

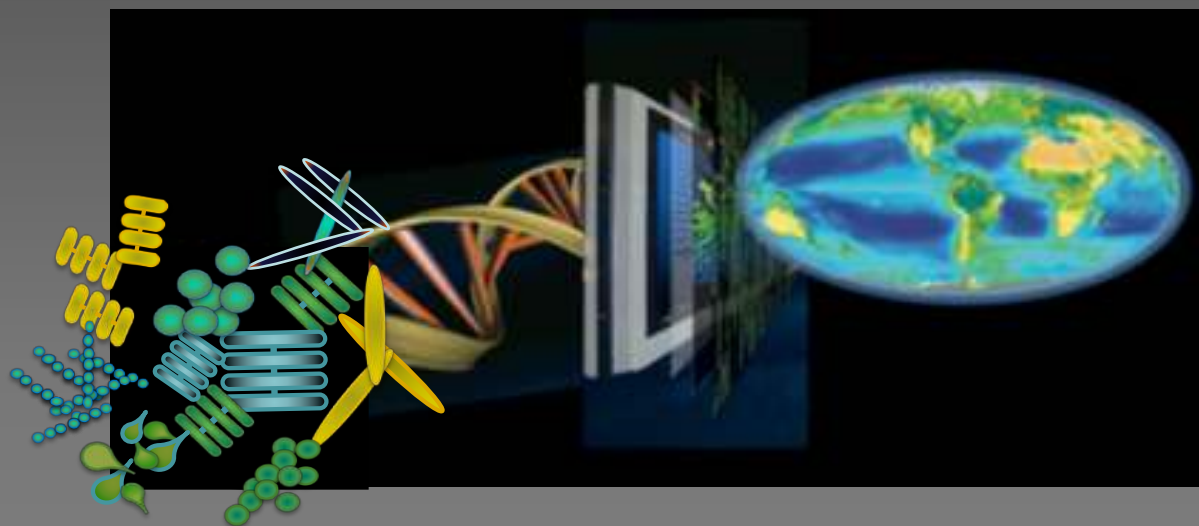
From flask to field: tracking the drivers of phytoplankton physiological ecology across marine ecosystems

Sonya Dyhrman

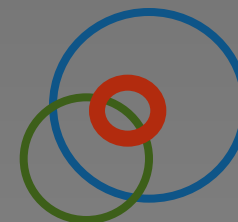
Department of Earth and Environmental Sciences

Lamont-Doherty Earth Observatory

Columbia University



COLUMBIA UNIVERSITY
IN THE CITY OF NEW YORK

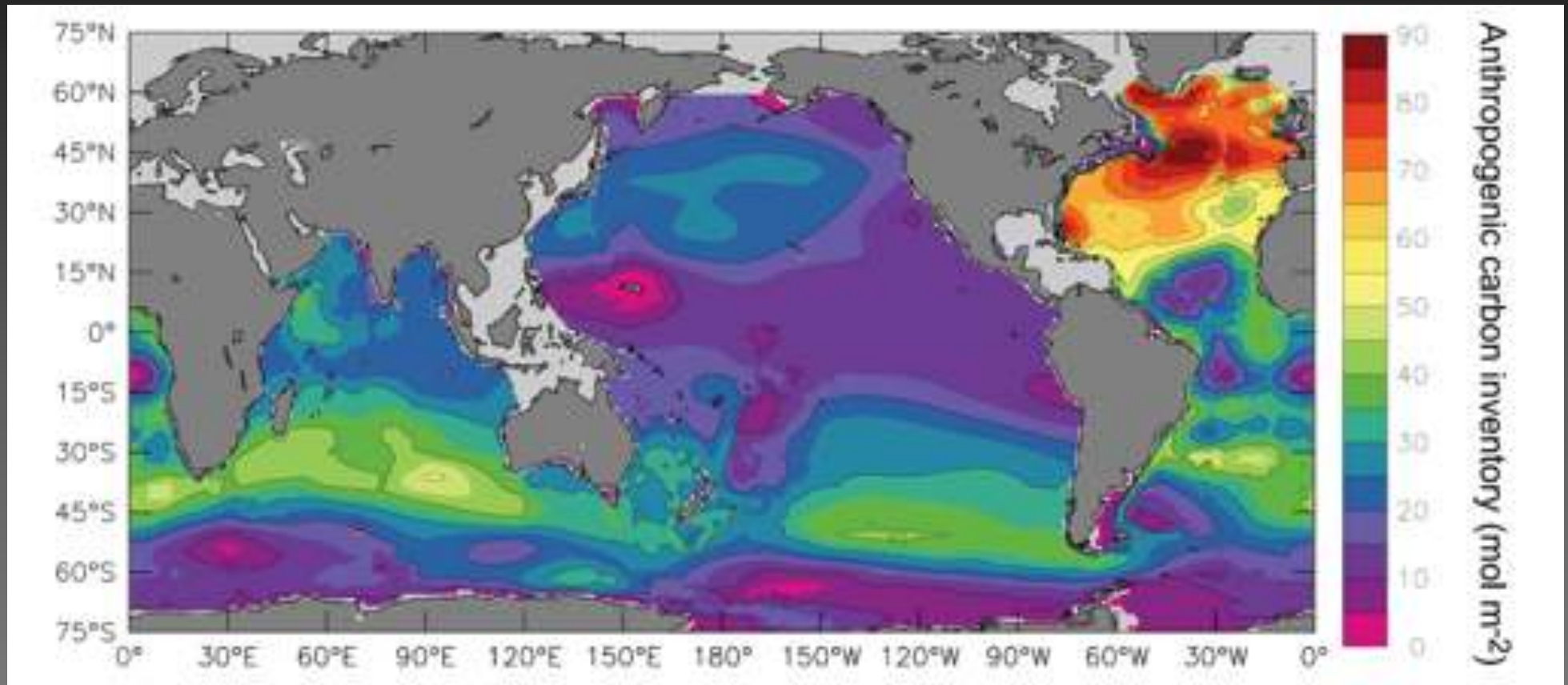


LAMONT-DOHERTY
EARTH OBSERVATORY

The ocean makes our planet livable



The ocean acts as a buffer for CO₂ in the atmosphere



Sabine et al. (2004) *Science*

Between 1800 - 1994, ocean has absorbed ~120 petagrams of CO₂
Oceanic sink accounts for ~48% of fossil-fuel emissions

The vast unseen microbial populations play a critical role in ocean function



Marine Microbes - fundamental to ocean ecosystem function

- Marine microbes...
 - Produce and consume green house gases
 - Supply the marine food web
 - Recycle organic matter
 - Account for roughly half of global primary production
- *make the planet habitable*

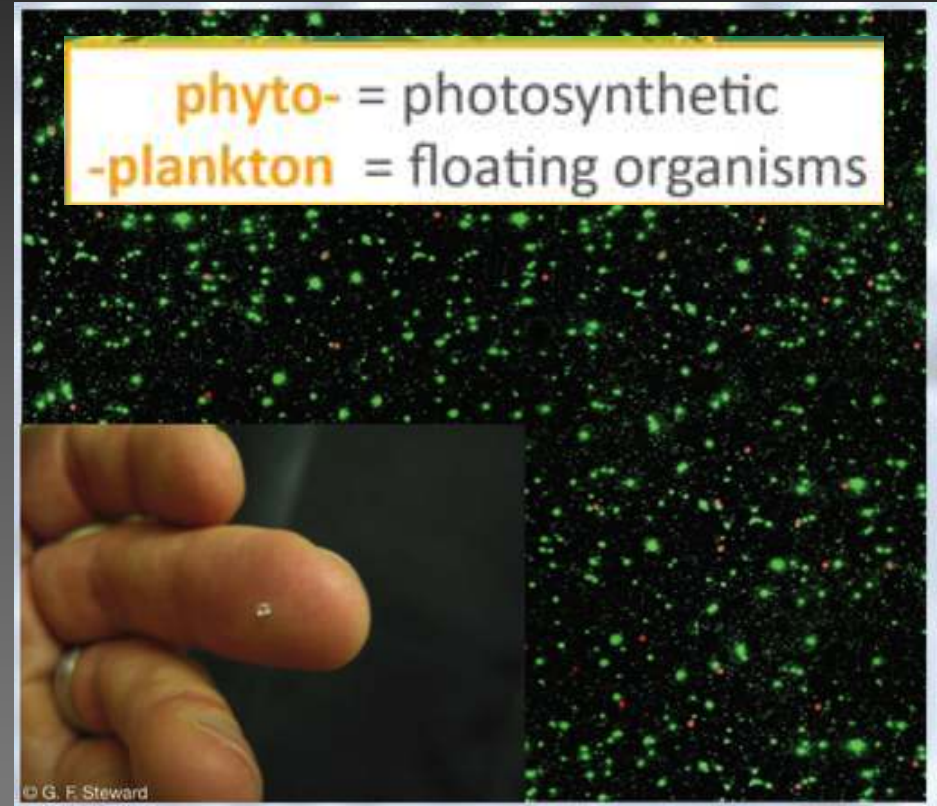
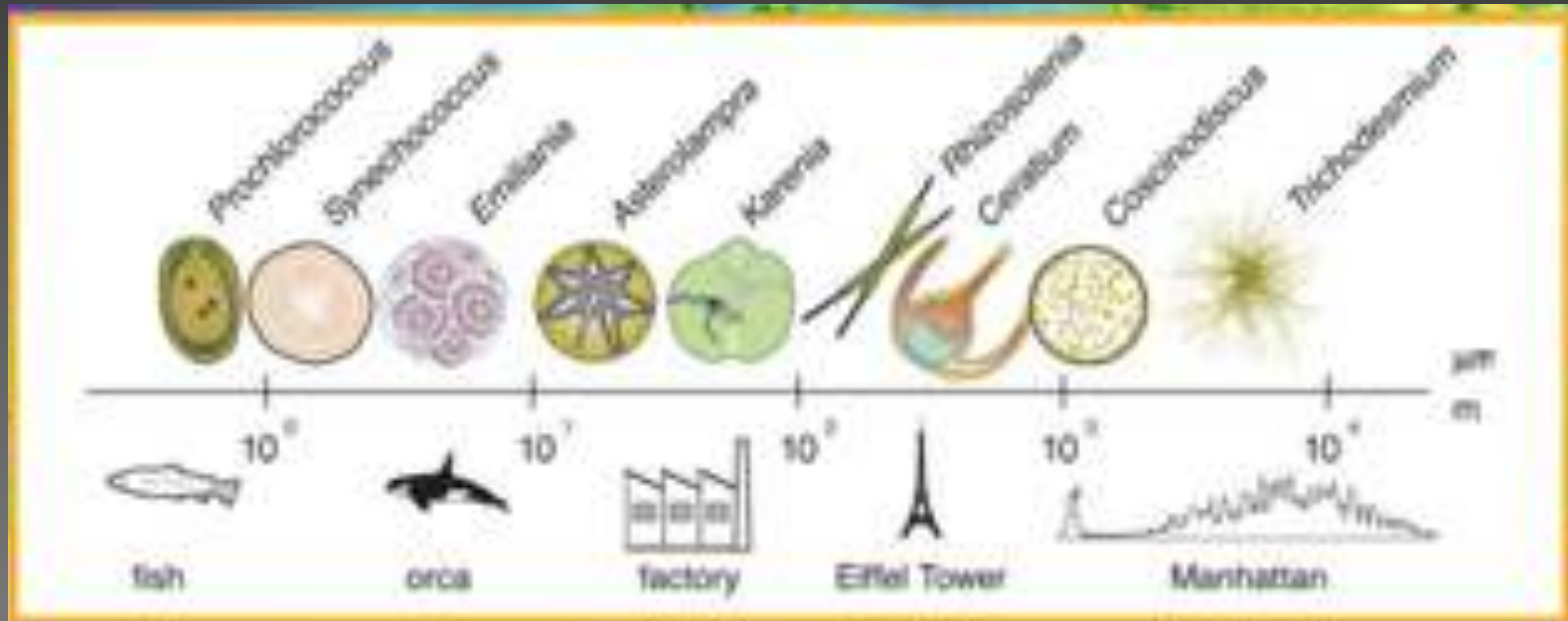
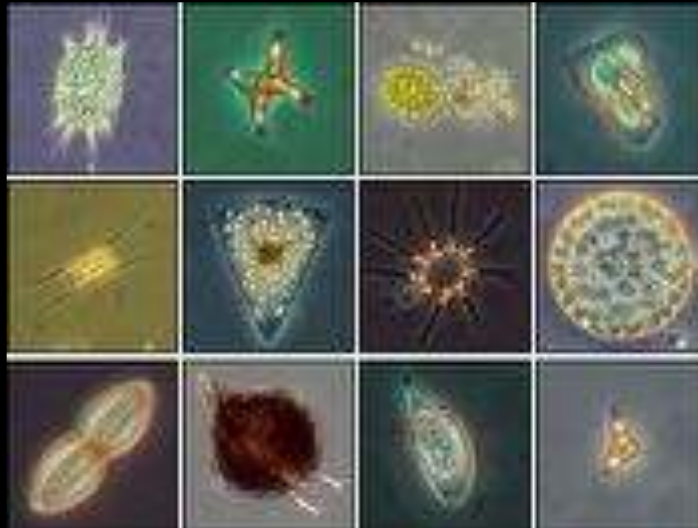
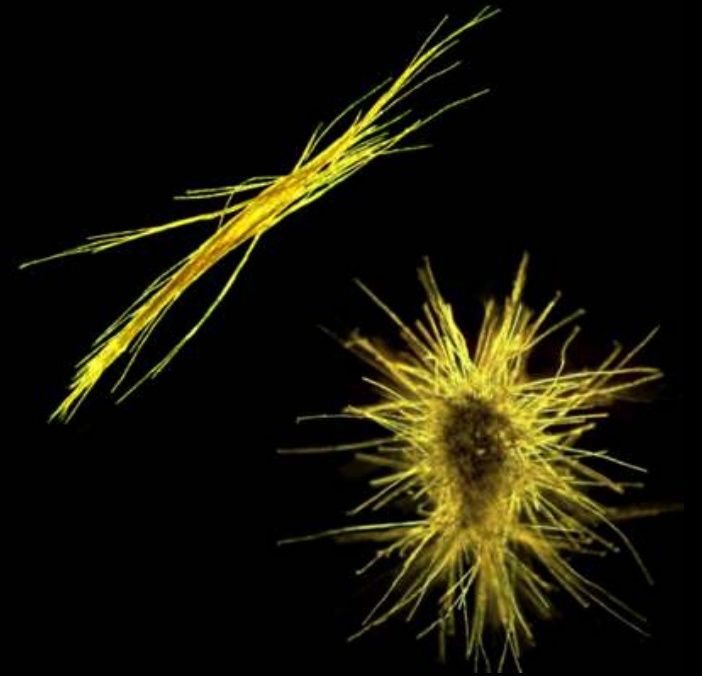
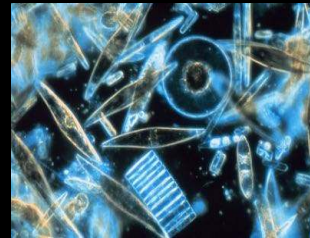
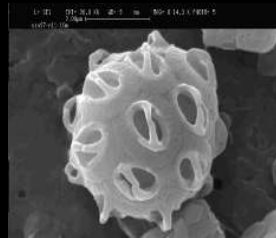
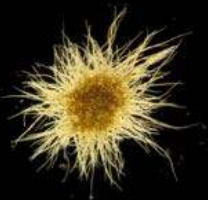
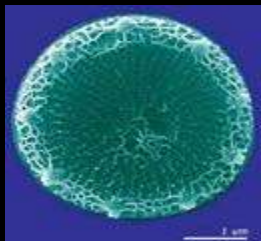


Image courtesy C-MORE

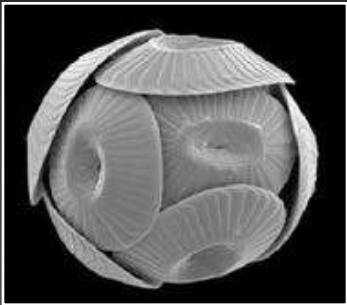
Marine phytoplankton are highly diverse





Phytoplankton underpin ocean ecosystem function

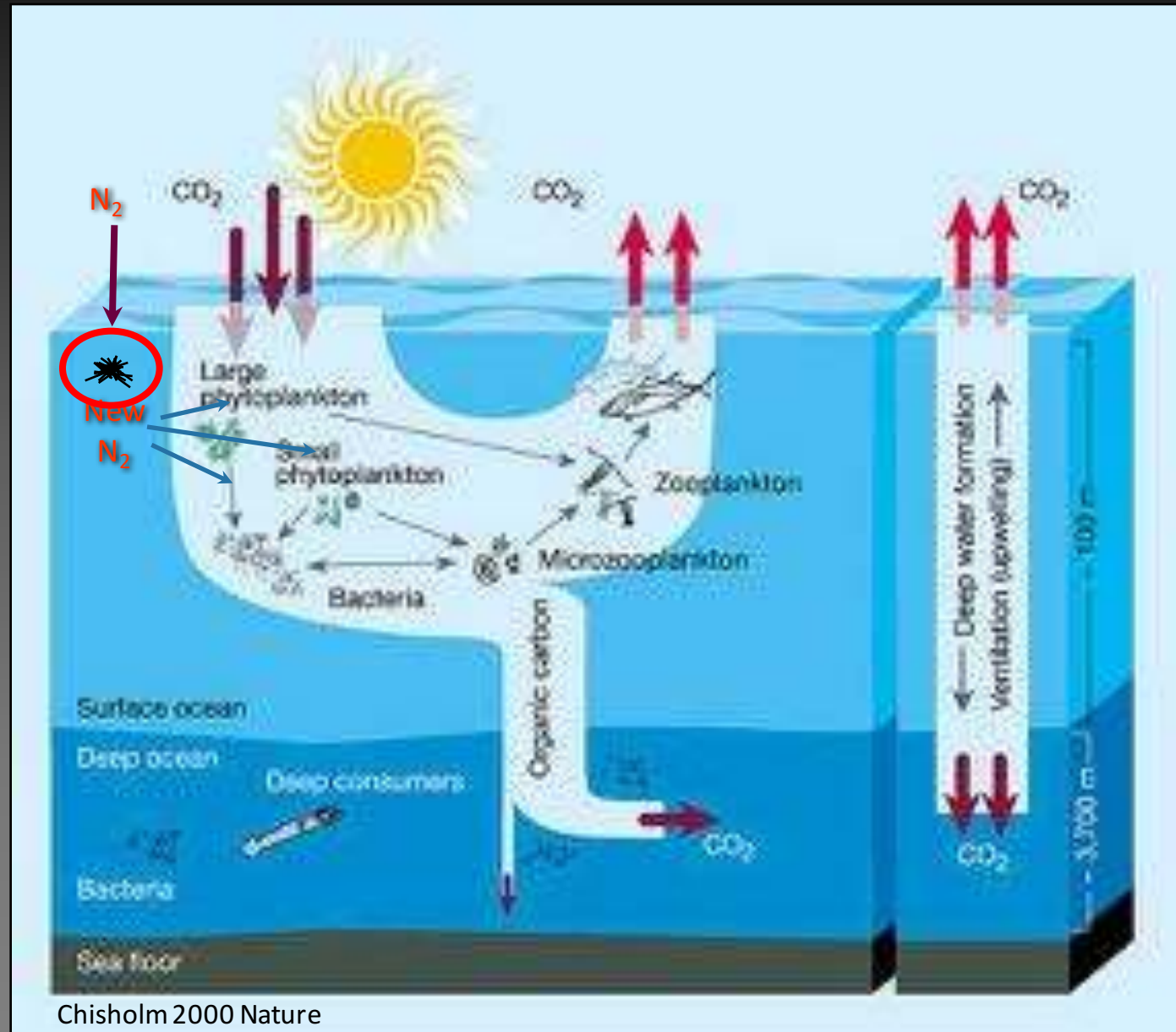
Haptophytes



Diatoms

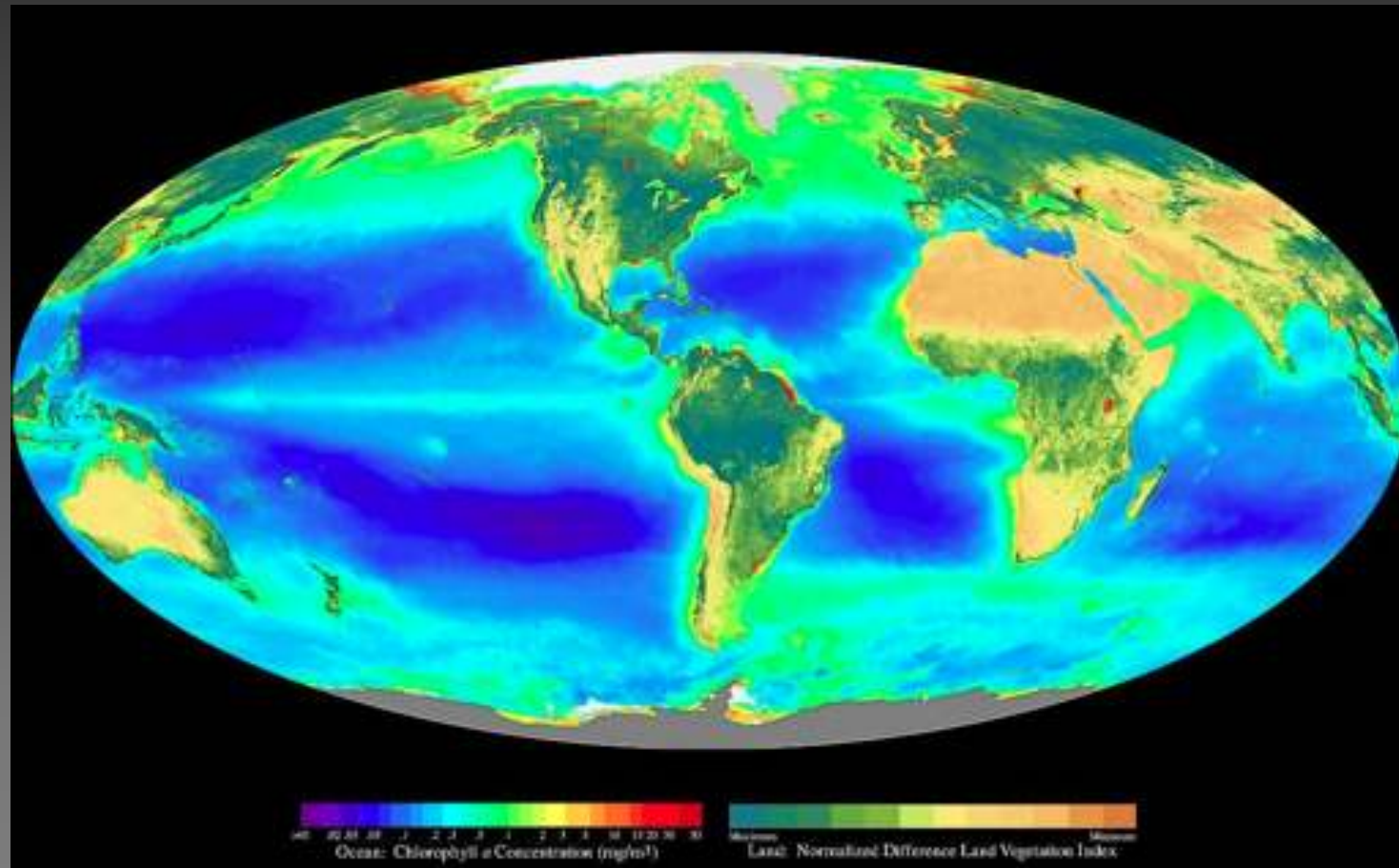


N₂ Fixers

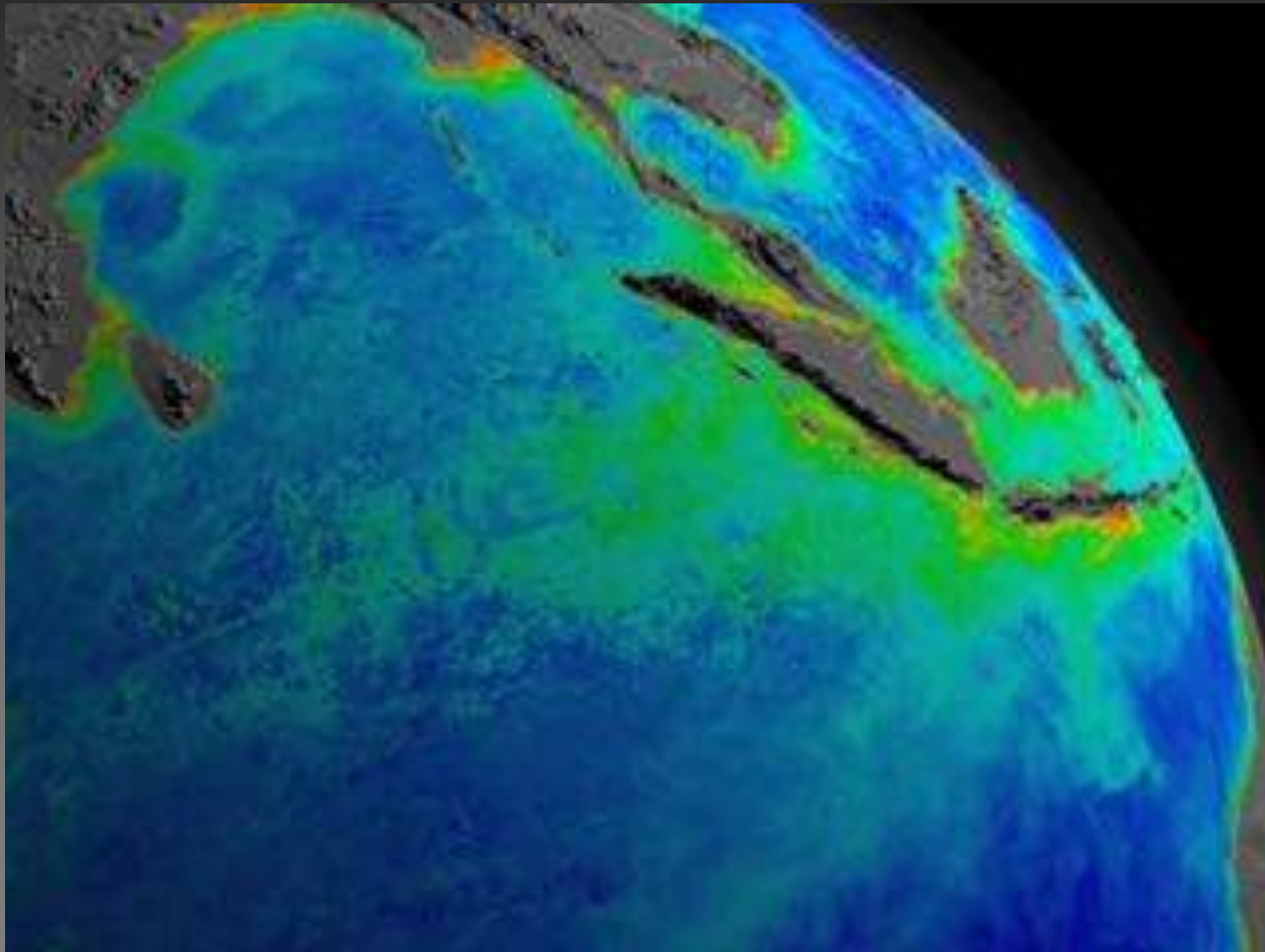


Phytoplankton play a profound role in the earth system

Half of global primary production



Seasonal chlorophyll distributions in the sea - highlights the global significance of phytoplankton



[illegible]

Tracking physiological ecology: from the flask to the field

Culture-based experiments

Species-specific responses to well-controlled environment

Limitations:

- Species must be in culture
- Time consuming
- Extrapolations to the field

Field-based studies

Assess whole community dynamics in a natural environment

Limitations:

- Not species-specific

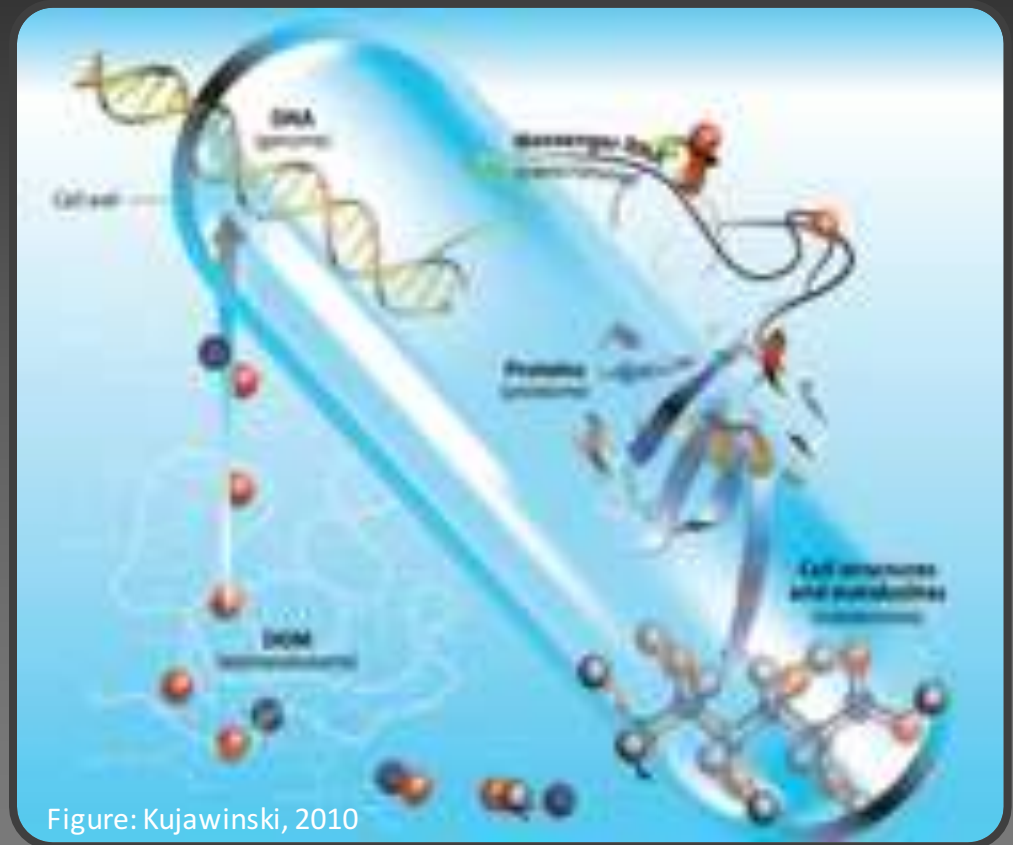
Micro/Mesocosm



‘Omic-enabled advances allowing to query cells in their environment in a species-specific way

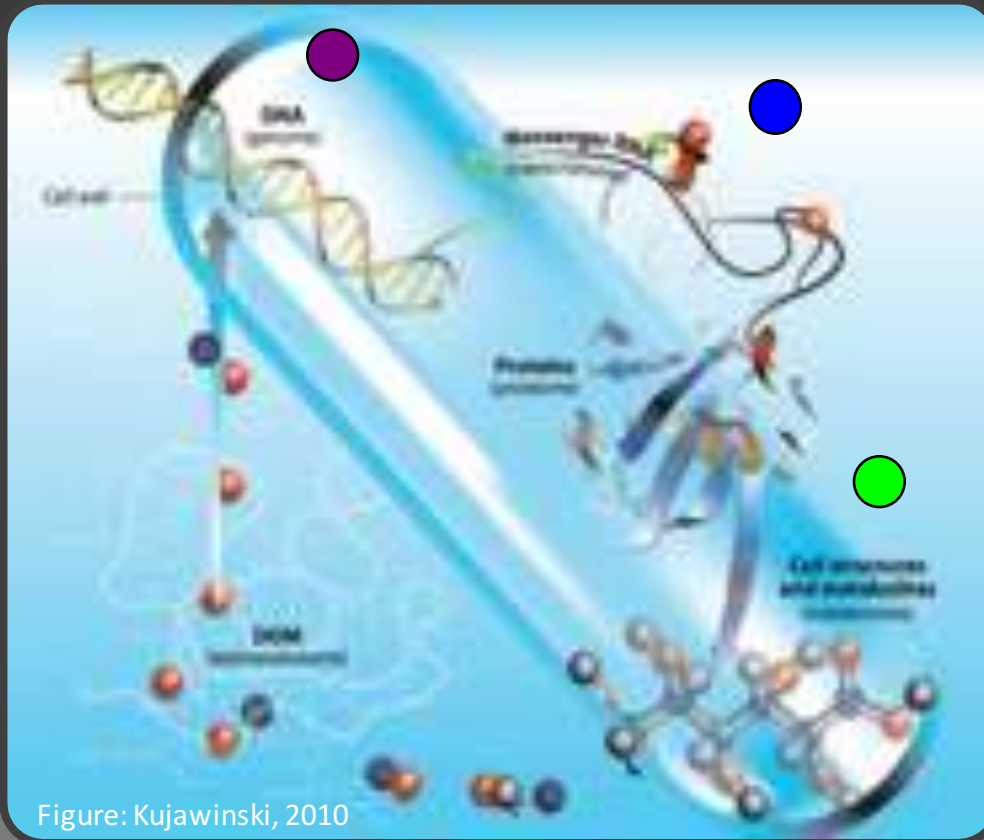
Challenges and opportunities in microbial oceanography

- Long standing challenges:
 - Populations are dilute
 - Few species-specific assays
 - Few genome or transcriptome sequences
- New opportunities
 - Novel concentration and detection strategies
 - Increases in whole genome sequences
 - Increases in transcriptomes for eukaryotic taxa



Increasingly able to use 'omic and 'metaomic approaches!

Leveraging 'omic data to study marine microbes

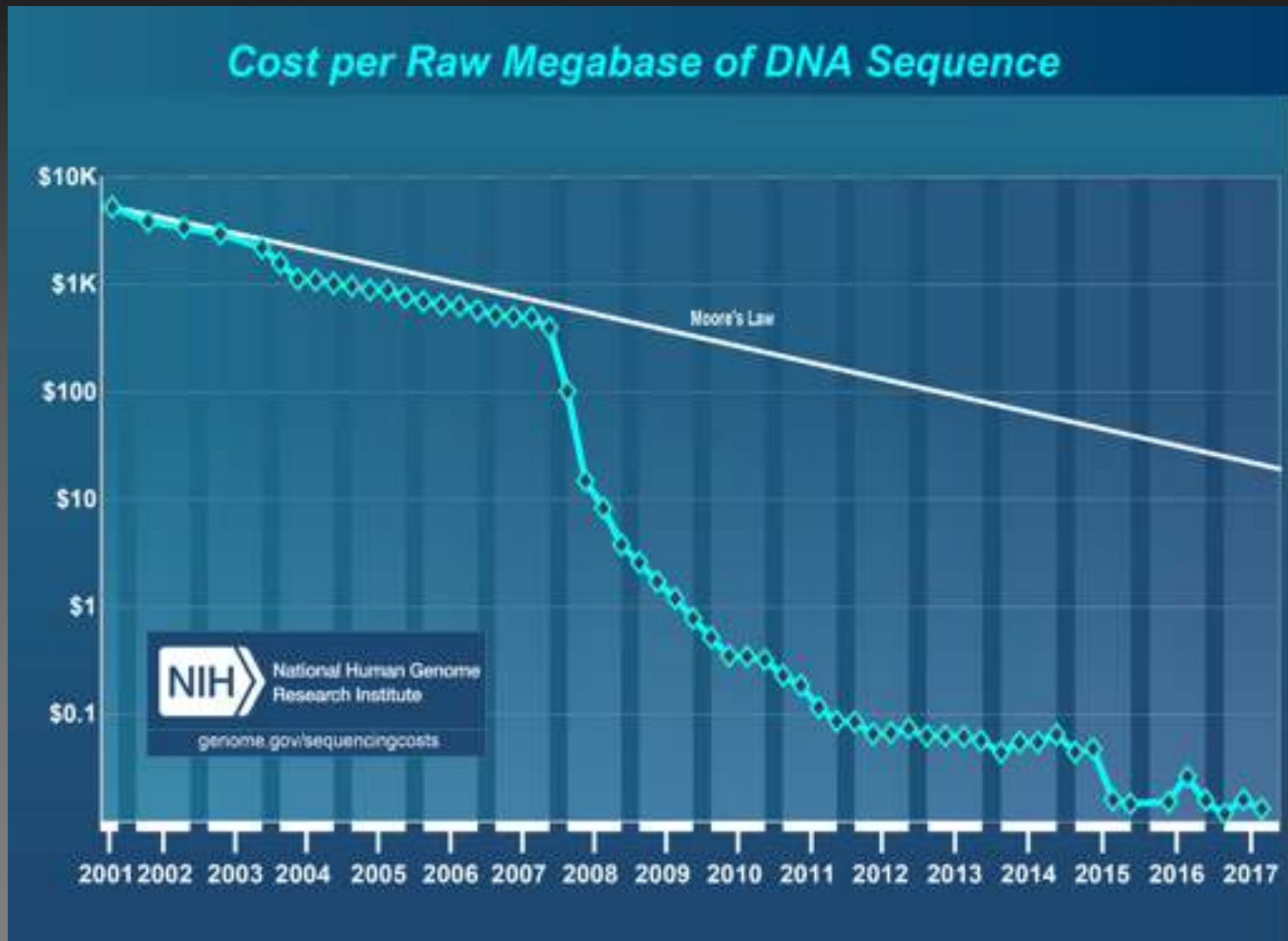


- **Taxonomic Diversity:** Who is there?
- **Metabolic capacity:** What are the molecular underpinnings of resource metabolism?
- **Metabolic plasticity:** How are those pathways regulated and expressed *in situ*?

