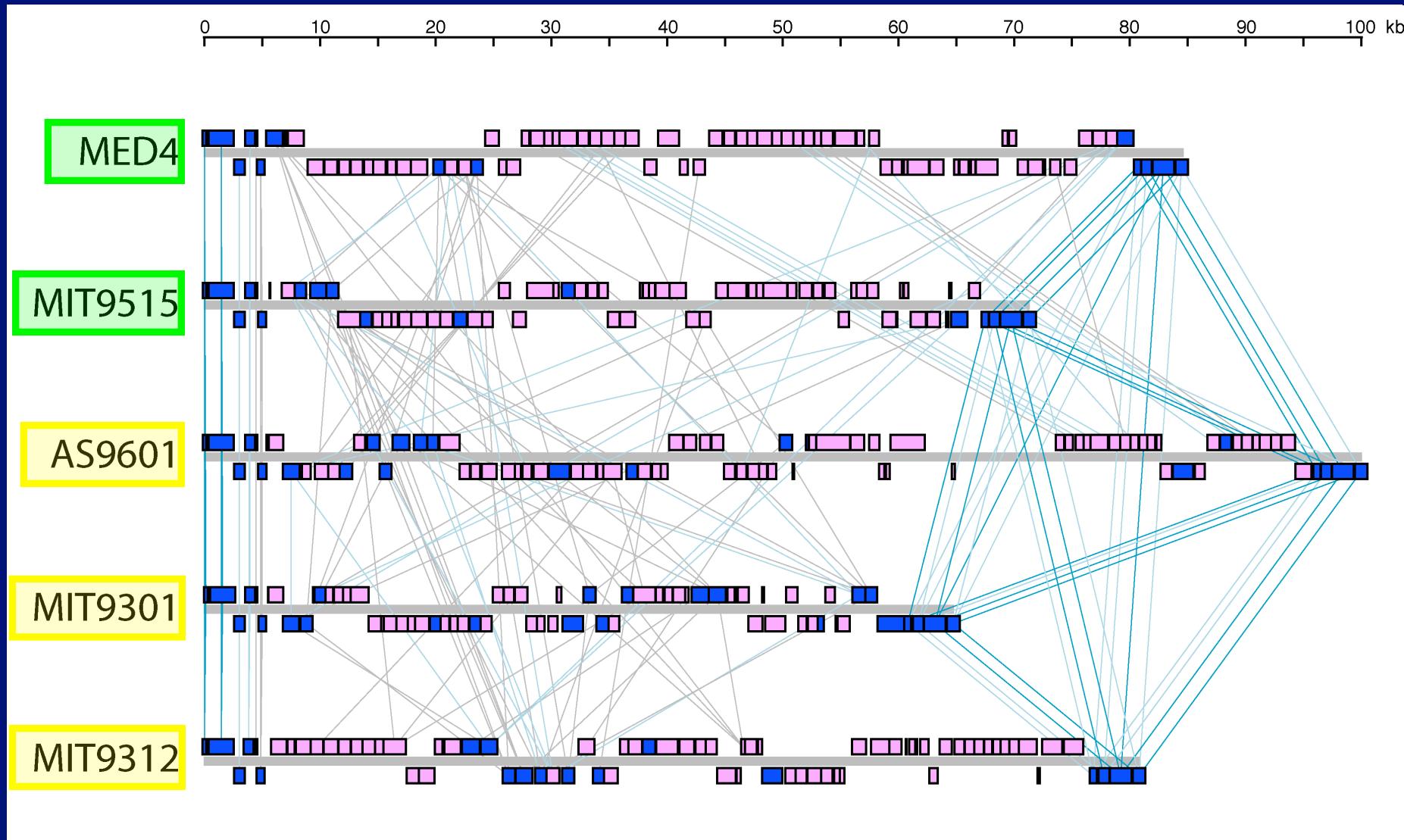
> 10% of the sequenced fragments are from *Prochlorococcus* at many stations



Core and flexible genes, and islands, visible in metagenomic data

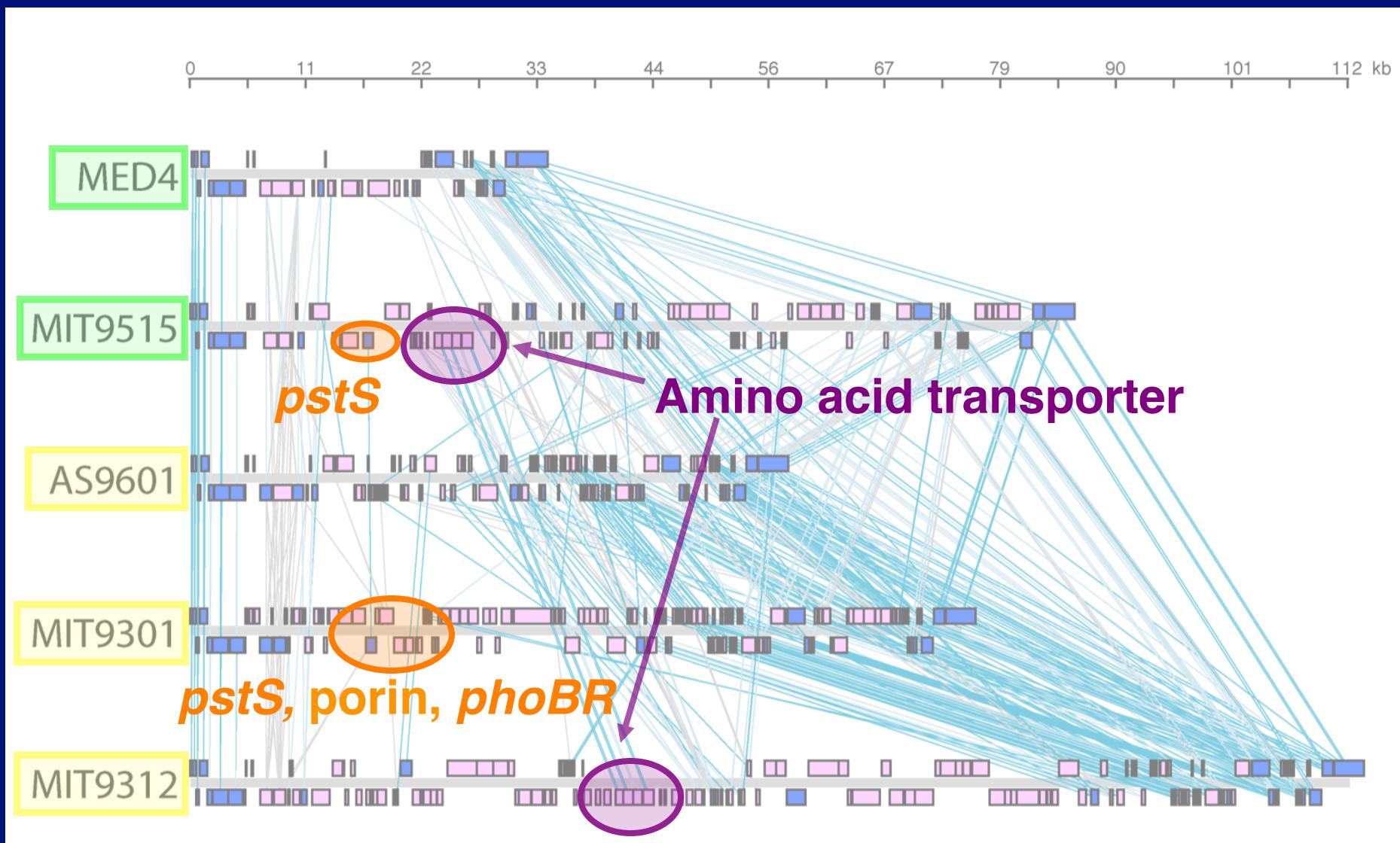


Island 4 - LPS Biosynthesis Genes



■ Found in all genomes

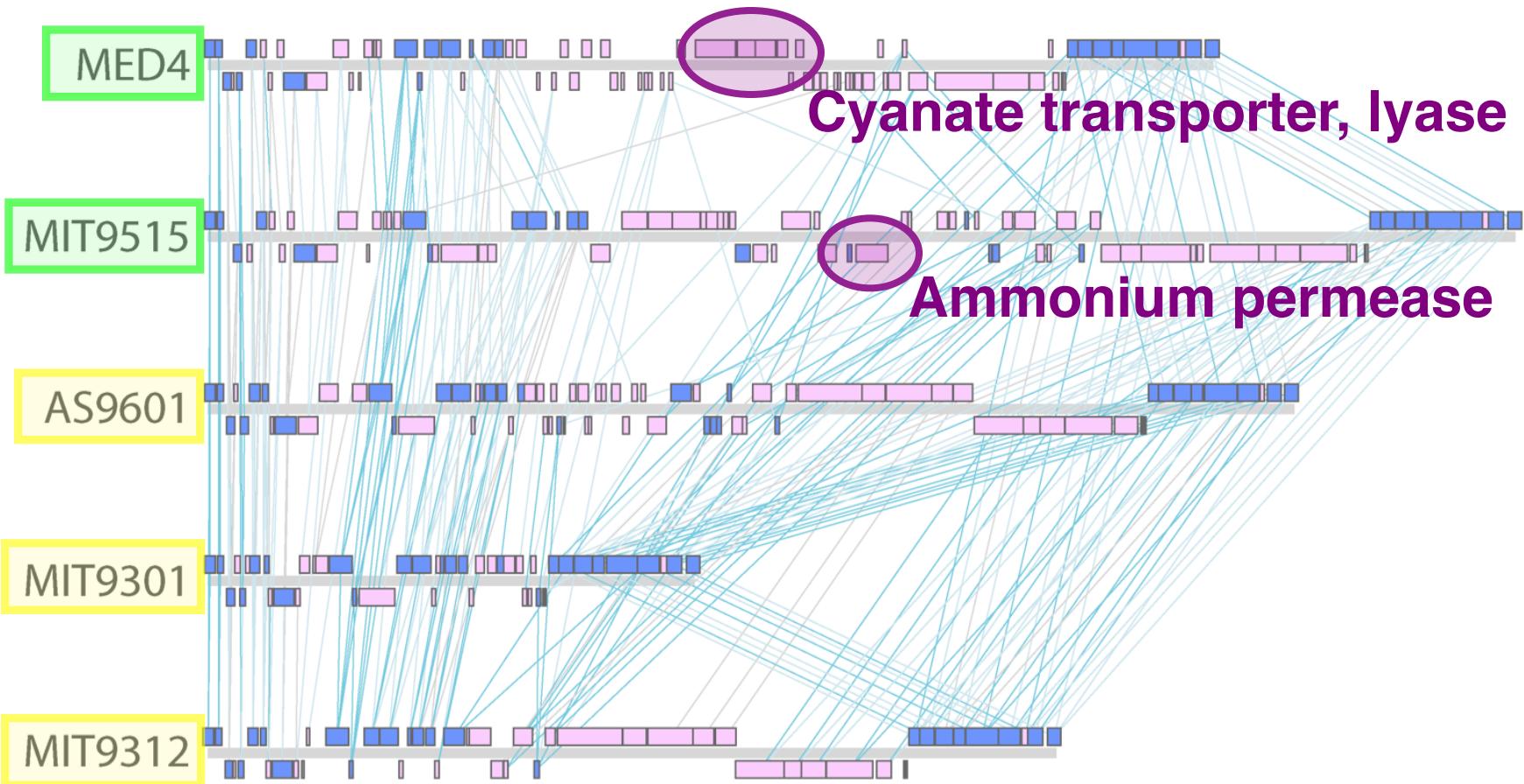
Island 3 – Genes involved in N and P acquisition



