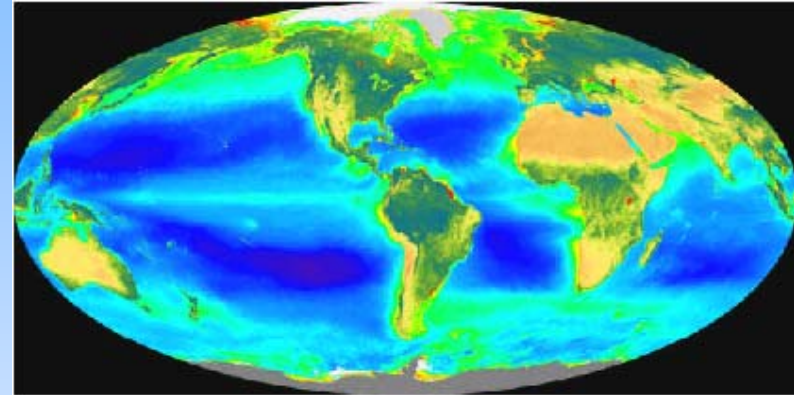
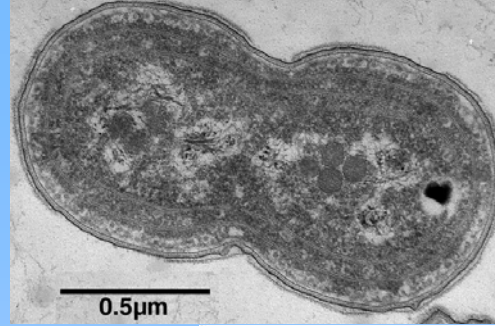


Marine Ecosystem Modeling & Genomics

Scott Doney, WHOI



Ecosystem State

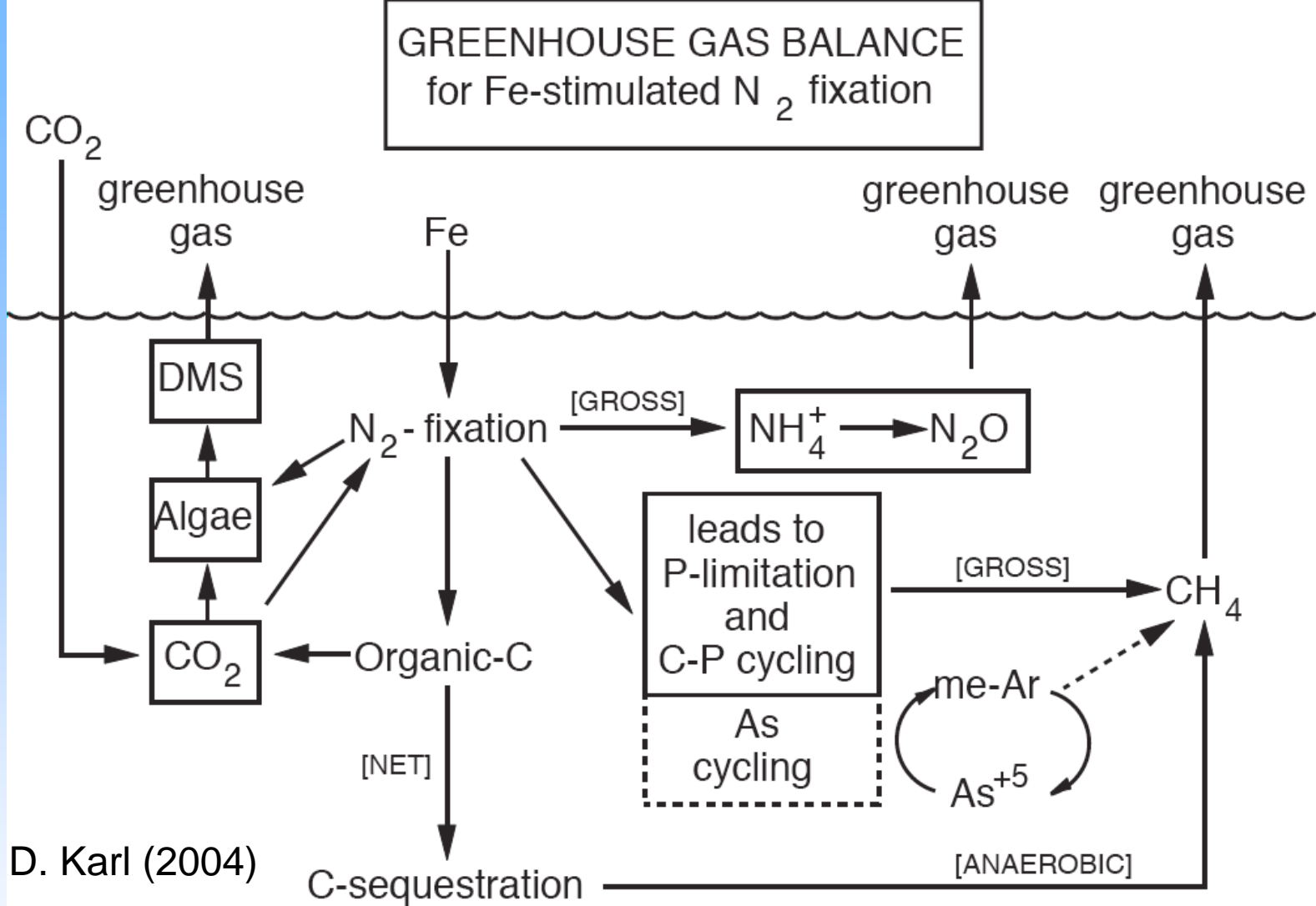
Biomass
Primary Productivity
Net Production/Export
Community Structure