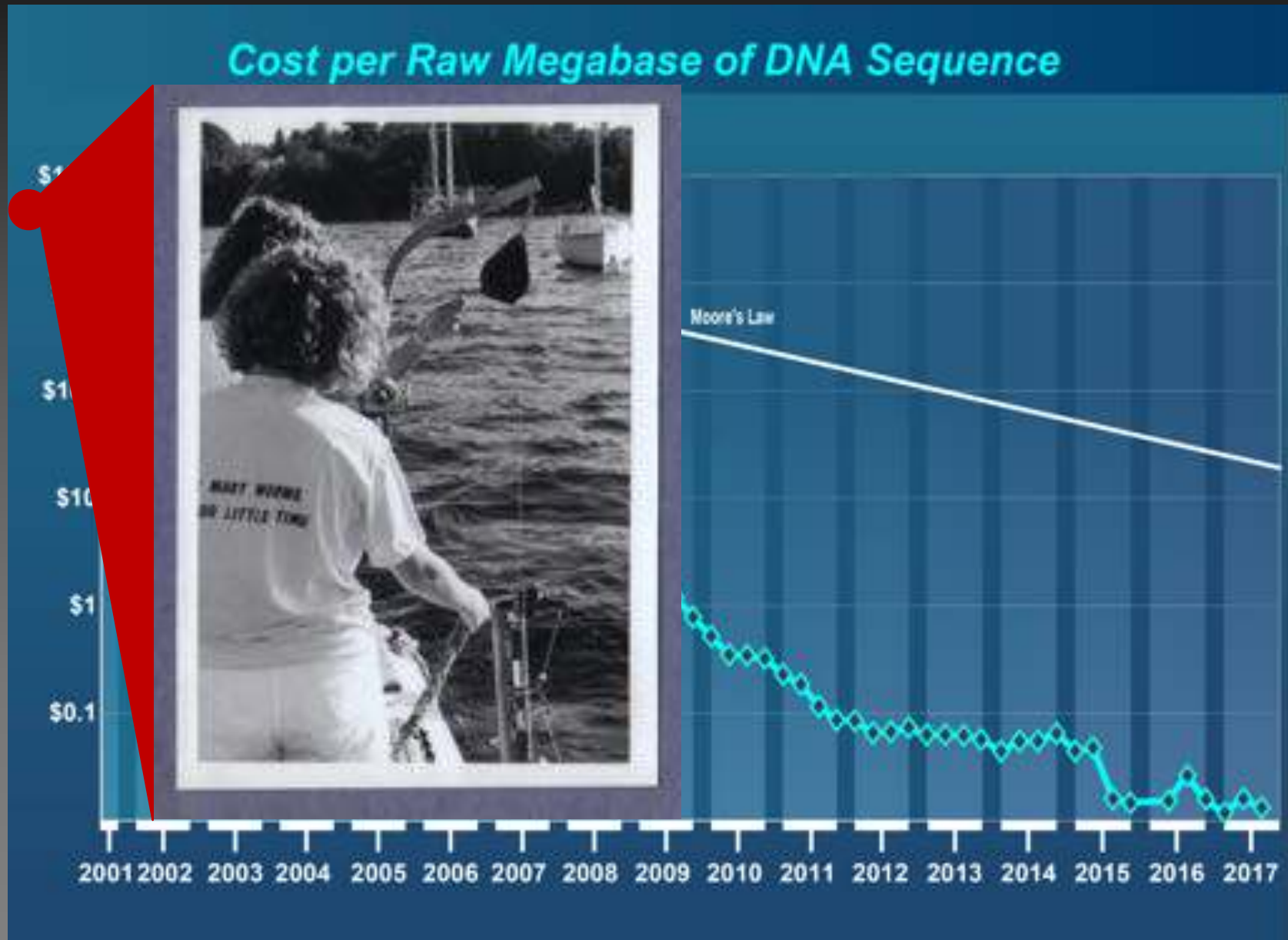
How did we get here?

- 1990s
 - First marine bacterial WGS
 - Fosmid cloning of community DNA
- 2000s
 - BAC libraries of community DNA
 - Sequencing and WGS assembly of whole community DNA
 - First marine microbial eukaryote WGS
- 2010s
 - Bacterial community RNA sequencing
 - Bacterial community proteomics and metabolomics
 - SAGs
 - MMETSP - marine microbial eukaryote transcriptomes
 - Eukaryotic community RNA sequencing

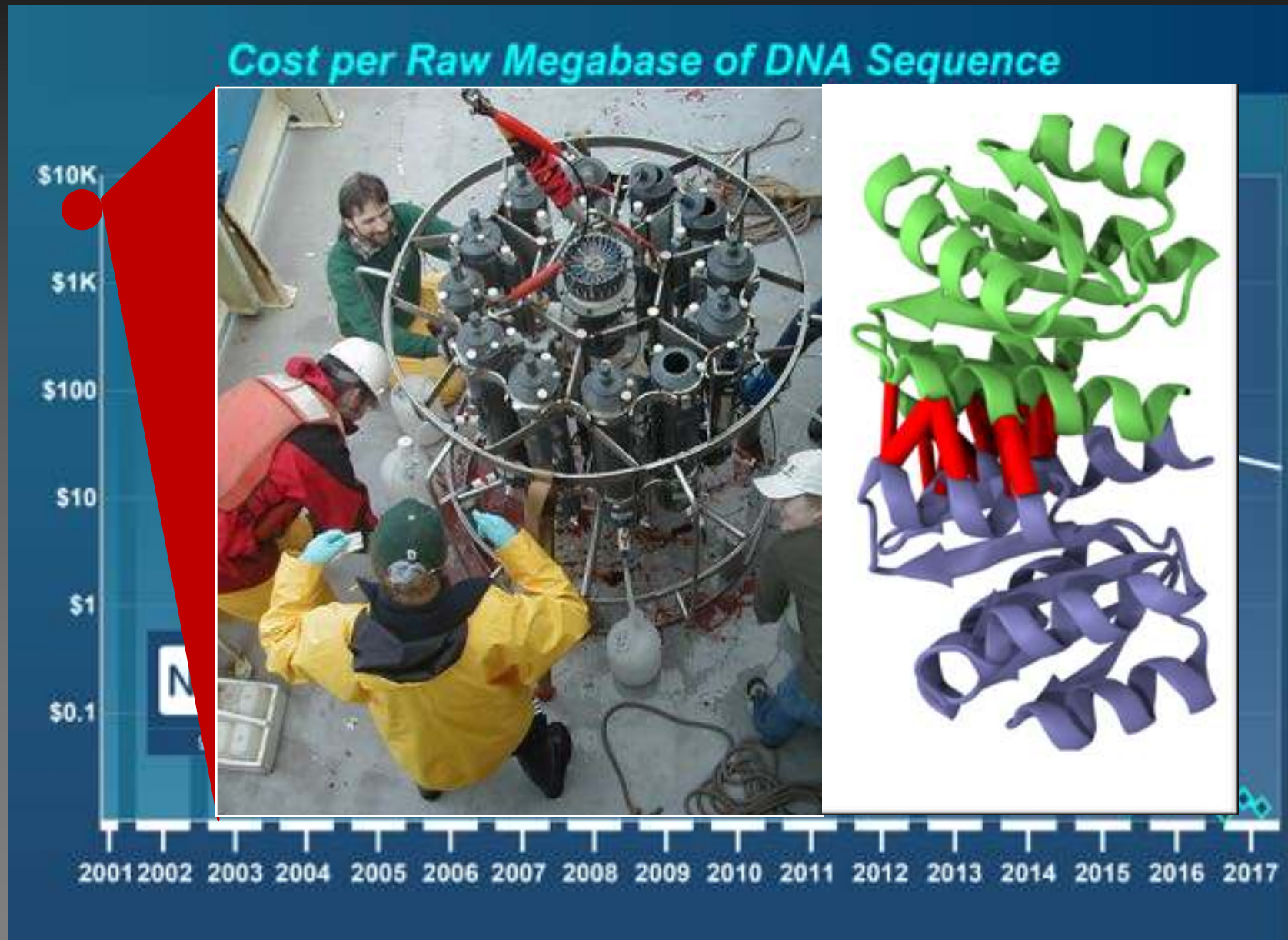
Sequencing advances opens new 'omic approaches



Sequencing advances opens new 'omic approaches

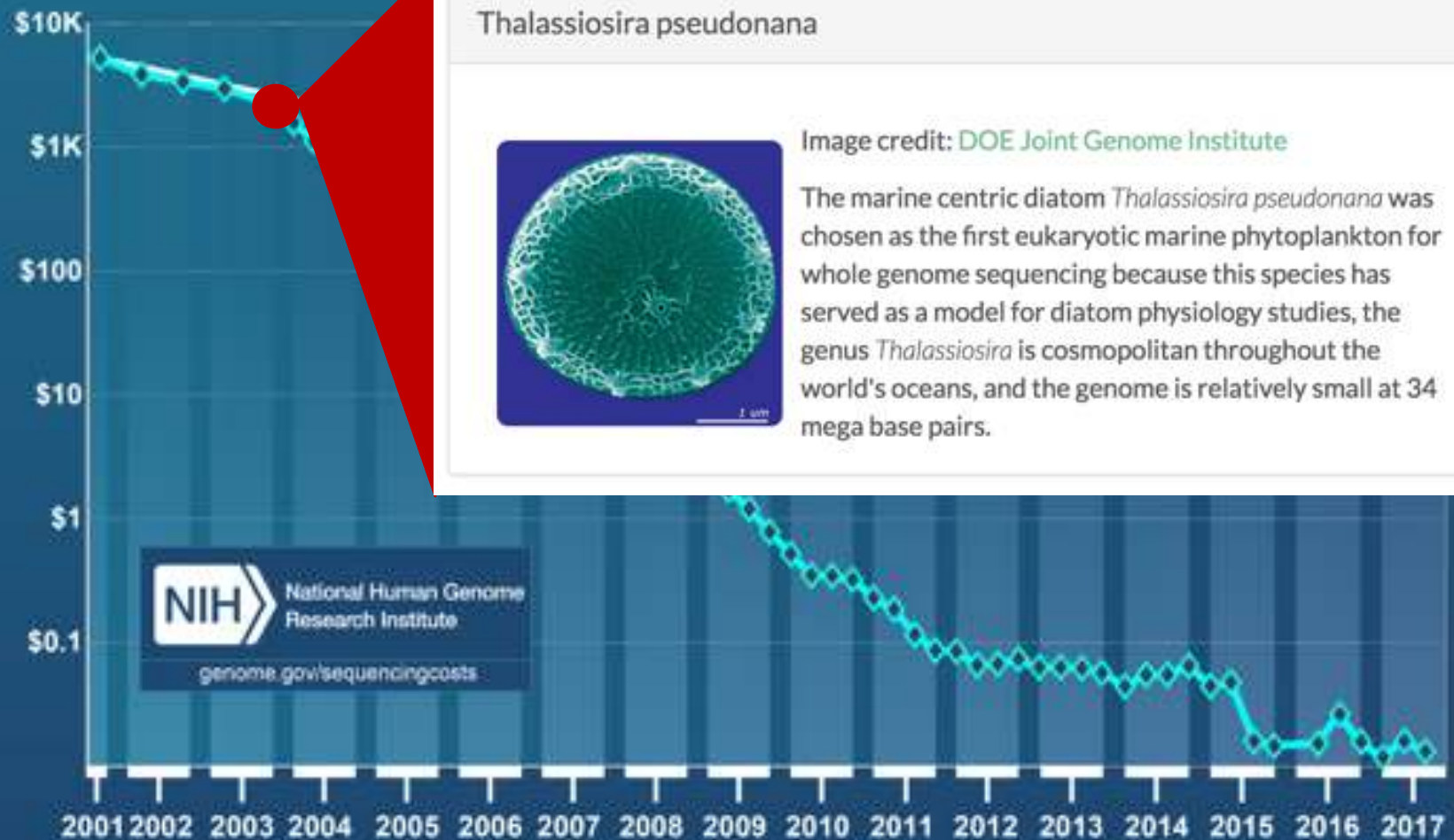


Sequencing advances opens new 'omic approaches

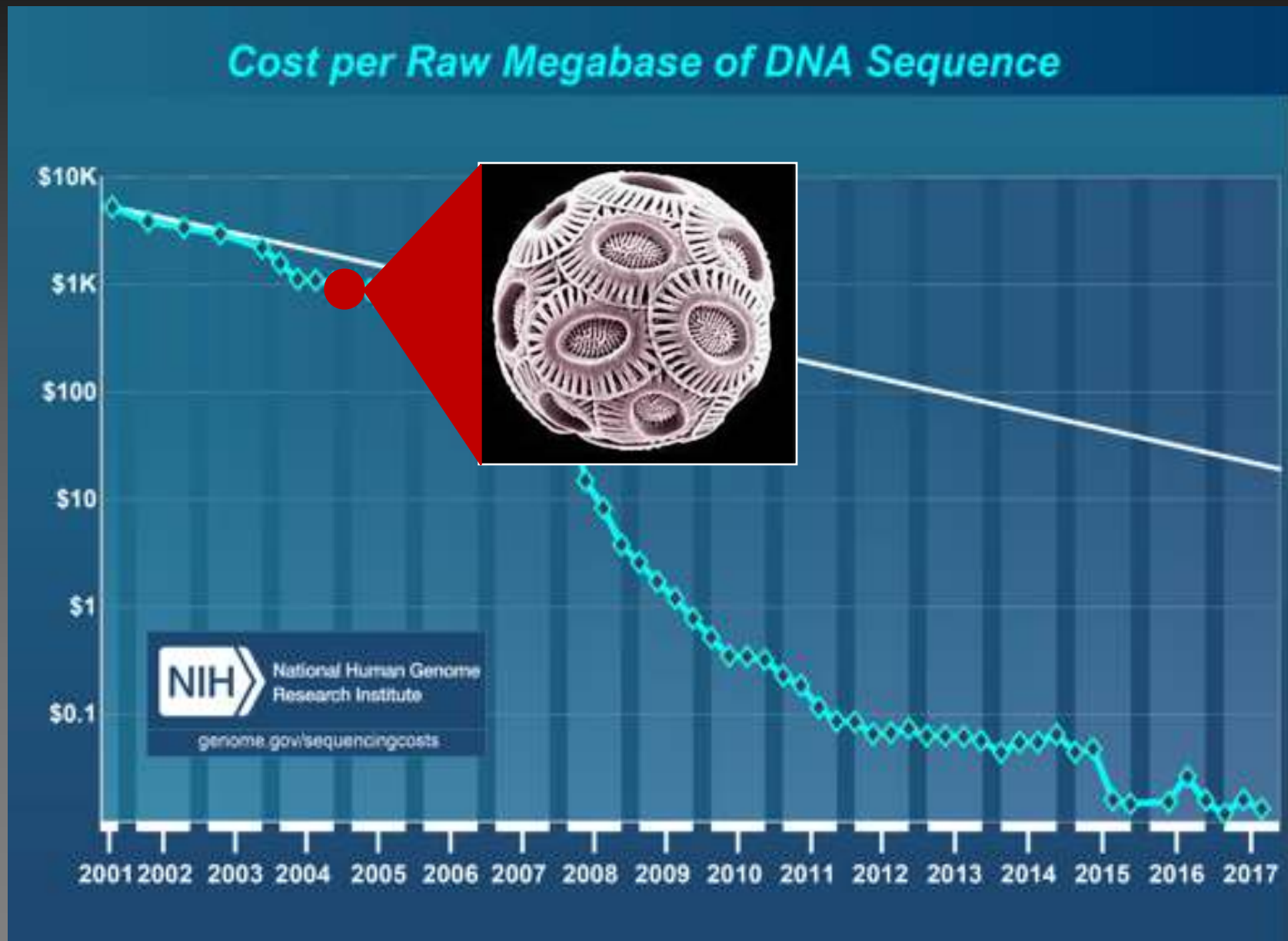


Sequencing advances opens new 'omic approaches

Cost per Raw Megabase of DNA Sequence



Sequencing advances opens new 'omic approaches



Sequencing advances opens new 'omic approaches

Cost per Raw Megabase of DNA Sequence

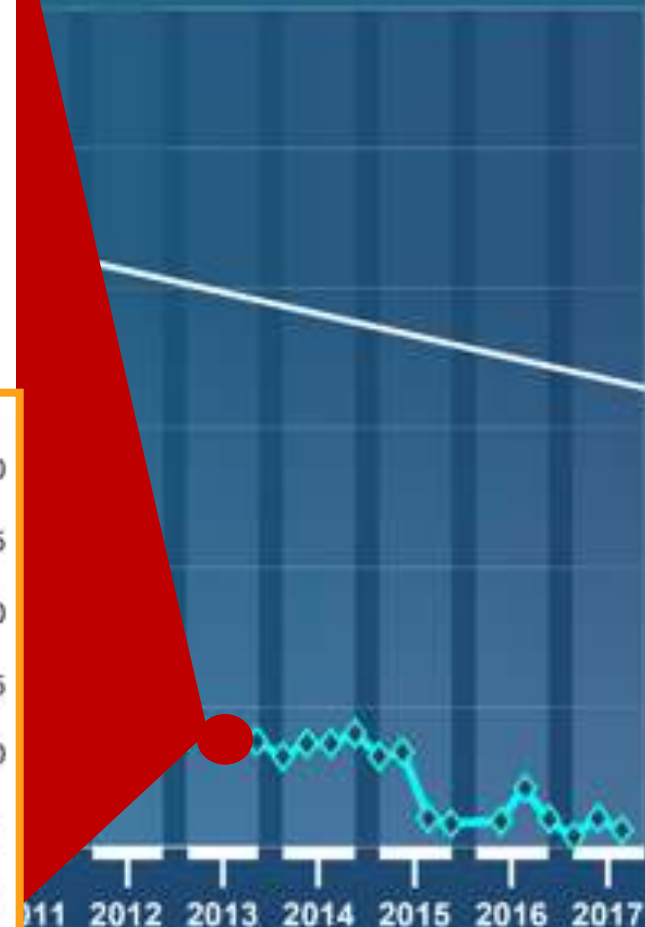
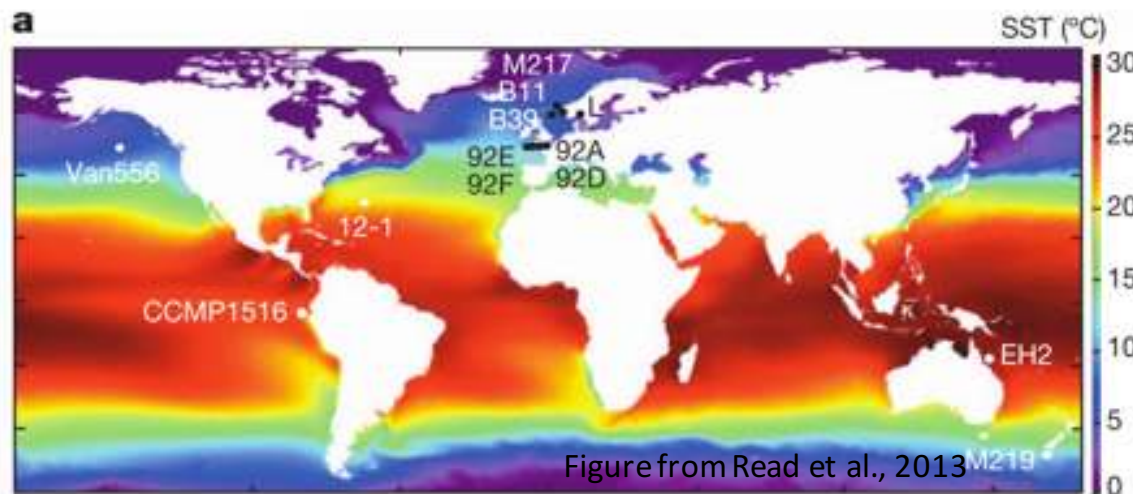
LETTER

OPEN

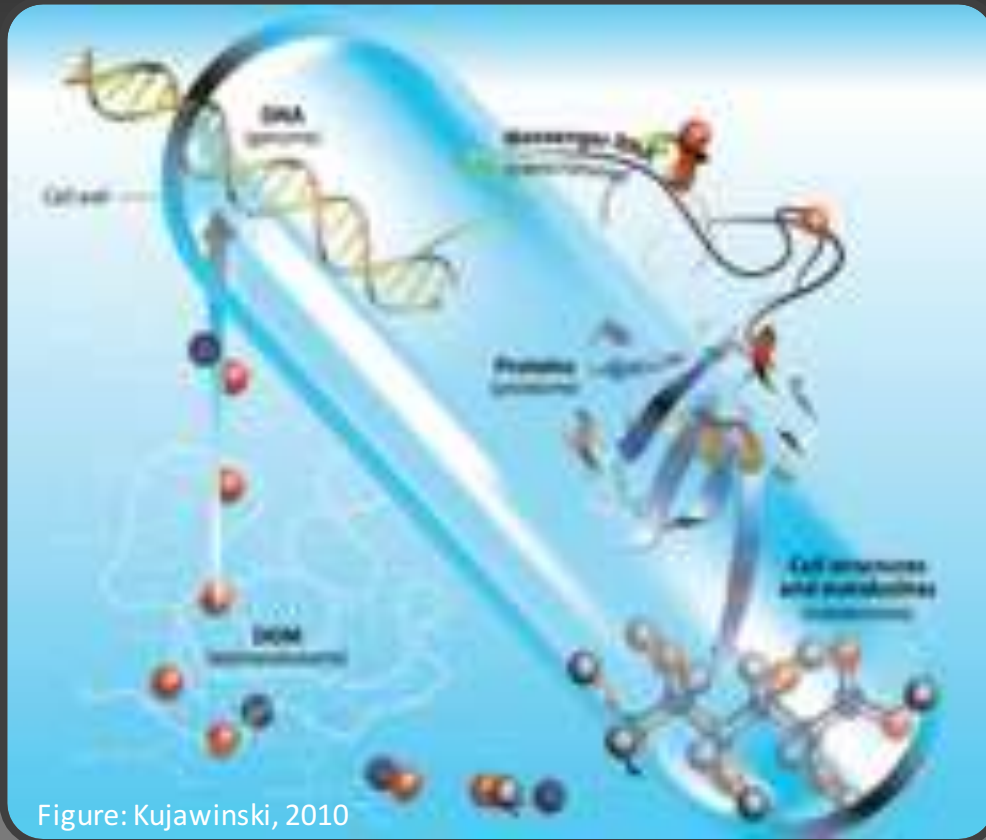
doi:10.1038/nature12221

Pan genome of the phytoplankton *Emiliana* underpins its global distribution

Betsy A. Read¹, Jessica Kegel², Mary J. Klute³, Alan Kuo⁴, Stephane C. Lefebvre⁵, Florian Maumus⁶, Christoph Mayer^{7,8}, John Miller⁹, Adam Monier¹⁰, Asaf Salamov⁴, Jeremy Young¹¹, Maria Aguilar³, Jean-Michel Claverie¹², Stephan Frickenhaus^{2,13}, Karina Gonzalez¹⁴, Emily K. Herman³, Yao-Cheng Lin¹⁵, Johnathan Napier¹⁶, Hiroyuki Ogata¹⁷, Analissa F. Sarno¹, Jeremy Shmutz^{4,17}, Declan Schroeder¹⁸, Colomban de Vargas¹⁹, Frederic Verret²⁰, Peter von Dassow²¹, Klaus Valentin², Yves Van de Peer²², Glen Wheeler^{18,22}, *Emiliana huxleyi* Annotation Consortium†, Joel B. Dacks^{2*}, Charles F. Delwiche^{9*}, Sonya T. Dyhrman^{23,24*}, Gernot Glöckner^{25*}, Uwe John^{2*}, Thomas Richards^{26*}, Alexandra Z. Worden^{10*}, Xiaoyu Zhang^{27*} & Igor V. Grigoriev⁴



Ongoing challenges



We need to grow the inventory of species and genes

We have too few samples, and too few contiguous datasets

Processing loses ecological context

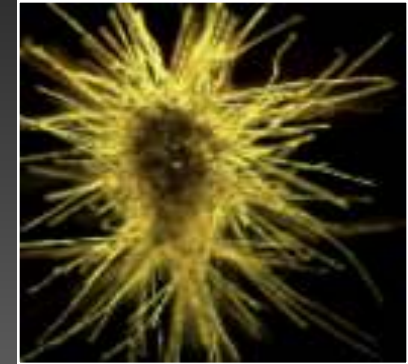
Lots of “dark matter”

Still too expensive to generate and store data

Vignettes

- From genome to biome: Tracking the metabolism and microbiome of a keystone N_2 fixer

Genome - enabled



- Co-existing in a sea of competition: Leveraging transcriptome data to track the physiological ecology of phytoplankton from key groups

Transcriptome - enabled



Thank you



Gwenn Hennon



Mónica Rouco



Sheean Haley



Kyle Frischkorn



Matt Harke



Maria Hernandez



Harriet Alexander



Core questions

Metabolic traits and trade-offs

- What phosphorus is bioavailable?
- What are the biogeochemical constraints on N_2 fixation?



Host microbiome interactions

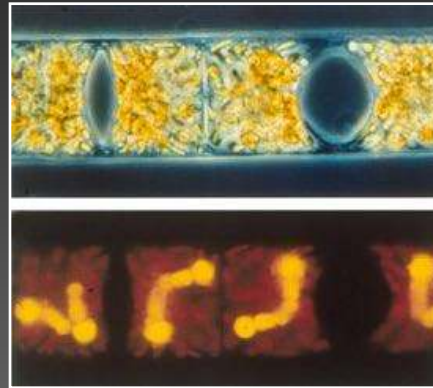
- Who is there? Microbiome diversity
- What are they doing? Microbiome functional diversity, holobiont physiology and controls on N_2 fixation



Nitrogen-fixing marine cyanobacteria

- Symbionts
 - UNCYN-A
 - *Richelia*
- Free-living
 - *Crococosphaera*
 - *Trichodesmium*
 - Trichodesmium contortum*
 - Trichodesmium erythraeum*
 - Trichodesmium tenue*
 - Trichodesmium thiebautii*
 - Trichodesmium spiralis*
 - Trichodesmium hildebrandtii*

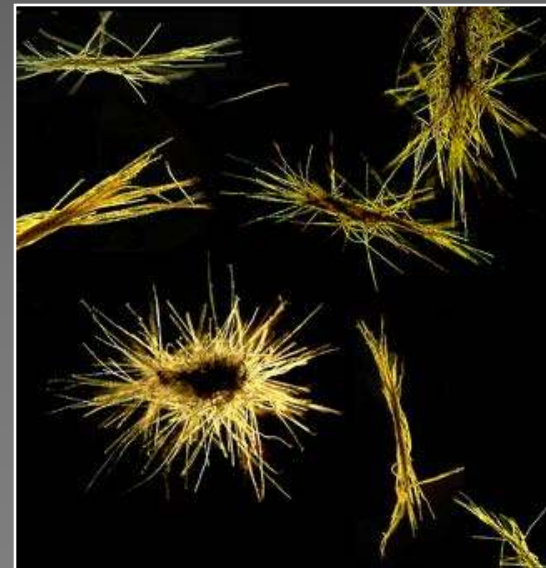
Richelia



Crococosphaera



Trichodesmium

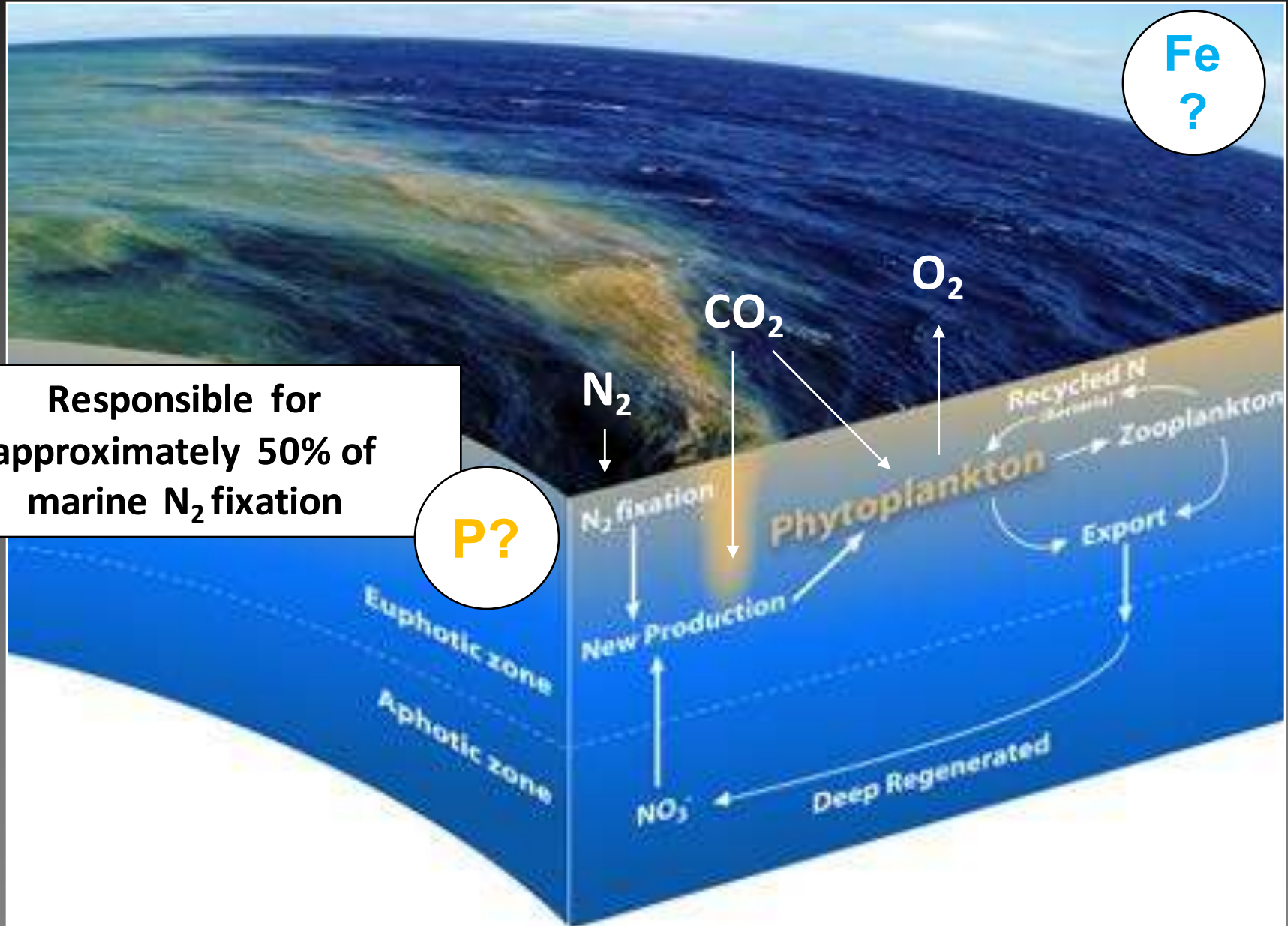


Trichodesmium: critical to ecosystem function

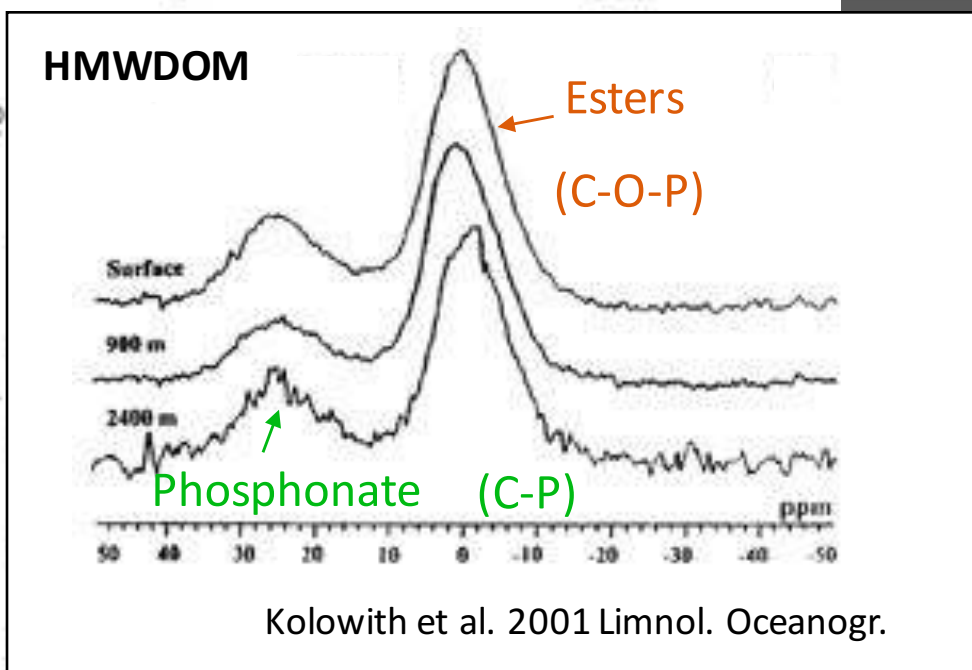
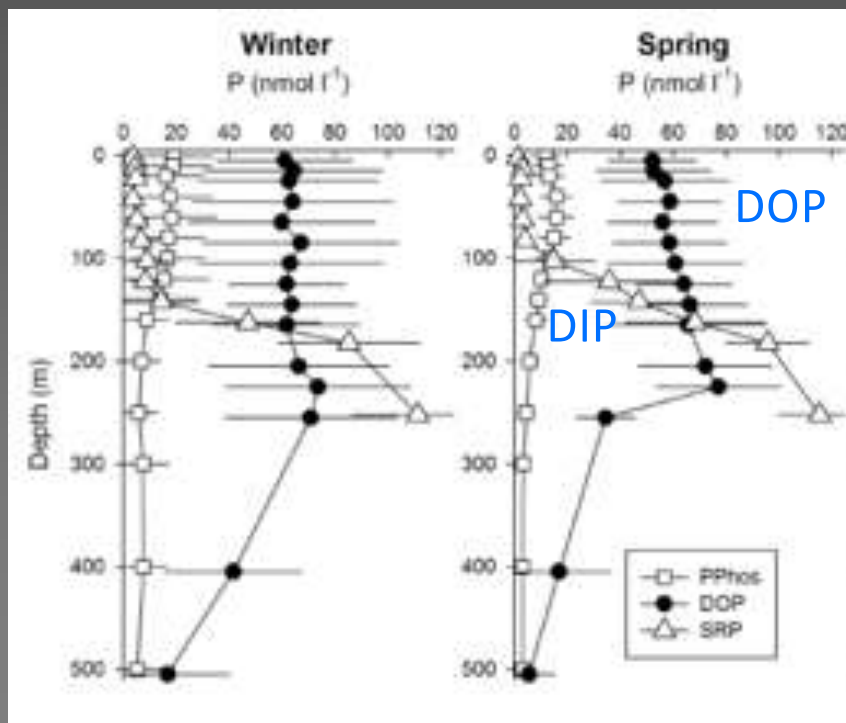
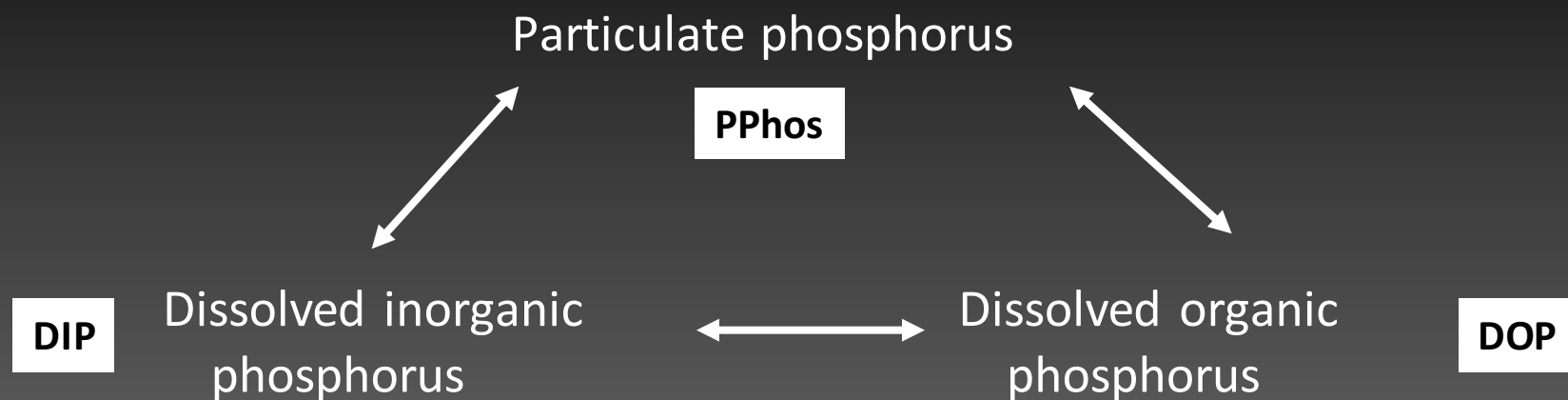


Photo: Chris Wade
Tricho. micrograph: WHOI

Trichodesmium: critical to ecosystem function



Phosphorus pools in the open ocean



Trichodesmium erythraeum IMS101 genome page

JGI Microbes

http://genome.jgi-psf.org/draft_microbes/Trich/Trich_Ery101.html

Apple Amazon eBay Yahoo! News Microsoft Mac OS X NCBI Webmail TV TV Listings

JGI Microbes *Trichodesmium erythraeum* DRAFT GENOME

| BLAST | Download | Draft Annotation | Info **Home**



Marine filamentous cyanobacteria of the genus *Trichodesmium* play a major role in the tropical and subtropical oceans both as primary producers and suppliers of "new" nitrogen through their ability to fix atmospheric dinitrogen (N₂) (Capone et al., 1997). They are simple undifferentiated filamentous forms that divide in a single plane. They may occur as single filaments but more commonly as macroscopic colonial aggregates (2-20cm) containing many filaments. The colonies vary in color from yellowish-brown to deep red because they contain phycoerythrin as their primary light harvesting pigment. *Trichodesmium* spp. are planktonic and owe their buoyancy to the possession of gas vacuoles. The genus currently contains five species characterized from natural populations (Carpenter et al., 1983; Jansson et al., 1995). The species are distinguished by cell and colony morphology, pigmentation and buoyancy.