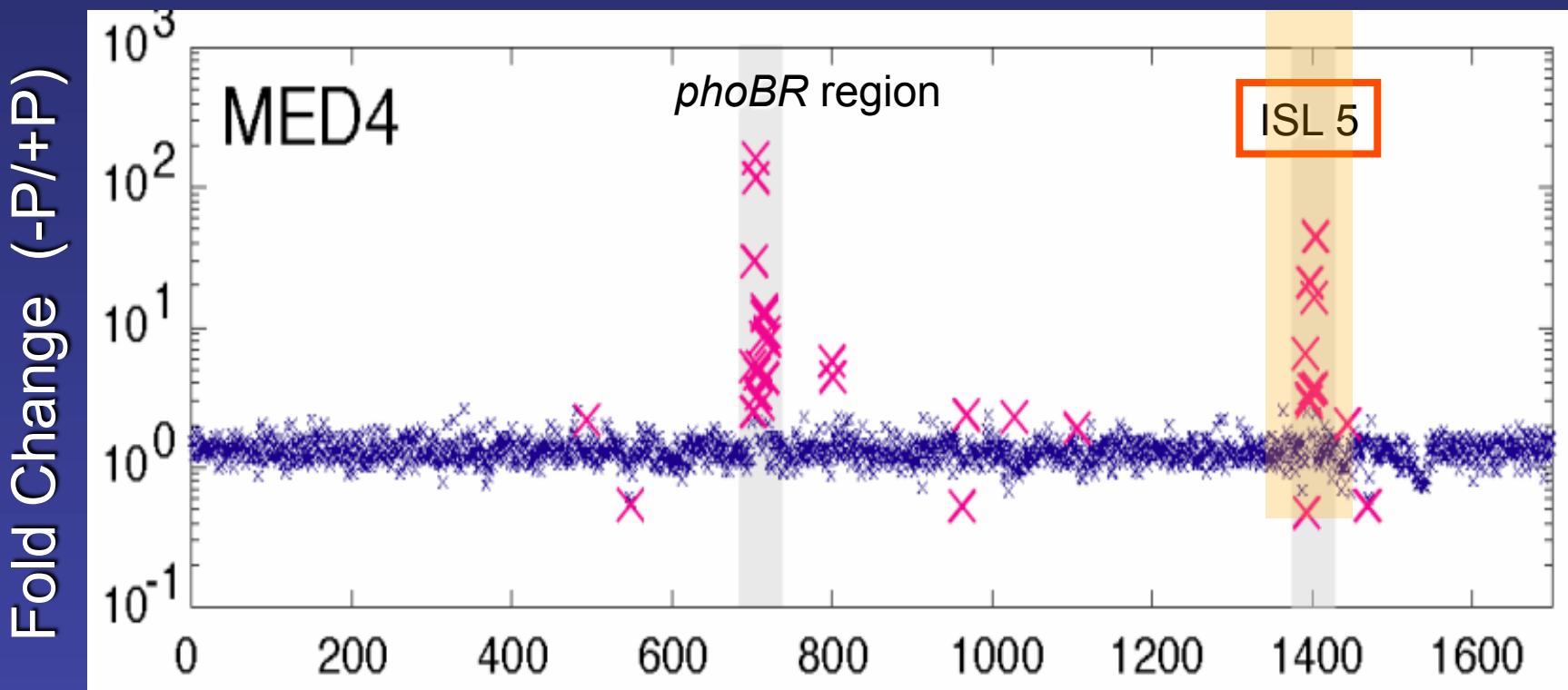
Island 1 – Genes involved in N acquisition

ISL1

0 5.5 11.0 16.5 22 27.5 33 38.5 44 49.5 55 kb



Island 5 genes (of unknown function) are upregulated under P-starvation in MED4
(but not in MIT9313)