Biological Dynamics

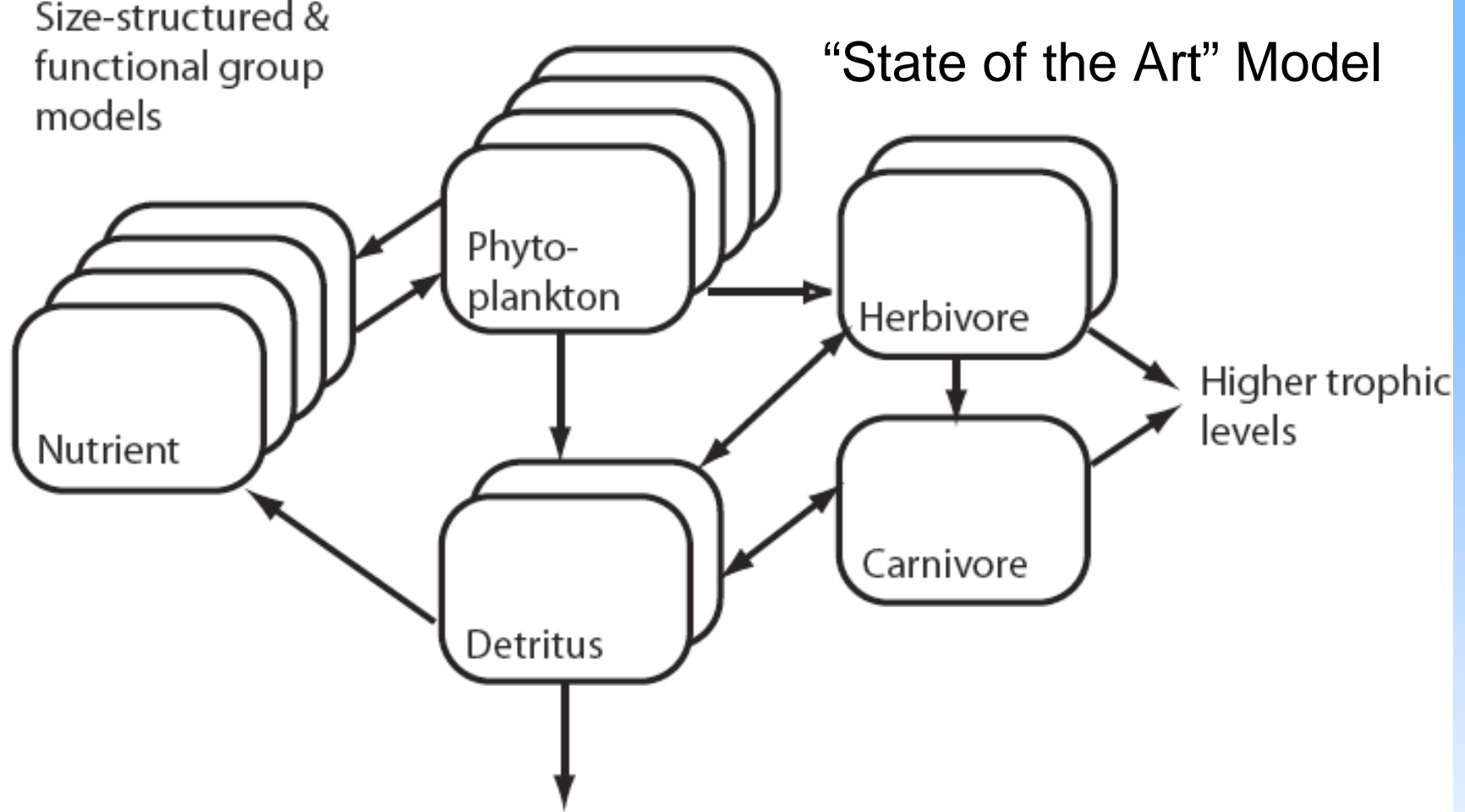
Environmental Genomics
Physiology
Population Ecology

Ocean & Climate

Atmospheric CO₂, DMS, ...
Ocean/Atmosphere Circulation
Dust-Iron Influx, pH
Ocean Nutrient Fields



- Regulation of atm. CO₂ & other radiative gases
- Responses & feedbacks to warming, dust, ...
- Predictions require mechanistic understanding



- Aggregate into trophic levels/functional groups
- Rates/processes from limited culture/field studies
- Many aspects empirically based
- Data poor for validation (rates, grazing, loss terms)

Marine Genomic Revolution

-Leverage advances in Biotech & Human Genome

-rapid gene sequencing

-O(10) => O(100) marine microbial genomes

-“microarrays” => 10^4 - 10^6 simultaneous samples

-Environmental genomics:

-sample whole

communities;

-“cultivation

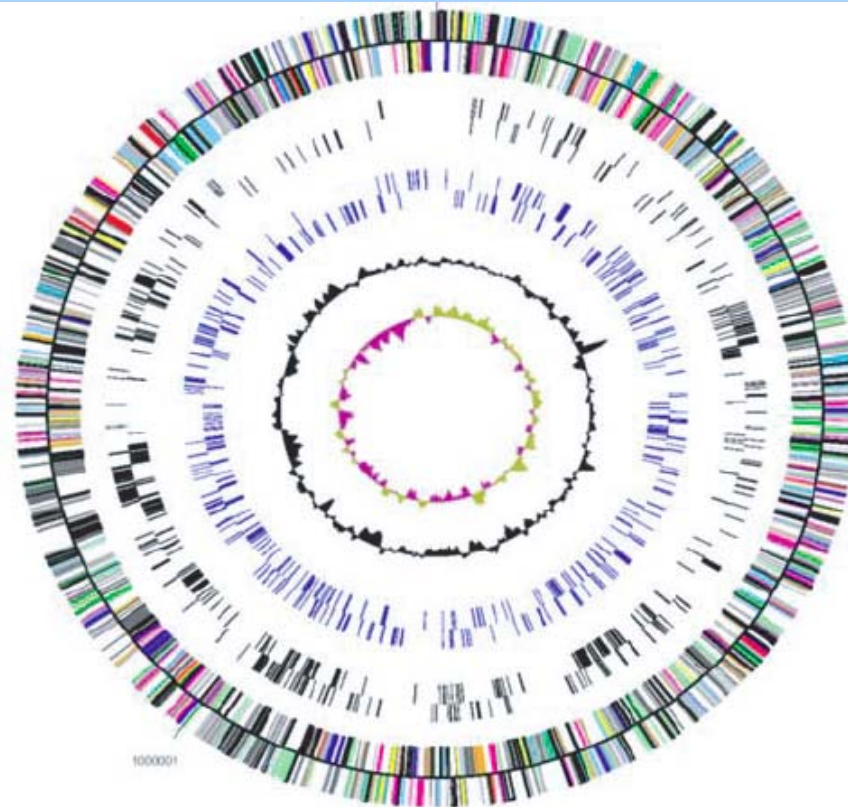
independent”

techniques

Prochlorococcus

Genome map

Rocap et al. (2003)



- Energy Metabolism
- Photosynthesis
- DNA replication
- Fatty Acid
- Biosynthesis of Cofactors
- Cellular Processes
- Transport
- Translation
- Regulation
- Amino Acid Biosynthesis
- Cell Envelope
- Transcription
- Purines, pyrimidines
- Central Metabolism
- Other
- Conserved Hypothetical
- Hypothetical

Brief Genomic Tutorial



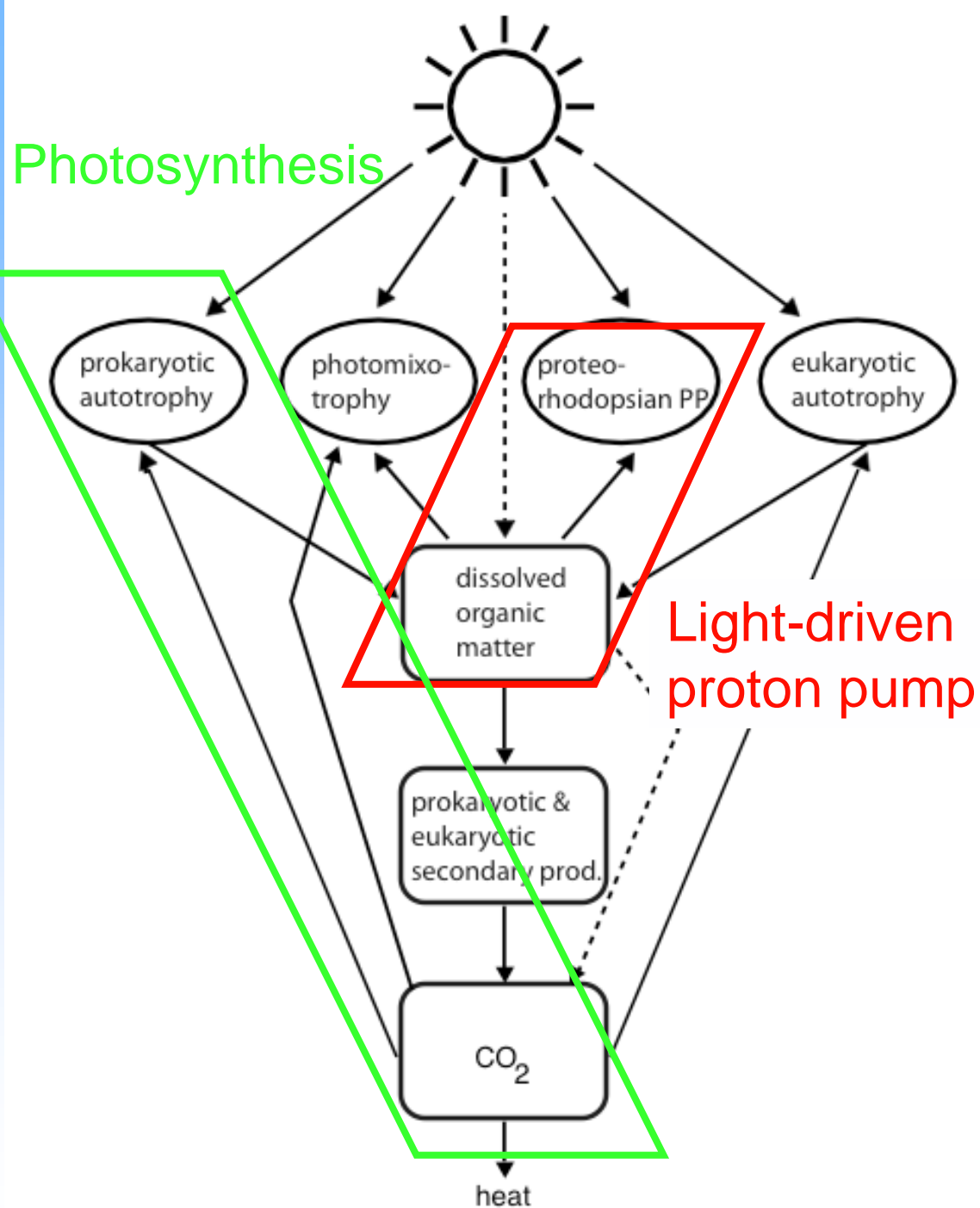
- Phylogeny
- Diversity
(DNA, rRNA)
- Metabolic
pathways