Questions about this project, contact: Paul Jansson
JGI, Joint Genome Institute #1000

Phosphorus metabolic traits and trade-offs

- Phosphonate

- C-P Lyase (Fe co-factor)

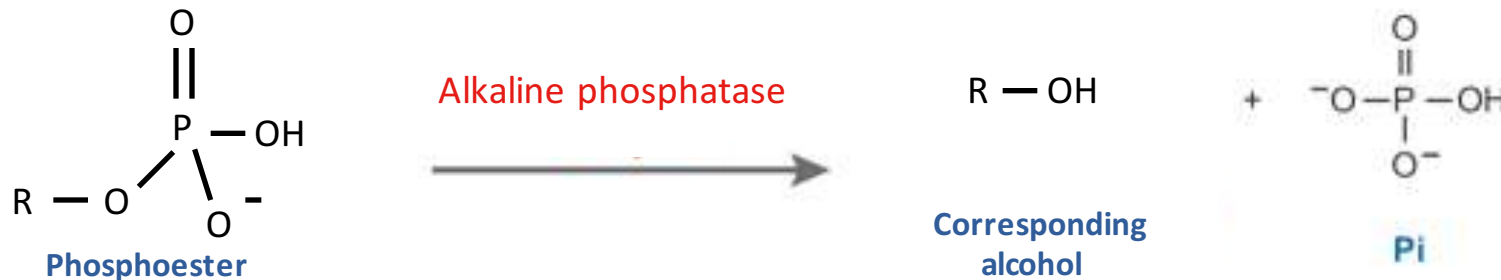
C-P

- Ester

- *phoX* type alkaline phosphatase (Ca Fe co-factor)
 - *phoA* type alkaline phosphatase (Zn co-factor)

COP

COP



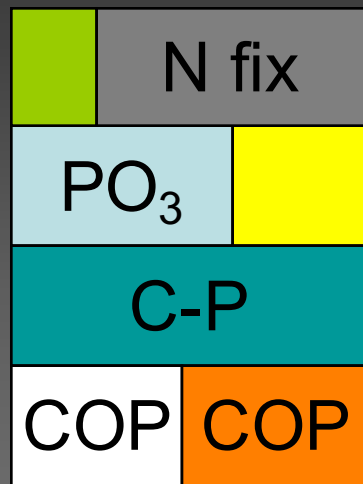
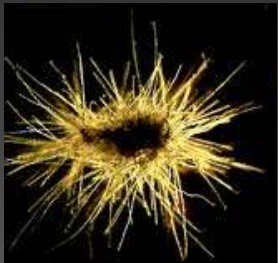
- Phosphite

- *ptxD* gene cluster

PO₃

Comparative genomics: phosphorus traits and trade offs

Trichodesmium



Crococosphaera



Other N_2 fixing cyanobacteria genomes do not encode the same pathways for phosphorus metabolism - less available substrates, but less metal requirement

Tracking genomic potential with expression studies



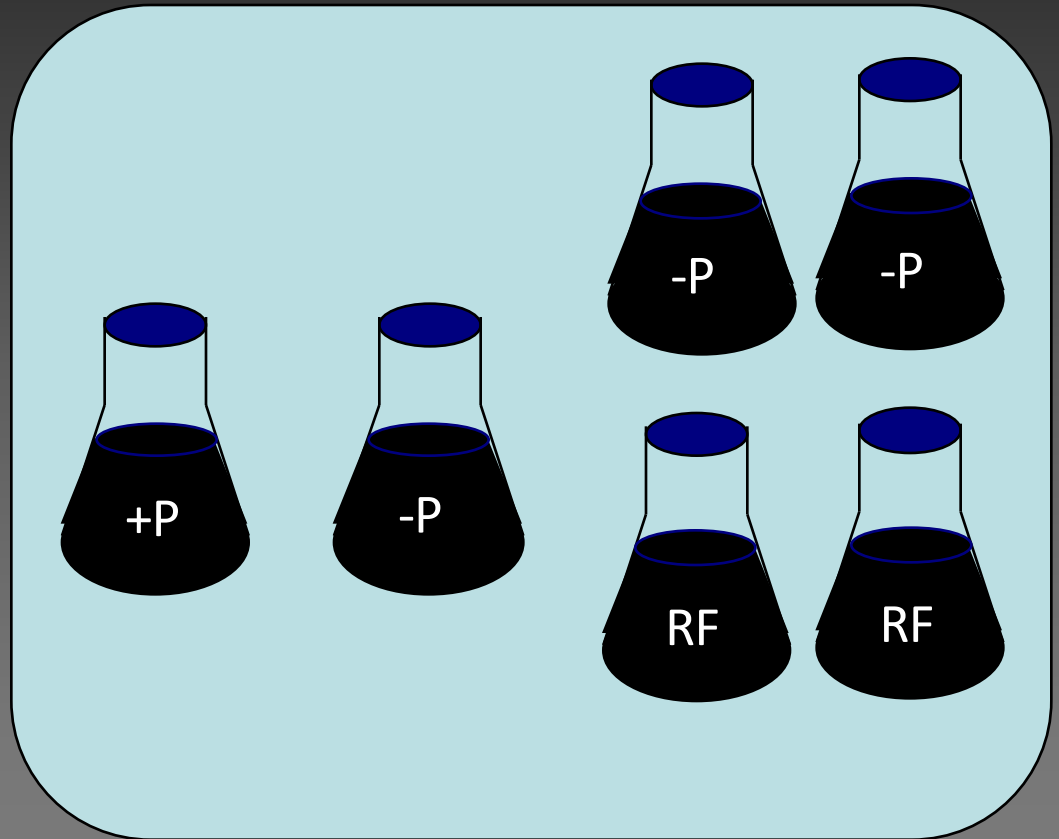
Culture cells

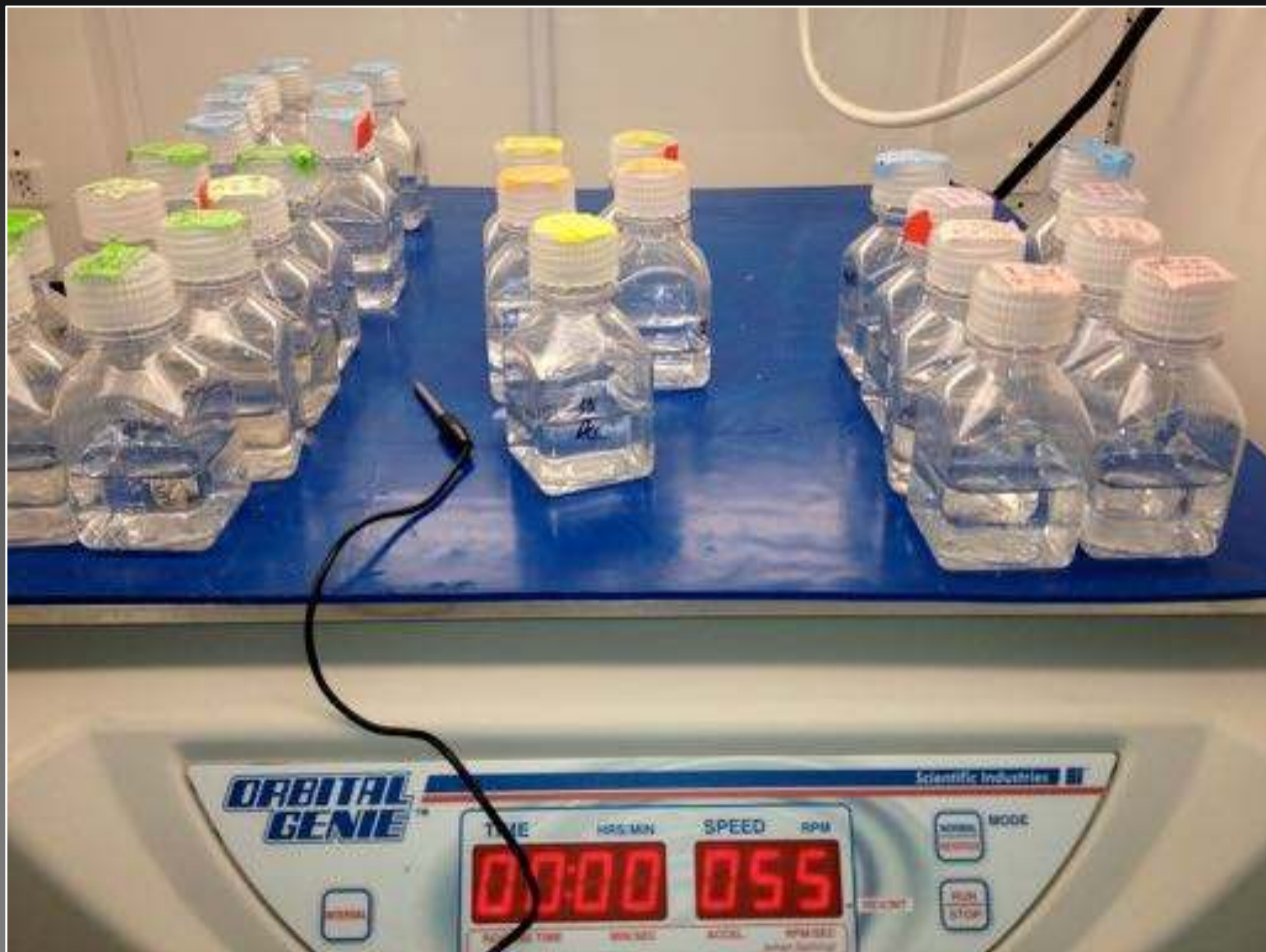


Harvest and preserve
samples

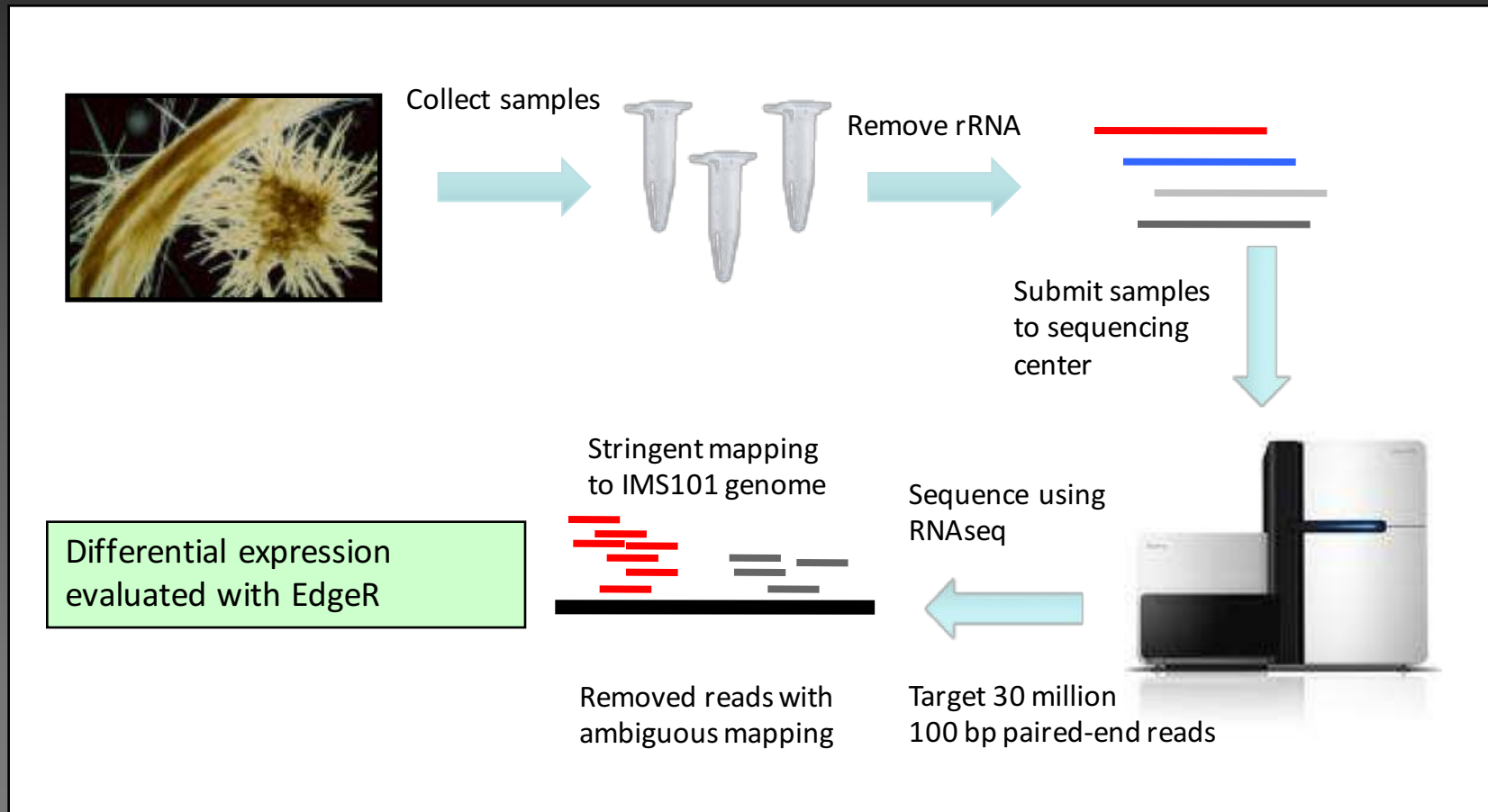


Transcriptome
Proteome

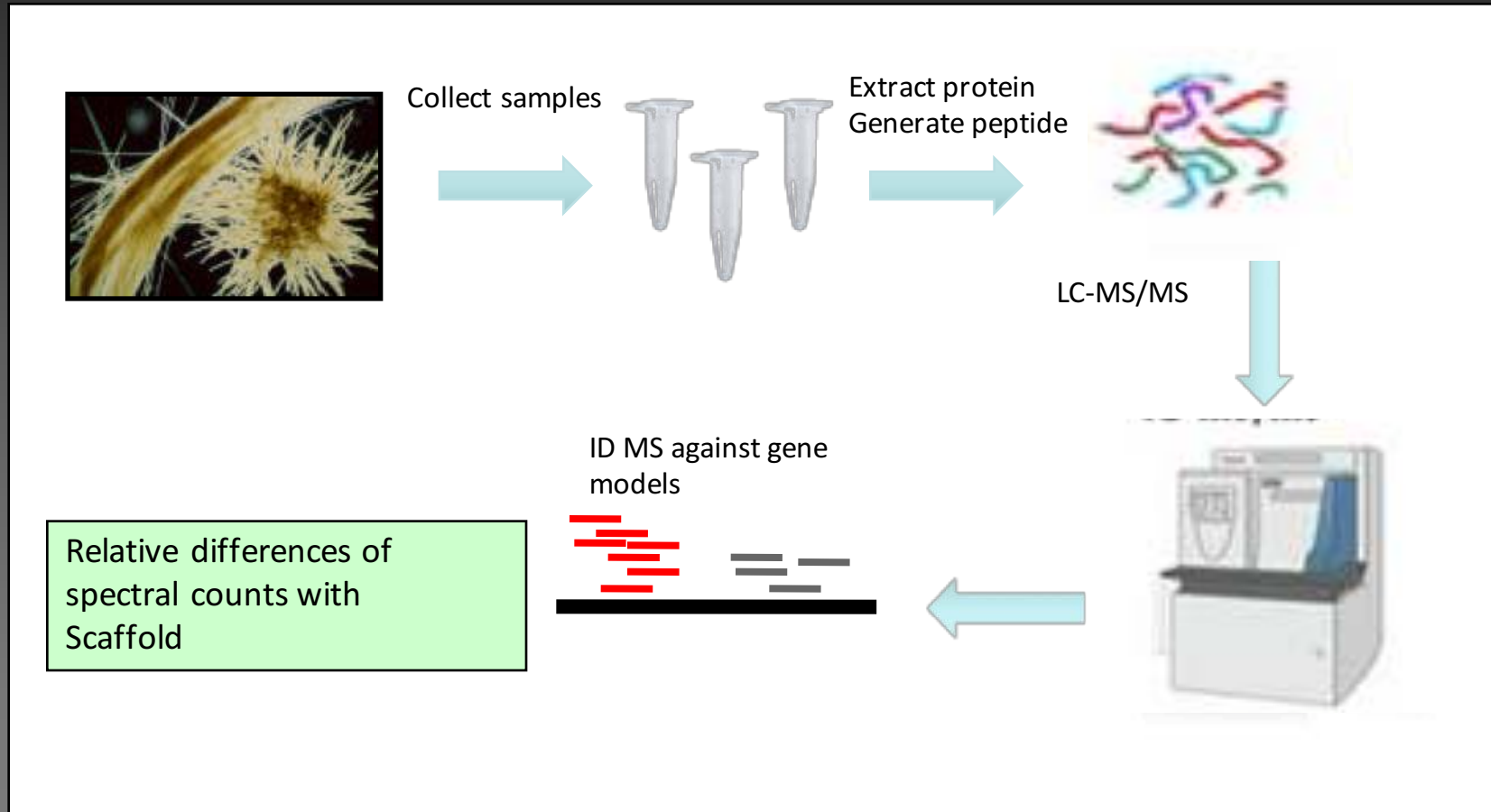




Tatranscriptome analysis pipeline

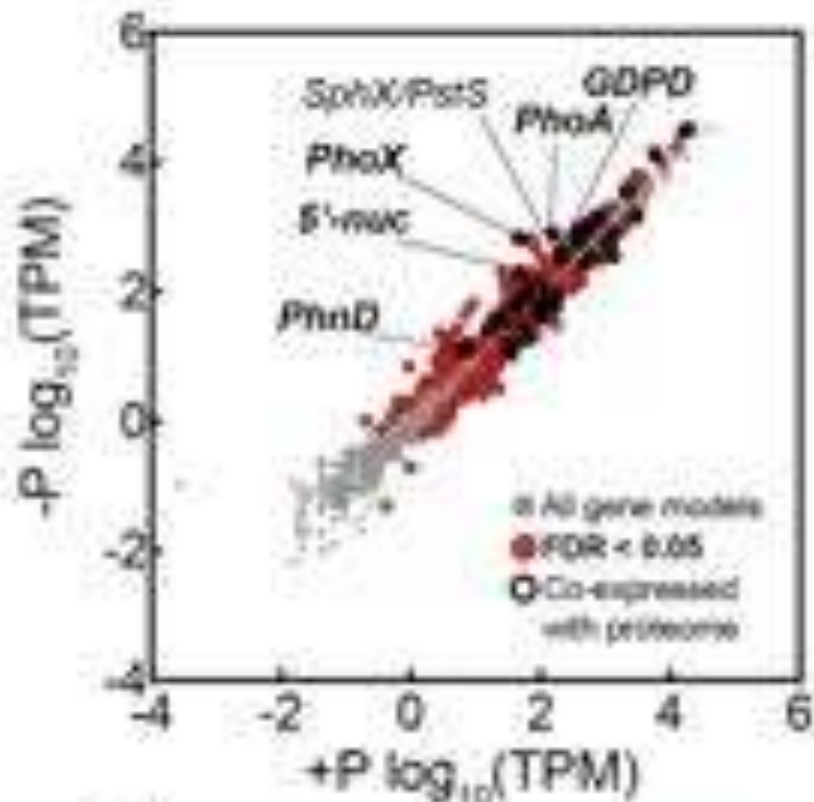


Proteome analysis pipeline

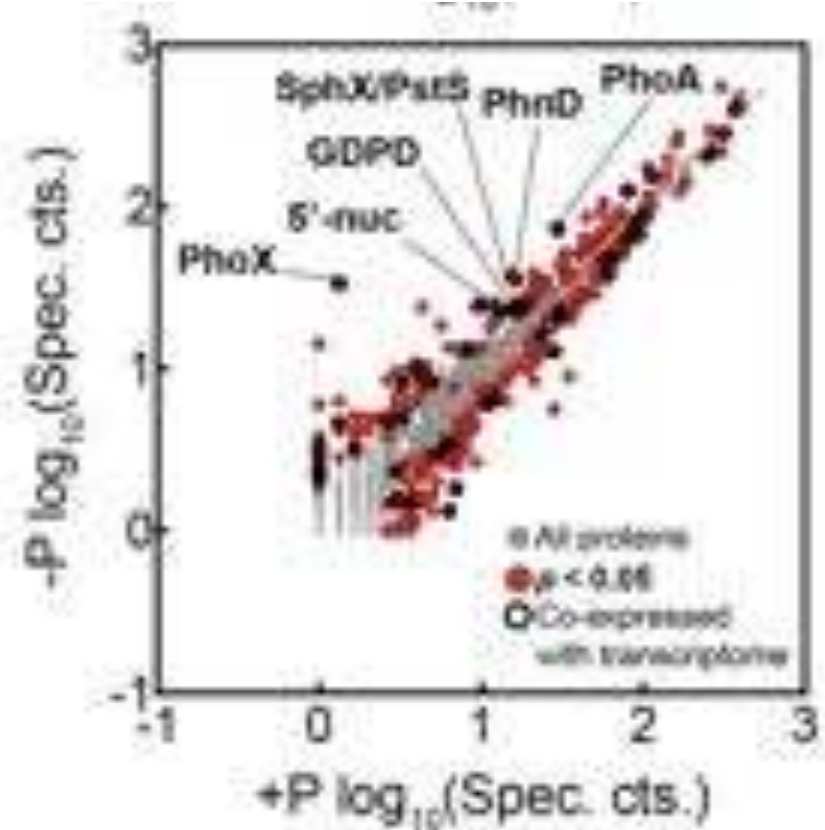


How does *Trichodesmium* respond to low phosphorus?

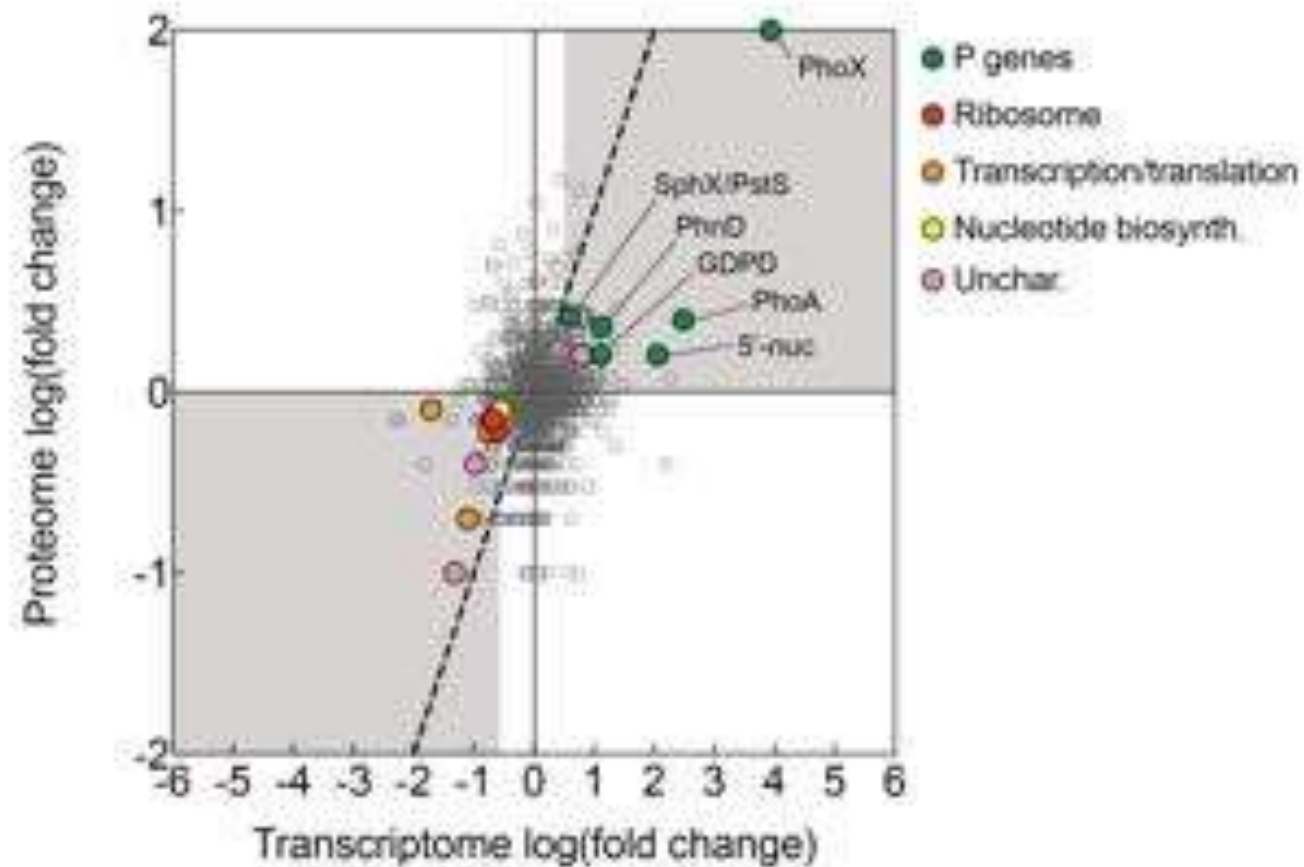
Transcriptome



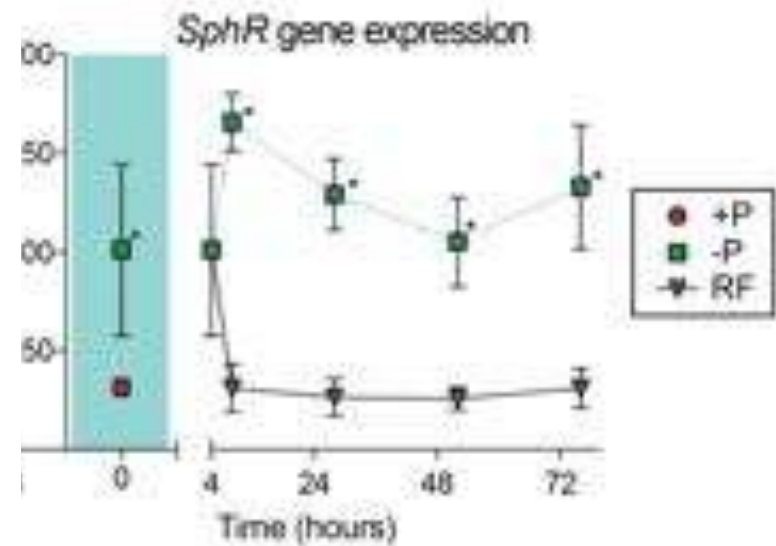
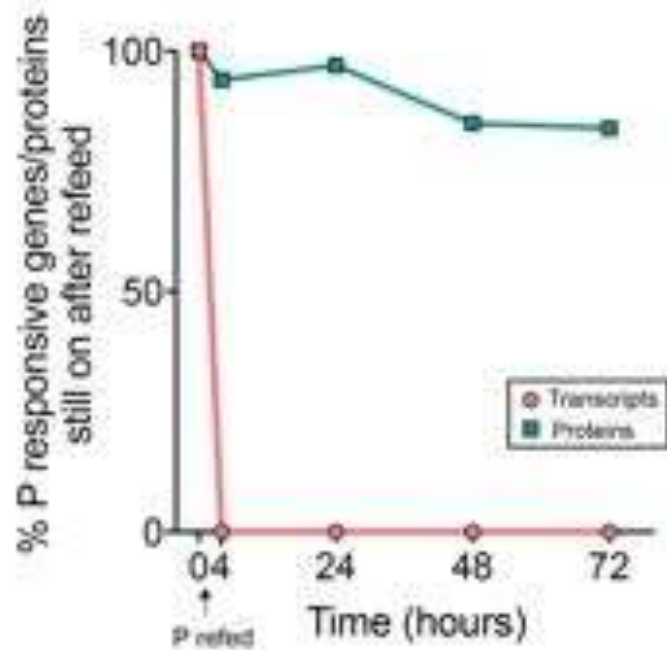
Proteome



Transcriptome - proteome coordination

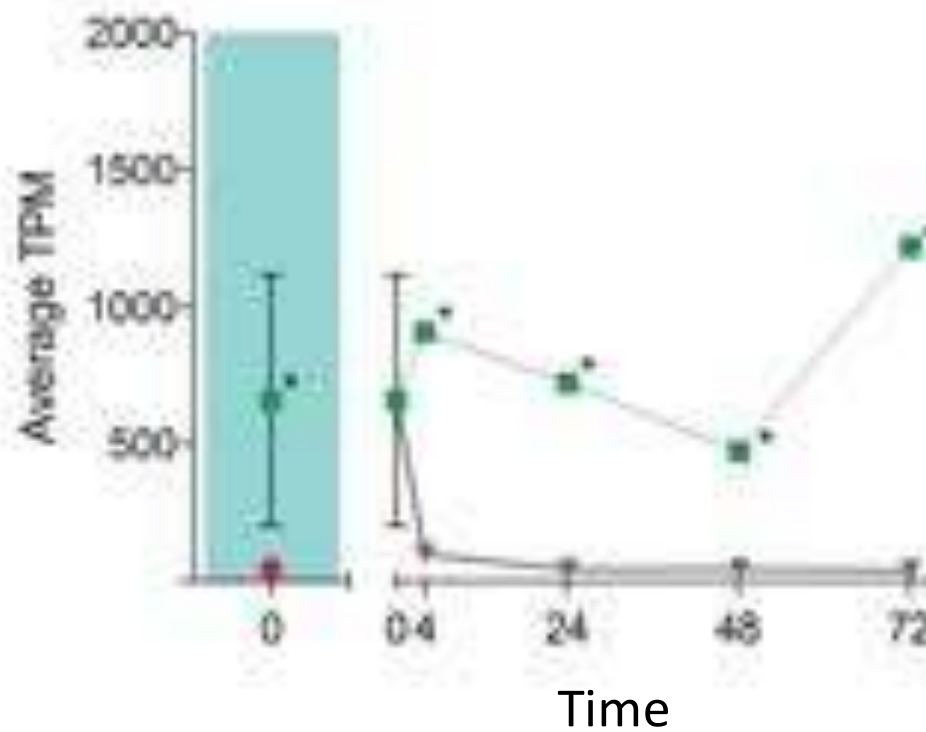


Transcripts turnover more quickly than proteins

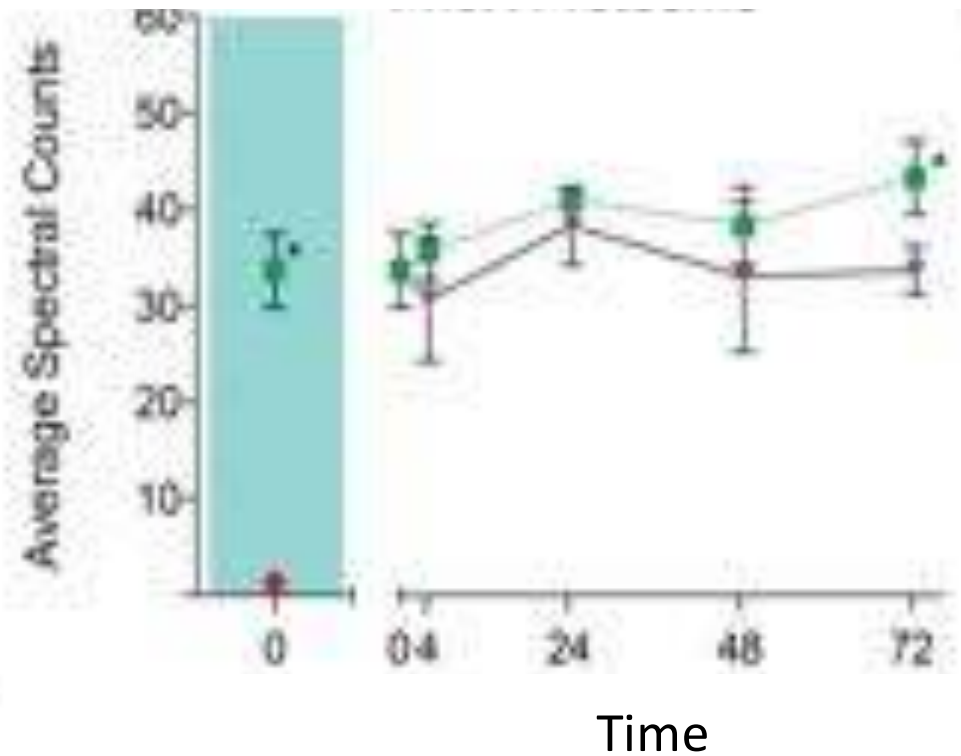


How does *Trichodesmium* respond to low phosphorus?