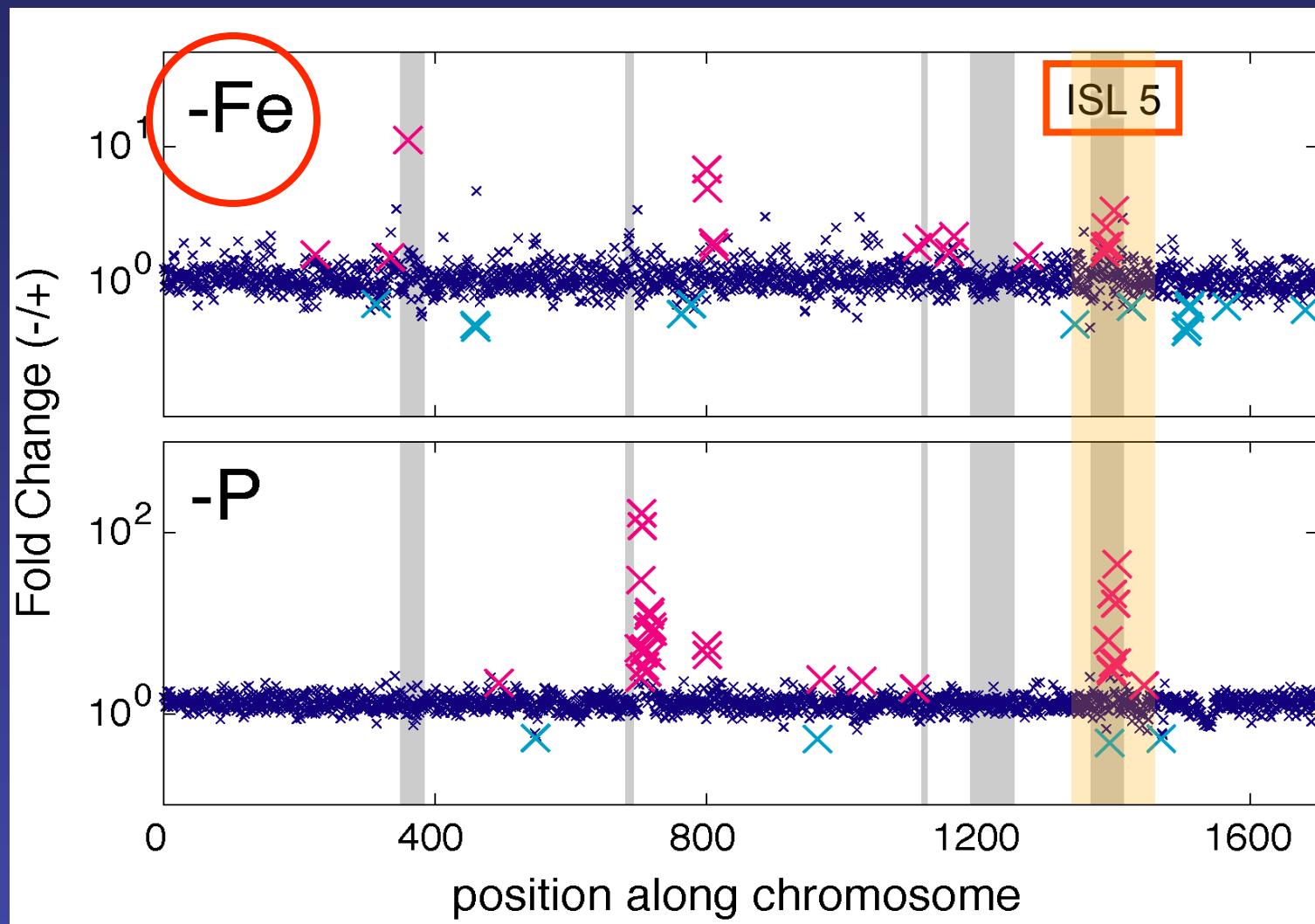


Position of Gene in Genome

31

Martiny/Coleman et al 2006

ISLAND 5 Genes are also upregulated under iron starvation



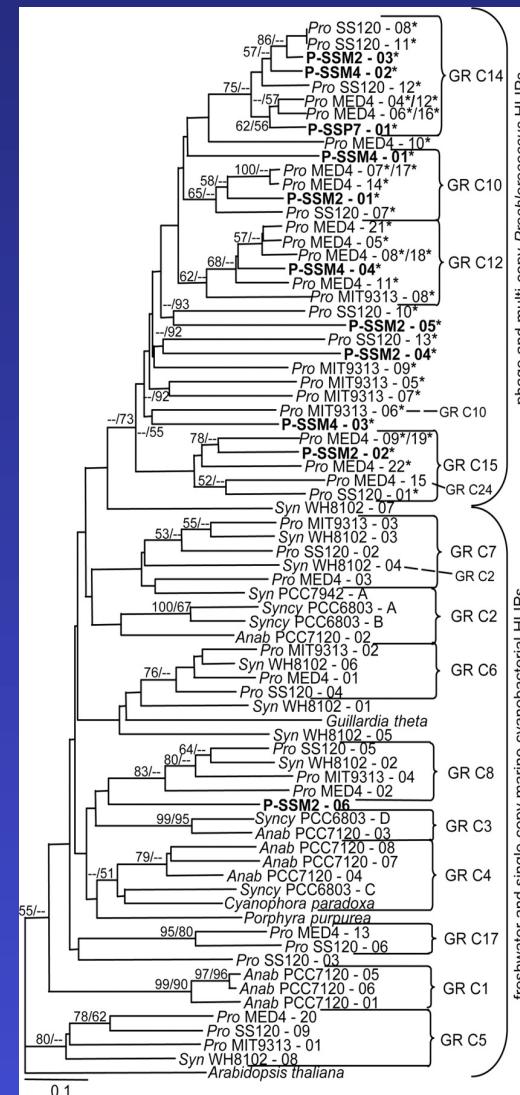
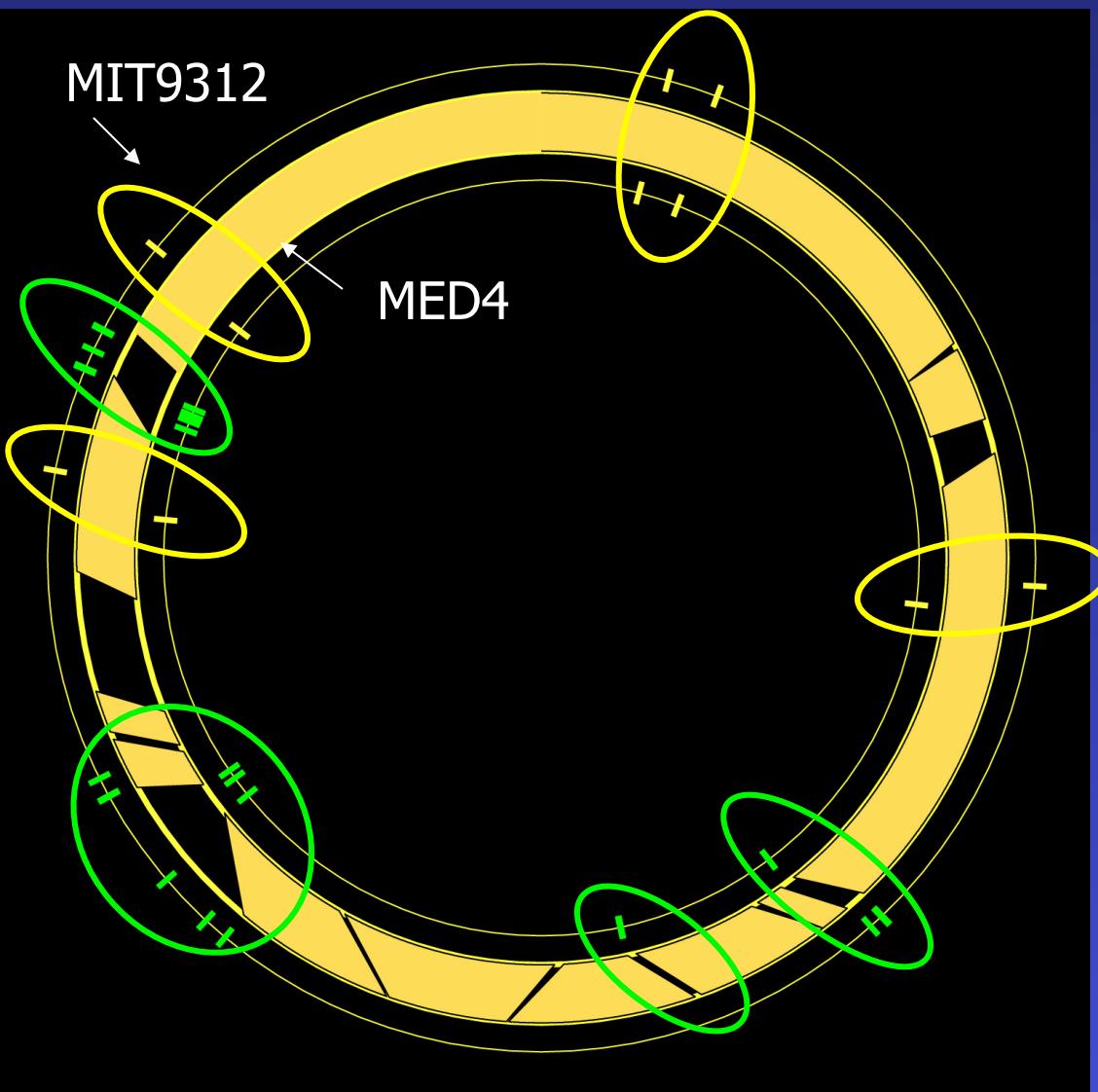
Components of two lectures

- ◆ The Cell
- ◆ Niche Dimensions of *Prochlorococcus*

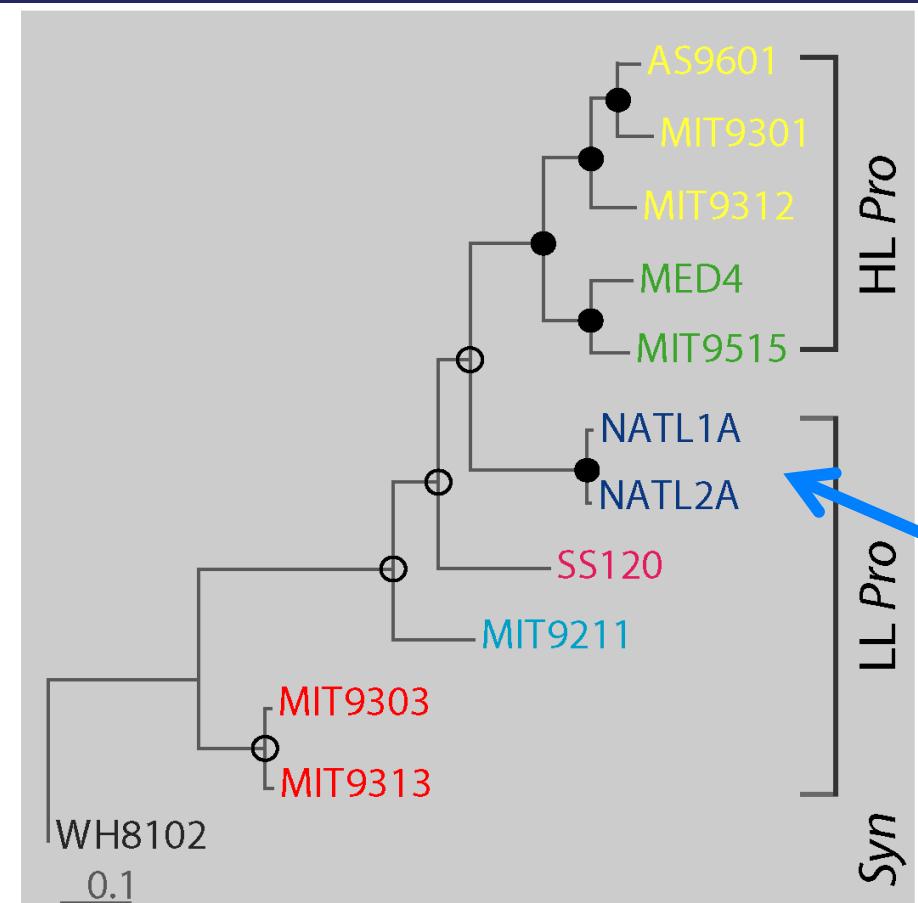
More on nutrients next time

- ◆ Single Cell Genomics
- ◆ Phage
- ◆ Interactions (and signaling?)

Phage-related HLIPs may play a role in island insertion

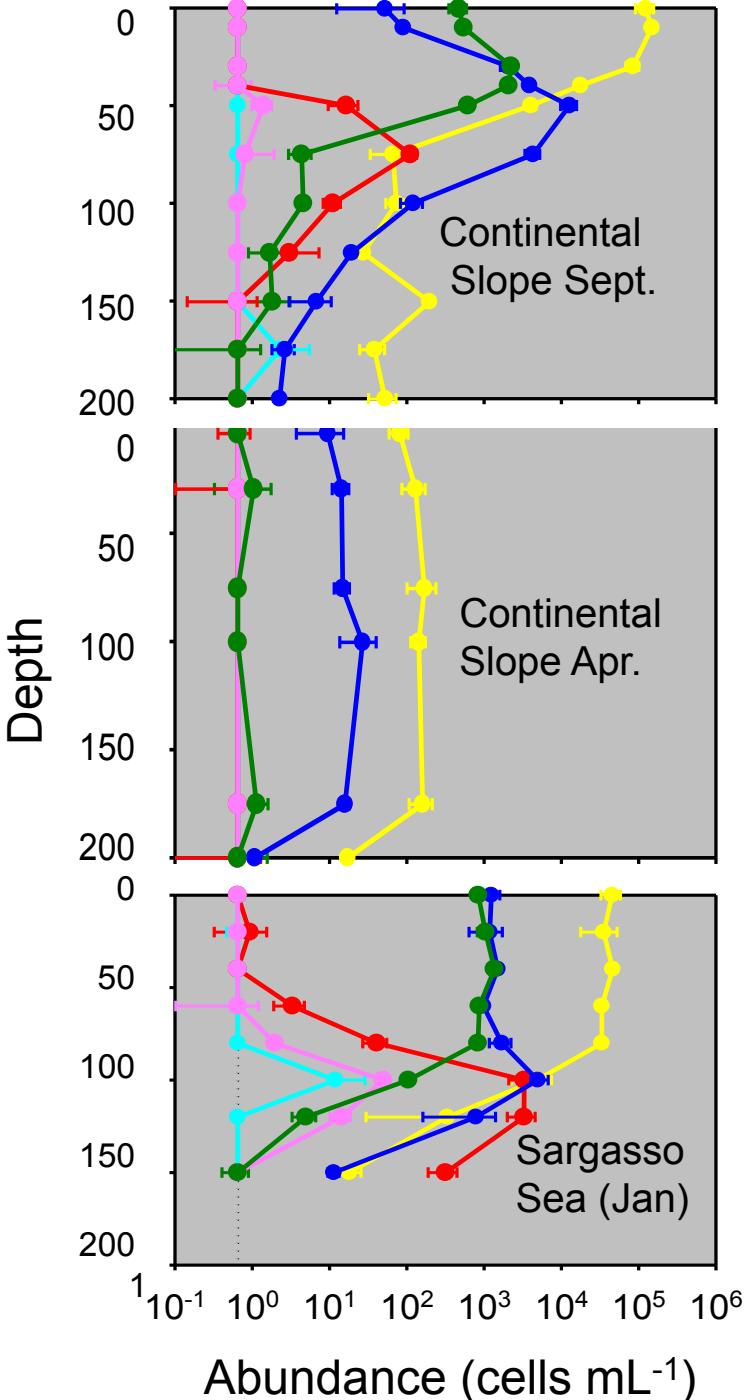


Speaking of HLIPs...