- Gene expression
- Response to
environmental
forcing

- Proteomics
- Physiological
rates

Recent Findings

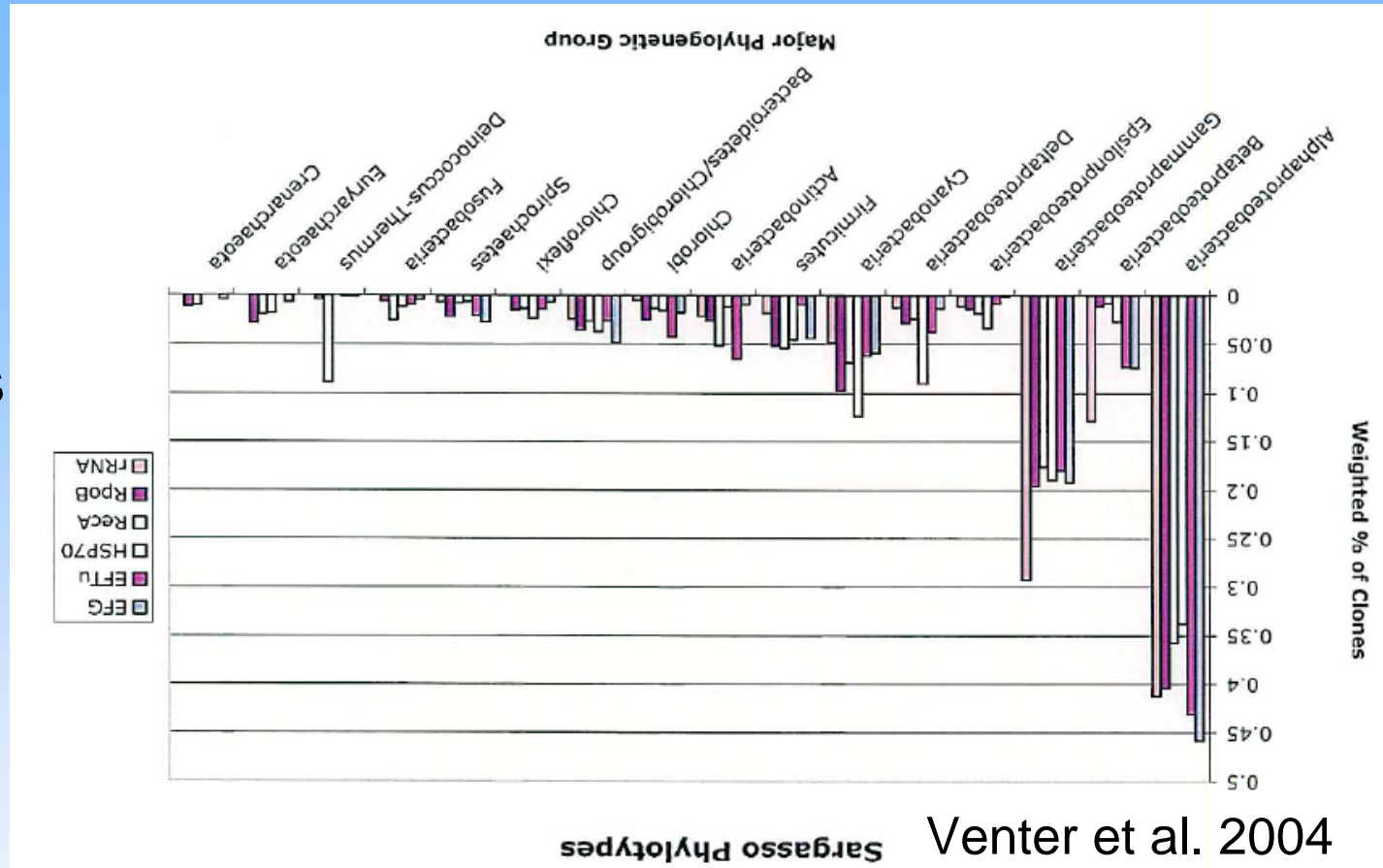
- dominance of uncultured microbes
- large number of species/taxa
- new metabolic pathways
- deeper genetic “potential” (genotype) often unexpressed