phoX transcripts



PhoX proteins



Tracking genomic potential with expression studies



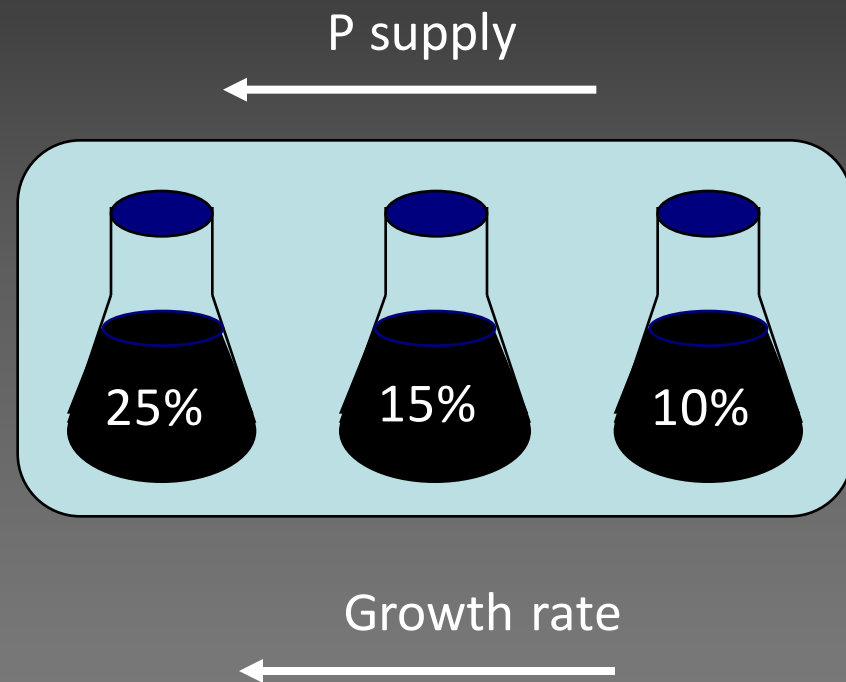
Culture cells



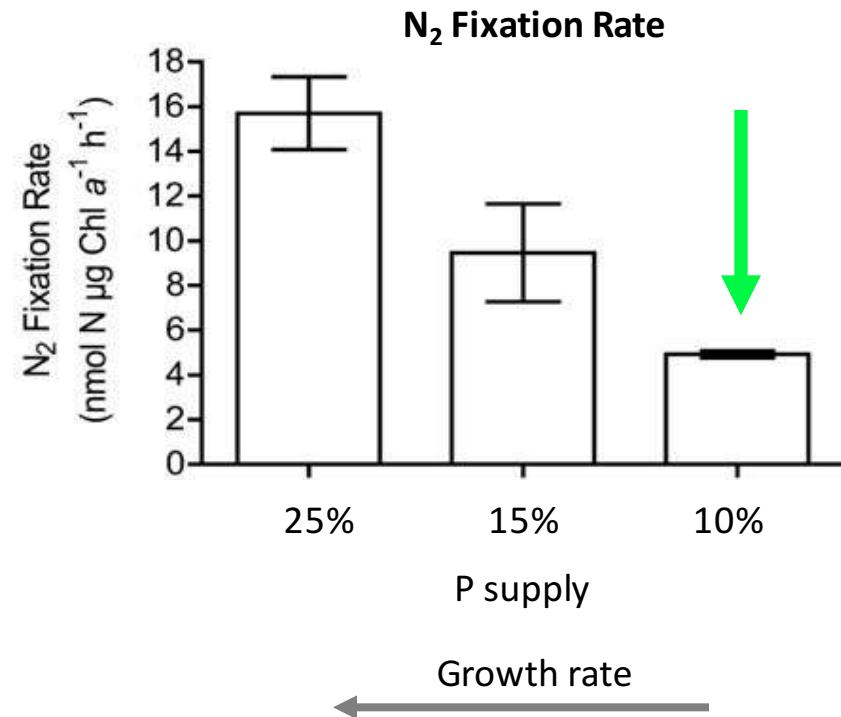
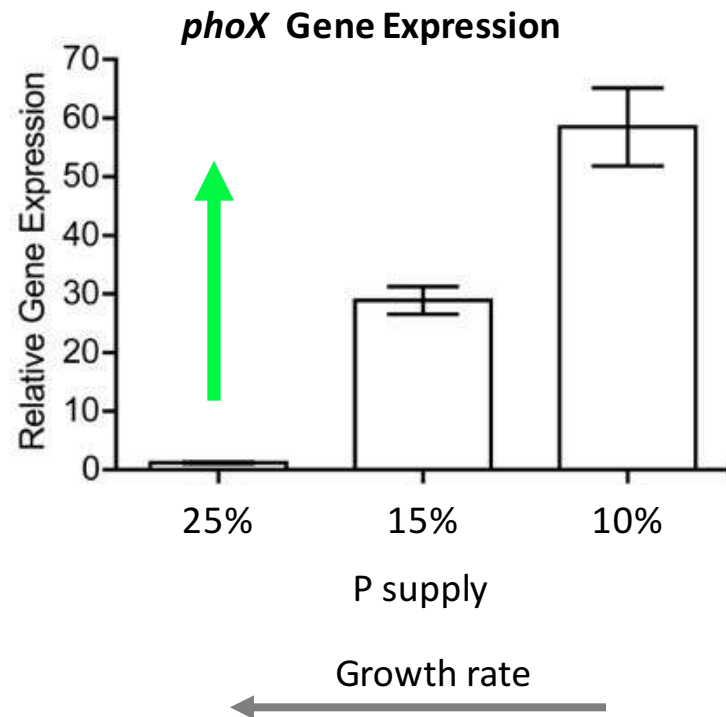
Harvest and preserve
samples



qRT-PCR of *phoX*
Activity

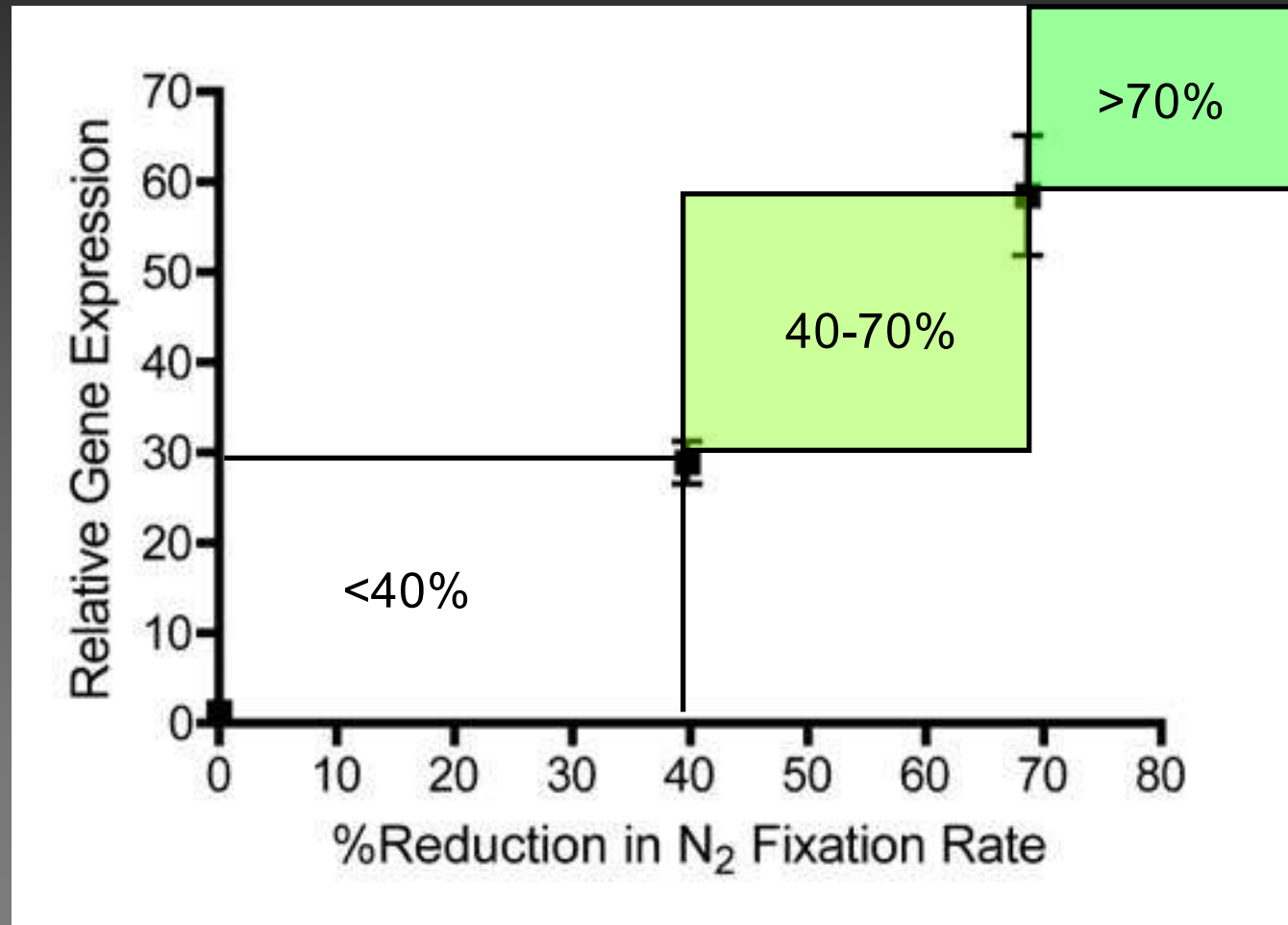


Calibrating gene expression to growth and N₂ fixation



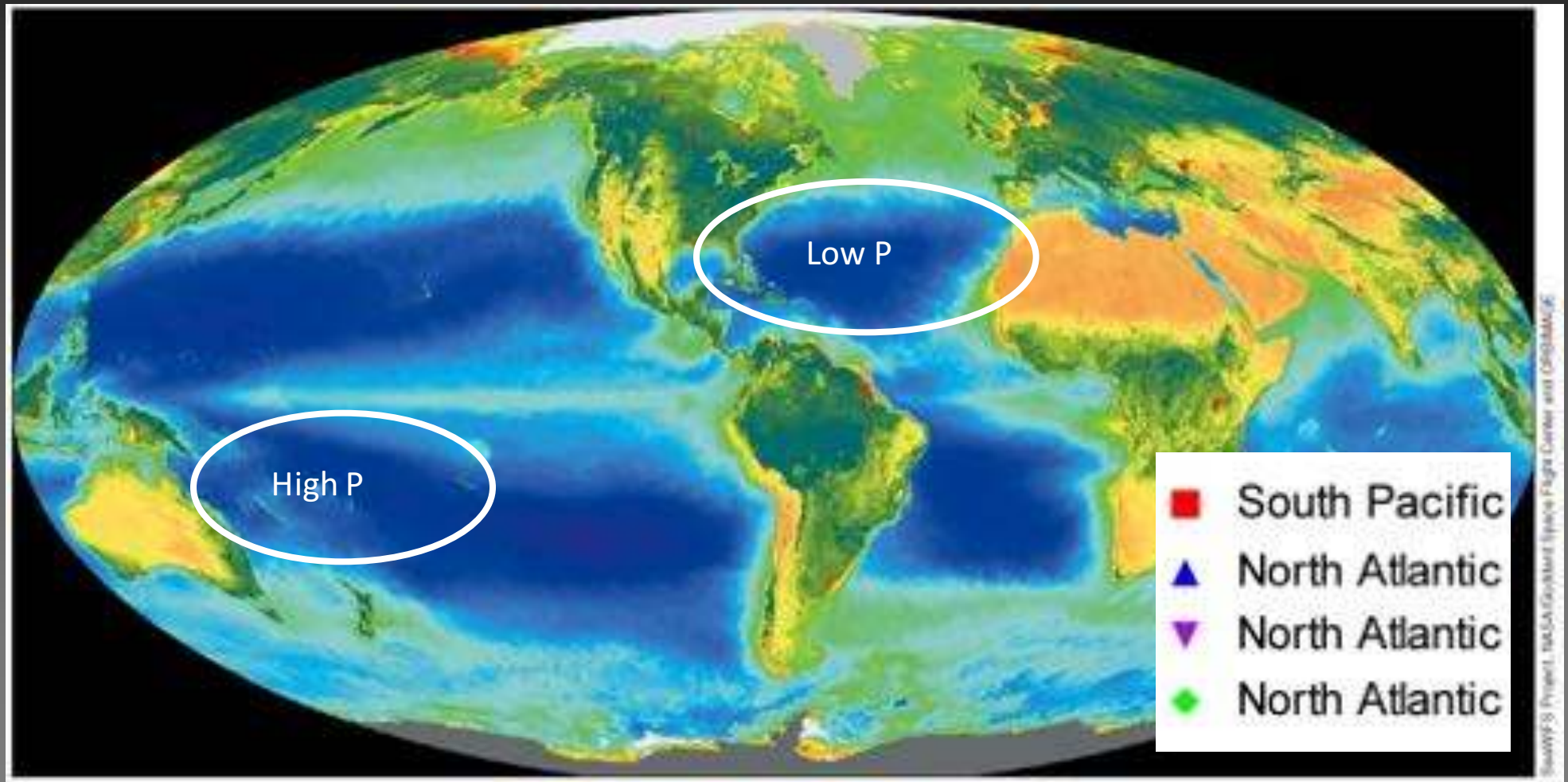
Orchard and Dyhrman unpublished

Calibrating gene expression to N₂ fixation



Orchard et al. in prep

Sampling different P regimes





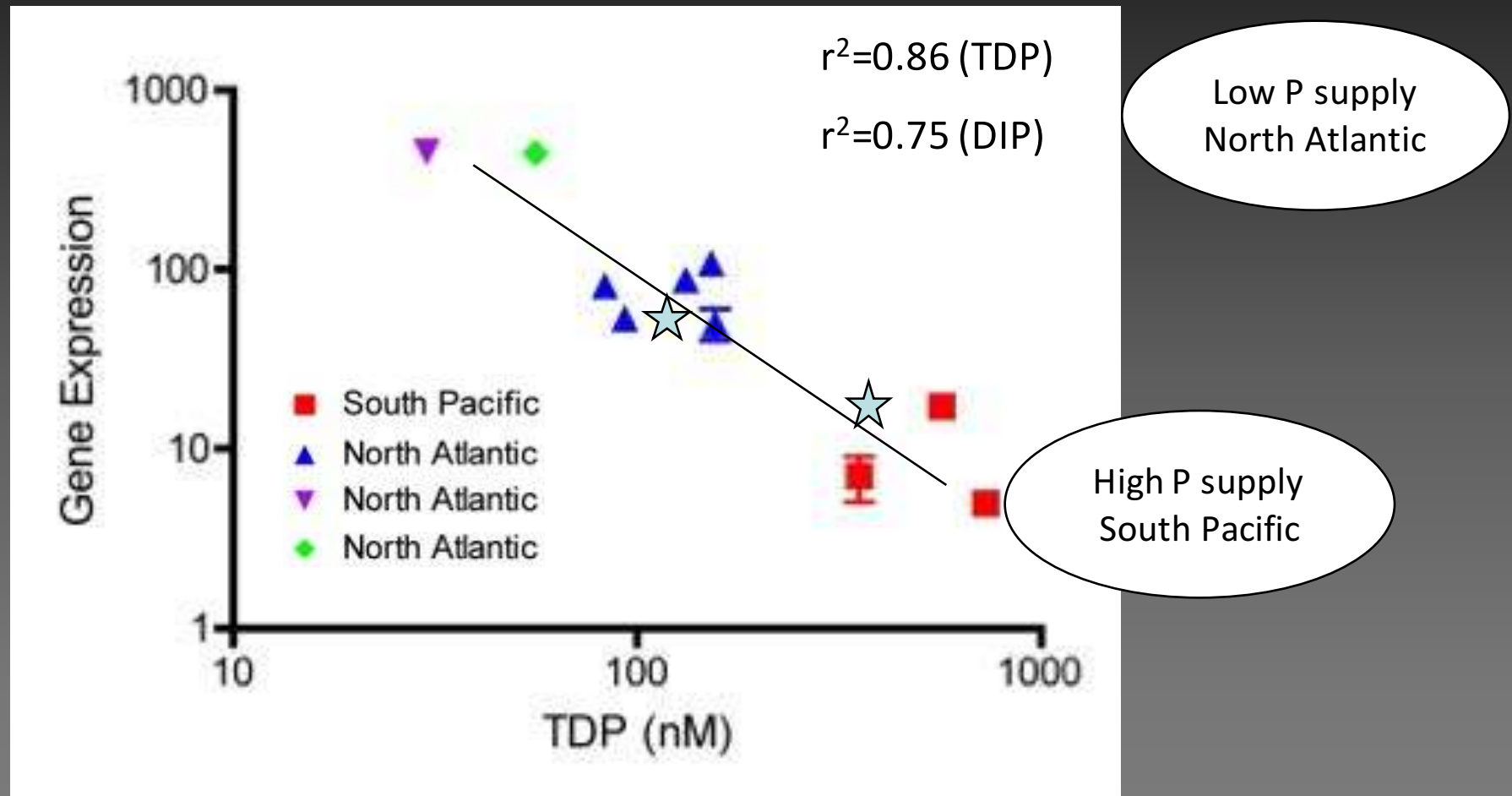


DIP, TDP
Measurements



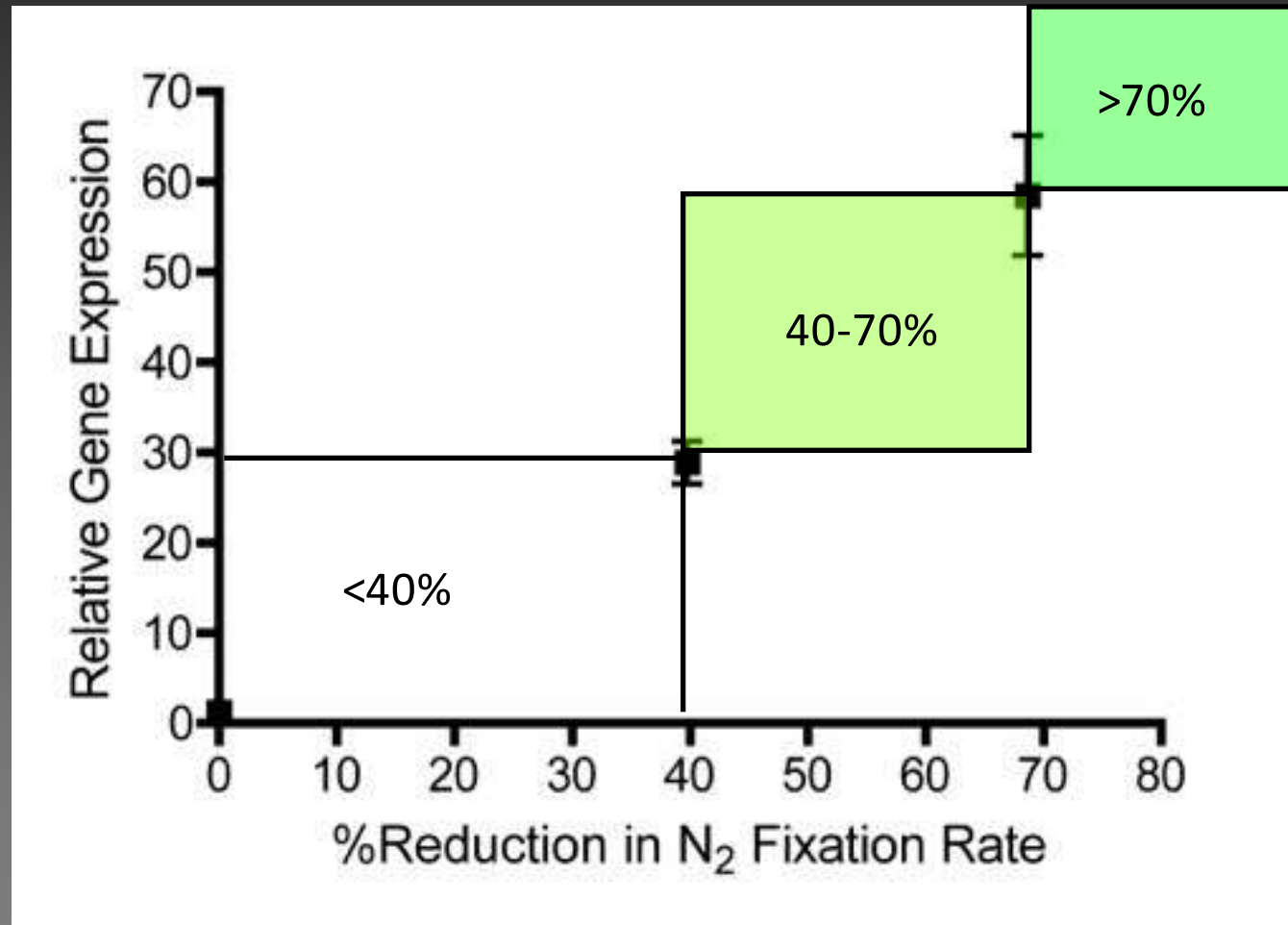
Measurements of
quantitative gene
expression for
Trichodesmium sp.

Gene expression increases at low phosphorus



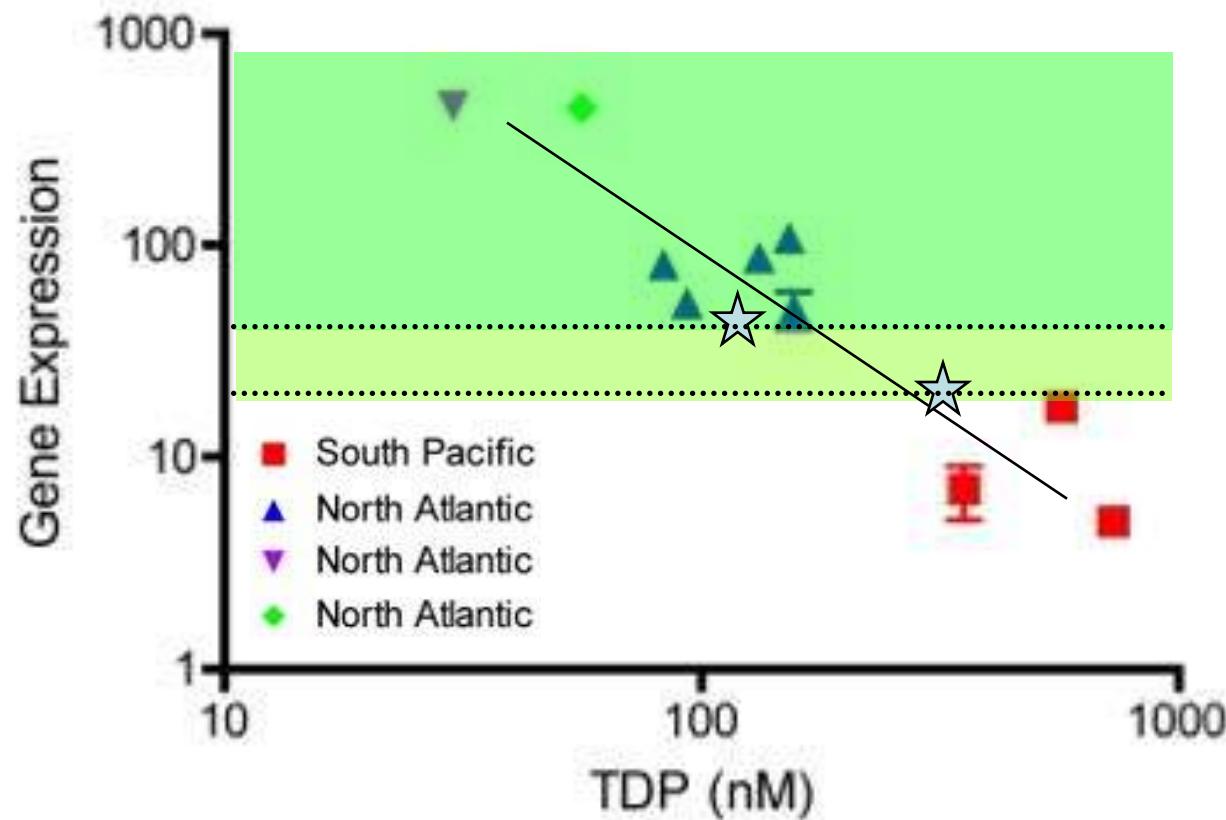
Orchard and Dyhrman unpublished

Calibrating gene expression to N₂ fixation



Orchard and Dyhrman unpublished

Data predicts that P supply limits N₂ fixation in the western N. Atlantic



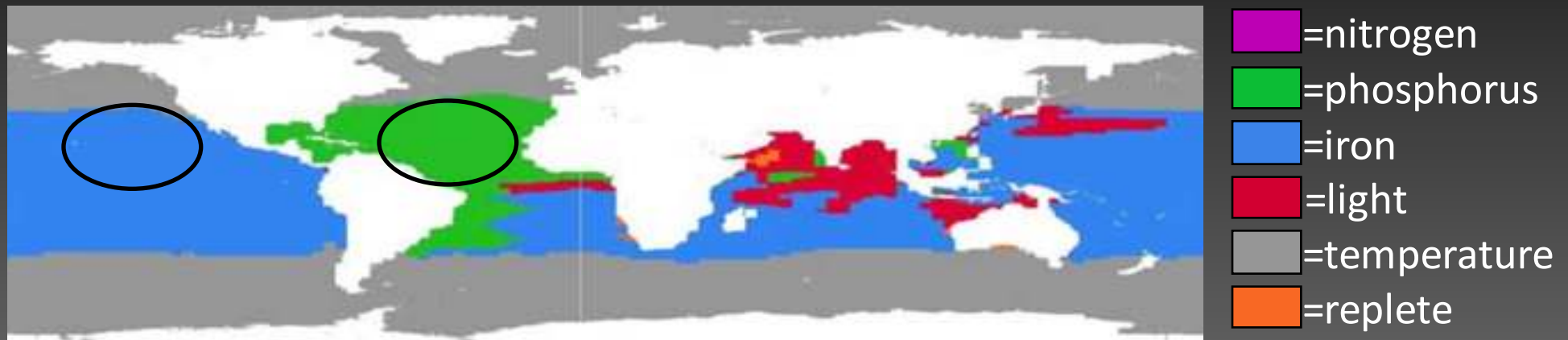
← >70%

← 40-70%

← <40%

Orchard and Dyhrman unpublished

Constraints on *Trichodesmium* N₂ fixation



(Moore et al. 2004)

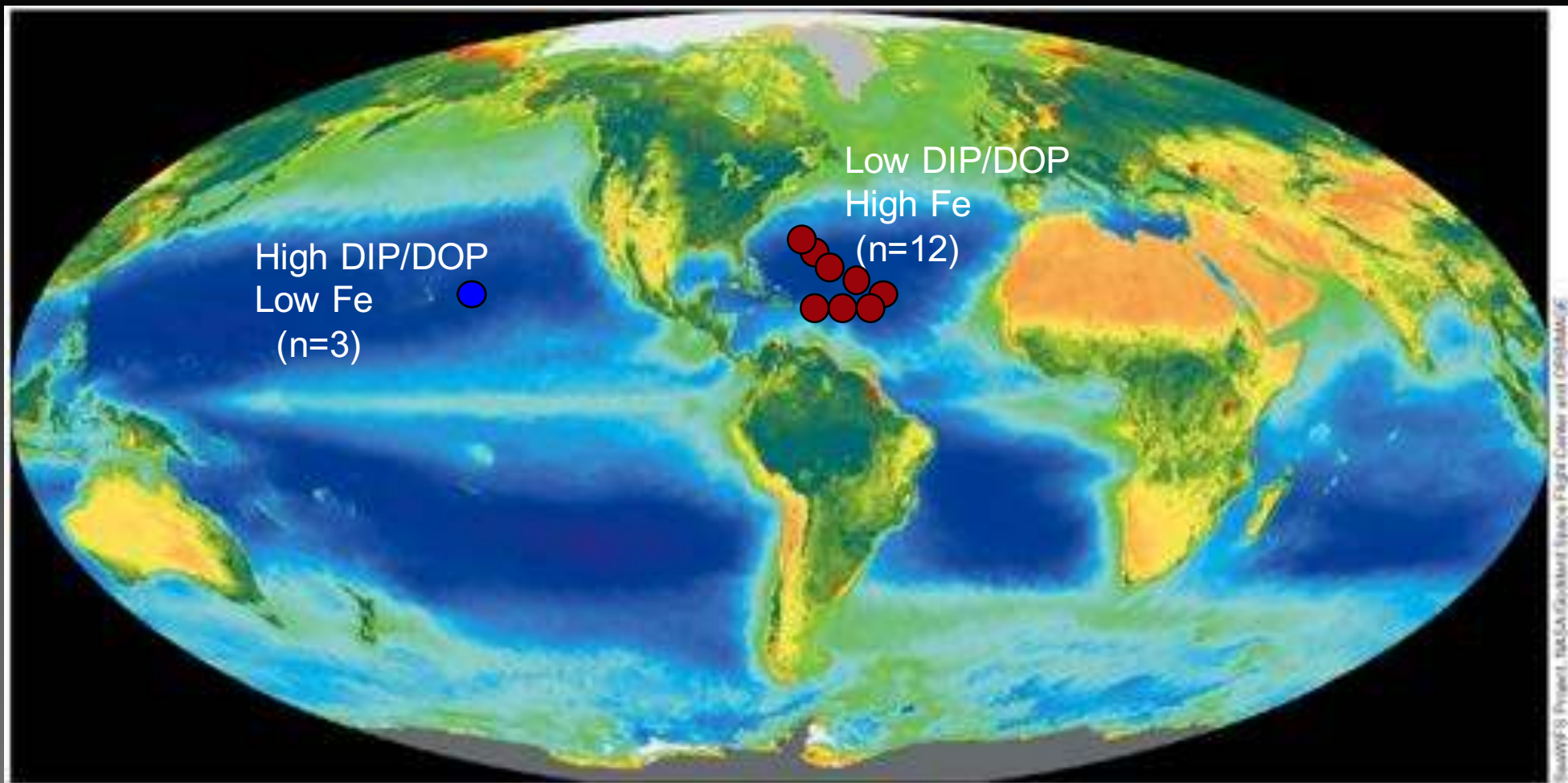
Molecular patterns corroborate predictive models in the western north Atlantic

phoX - P regulated ester metabolism (Orchard et al. 2009 *Environ. Micro.*)

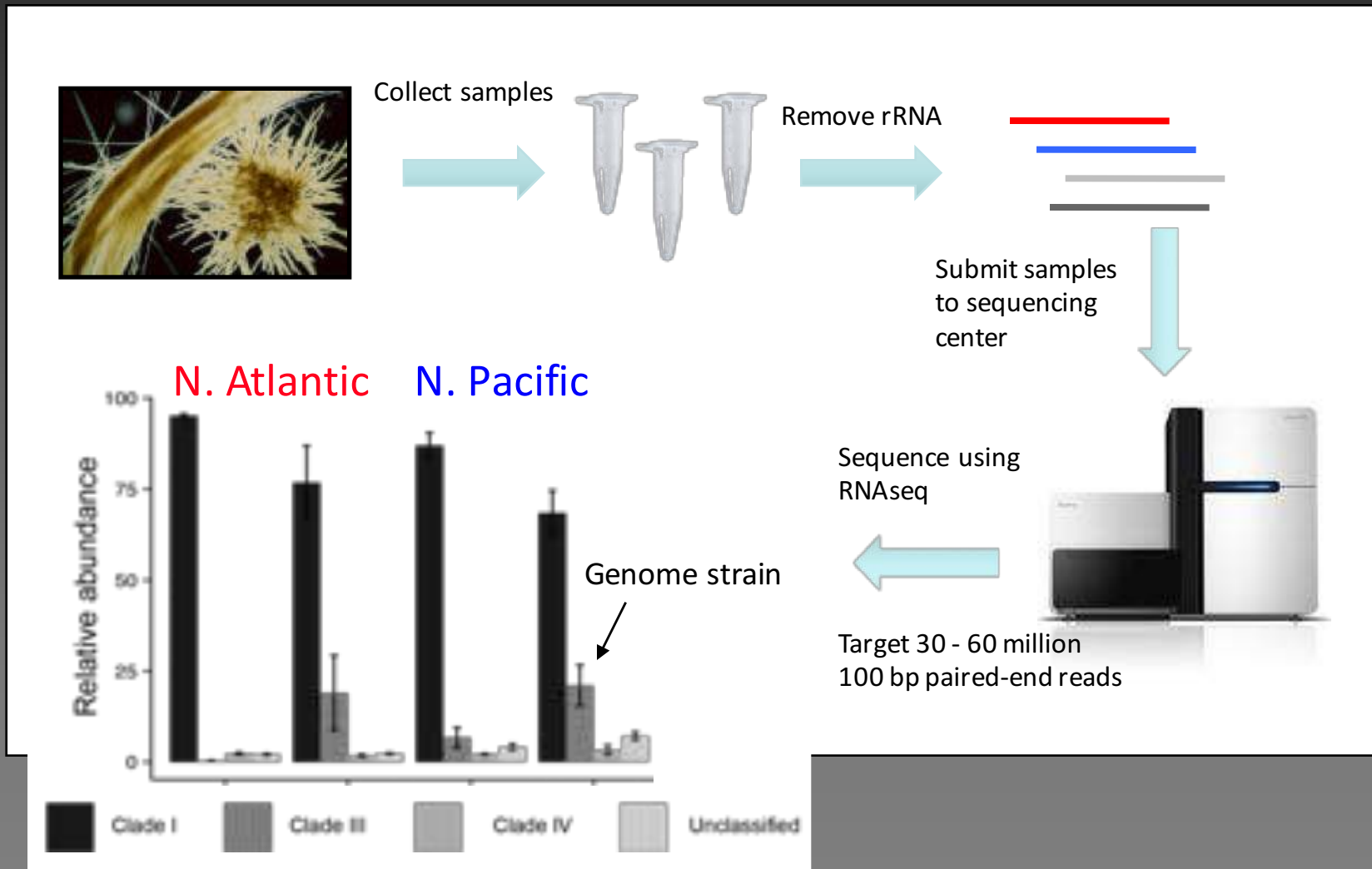
idiA - Fe regulated iron metabolism (Chappell et al. 2013 *ISME J.*)

rnpB - reference gene

nifH - N₂ - fixation

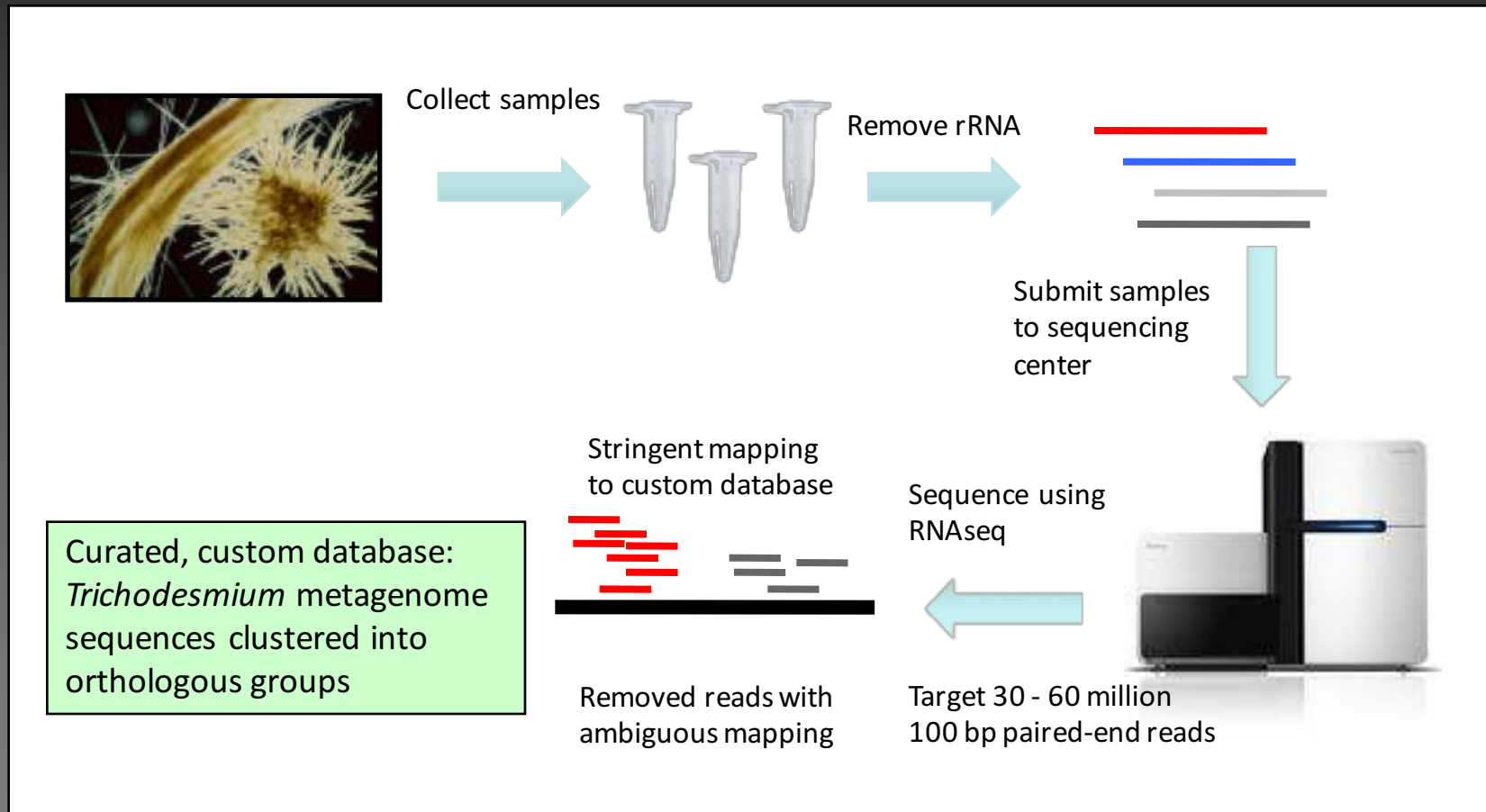


Metatranscriptome analysis pipeline



Rouco et al. (2016) *Environ. Micro.*

Metatranscriptome analysis pipeline



The reality.....

```
@DHT4KXP1:1:1101:5930:2353#0/1
CAACAACATCATACCTTCCAAGGCACGGGCTTCAACGCCCGCCAAATCTCC
TGCGGCAGCAGGGATGGGACCCTGGGACTGTGTGGCGCTGTGGAGGCCG
+DHT4KXP1:1:1101:5930:2353#0/1
\W\^aac^[`[cfhh_Z`^eg[RJ`W~000^aeae0_eehhULVMV\H\
\`ZSNWw^aaQTRGX^BBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBB
@DHT4KXP1:1:1101:5904:2385#0/1
CTACCATTTTCATTTTCCATGTCTCTCCCCATCTTGACACATTATTTTTCT
ACCTCCATCACATCATGATCACGTTATACGATCTCTACAGTAGCCCCCA
+DHT4KXP1:1:1101:5904:2385#0/1
bbbeeeeeggggegiiiiiiiighhhhiiiiifhihiifgiifhiiiihihi
iihihihihihihihihihiidgggggeeeecdddddccbcccccccc_
@DHT4KXP1:1:1101:5781:2386#0/1
CTTTCAGATACAGTAGGATTTATTTCAGGATCTTCCGACGACATTGATTGCTG
CATTCCGCTCAACGCTTGAGGAAGTAAAAGAAGCGGATTTAATTCTGCA
```