“The NATLs” are very interesting in this regard

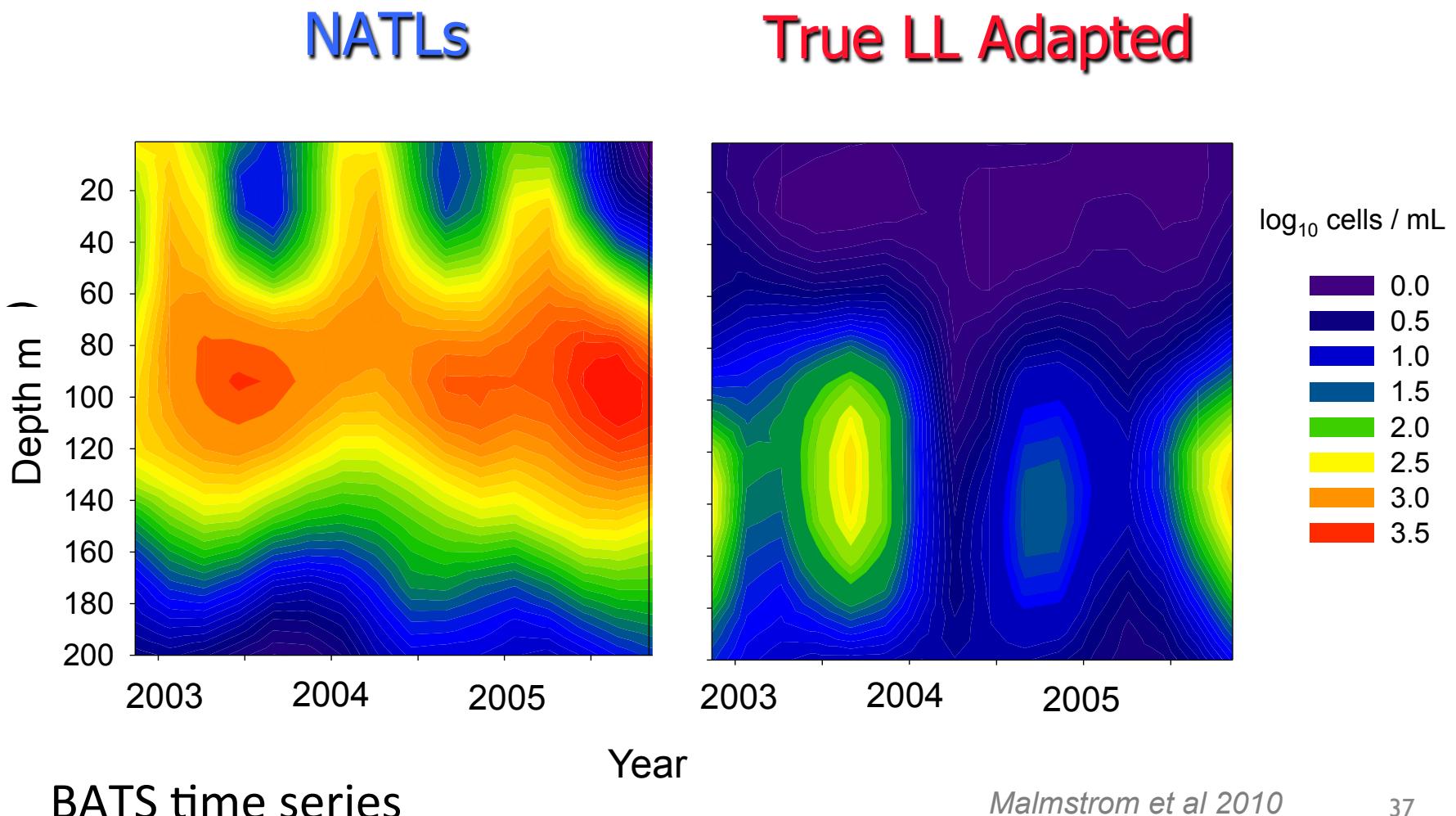
(note intermediate taxonomic position)



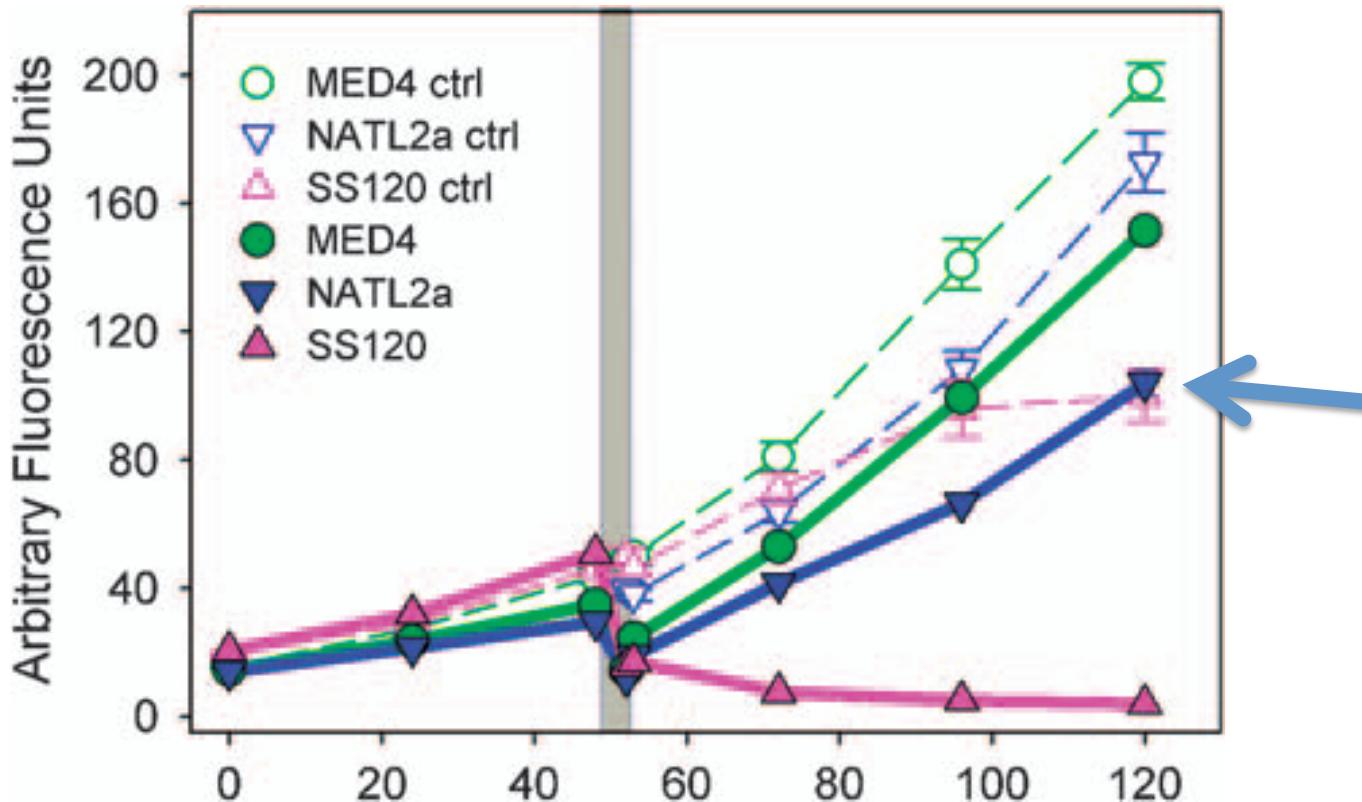
Handle high light better than
other LL ecotypes...

...and deep mixing better than
some HL ecotypes

HYPOTHESIS: NATLs better adapted to fluctuating light

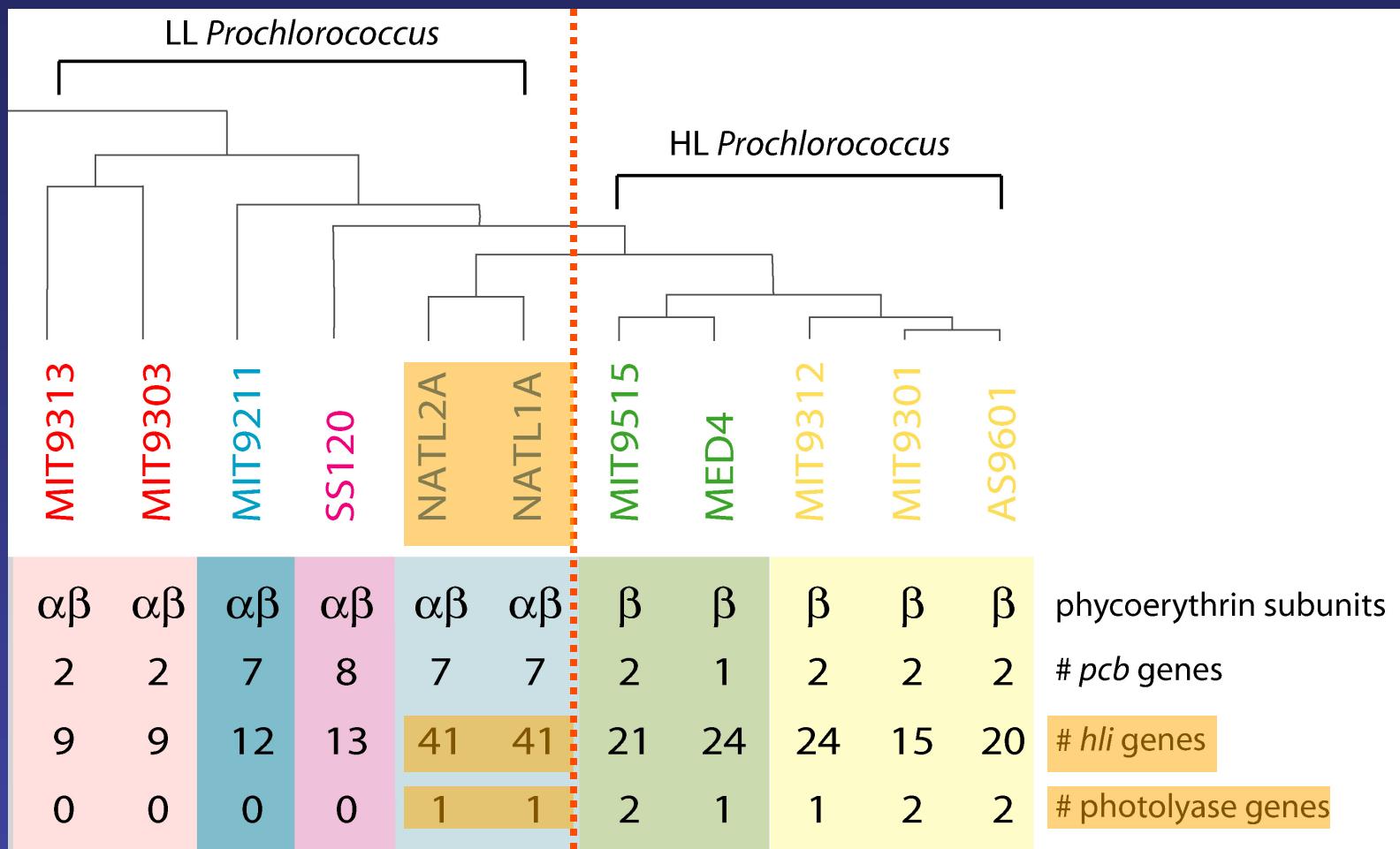


Back to the lab...



“The NATLs” are more resistant to light shock than other LL strains

What do the genomes tell us?