Sargasso Sea “Shotgun” Analysis (C. Venter)

- filter 2000 liters
- collect genome fragments
- assemble *in silico*

- ~1.2M genes
- ~1800 new “species”

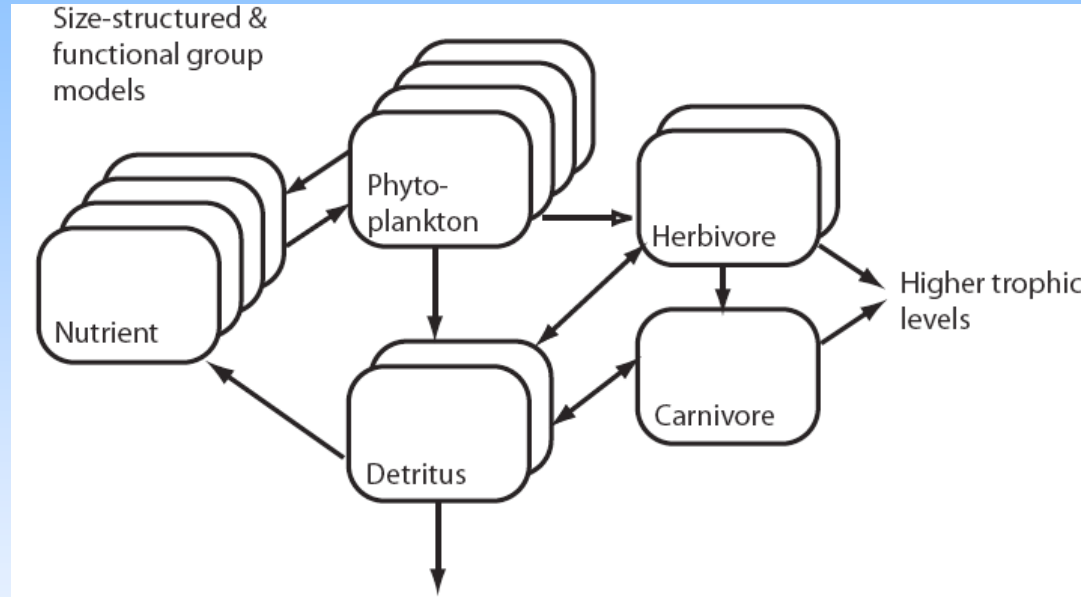


Bridging Genomics & Ecosystem Modeling

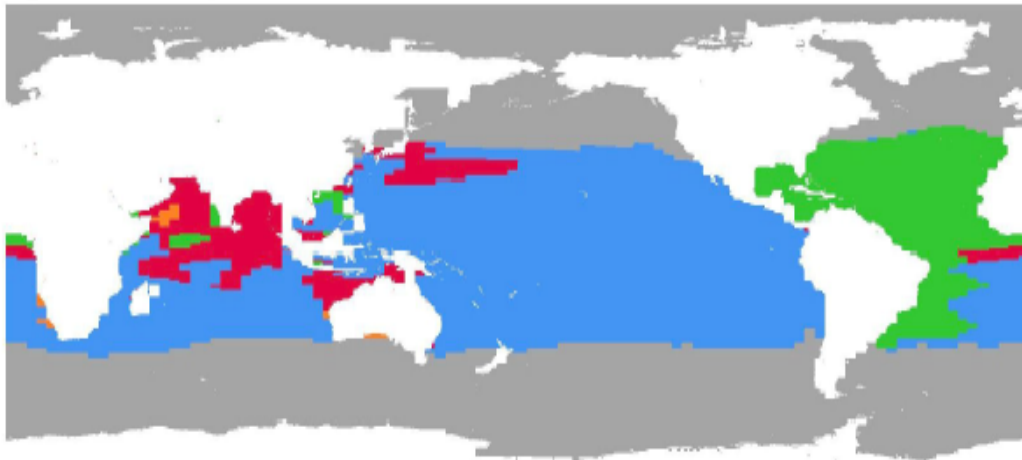
- New processes/dynamics
- Data for model evaluation

species composition
metabolic rates

- Adapt current models
- expand predicted variables
increase species diversity
(more boxes)
model cellular metabolism
(more complex boxes)