Metatranscriptome analysis

RNA extraction

Bacterial mRNA enrichment:

- Euk RNA removal- MICROBEnrich kit (Ambion)
- Bacterial rRNA removal- Ribo-Zero (Epicentre)

Sequencing:

Single-end reads 100bp
Illumina HiSeq. 2000
Depth coverage: 30M

Output:
.fastq

Preparation of reference metagenome:

- Extraction of *Trichodesmium*-only scaffolds from metagenome data

Read mapping

RSEM (Li and Dewey, 2011) with
Bowtie2 (Langmead et al. 2012)

Sequence processing:

- Sequence quality - FASTQC (.fastq)
- Trimming - Trimmomatic (.fastq)

Differential expression analyses:

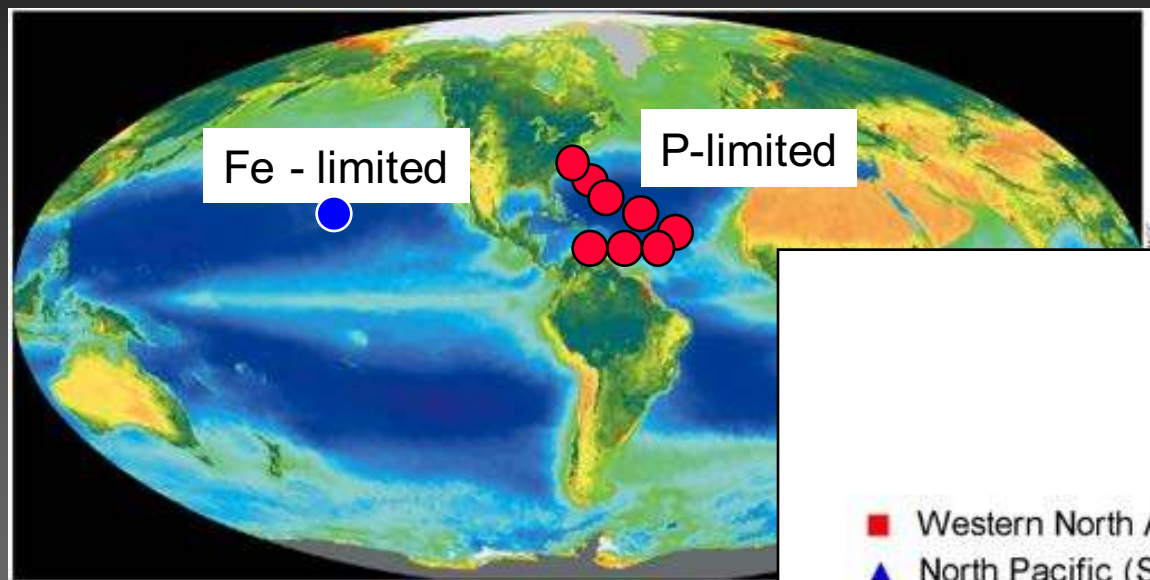
R (vegan package – Oksanen et al. 2016)

- Correspondence analysis (CA) + envit function
- PERMANOVA (adonis function)

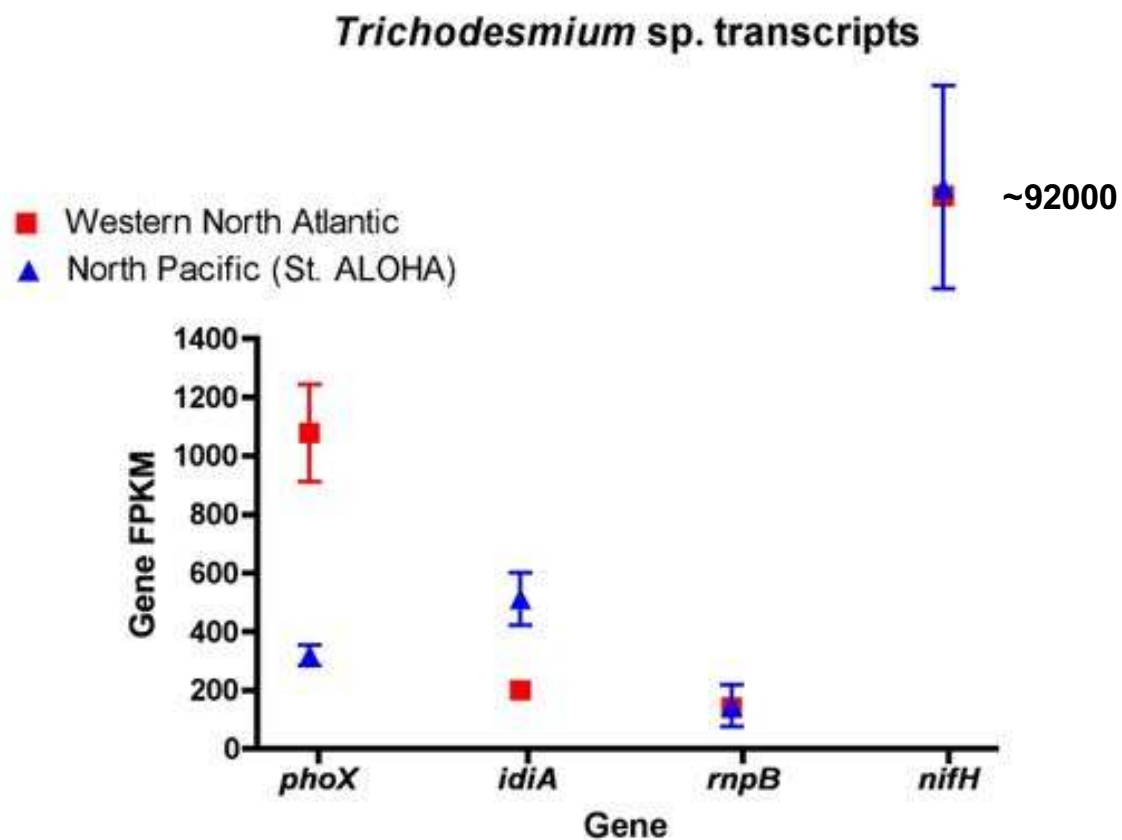
R (EdgeR package– Robinson et al. 2010)

- Assessment of differential abundance of individual OG

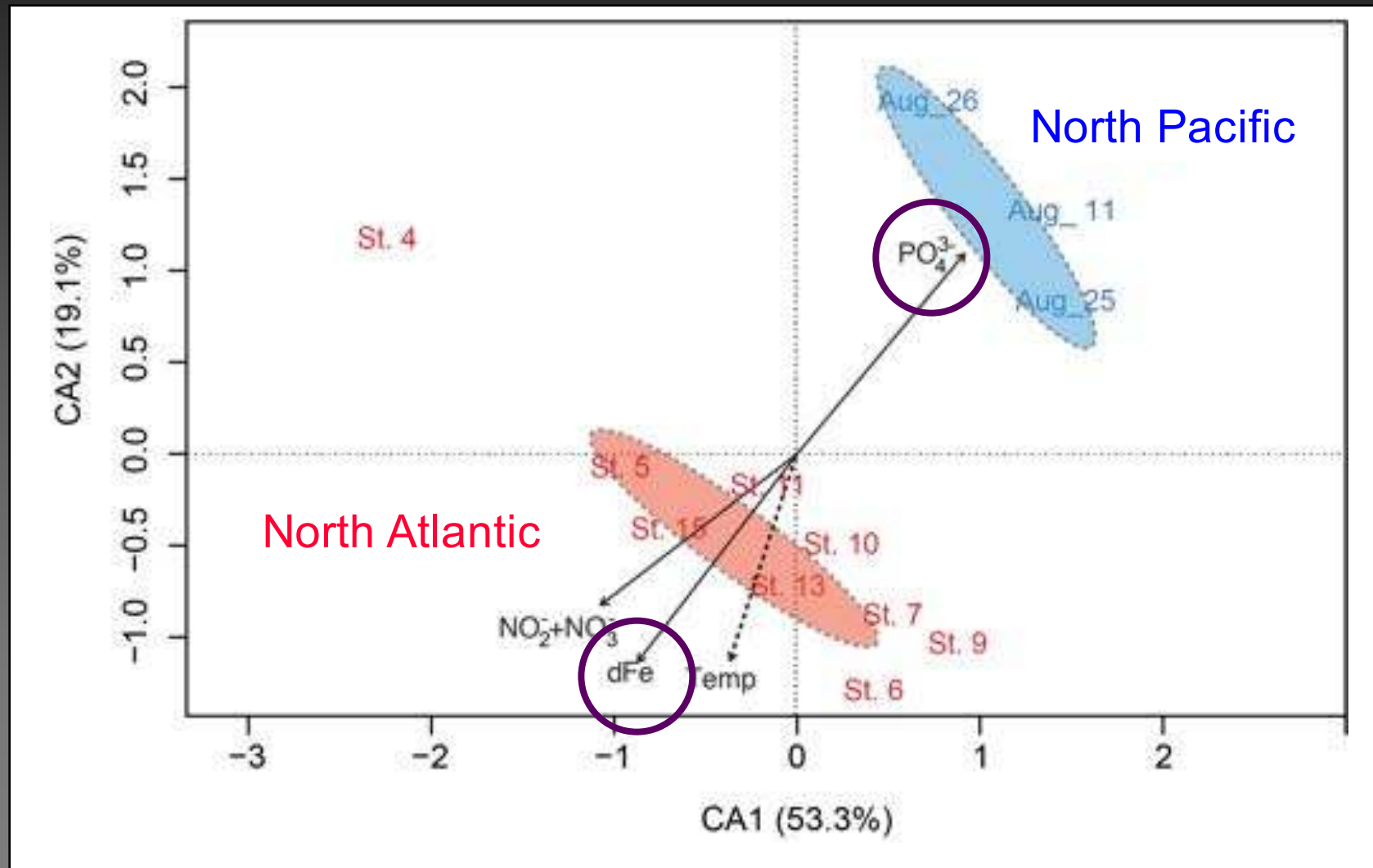
Biomarkers consistent with model prediction



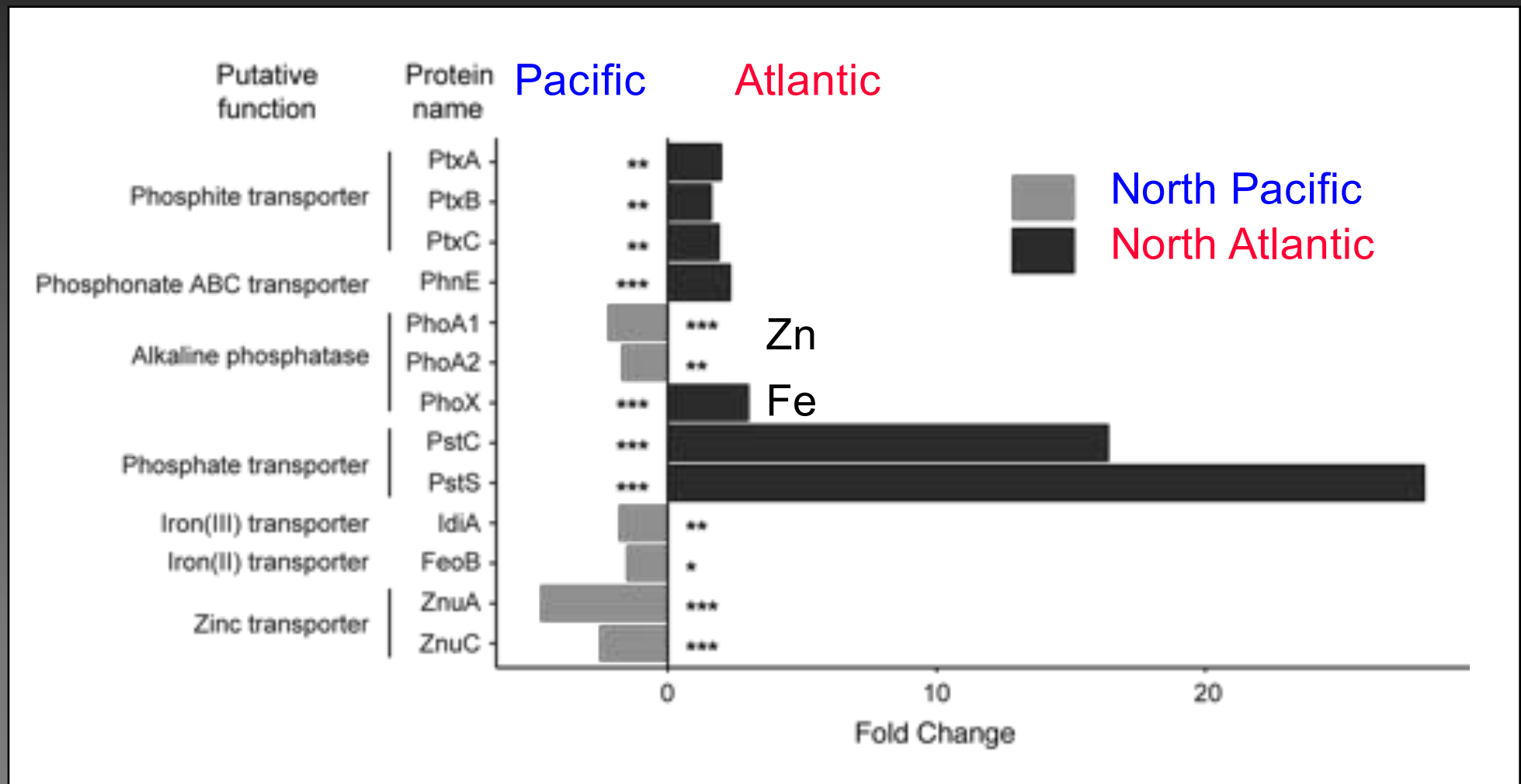
Biomarkers confirm
model predictions.



Significant differences in global transcription between the North Pacific and the North Atlantic



Transcription patterns indicate metalloenzyme trade-offs and geochemical controls



Summary - Metabolic traits and trade-offs

What phosphorus forms are bioavailable?

What are the biogeochemical constraints on N₂ fixation?

- **Genome:** *Trichodesmium* genome suggests bioavailability of phosphonate, ester, and phosphite
- **Marker transcripts:** *Trichodesmium phoX* expression levels suggests that supply of bioavailable P is low in the western N. Atlantic, which could constraint N₂ fixation
- **Metatranscriptome:** Predicted biogeochemical drivers of N₂ fixation are reflected in *Trichodesmium* transcriptional signals including likely metalloenzyme switching

Core questions

Metabolic traits and trade-offs

- What phosphorus is bioavailable?
- What are the biogeochemical constraints on N_2 fixation?



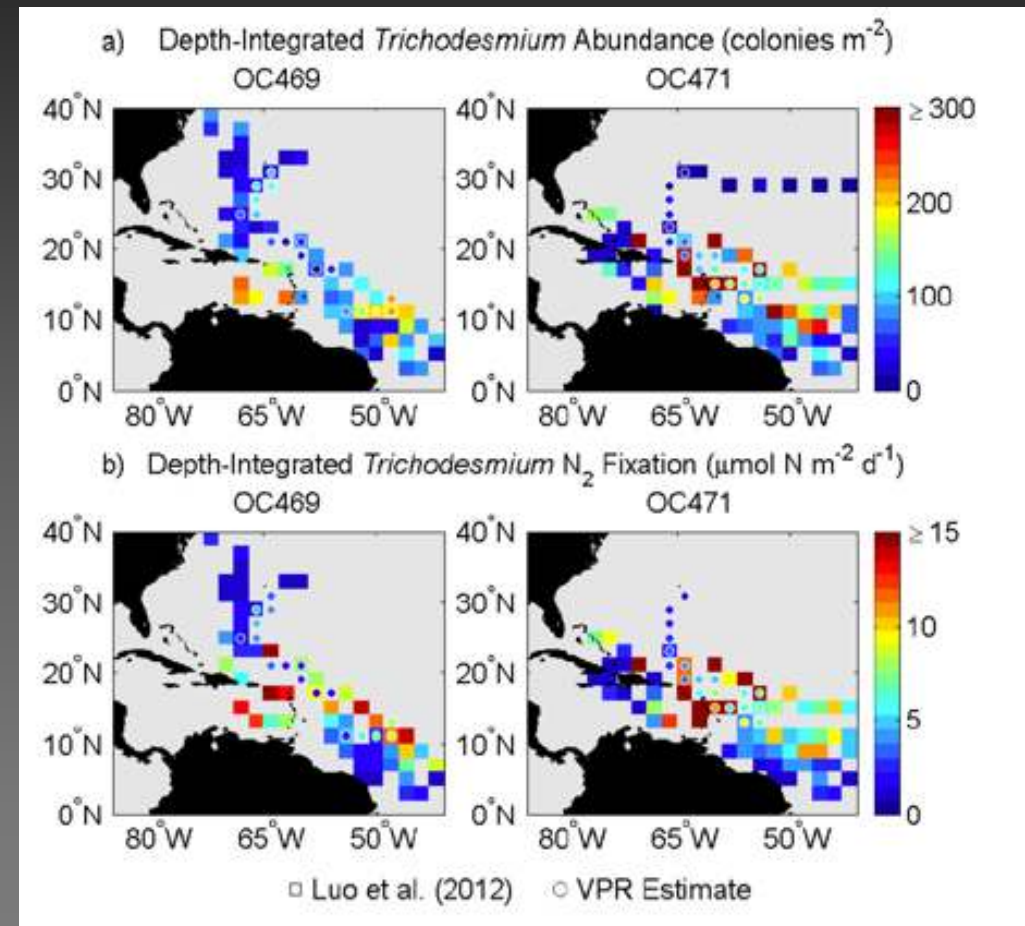
Host microbiome interactions

- Who is there? Microbiome diversity
- What are they doing? Microbiome functional diversity, holobiont physiology and controls on N_2 fixation



Modeling N₂ fixation is still a challenge

- Models do not balance the N cycle in the ocean or recapitulate patterns well
- Assays of nitrogen fixation are technically difficult = variability
- Information on distribution over time and with depth is still patchy
- Geochemistry is not necessarily a good predictor of distribution or N₂ fixation



Olson et al. 2015 *DSR II*

Host microbiome interactions

- *Trichodesmium* colonies harbor epibionts in cultures and field populations (Ruoco et al. 2016 *EM*)
- Quorum sensing communication molecules (acylated homoserine lactones - AHL) detected in colonies (Van Mooy et al. 2012 *ISME J*)
- Addition of AHLs to field colonies changes activity independent of geochemistry (Van Mooy et al. 2012 *ISME J*)

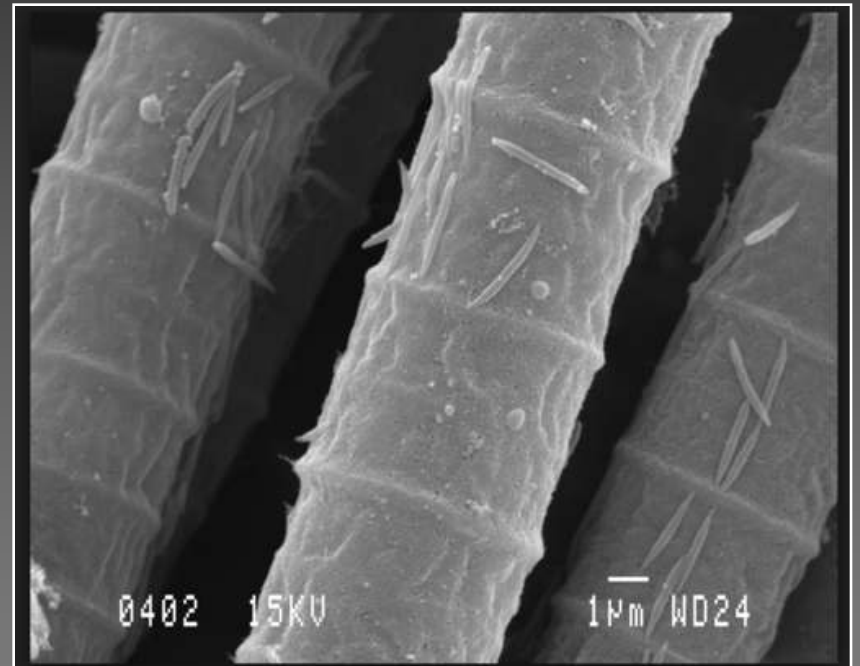
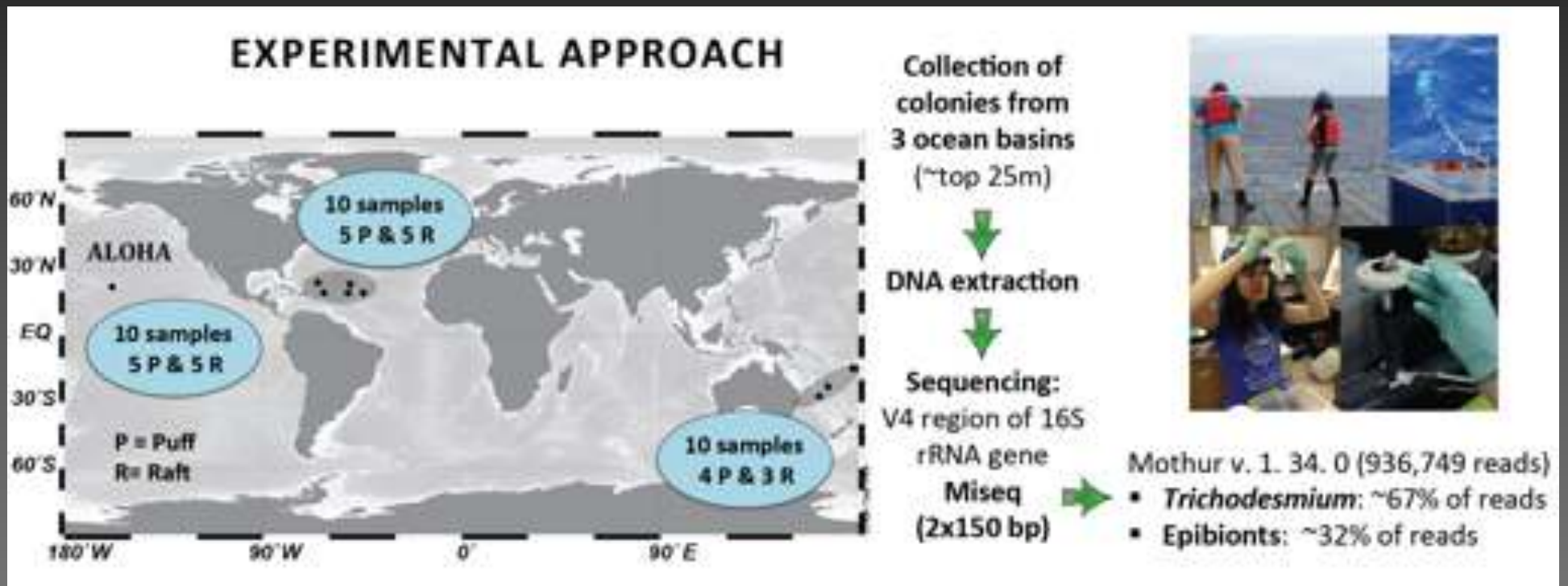


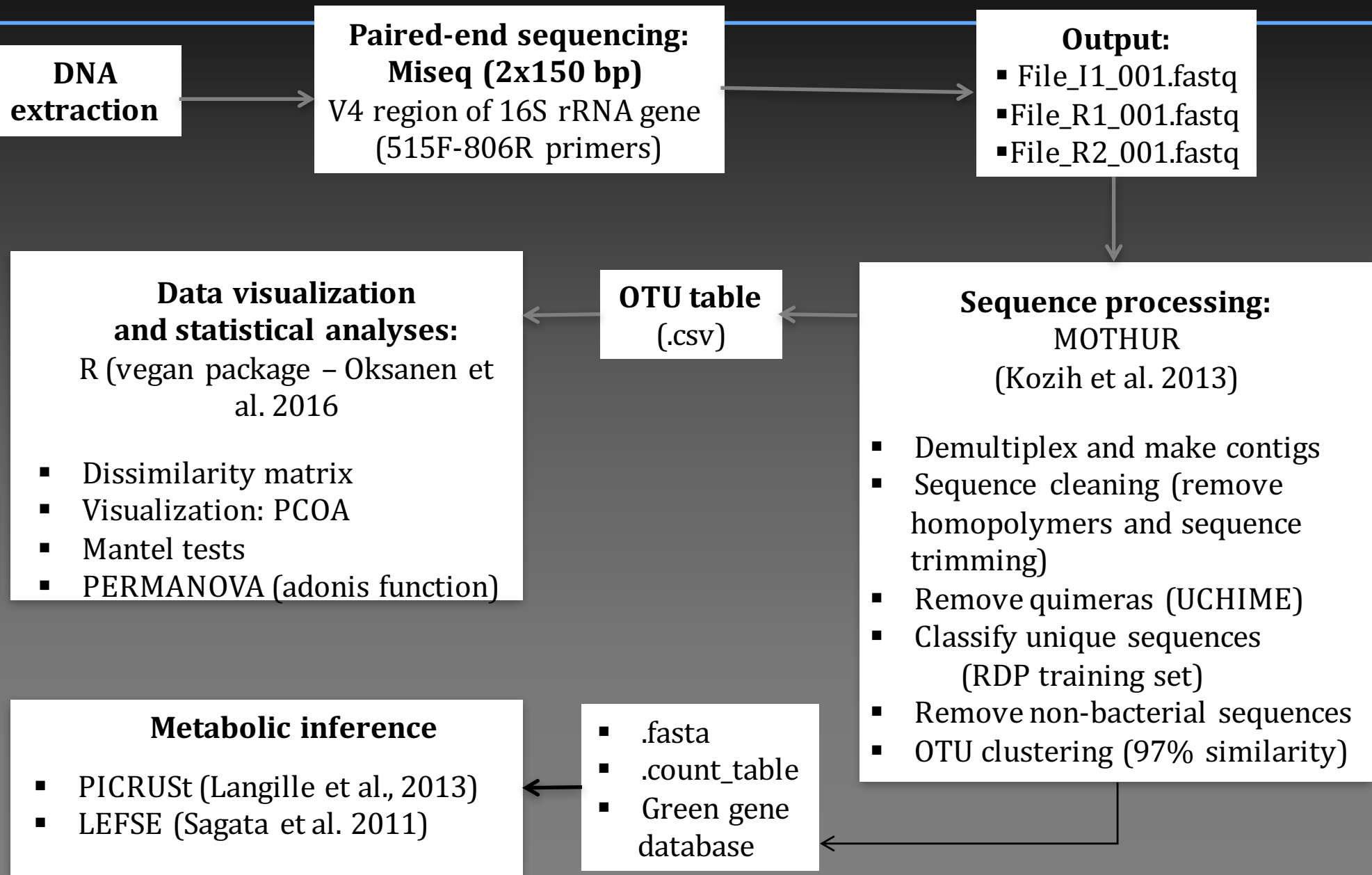
Image courtesy Tracy Mincer

Epibiont diversity

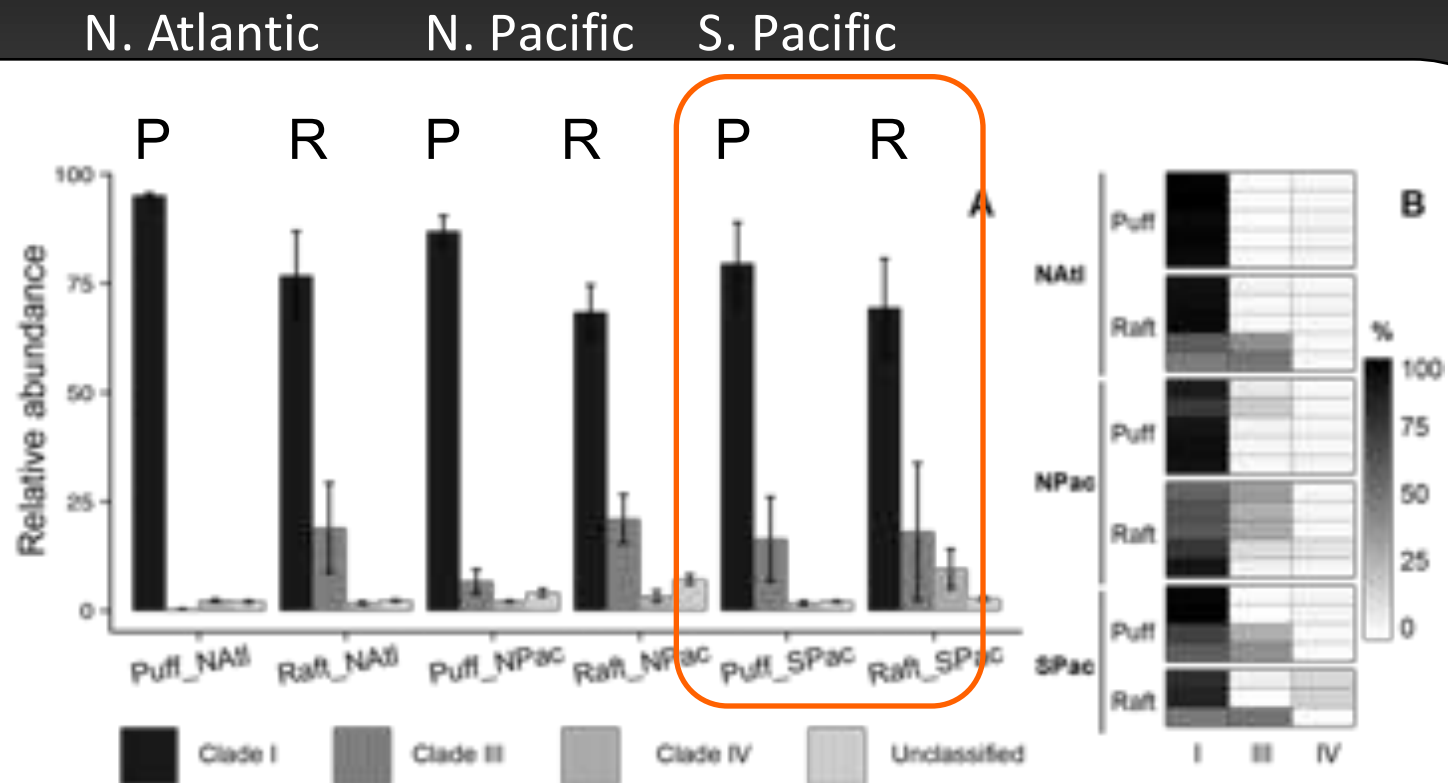


Are epibiont communities distinct as a function of colony morphology or environment?

16S rDNA analyses



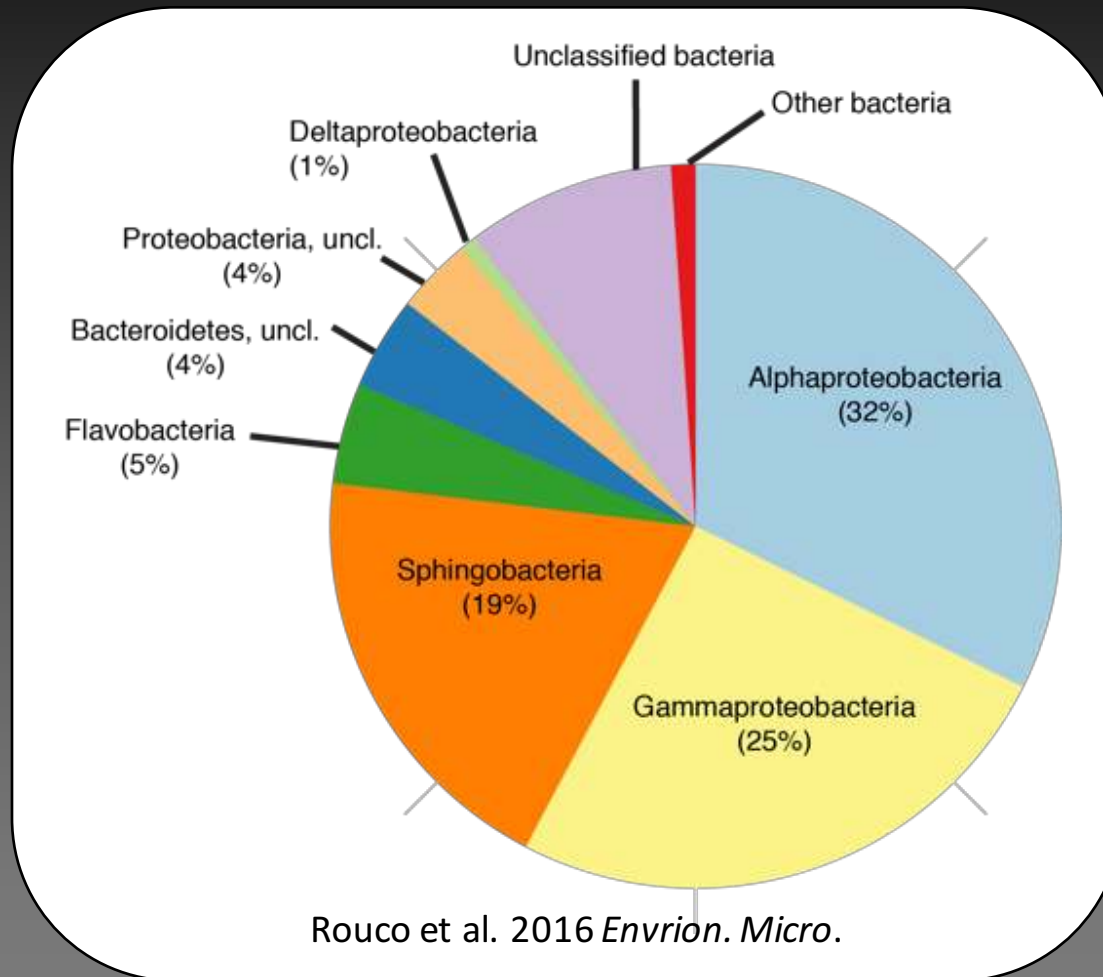
Colony composition by region



Rouco et al. 2016 *Environ. Micro.*

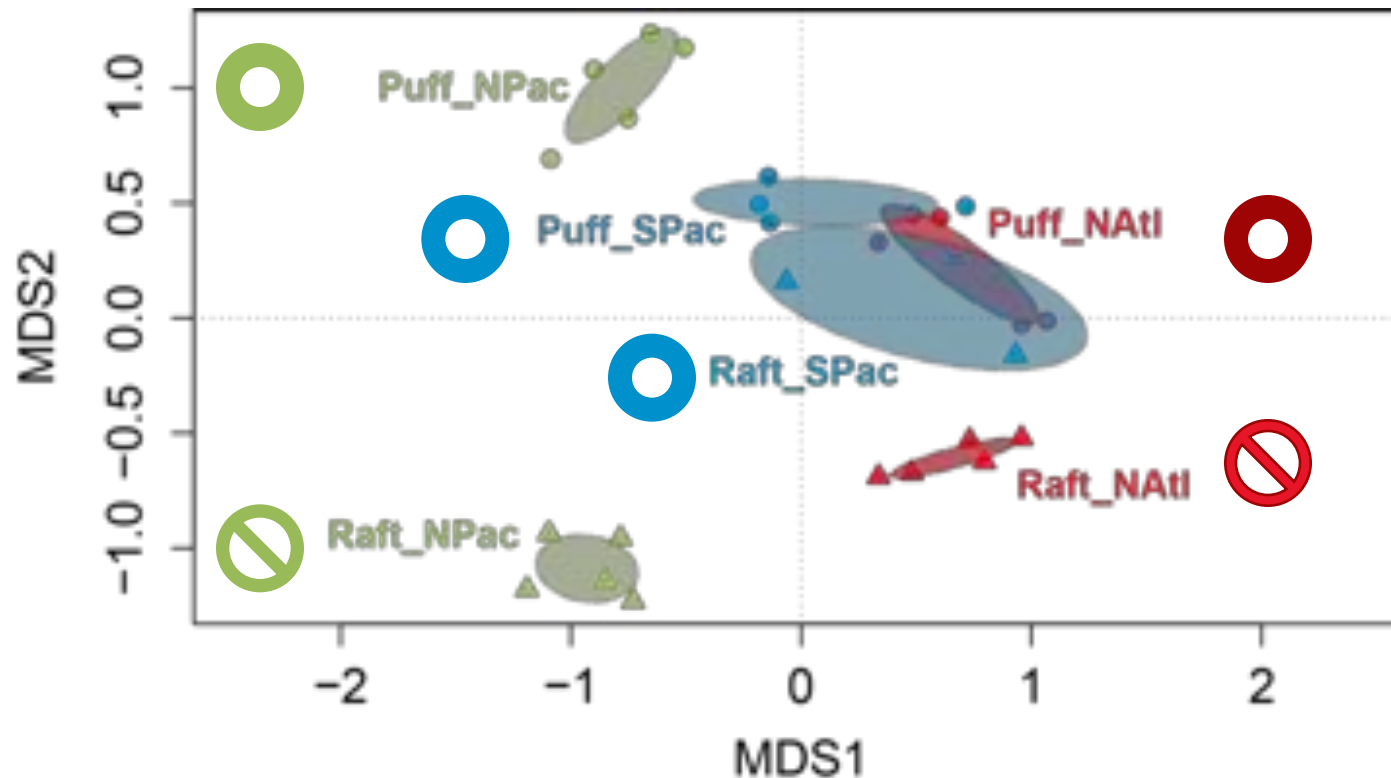
Colonies are not likely species specific, the raft morphology is more diverse except in the S. Pacific

Average epibiont community



16S amplicon sequencing indicates that *Trichodesmium* colonies harbor diverse epibionts distinct from common water column bacteria, and those found on sinking particles.