Components of two lectures

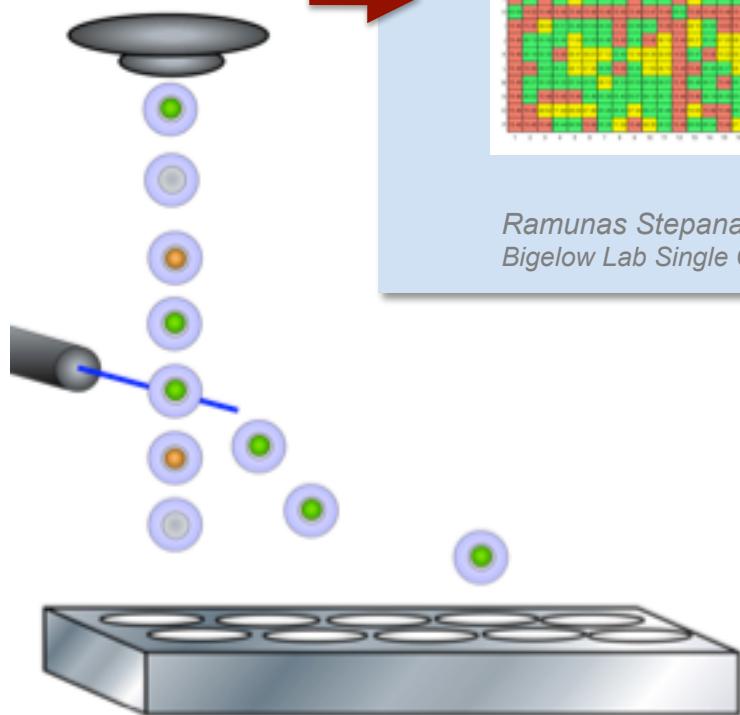
- ◆ The Cell
- ◆ Niche Dimensions of *Prochlorococcus*

More on nutrients next time

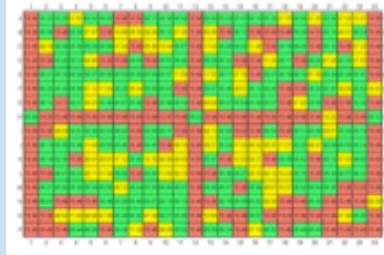
- ◆ Single Cell Genomics
- ◆ Phage
- ◆ Interactions (and signaling?)

Single Cell Genomics Pipeline

Flow Sort



MDA Amplification



Ramunas Stepanauskas
Bigelow Lab Single Cell Facility

Amplify and sequence identifier gene of interest:
eg. *rRNA ITS, narB, etc.*

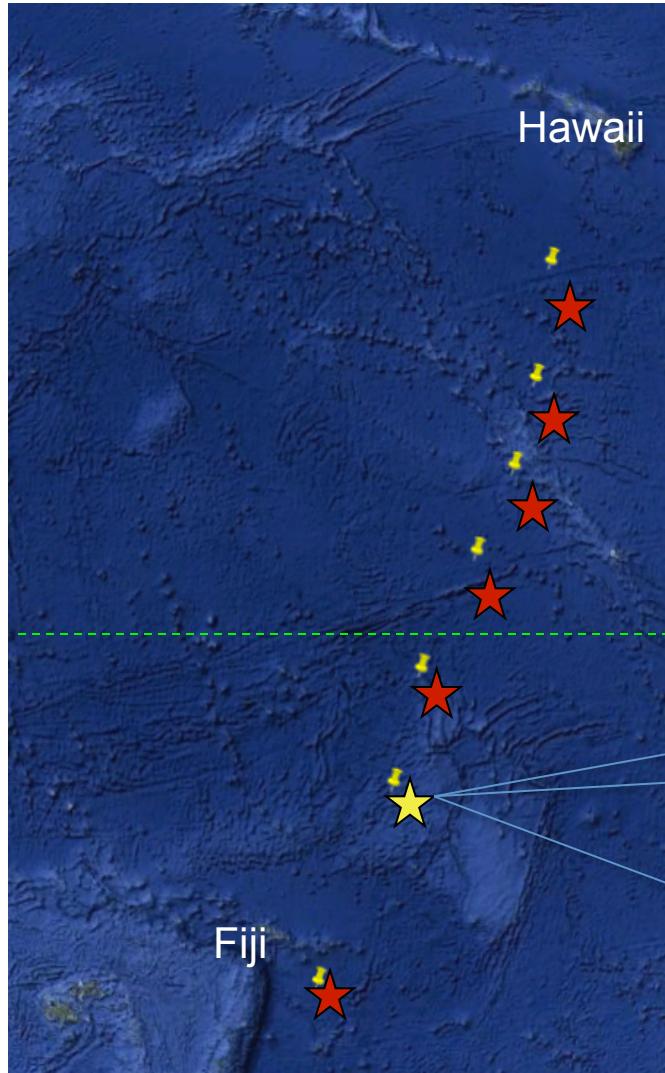
Select candidates for sequencing

Re-amplify and make sequencing libraries

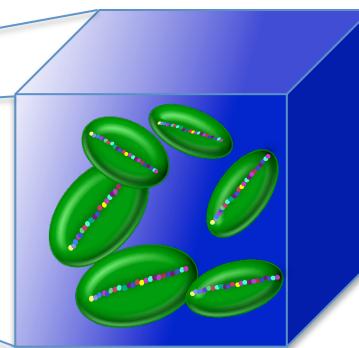
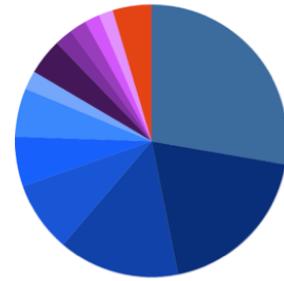
Illumina Sequencing

Assembly

Genomes of 5 Wild *Prochlorococcus* Cells



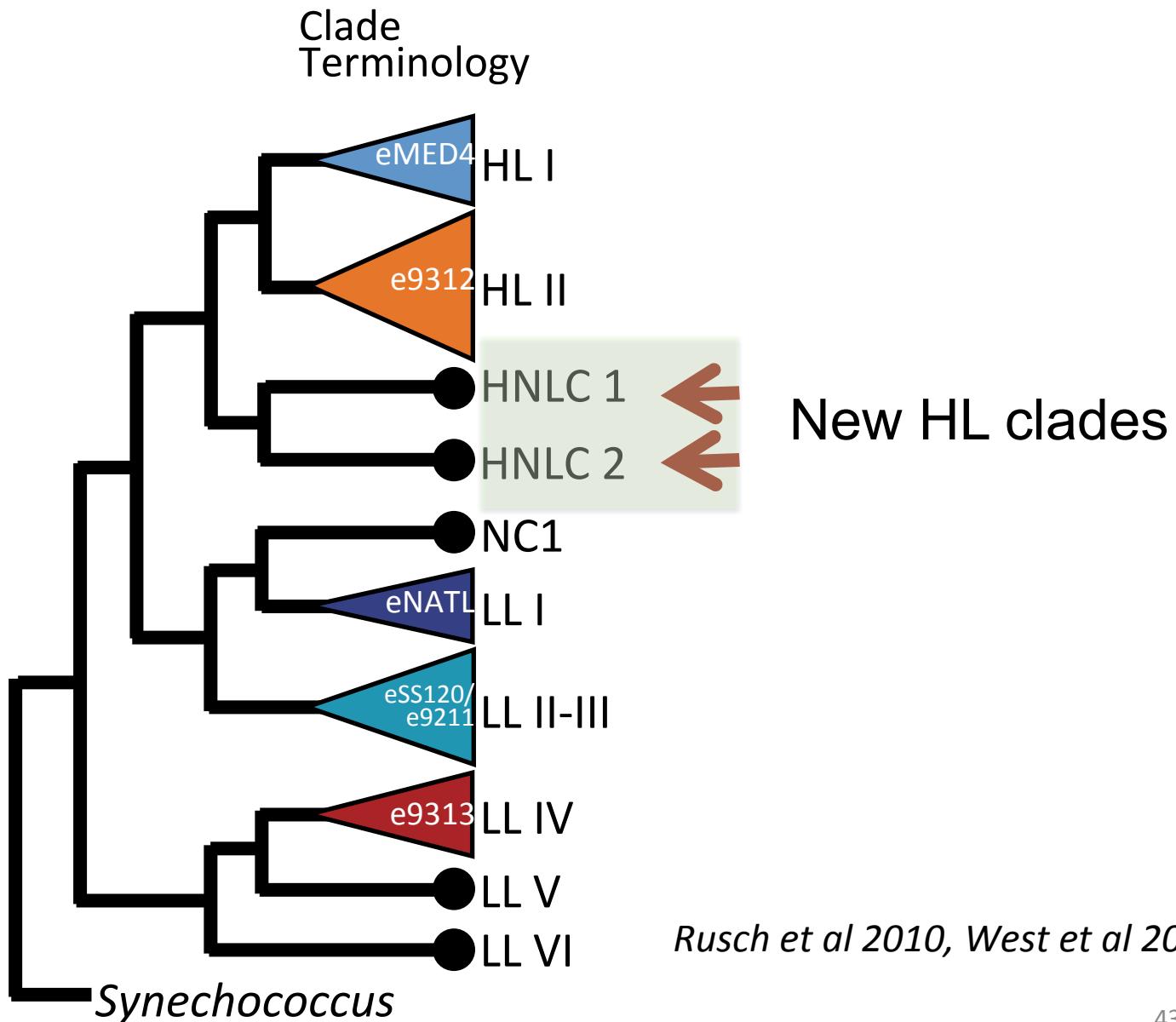
- ❑ Expanded recruited GOS reads by 15%
- ❑ Added to **641 new genes** to *Prochlorococcus* pan-genome
- ❑ New functions