C) Diazotroph Growth Limitation



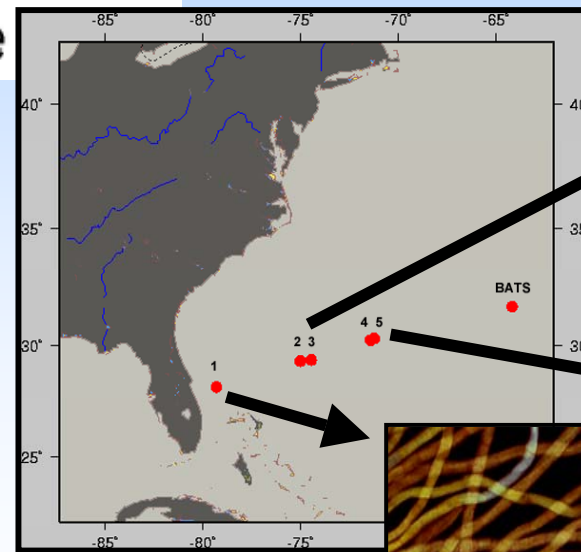
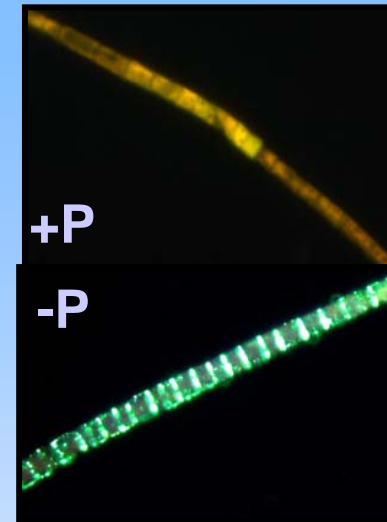
Nitrogen 0.000%, Iron 44.06%, Phosphorus 11.66%
Light 7.072%, Temperature 36.81%, Replete 0.376%

■ Nitrogen ■ Iron ■ Phosphorus ■ Silicon
■ Light ■ Temperature ■ Replete

Molecular Detection of *Trichodesmium* Phosphorus Stress

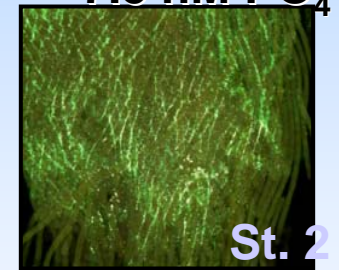
Dyhrman et al. 2002

Assay development:
Cultures grown with (+P) or without (-P) phosphorus.



12.1 nM PO_4^{3-}

7.5 nM PO_4^{3-}



7.5 nM PO_4^{3-}



Genomics & Modeling

New model paradigms

-multi-scale models

(e.g., individual based models;
continuous distributions)

(more flexible “boxes”)

nesting; SGS parameterization

-simulate ecological functions,
not species

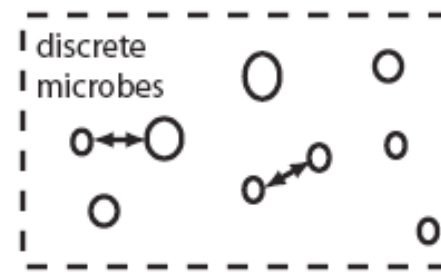
“genotype” => “phenotype”

(abandon boxes)

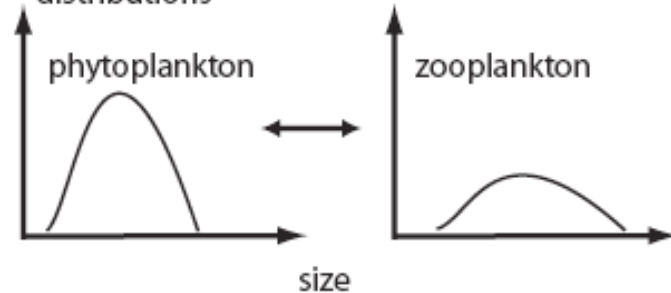
-ecological/evolutionary rules
for ecosystem assembly

(e.g., resilience; optimal
energy/mass flow)

Individual-based &
multi-scale models

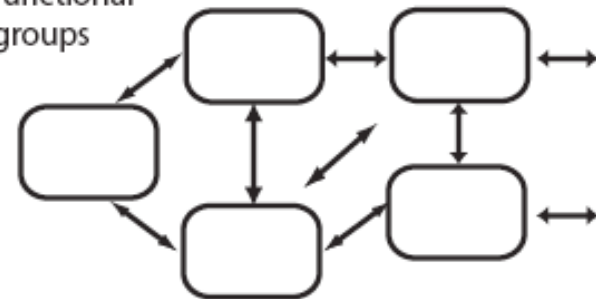


continuous
distributions



size

functional
groups



How do we build a credible model?
How much complexity is enough?
Do we know the key processes for
climate change?