Microbiome community diversity (16S)



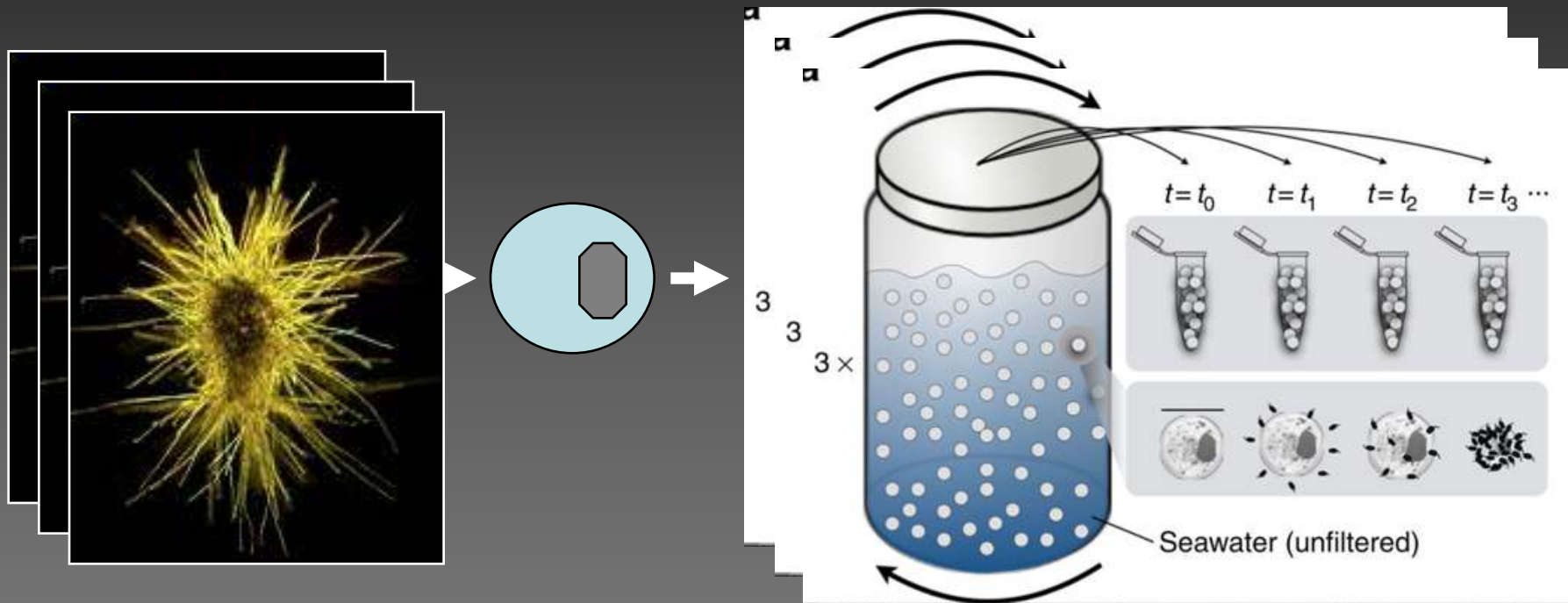
Rouco et al. (2016) *Environ. Micro.*

Microbiome communities significantly differ by ocean basin, and with colony morphology, except for the S. Pacific. Communities are distinct from the water column, and sinking particles.

What drives community assembly?

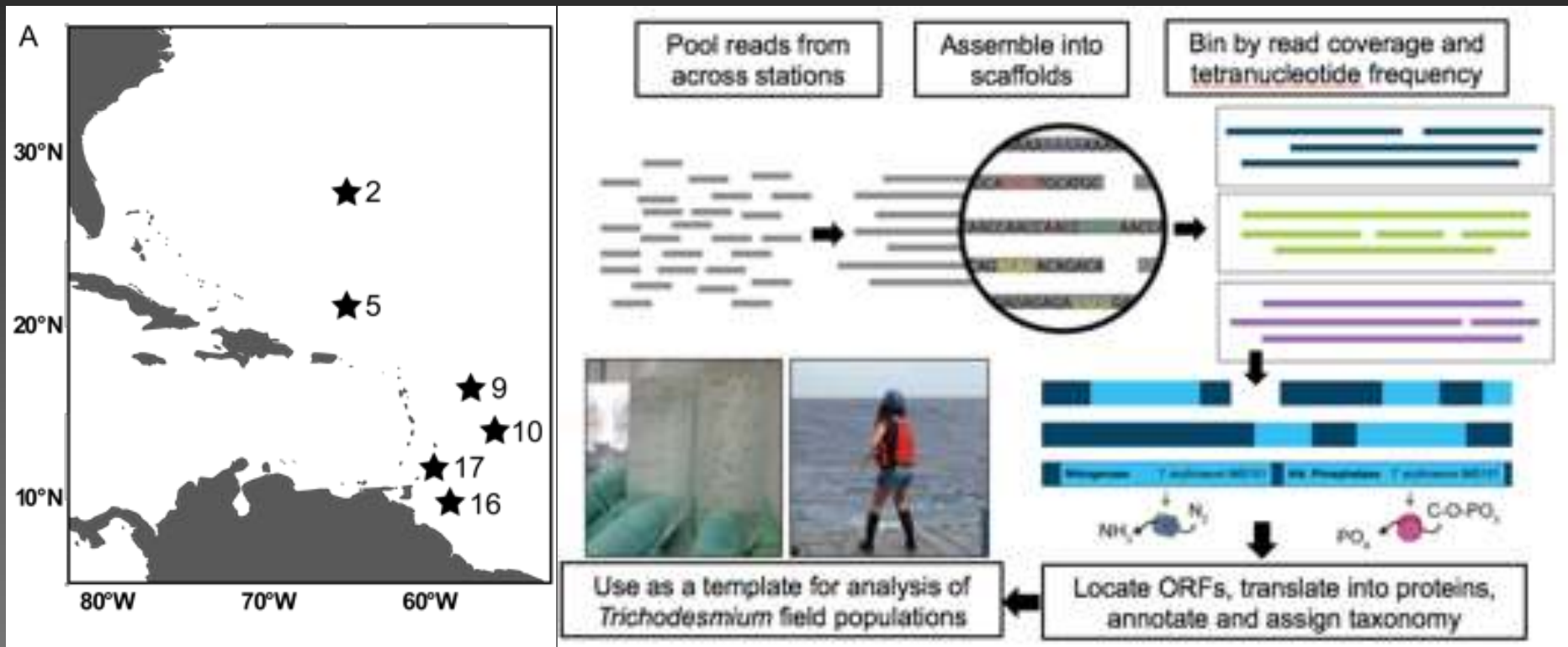
- *Niche?* What type of *Trichodesmium*, physiological ecology in the colony, environment..
- *Lottery?* Random selection of potential copiotrophs, role of taxonomic v. functional group uncertain...
- Working to examine the *Trichodesmium* holobiont with metagenomics/metatranscriptomics and “germ-free” *Trichodesmium*

Drivers of community assembly



Initial trial of “germ-free” *Trichodesmium* ran into problems - phase two scheduled for spring 2019.

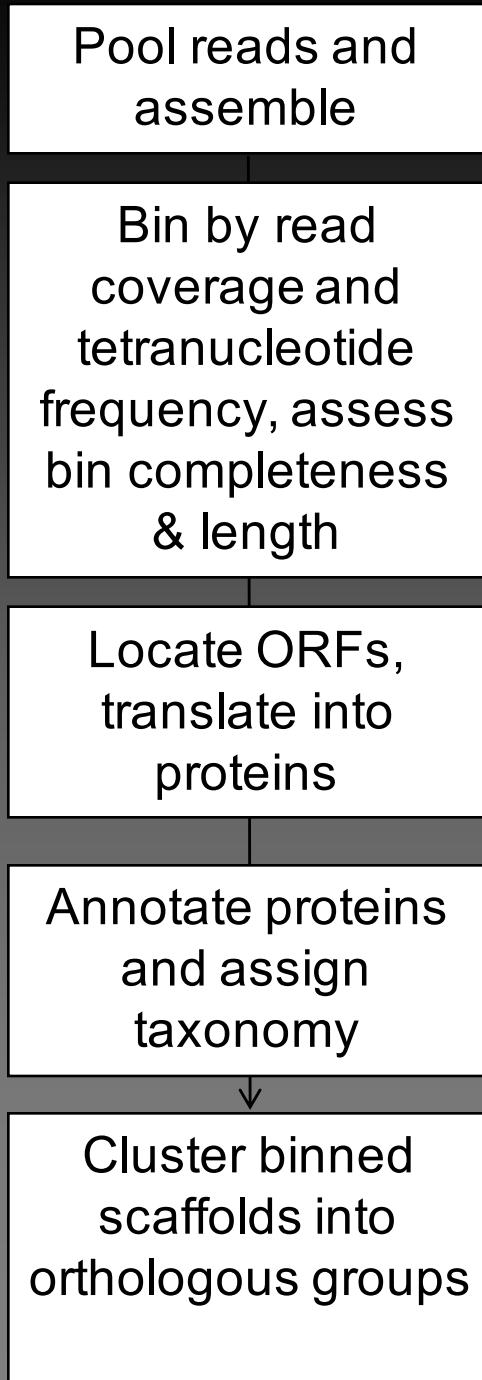
Metabolic potential in the *Trichodesmium* holobiont



Each sample:

- 20 gigabytes
- ~120 million reads
- >200,000 protein coding genes

Metagenome Pipeline



IDBA-UD

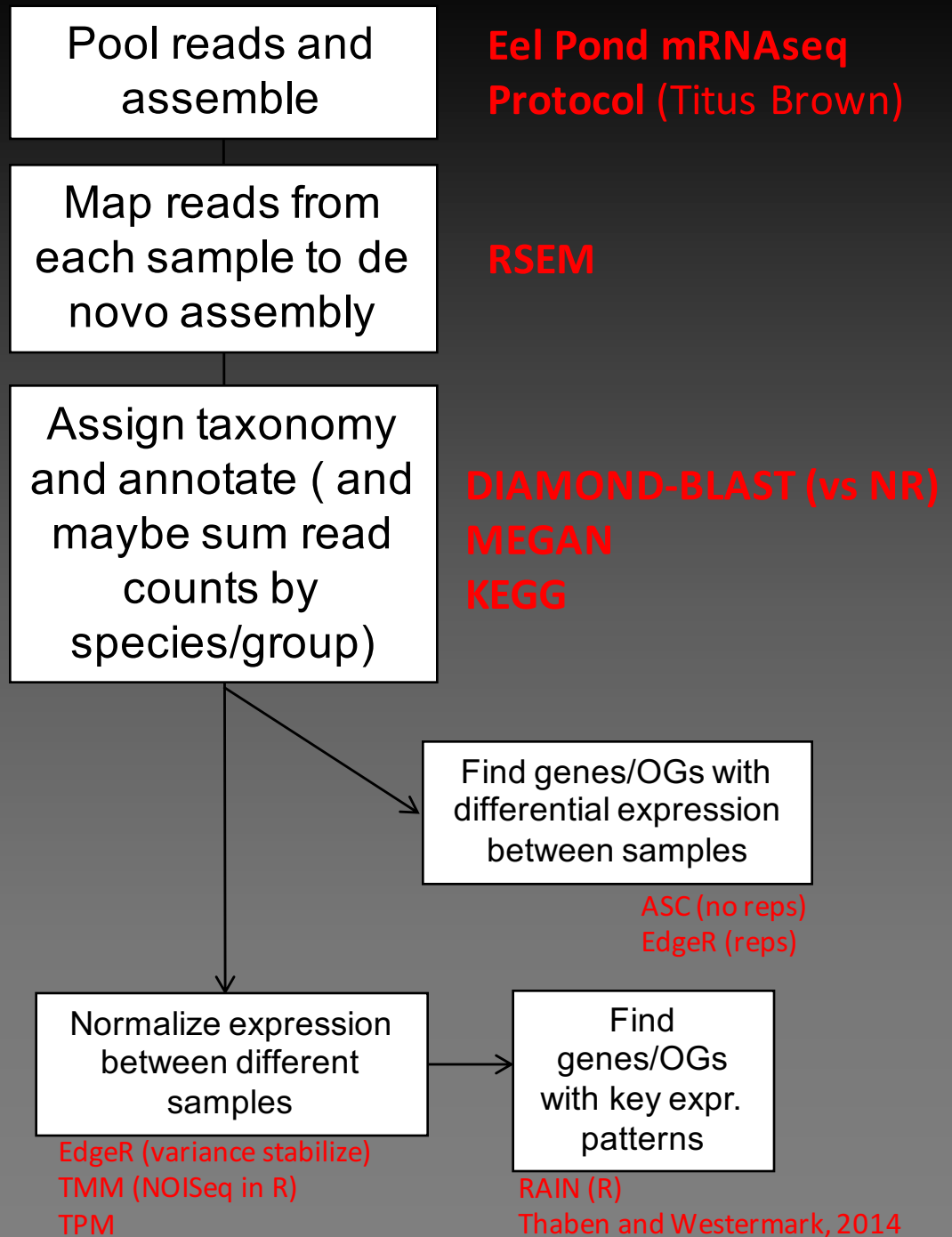
MaxBin

Prodigal

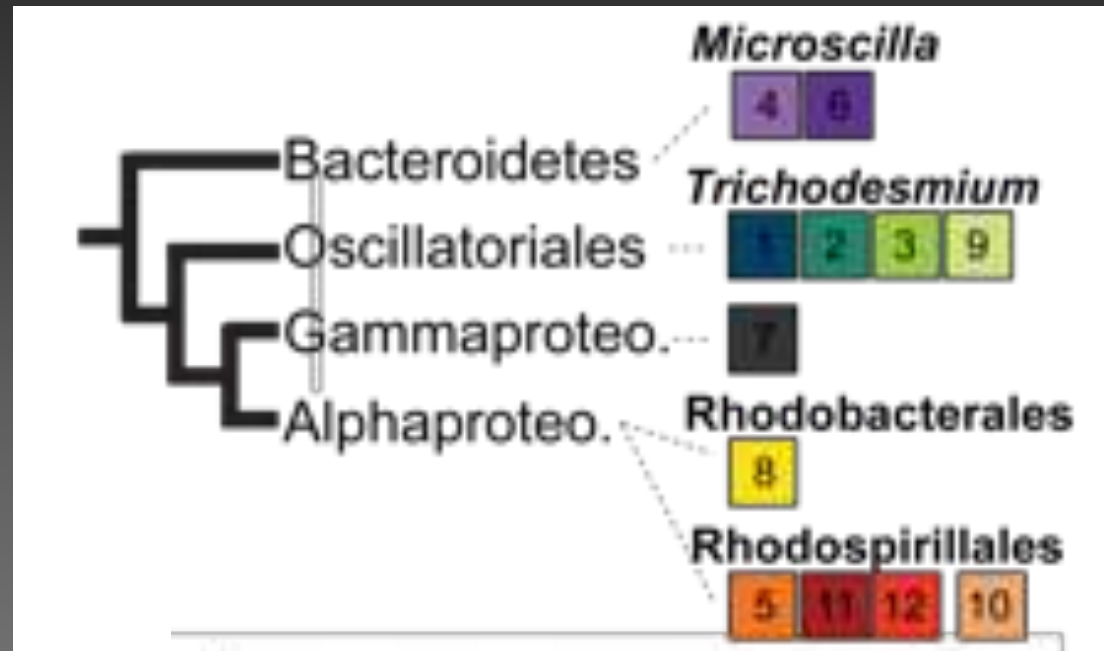
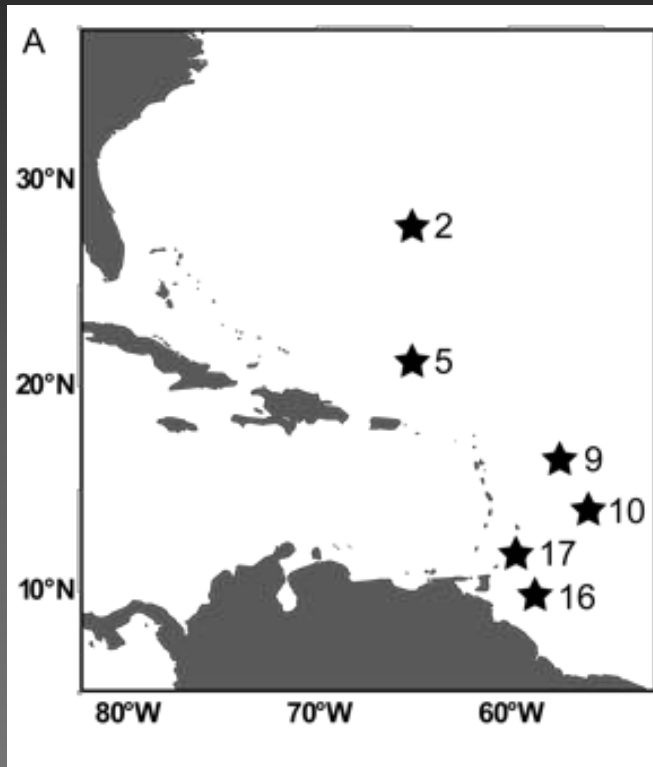
DIAMOND-BLAST
MEGAN?
KEGG

MCL

Metatranscriptome Pipeline



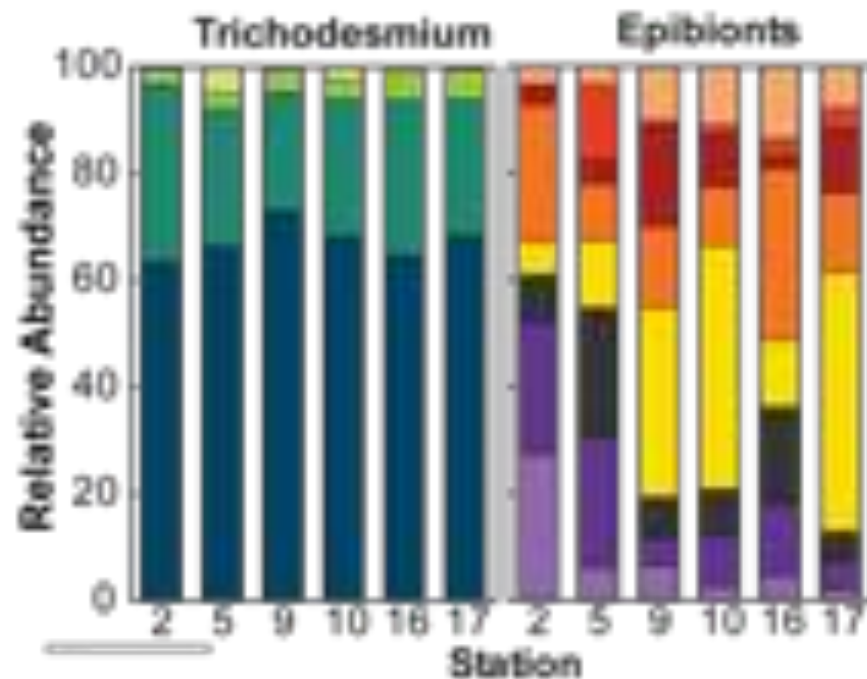
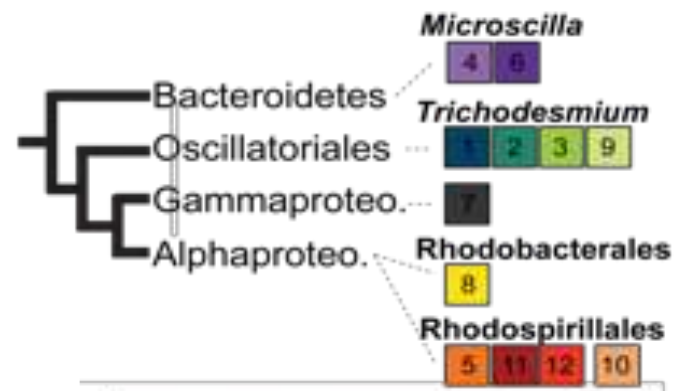
Composition of the holobiont



Frischkorn et al. (2017) *ISMEJ*

Nearly complete (65-90%) genome bins were reconstructed from a merged assembly and results are consistent with 16S data

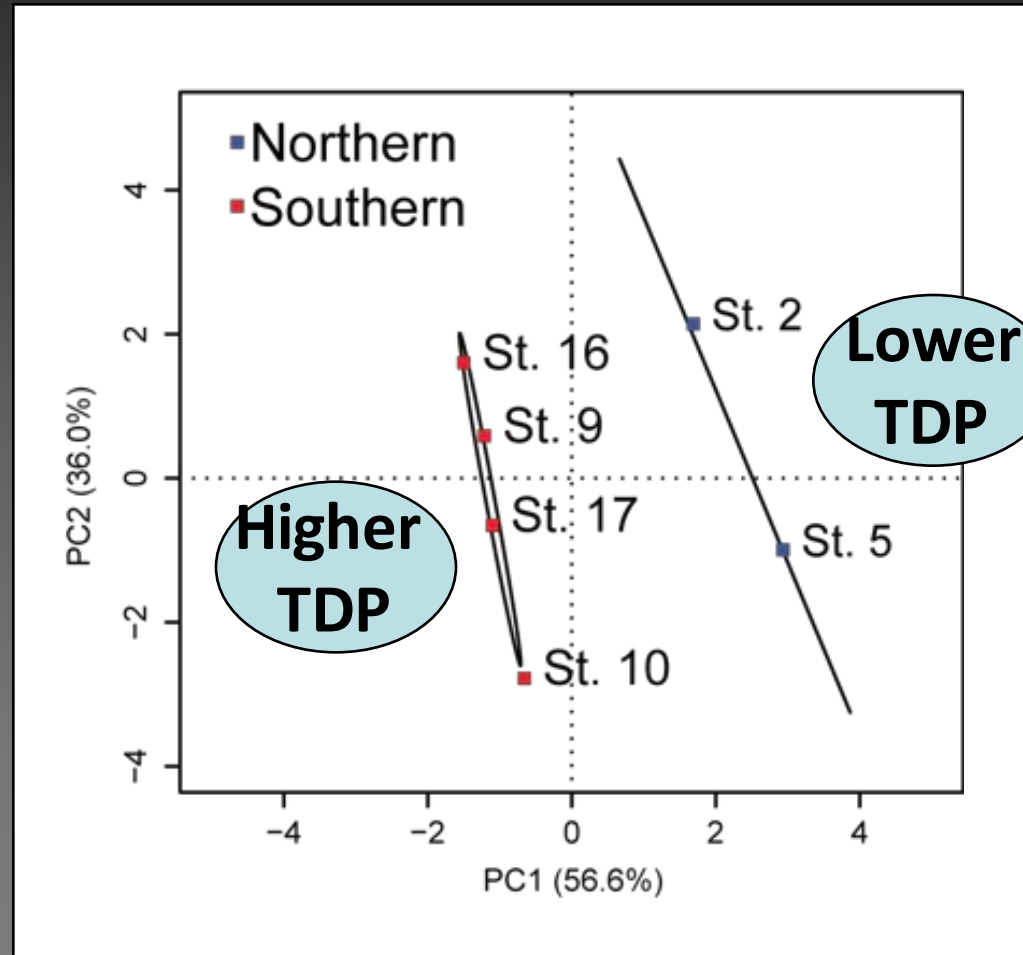
Distribution of holobiont



Frischkorn et al. (2017) *ISMEJ*

Epibiont genome bins are detected at all stations, but the relative abundance varies

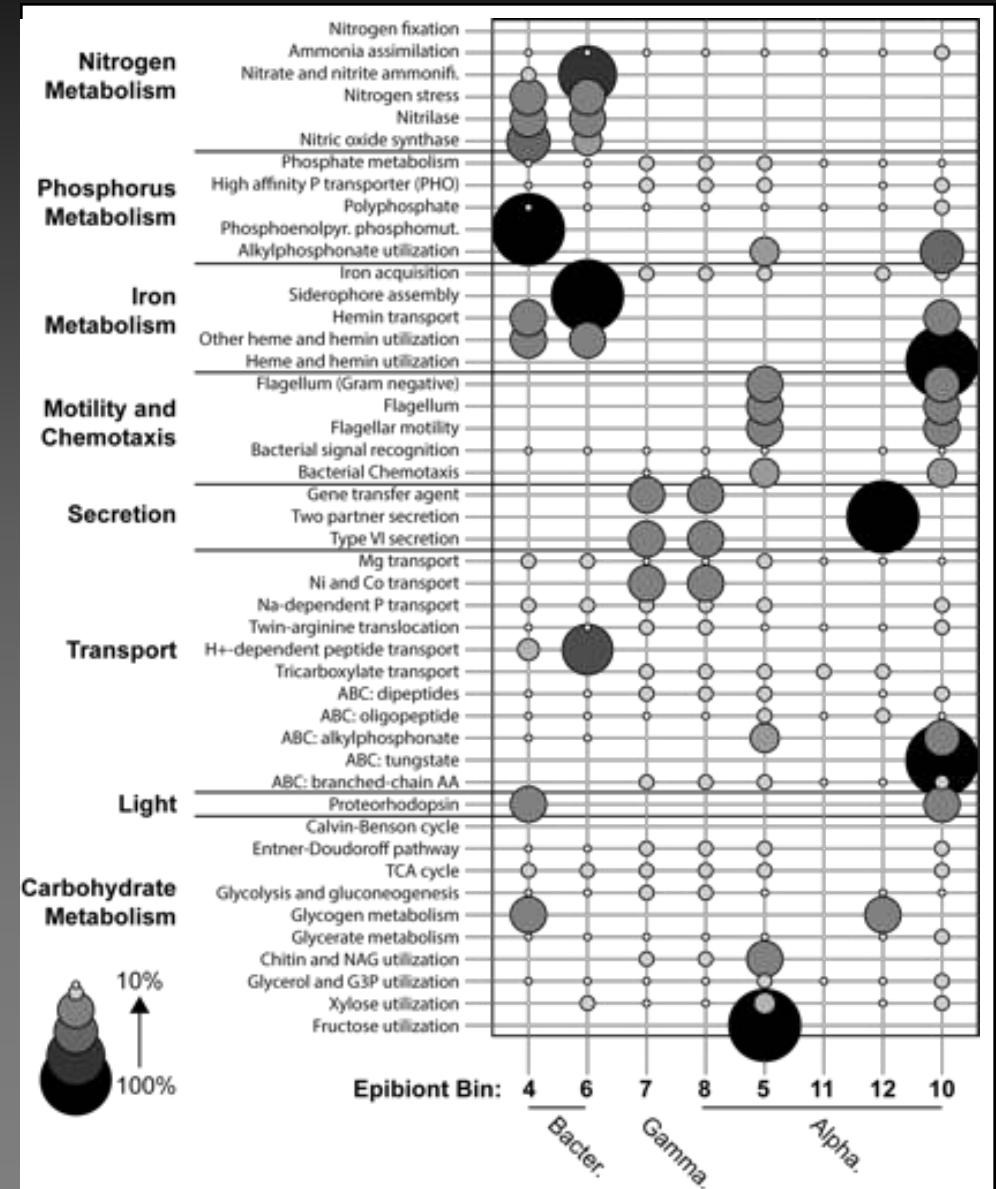
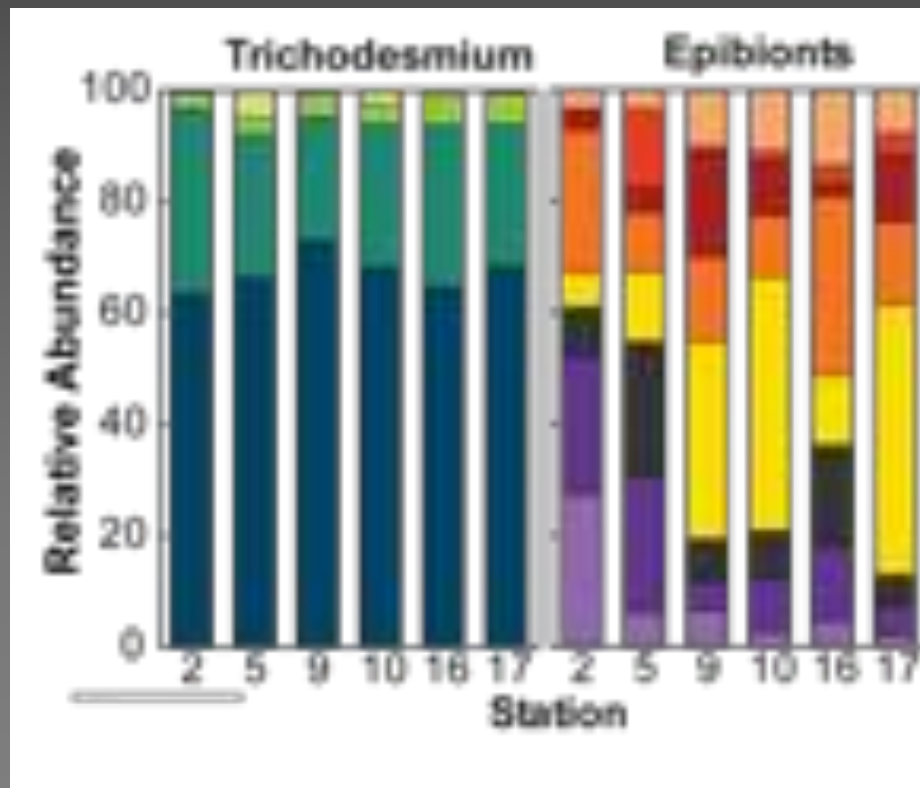
Microbiome diversity differs significantly between regions



Frischkorn et al. (2017) *ISMEJ*

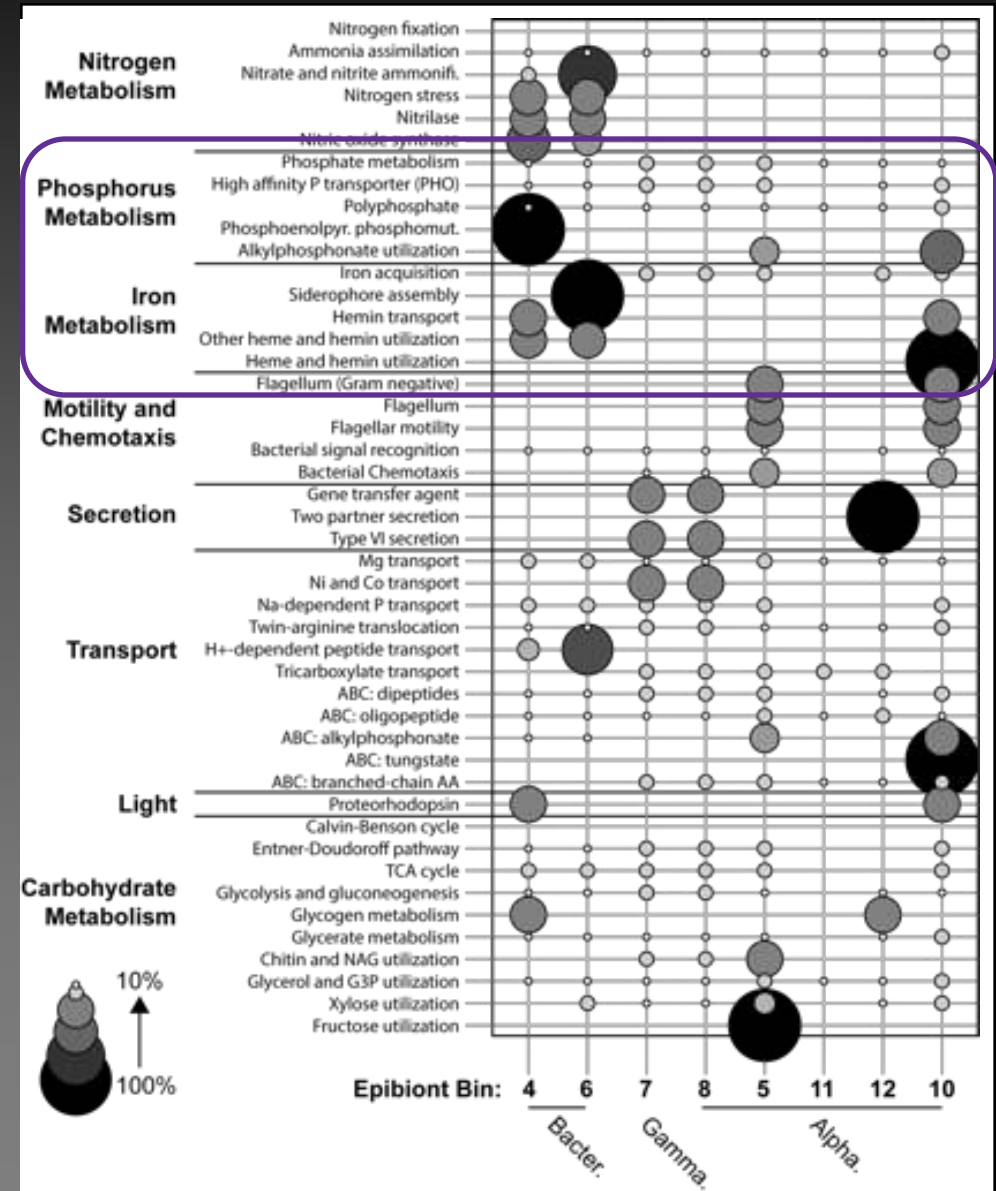
Variable distribution of functional pathways among epibionts

- Differential pathway enrichment consistent with a microbiome that is modulated as a function of environment



Variable distribution of functional pathways among epibionts

- Differential pathway enrichment consistent with a microbiome that is modulated as a function of environment
- Phosphonate, heme and siderophore functions are enriched relative to water column microbes in the Sargasso Sea.