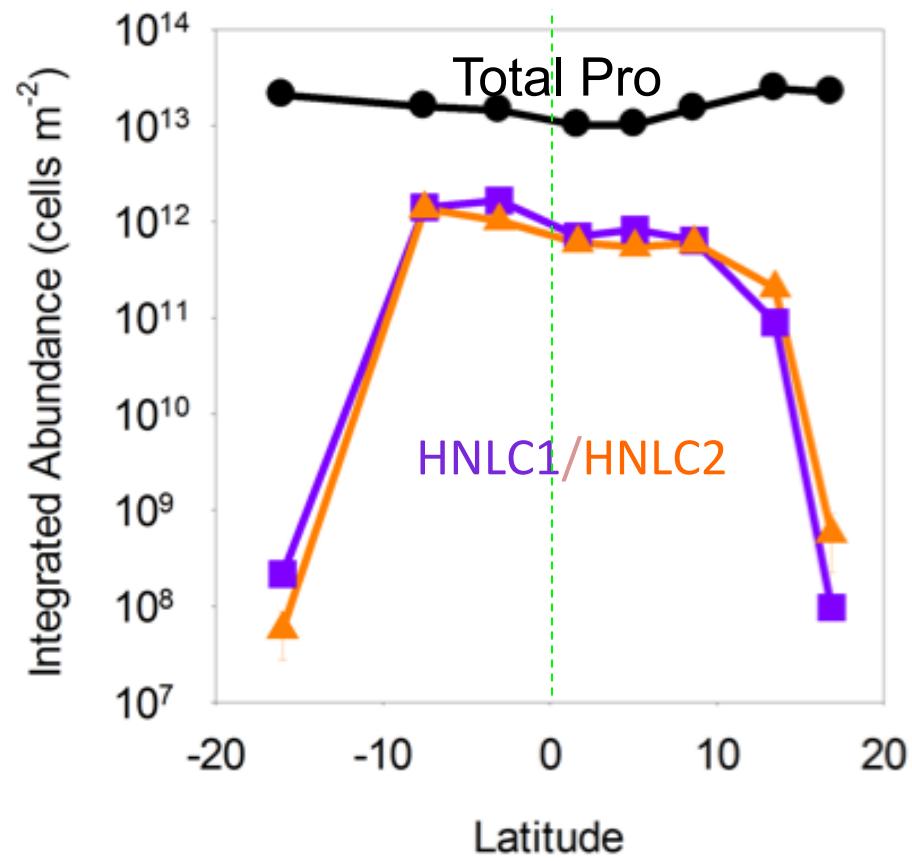
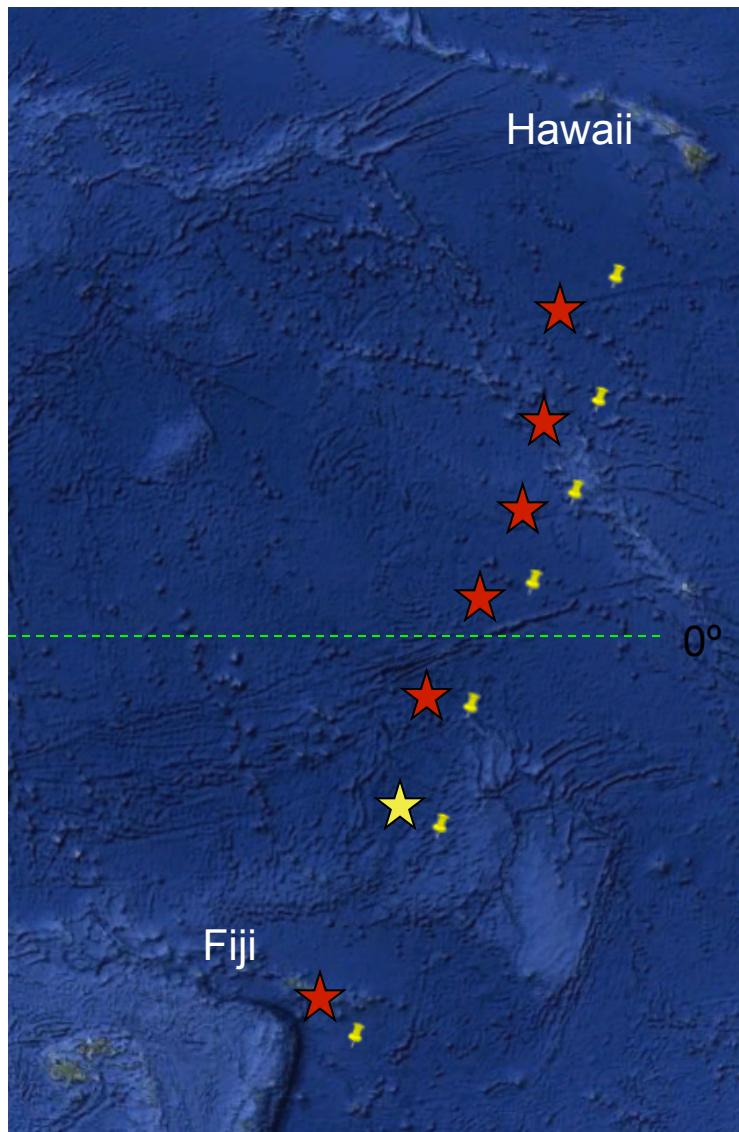
Malmstrom, Rodrigue, 2012 in revision

Two new clades

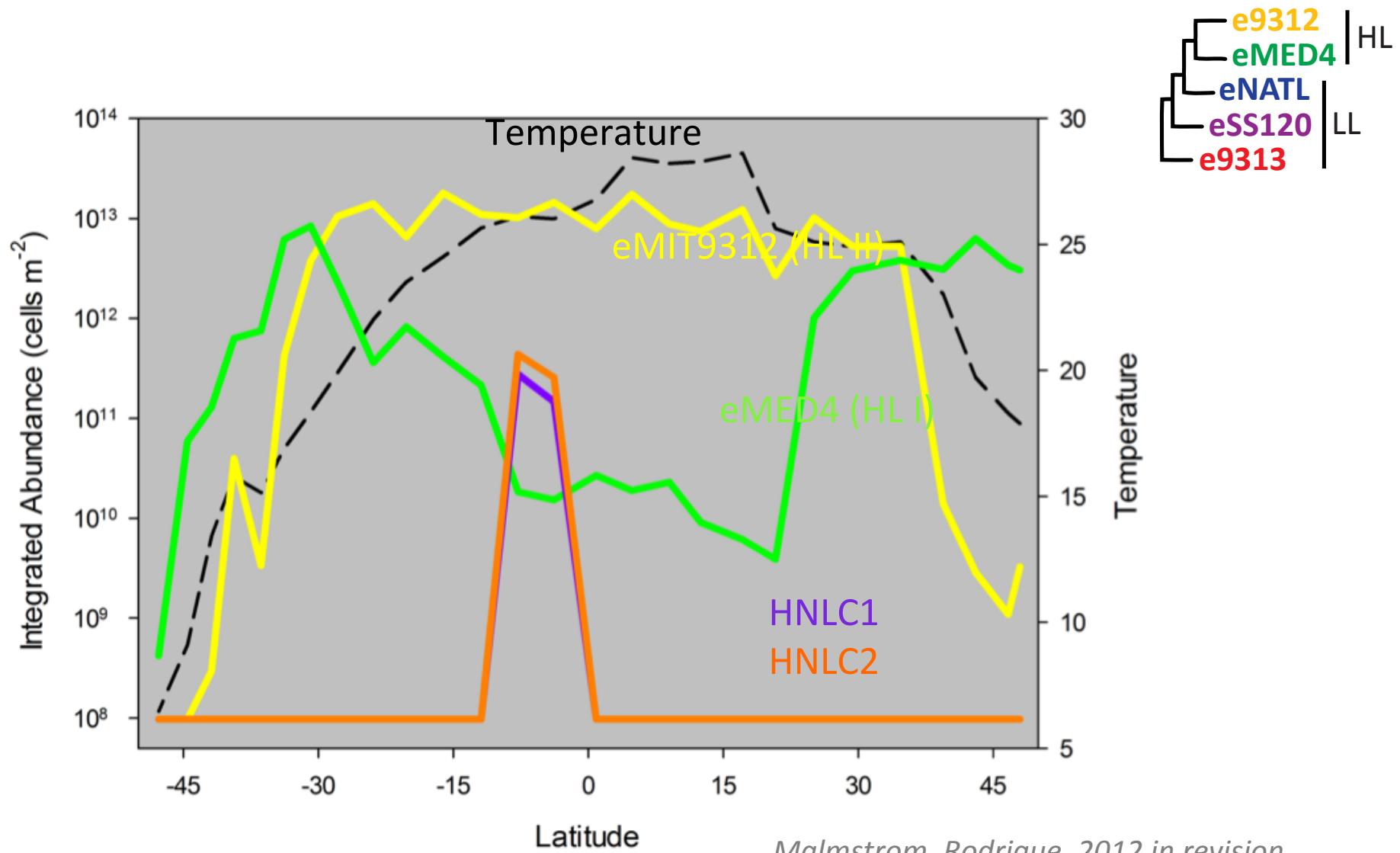
ITS and whole genome tree



New HL clades restricted to equatorial waters

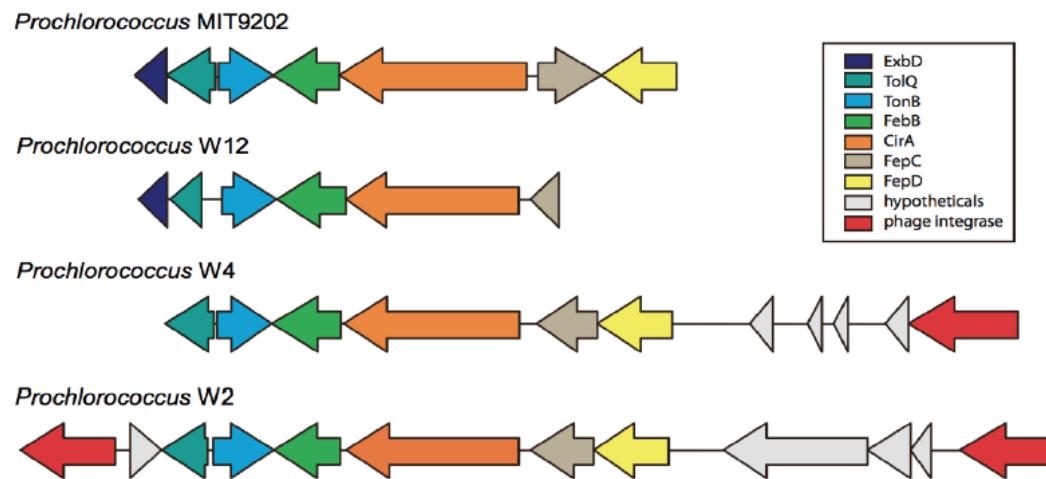


What is their distribution in the Atlantic?