Genomic data will help to quantify
processes & environmental sensitivity

Ecosystem State

Biomass
Primary Productivity
Net Production/Export
Community Structure

Biological Dynamics

Environmental Genomics
Physiology
Population Ecology

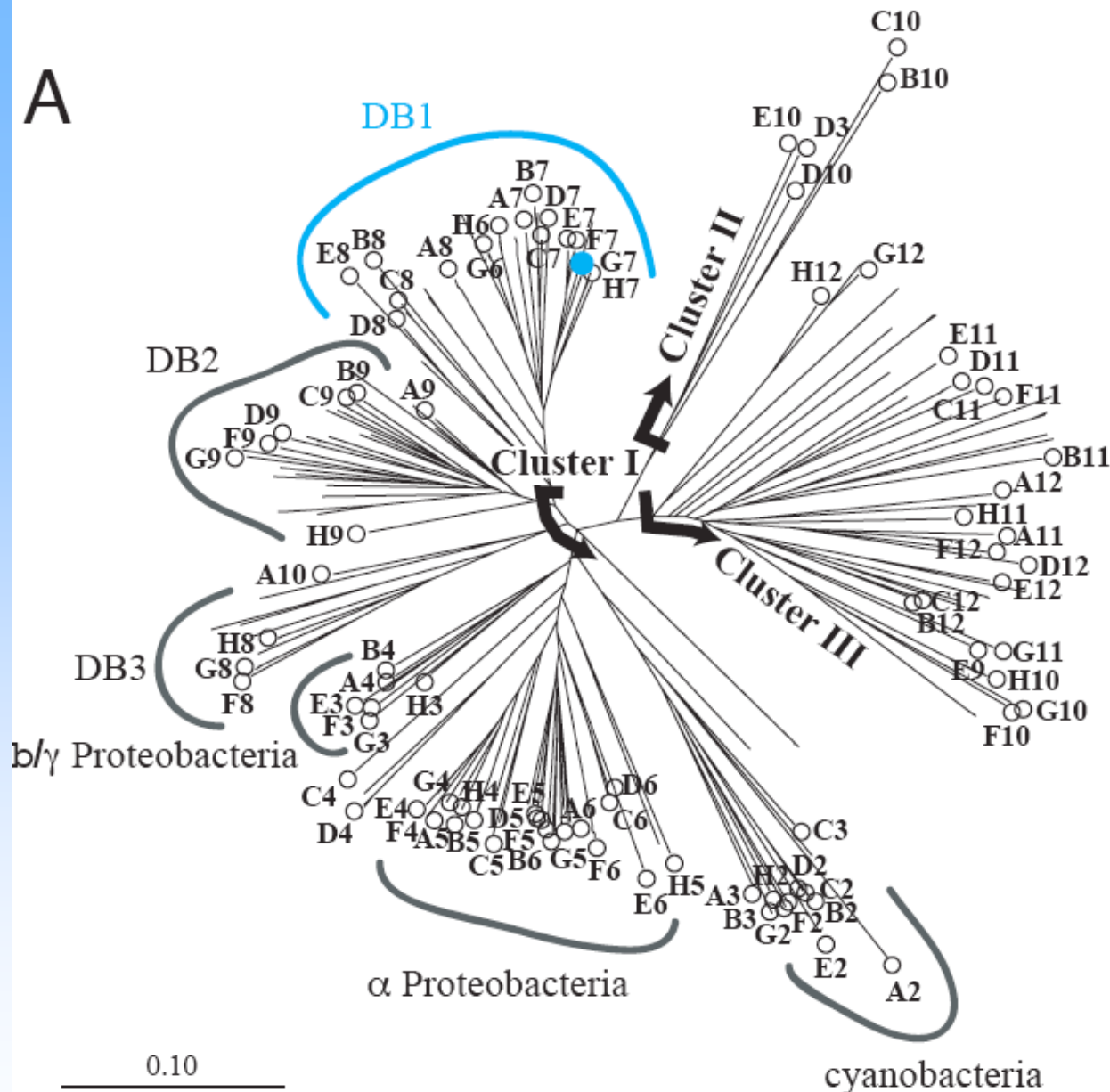
Ocean & Climate

Atmospheric CO₂, DMS, ...
Ocean/Atmosphere Circulation
Dust-Iron Influx, pH
Ocean Nutrient Fields