Comparing metabolic potential in the holobiont



Metagenomes



Orthologous group
analysis



Epibionts v. *Trichodesmium*

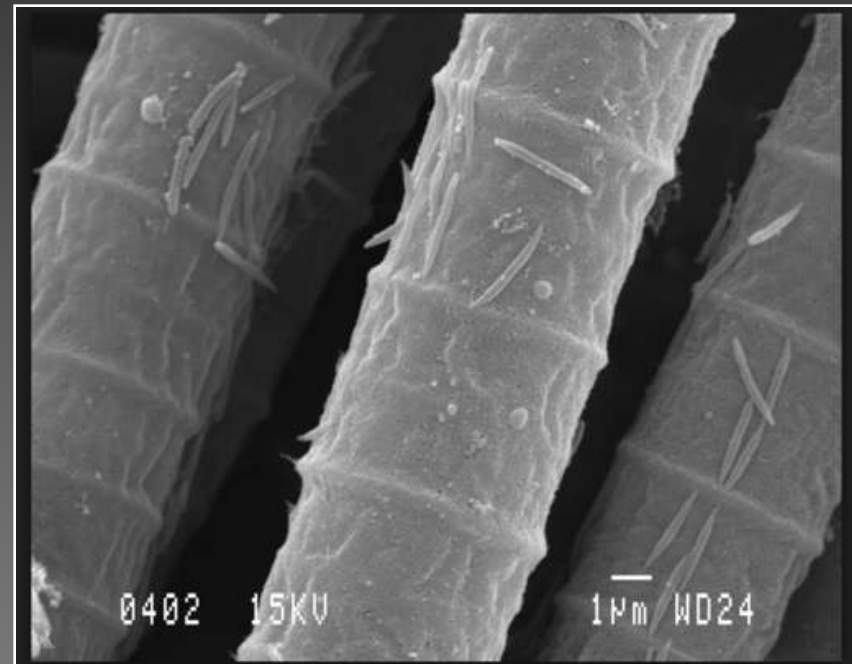
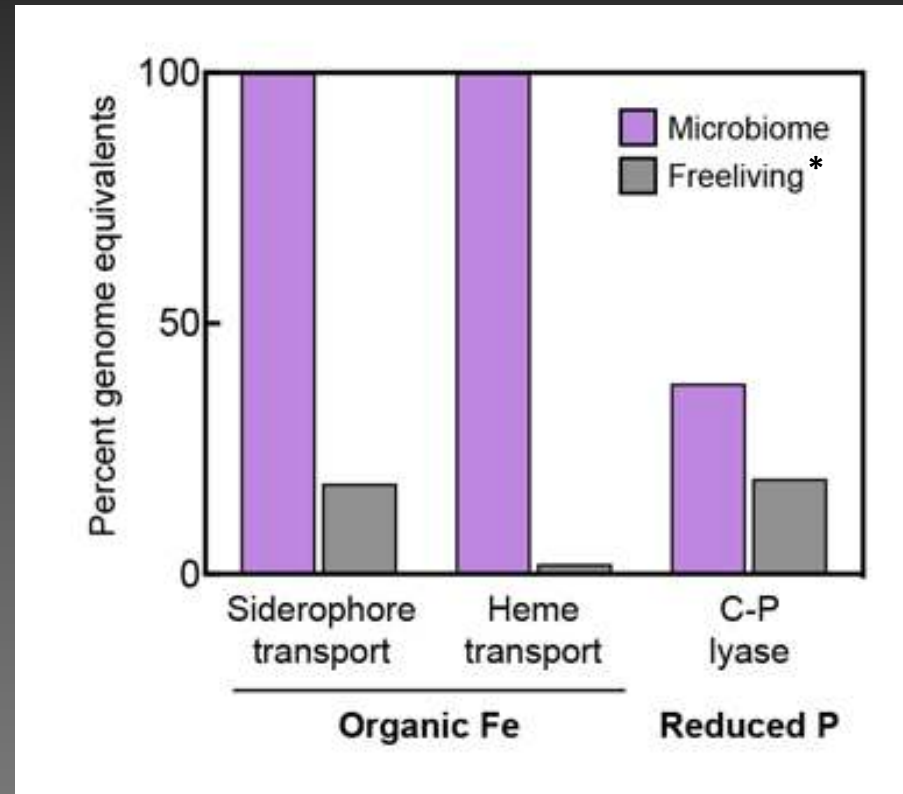
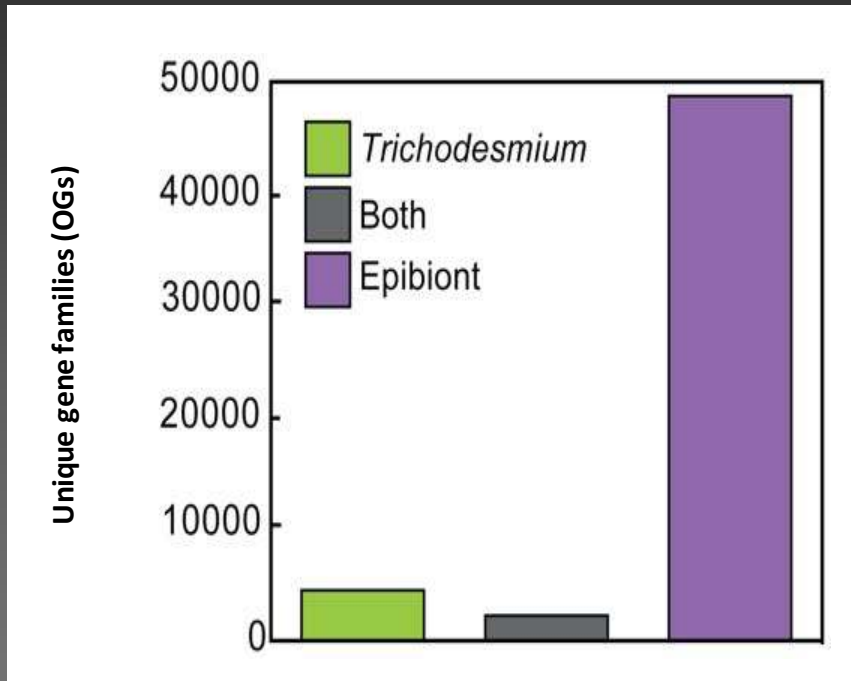


Image courtesy Tracy Mincer

Epibionts confer the majority of the metabolic potential

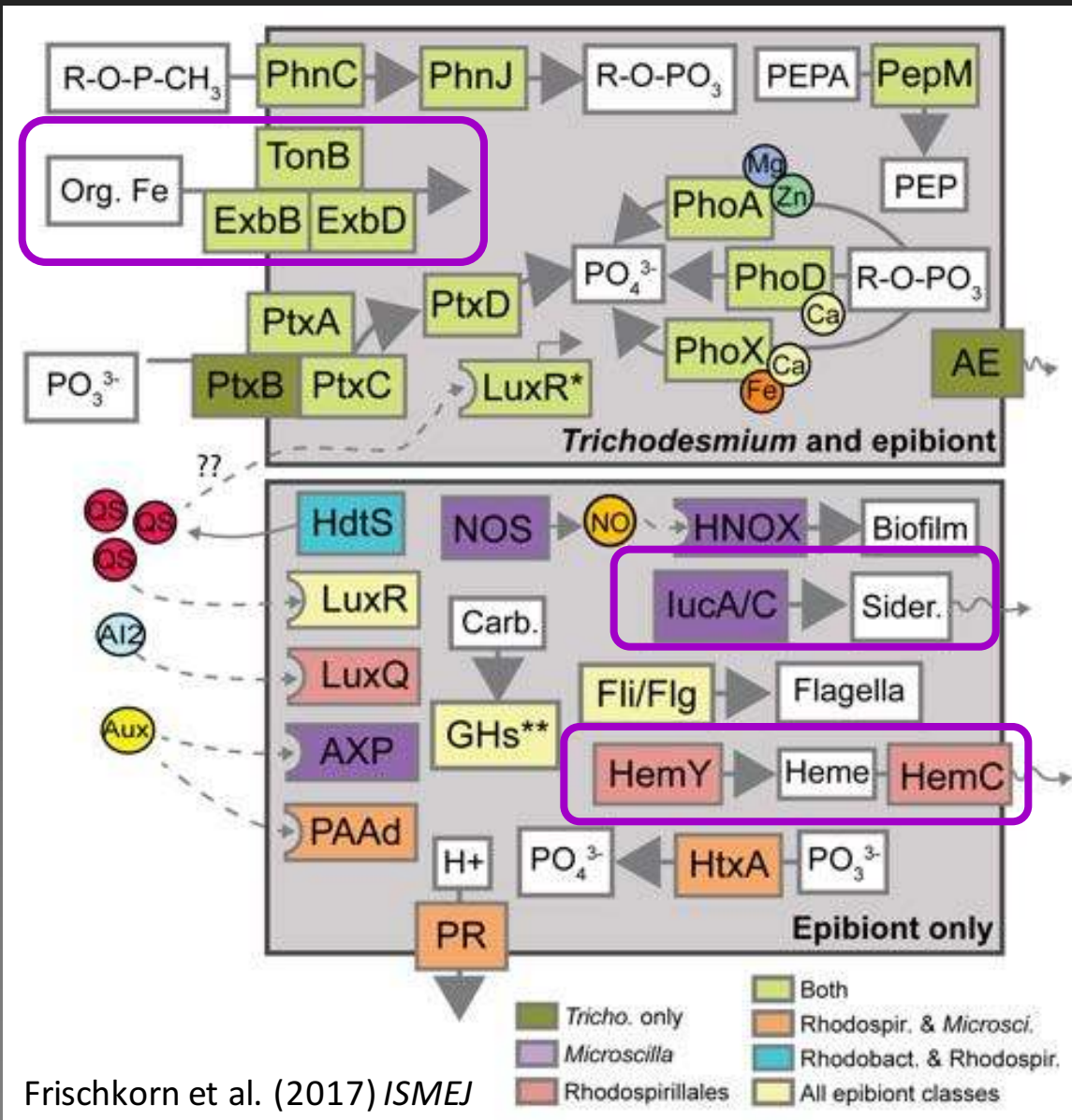
>90% OGs



Orthologous (OG) group analysis suggests that epibionts confer the vast majority of metabolic functions to the holobiont.

Epibiont metabolism expands Fe and P functions for the holobiont.

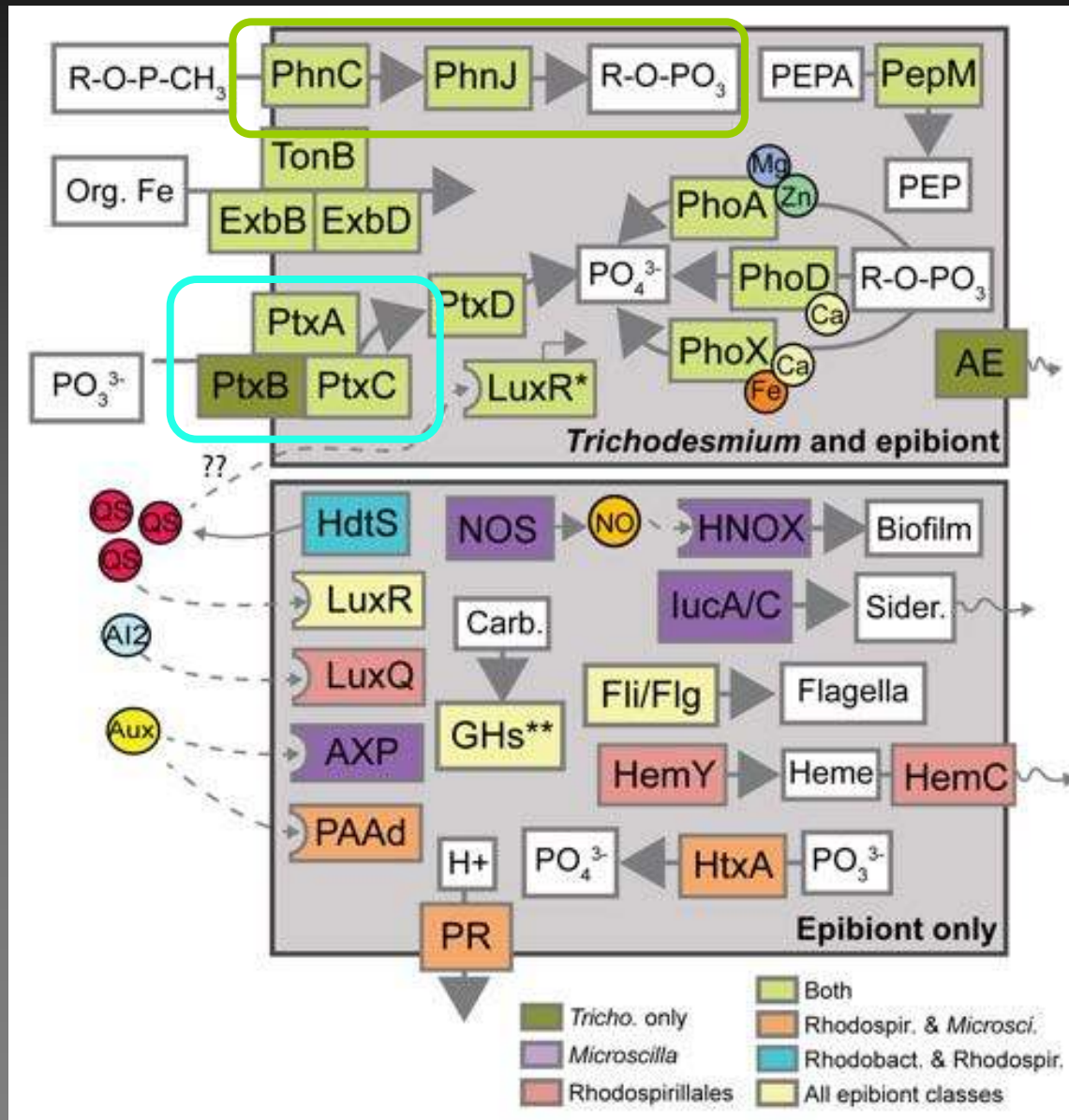
Metabolic partitioning within the *Trichodesmium* holobiont



Organic Iron

Epibionts can produce organic iron complexes that likely modulate iron in the holobiont microenvironment

Uptake and metabolism of reduced phosphorus forms



C-P Lyase
PhoX
PhoA

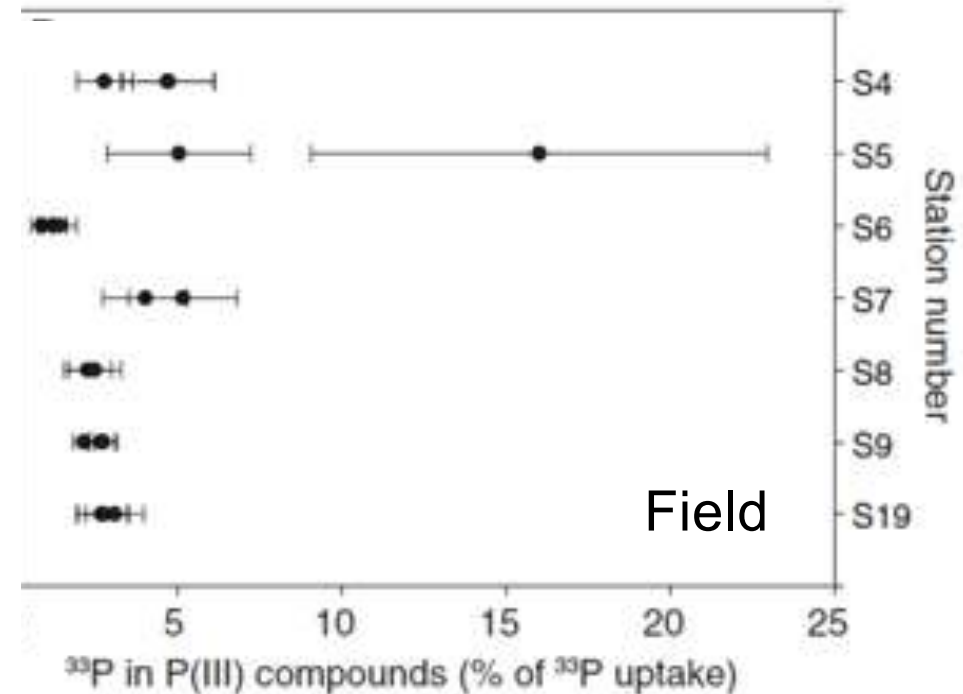
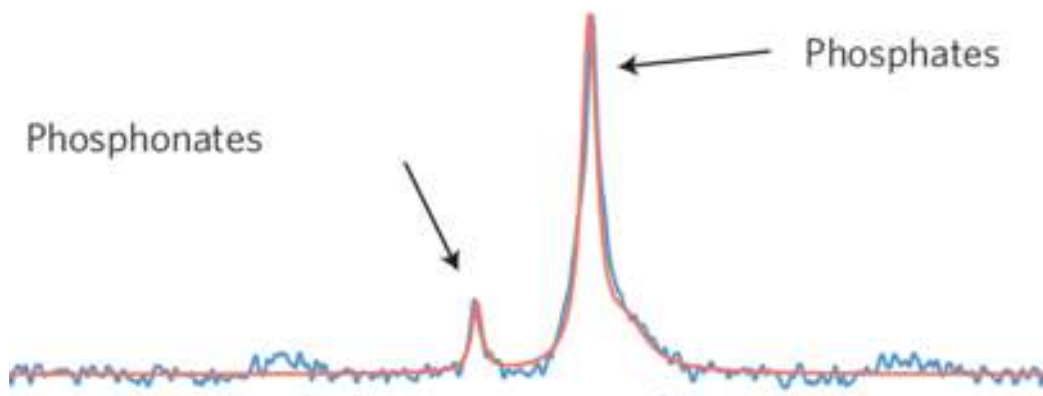
Phosphite
uptake

Phosphorus metabolisms are present in both *Trichodesmium* and the microbiome.

Answers to enduring mysteries... who makes C-P compounds?

Phosphonate (C-P) biosynthesis

Culture

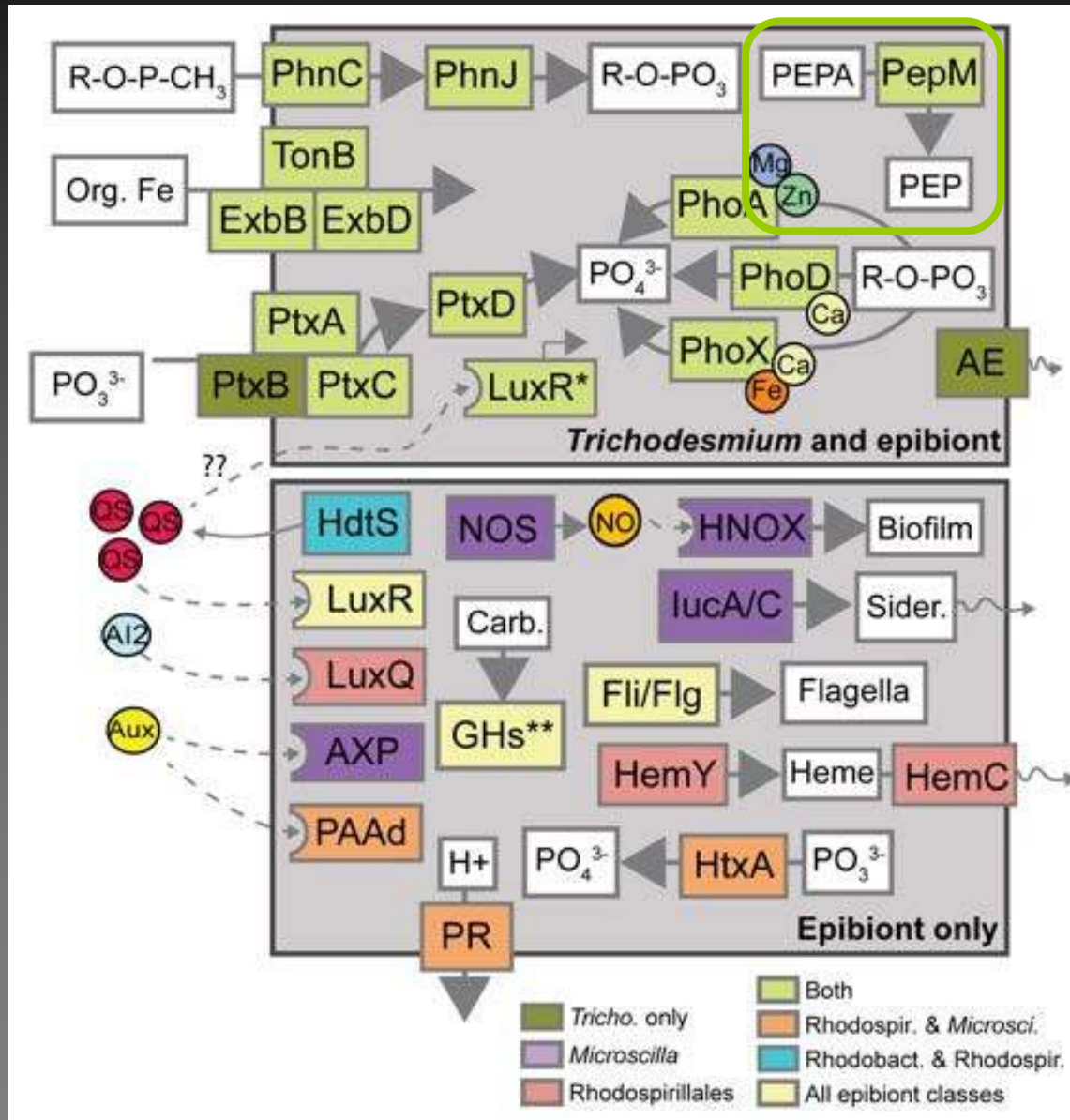


Dyhrman et al. (2009) *Nature Geo.*

Van Mooy et al. (2015) *Science*

Phosphonates are produced at high rates in the holobiont - hot spot for reduced phosphorus cycling. Is it *Trichodesmium* or the epibionts?

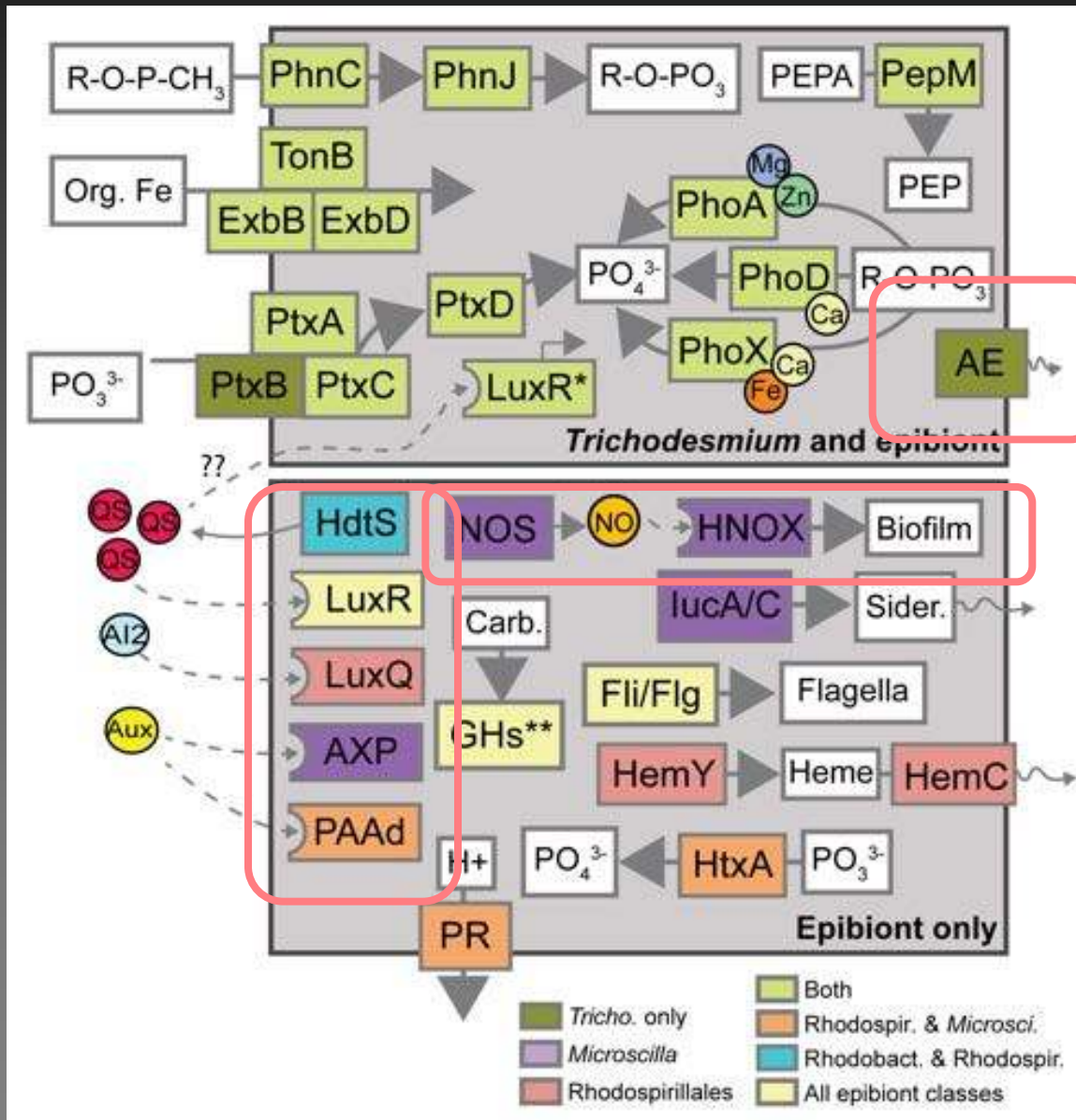
Phosphonate production is a shared metabolism



Phosphonate biosynthesis

Phosphonate produced by both *Trichodesmium* and the epibionts – at least in this environment

Microbial cross talk within the *Trichodesmium* holobiont



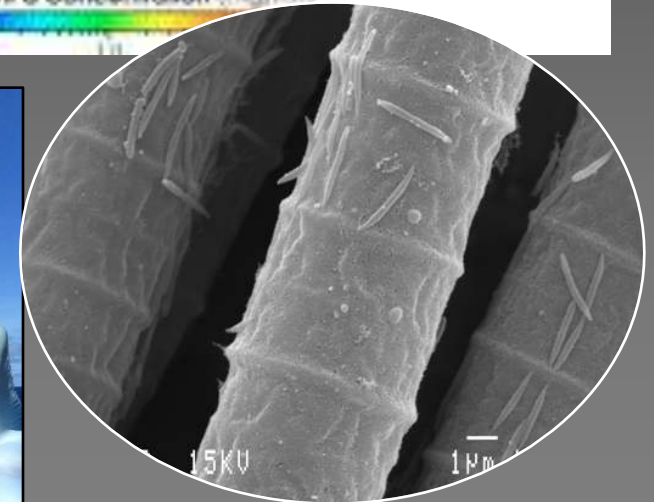
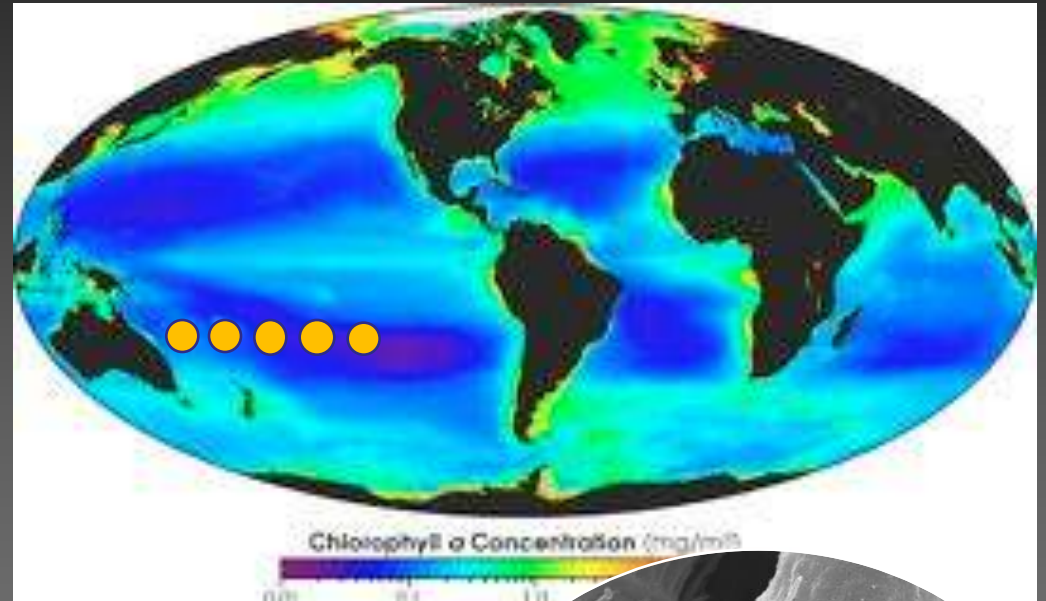
Tracking the interactome... with metatranscriptome profiling after addition of NO and QS molecules

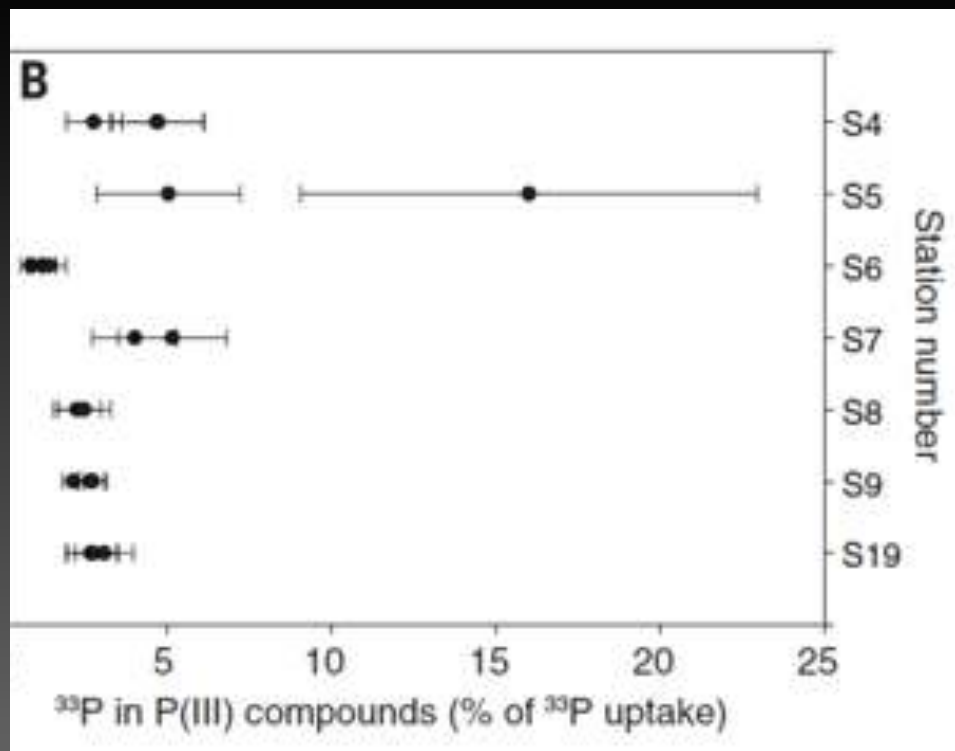
QS and cell signaling

Joint metagenome and metatranscriptome analysis

- South Pacific is undersampled and the dynamics of the *Trichodesmium* holobiont are not well understood
- Unique opportunity to sample metagenome, metatranscriptome, and key activities.
- Is there evidence of phosphorus reduction and cycling in this environment?

OUTPACE

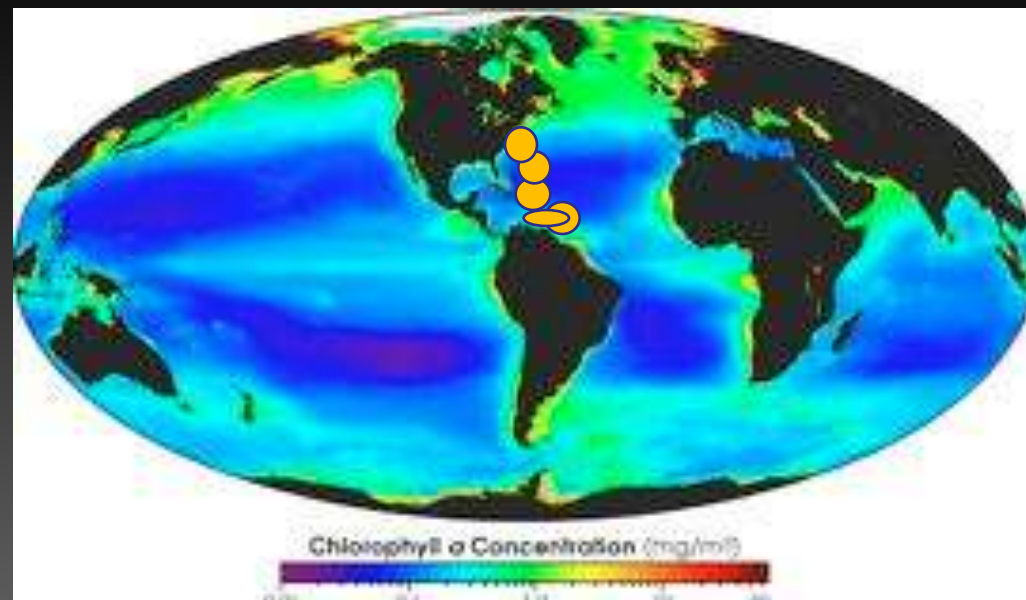




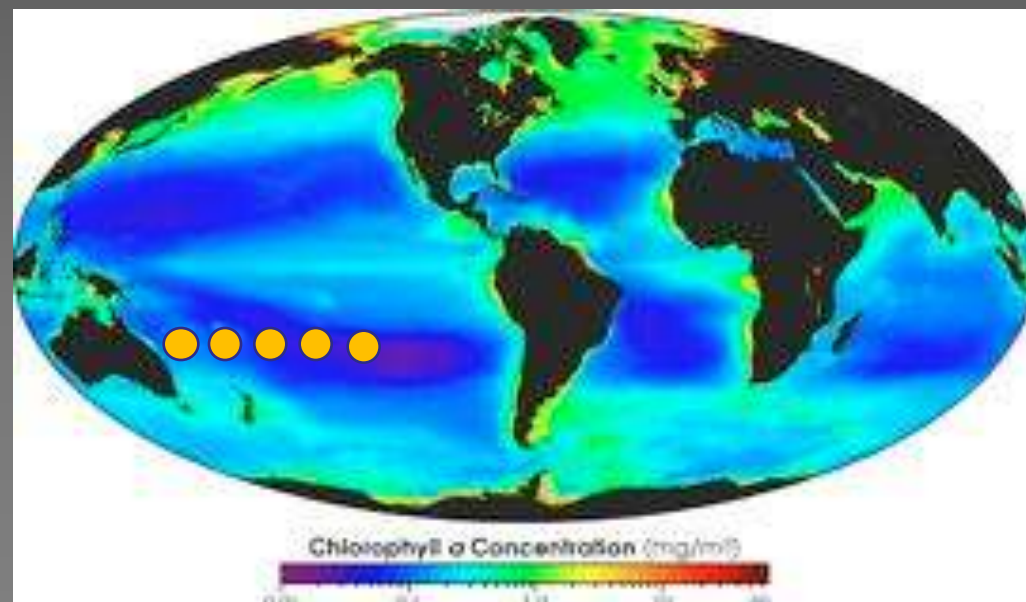
Van Mooy et al. (2015) *Science*

?