Siderophore transport genes found in wild cells, and in one of our cultures (9202)

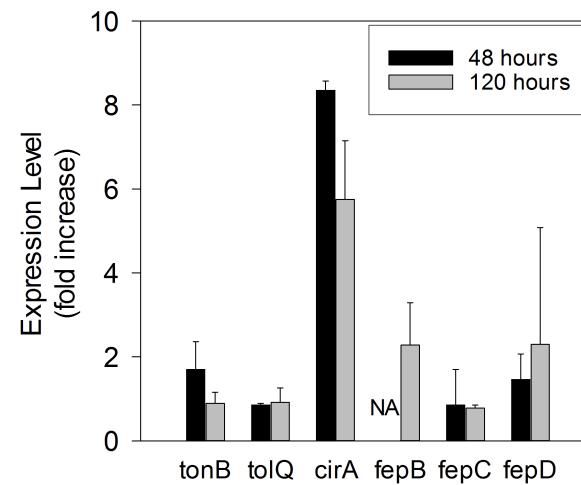
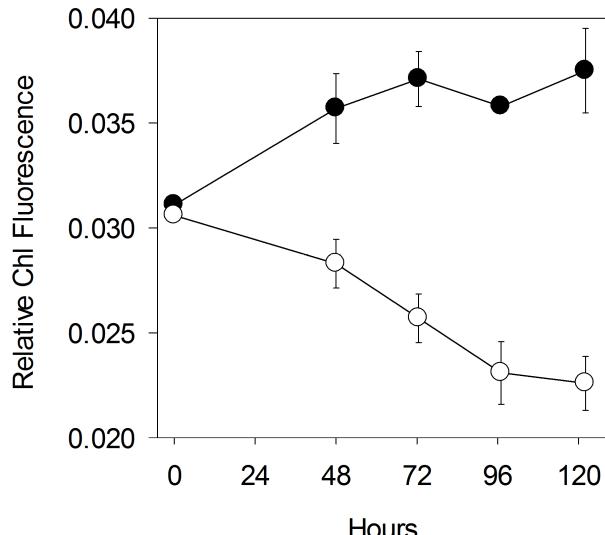
Culture



Wild single cell

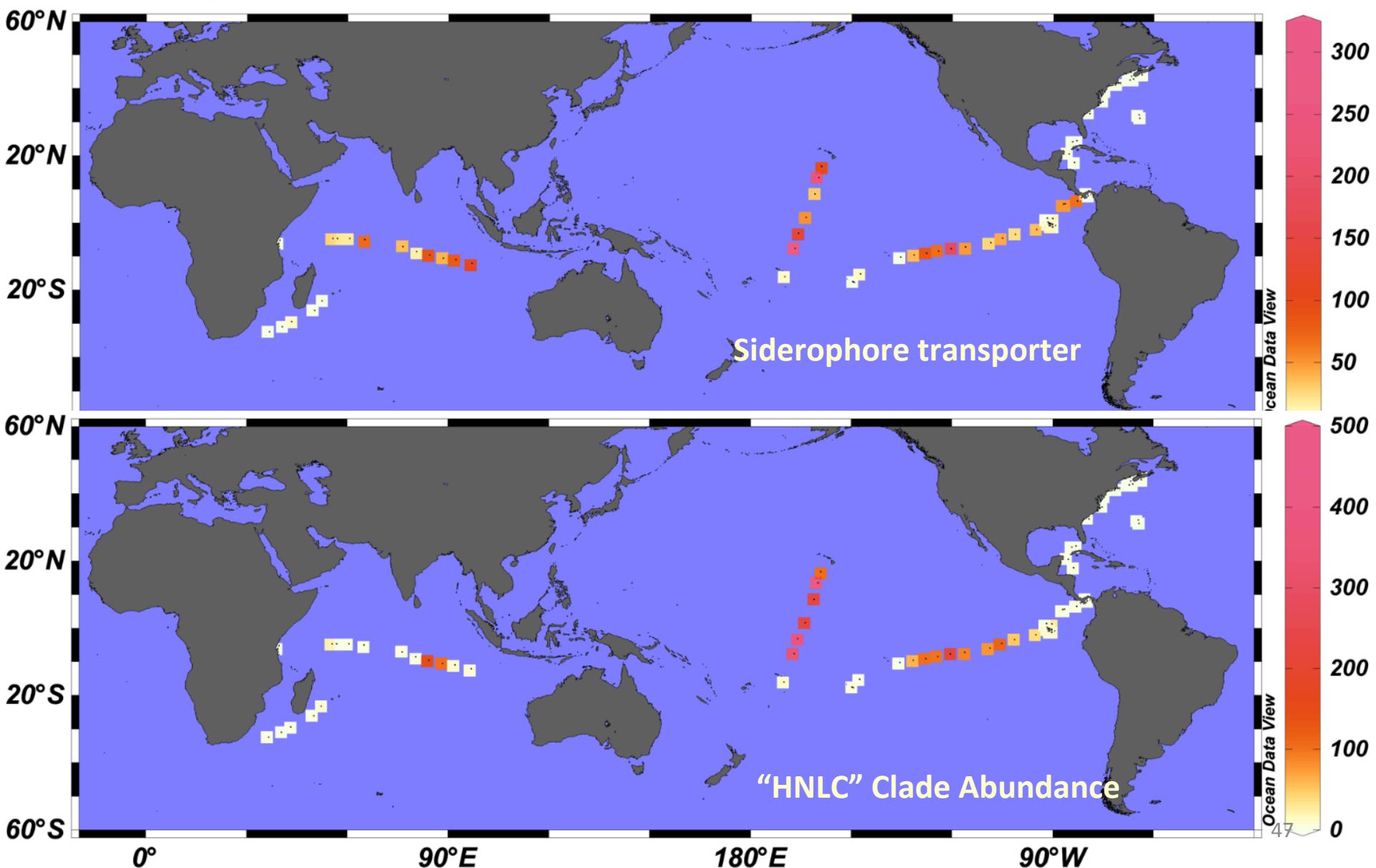
Wild single cell

Wild single cell

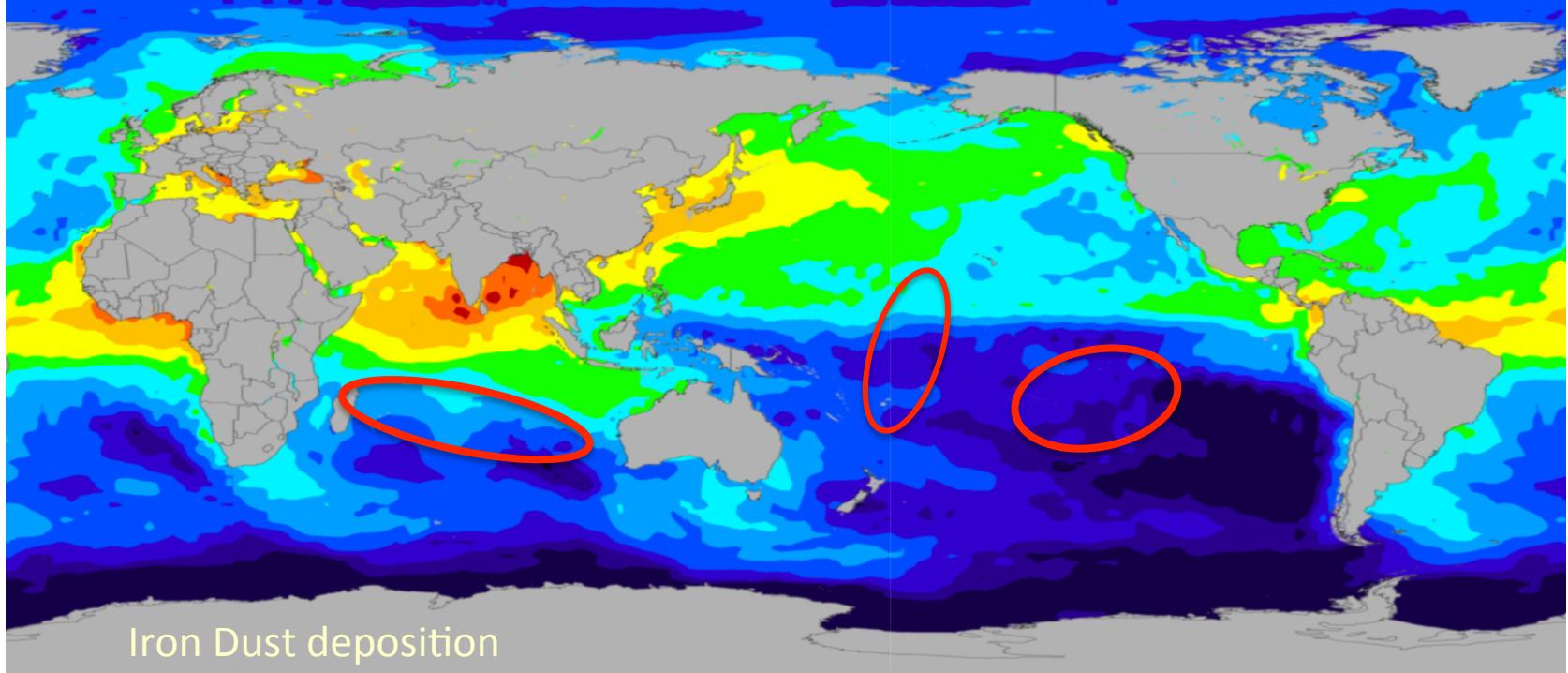
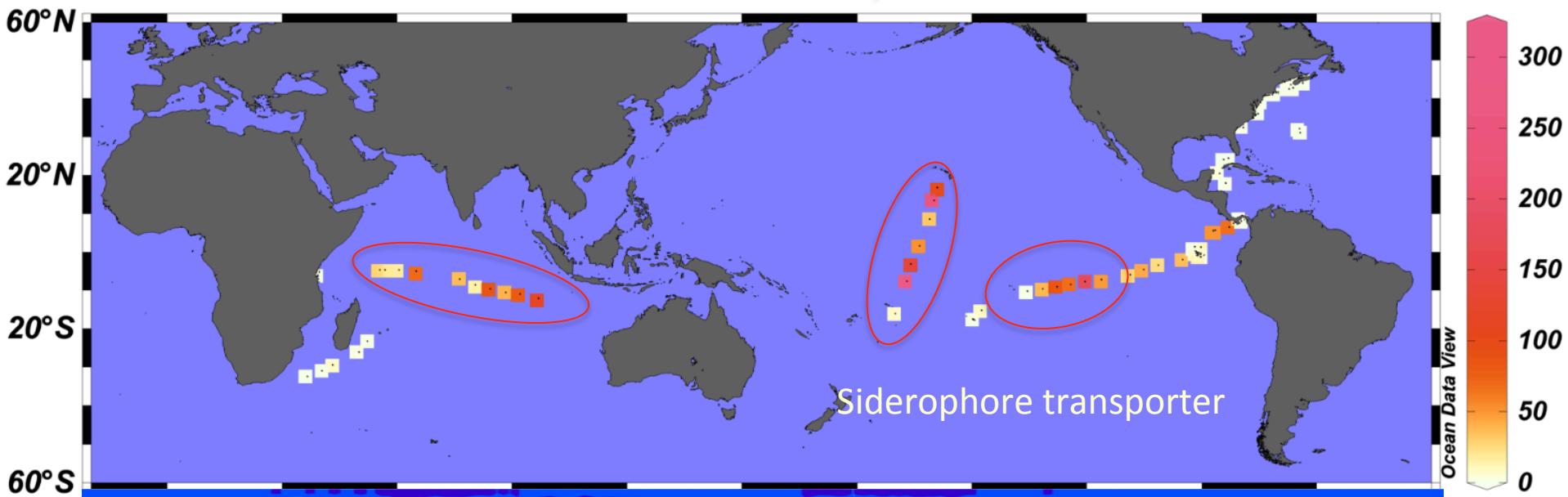