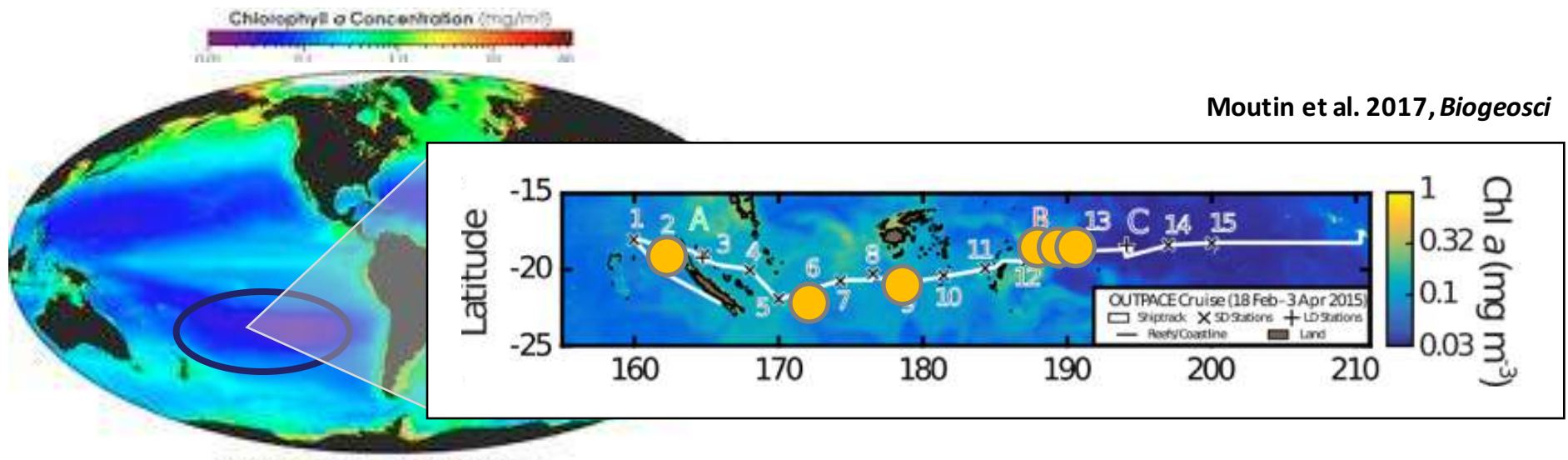
PABST



OUTPACE



Physiological ecology of *Trichodesmium* and its microbiome in the western tropical South Pacific

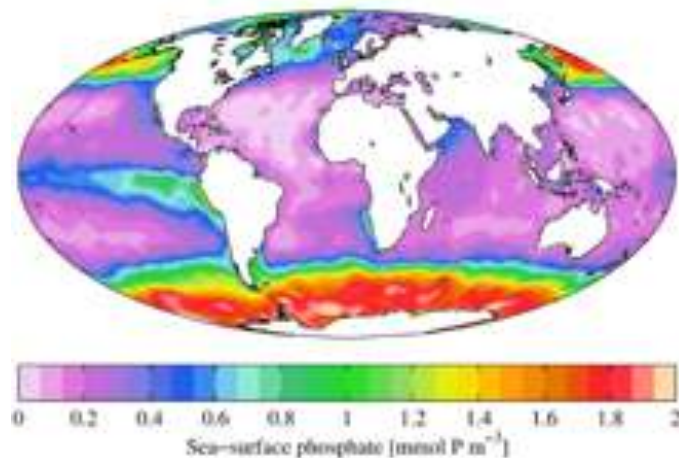
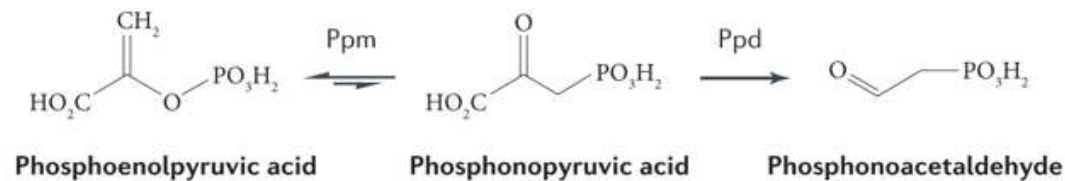
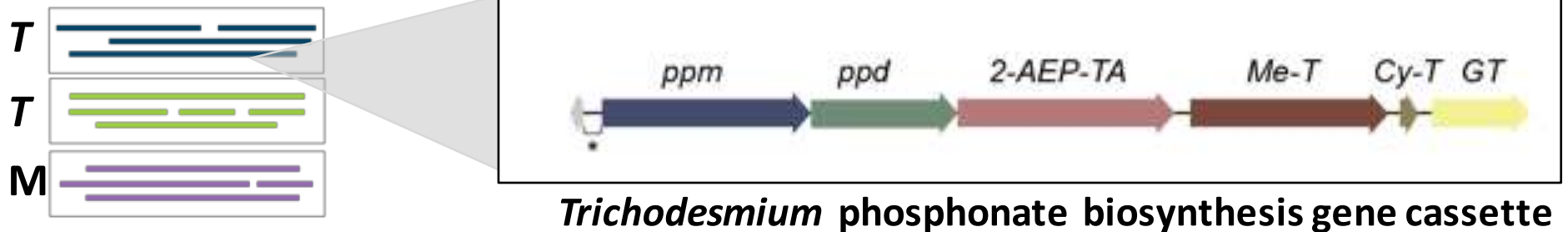


● *Trichodesmium* samples taken

Metatranscriptomes



Metagenomic evidence of P reduction



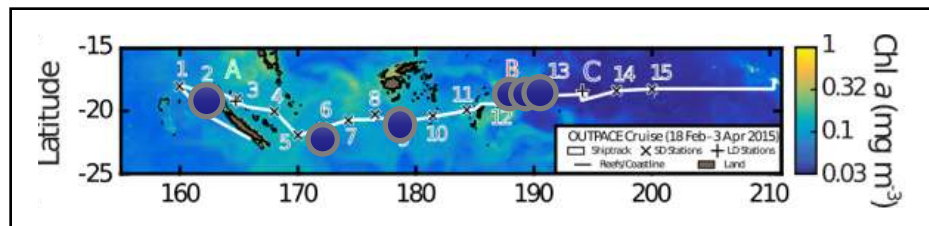
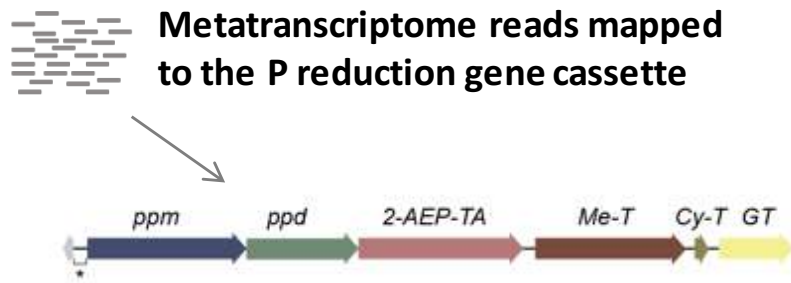
Phosphonates in the oligotrophic ocean

- 25% DOP is in the C-P bond class
- Recalcitrant
- Mysterious origins
- *Trichodesmium* colonies are hotspots

McGrath et al. 2013
 Dyhrman et al., 2006
 Van Mooy et al., 2015

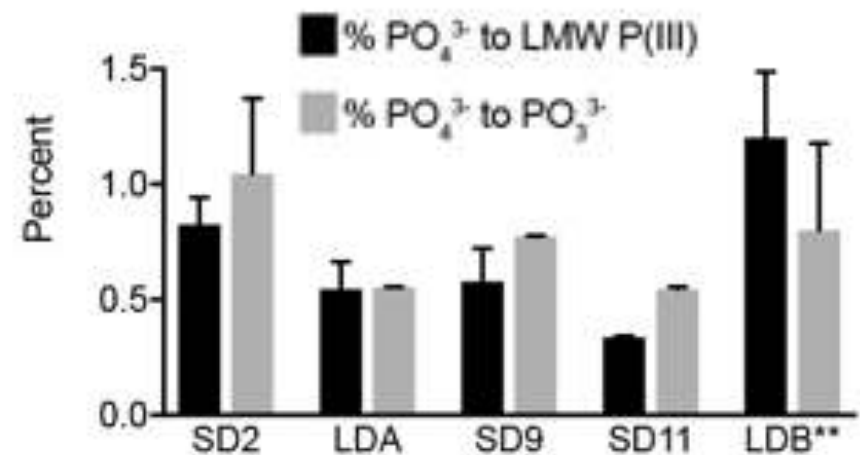
Genes are expressed with P reduction

Measure gene expression



Measure phosphate reduction

Percentage of radiolabeled phosphate taken up and reduced by *Trichodesmium* colonies



*methylphosphonate, phosphonoacetylaldehyde, or 2-aminoethylphosphonate

- ✓ Genes detected
- ✓ Genes expressed
- ✓ Activity measured
- ? Interactions & ecology?

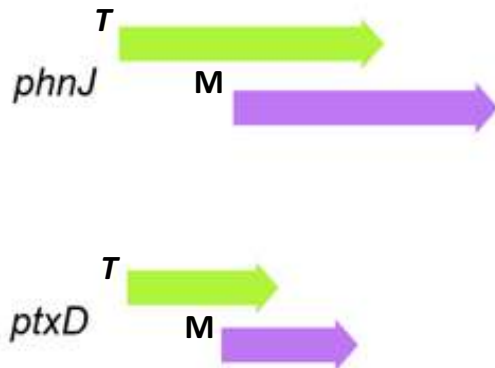
Evidence for use of reduced phosphorus compounds in *Trichodesmium* and the microbiome



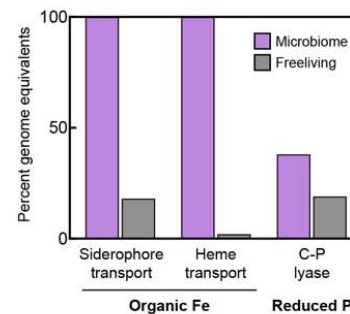
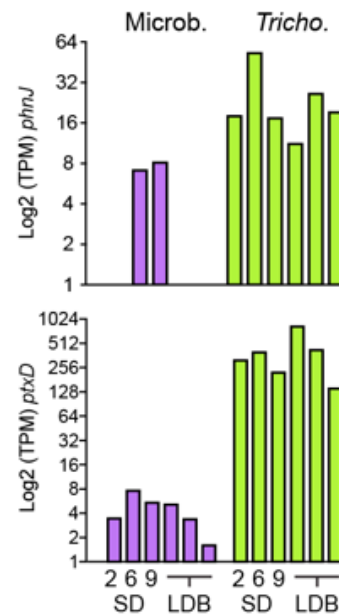
Query for genes:

- Phosphonate C-P lyase (*phnJ*)
- Phosphite dehydrogenase (*ptxD*)

✓ Genes detected



✓ Genes expressed



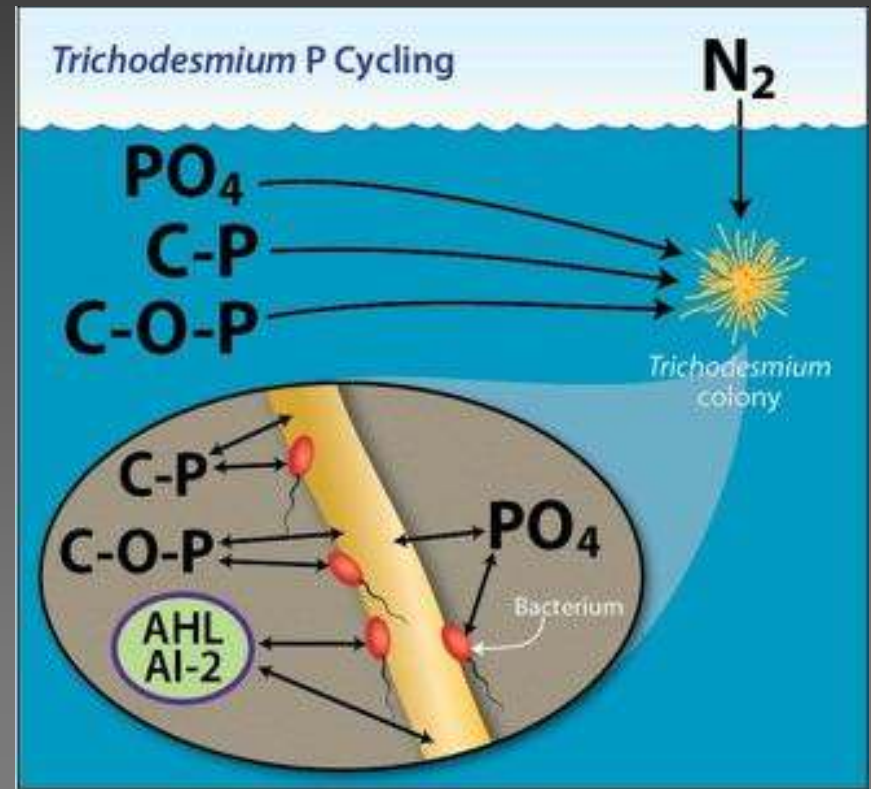
Ability to access reduced P is enriched in *Trichodesmium* consortia

A cryptic P currency?

Summary - Host microbiome interactions

What is the role of the microbiome in *Trichodesmium* physiological ecology?

- **16S community amplicon sequencing:** Colonies harbor diverse epibionts distinct from water column, that are dynamically curated across gradients in the environment
- **Metagenomics:** Epibionts confer substantial metabolic potential which likely underpins *Trichodesmium* fitness
- **Metatranscriptomics:** Distinct physiology and interactions between *Trichodesmium* and its microbiome



Core questions

Metabolic traits and trade-offs

- What phosphorus is bioavailable?
- What are the biogeochemical constraints on N_2 fixation?

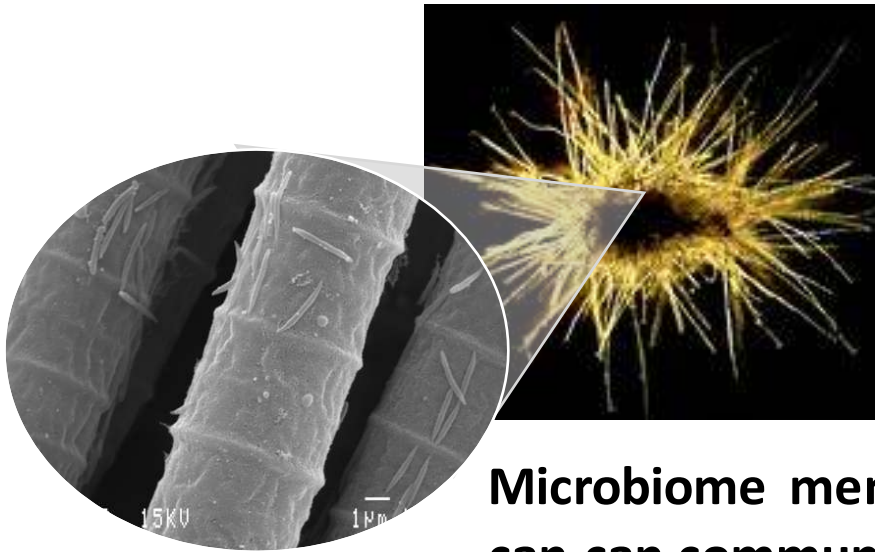


Host microbiome interactions

- Who is there? Microbiome diversity
- What are they doing? Microbiome functional diversity, holobiont physiology and **controls on N_2 fixation**

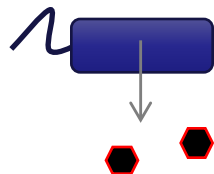
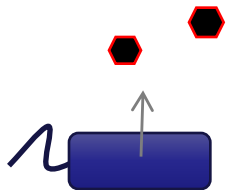


A strategy for assessing the physiological impact of the microbiome on *Trichodesmium* N₂ fixation

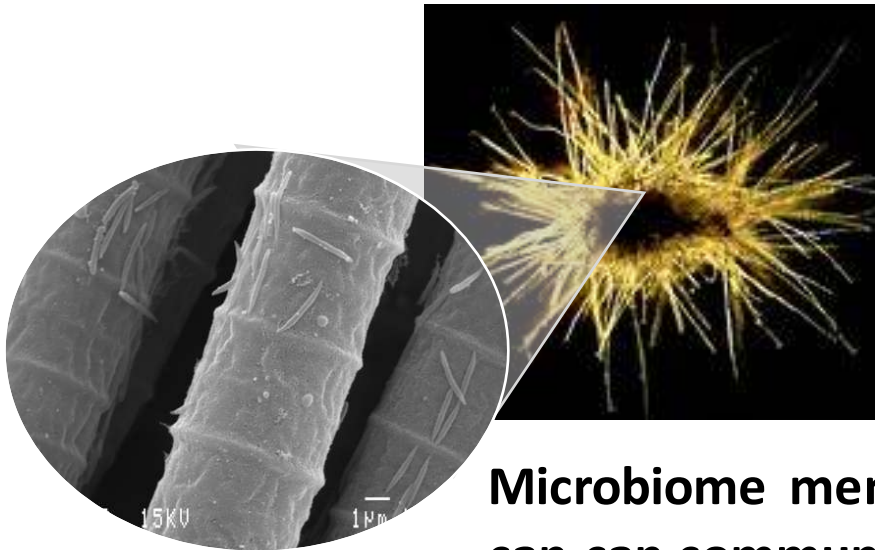


● AHLs

Microbiome members
can communicate
using a mechanism
called quorum
sensing

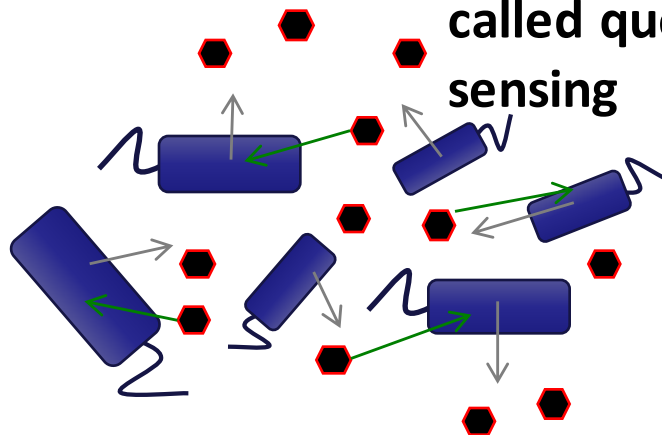


A strategy for assessing the physiological impact of the microbiome on *Trichodesmium* N₂ fixation

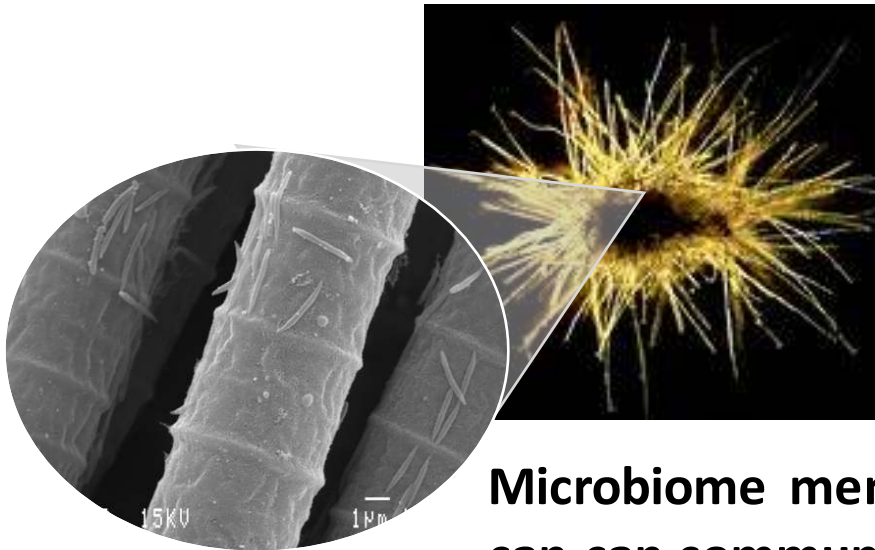


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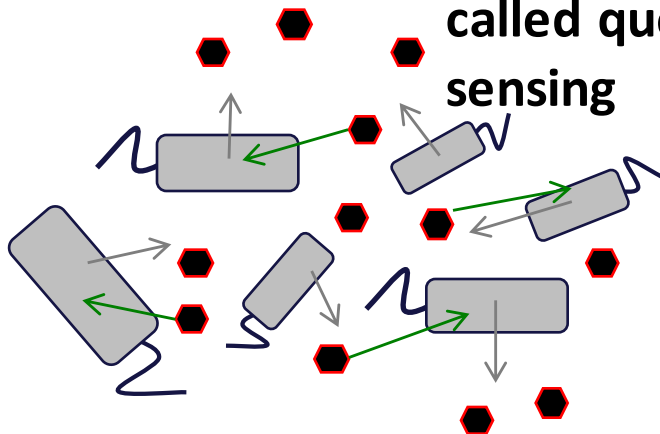


A strategy for assessing the physiological impact of the microbiome on *Trichodesmium* N₂ fixation

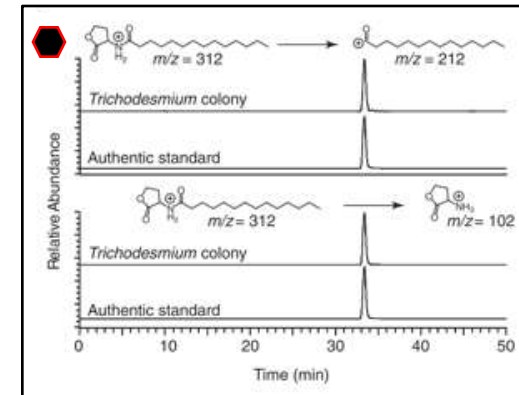


● AHLs

Microbiome members can communicate using a mechanism called quorum sensing



AHLs found in colonies



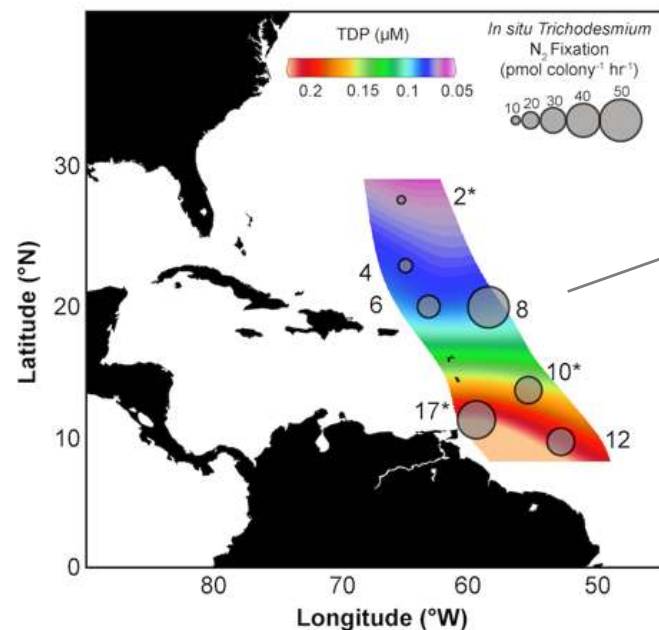
Van Mooy et al., 2012

****Trichodesmium* can't "hear" QS molecules***



AHLs can be used to selectively modify microbiome behavior

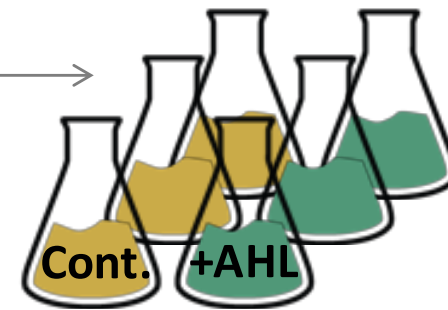
Selectively modifying the *Trichodesmium* microbiome with AHLs in the North Atlantic



Isolate
Trichodesmium



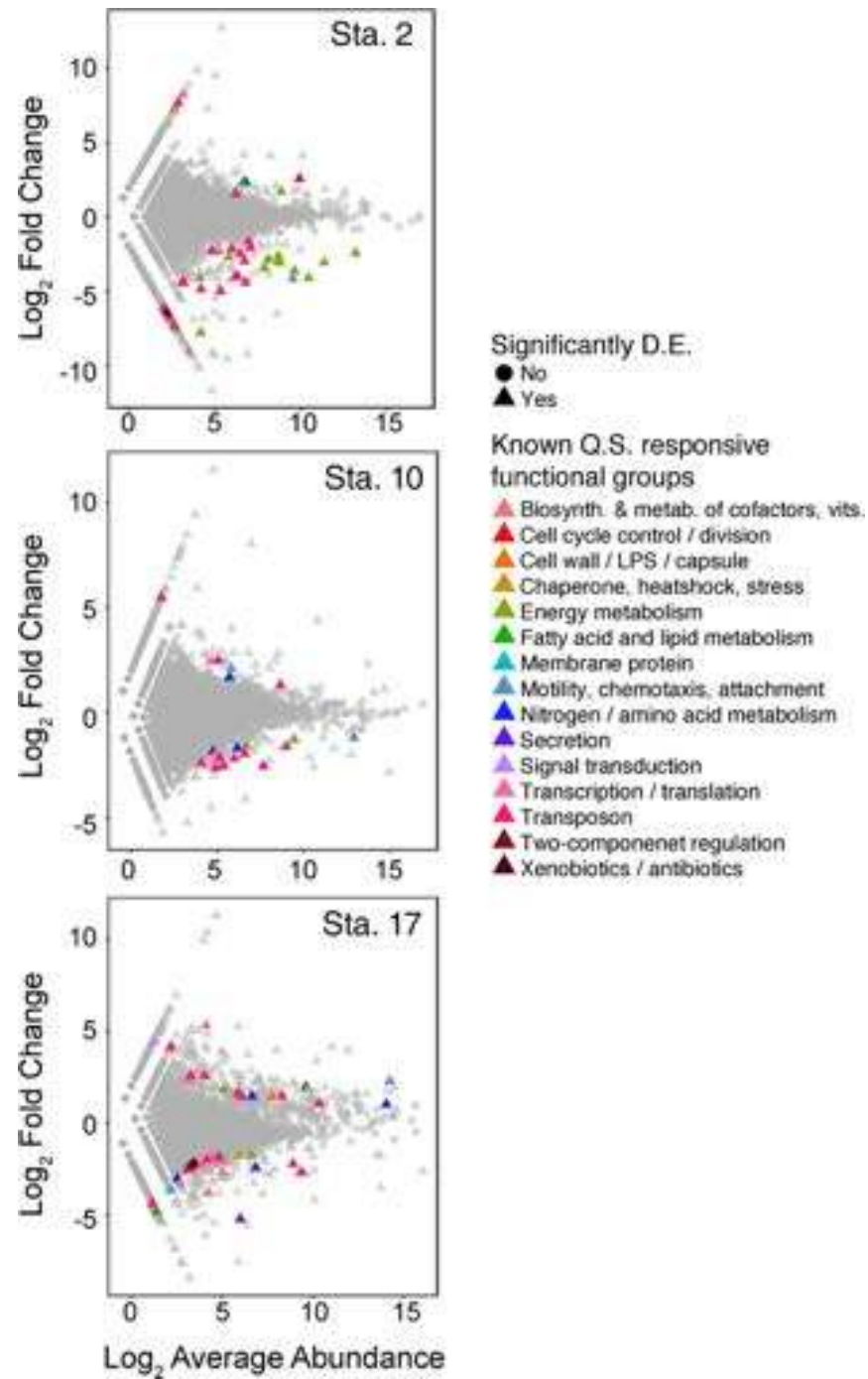
Incubate with a cocktail
of AHL molecules



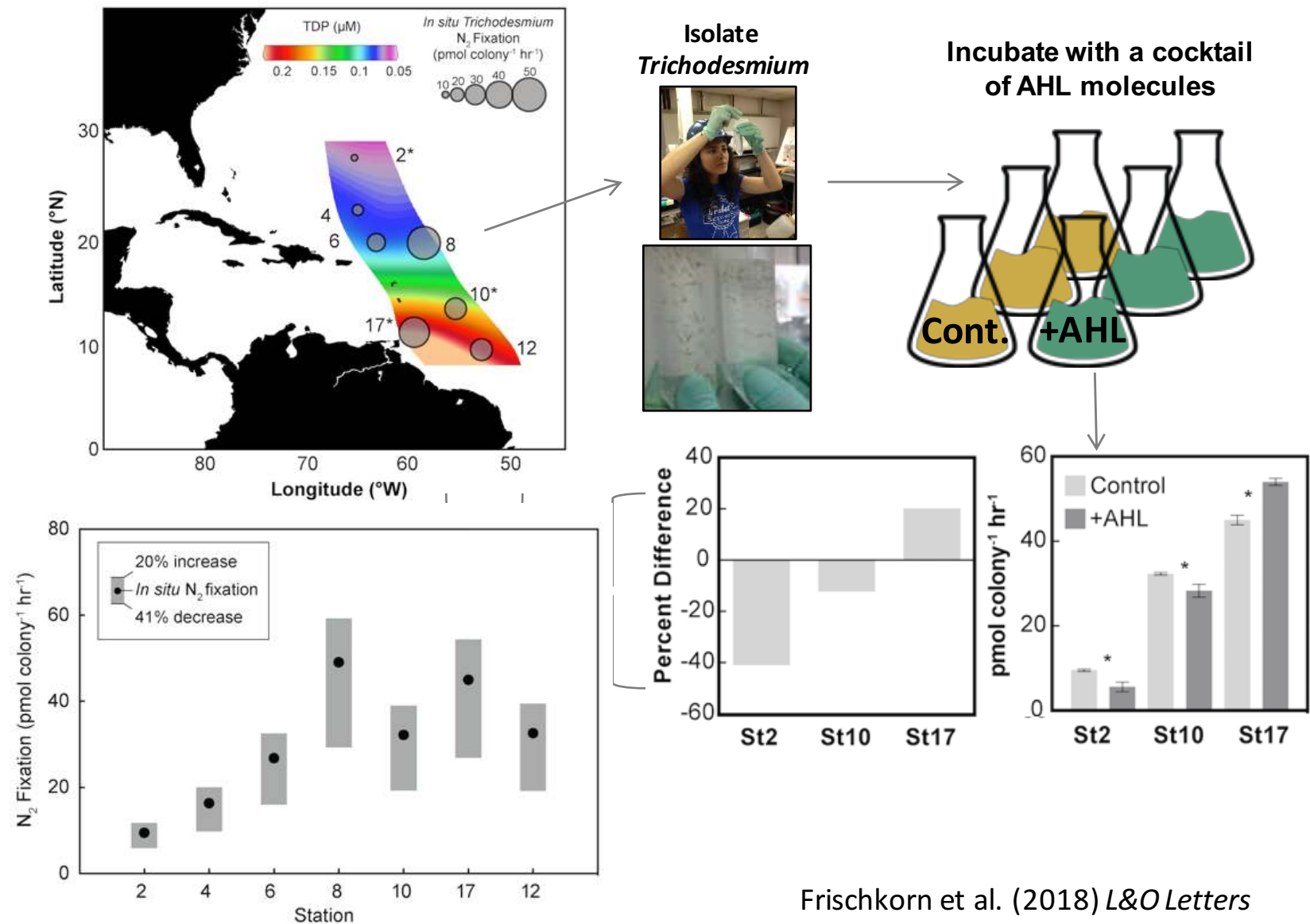
Does AHL addition
influence microbiome gene
expression?







Microbiome modulates N₂ fixation

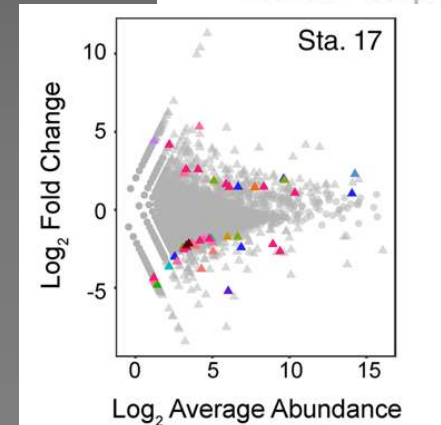
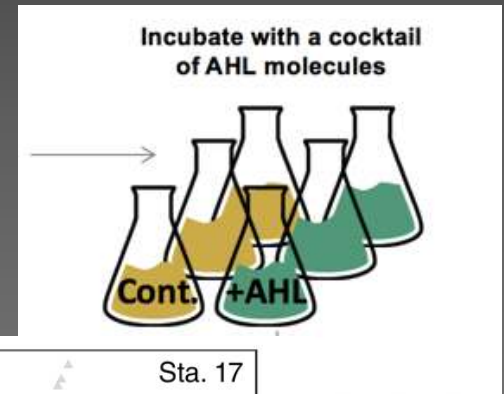
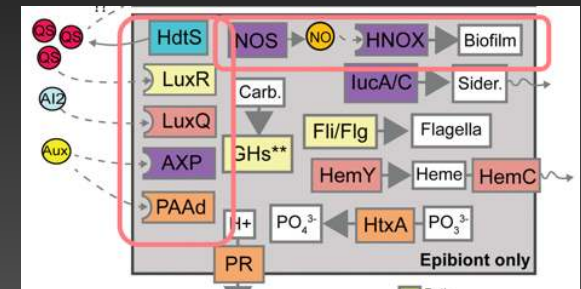


Frischkorn et al. (2018) *L&O Letters*

Summary – host microbiome interactions focus on N₂ fixation

Can the microbiome modulate host N₂ fixation?

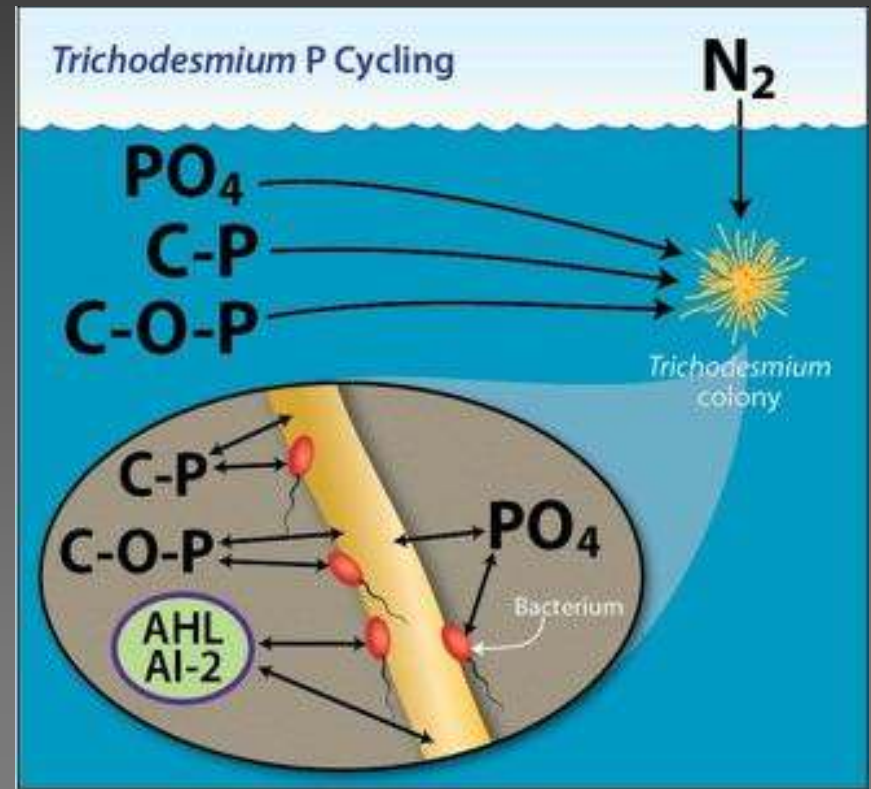
- **Metagenome:** *Trichodesmium* can't “hear” AHLs, while the microbiome can
- **Metatranscriptome:** AHL addition induces known quorum sensing responses and shifts host N₂ fixation
- Understanding the mechanisms that underlying interactions will help models and predictions of *Trichodesmium* distribution and N₂ fixation



Summary - Host microbiome interactions

What is the role of the microbiome in *Trichodesmium* physiological ecology?

- **16S community amplicon sequencing:** Colonies harbor diverse epibionts distinct from water column, that are dynamically curated across gradients in the environment
- **Metagenomics:** Epibionts confer substantial metabolic potential which likely underpins *Trichodesmium* fitness
- **Metatranscriptomics:** Distinct physiology and interactions between *Trichodesmium* and its microbiome



Conclusions

Genome-enabled approaches are providing new tools to trace the activities and physiological ecology of *Trichodesmium* and its microbiome.

Lessons learned: There is value in comparisons/time-series and having coincident datasets (Multit-omics)