Genes are expressed under conditions of iron starvation in cultures

Global distributions through GOS metagenomics

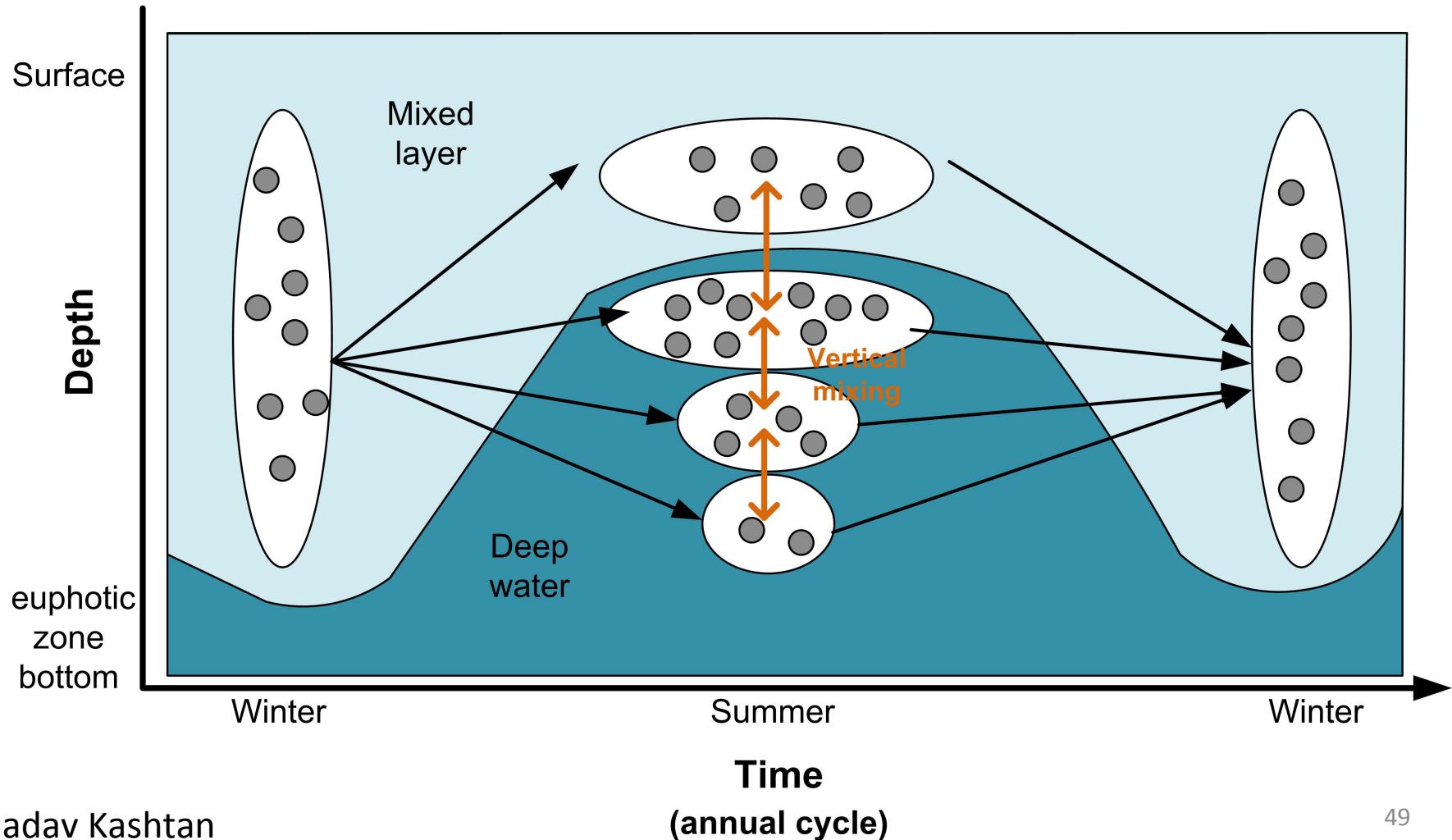


Makes sense, so far...

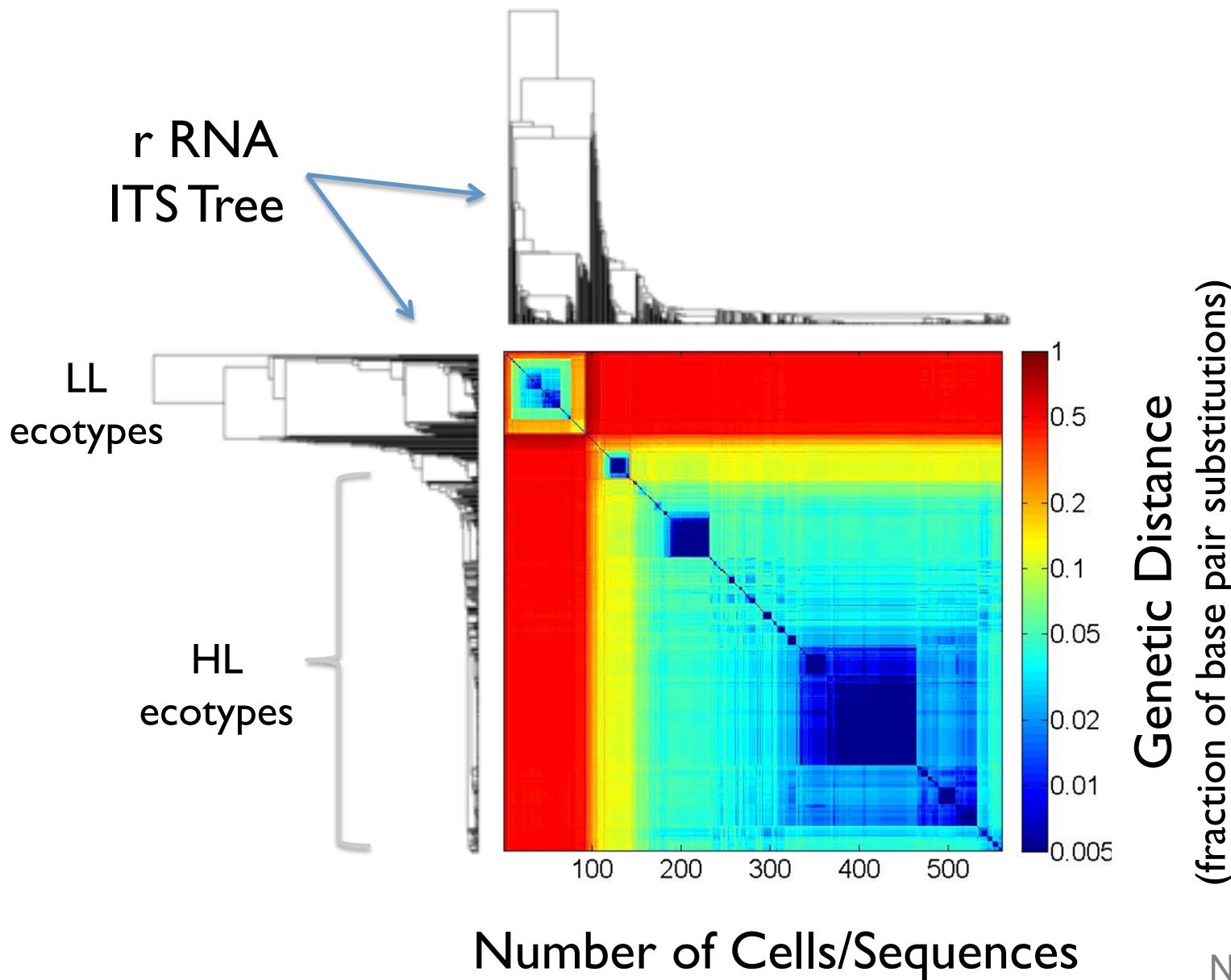


Iron Dust deposition

Population genetics of wild *Prochlorococcus* cells through single cell genomics



Representing the data



Prochlorococcus seasonal population dynamics in the Atlantic Ocean

(based on ribosomal ITS sequences analysis of samples from Bermuda)

Autumn

(November 2008)

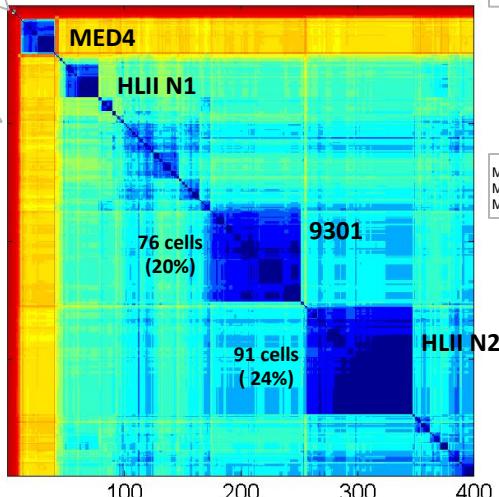
MIT 9313
MIT 9301
MIT 9211
SS120

NATL 1A
NATL 2A

MIT 9515
MED 4

MIT 9312
MIT 9202
MIT 9215

Sequences



Sequences

(386 in total)

Winter

(February 2009)

MIT 9313
MIT 9301
MIT 9211
SS120

NATL 1A
NATL 2A

MIT 9515
MED 4

MIT 9312
MIT 9202
MIT 9215

AS 9601

MIT 9301

NATL

MED4

HLII N1

9301

HLII N2

Sequences

(422 in total)

Spring

(April 2009)

MIT 9313
MIT 9301
MIT 9211
SS120

NATL 1A
NATL 2A

MIT 9515
MED 4

MIT 9312
MIT 9202
MIT 9215

AS 9601

MIT 9301

NATL

MED4

HLII N1

9301

HLII N2

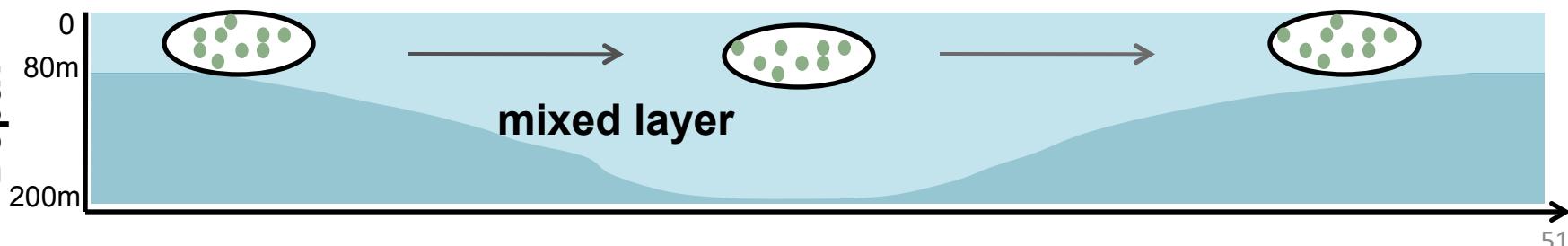
Base pair difference
250
200
150
100
50
0

Sequences

Sequences

(523 in total)

Depth



Knee-deep in Genomes

- 50 cultured *Prochlorococcus* strains
- 100's of wild single cells
- 100's of virus strains
- Megagenomic data
- Endless Ocean

Genome sequencing
Fast & Cheap!



Staggering amounts
of data