Phylogenetic Tree for *nifH* (N₂ fixation) gene

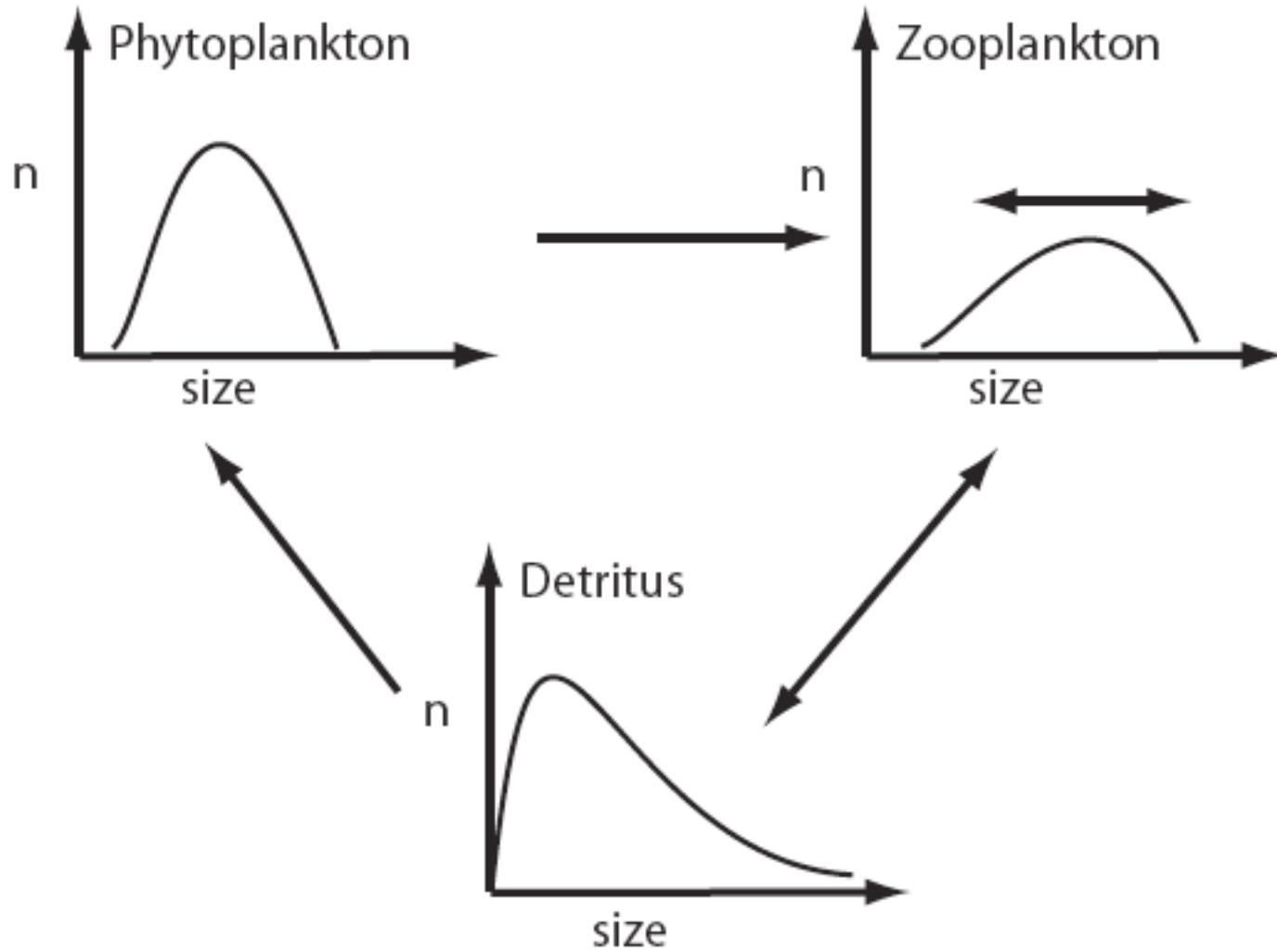
Chesapeake Bay

A

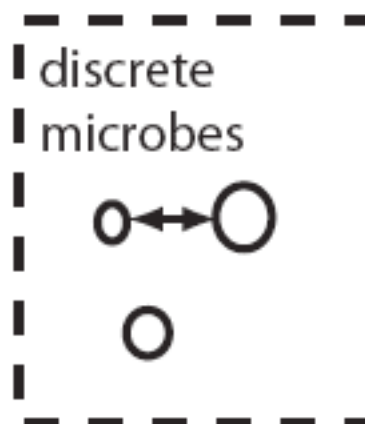


Jenkins et al. (2004)

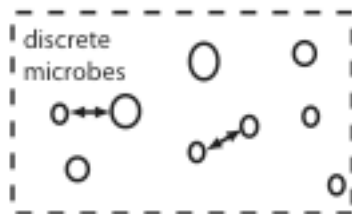
Continuous distribution models



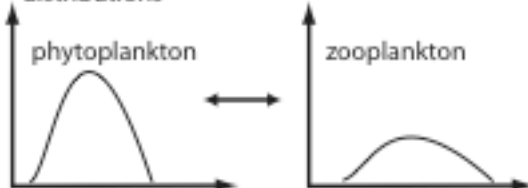
Individual-based & multi-scale models



Individual-based & multi-scale models

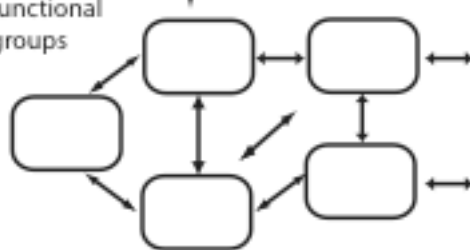


continuous distributions

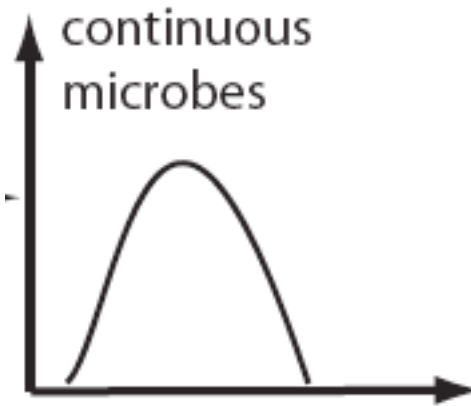


size

functional groups



continuous microbes

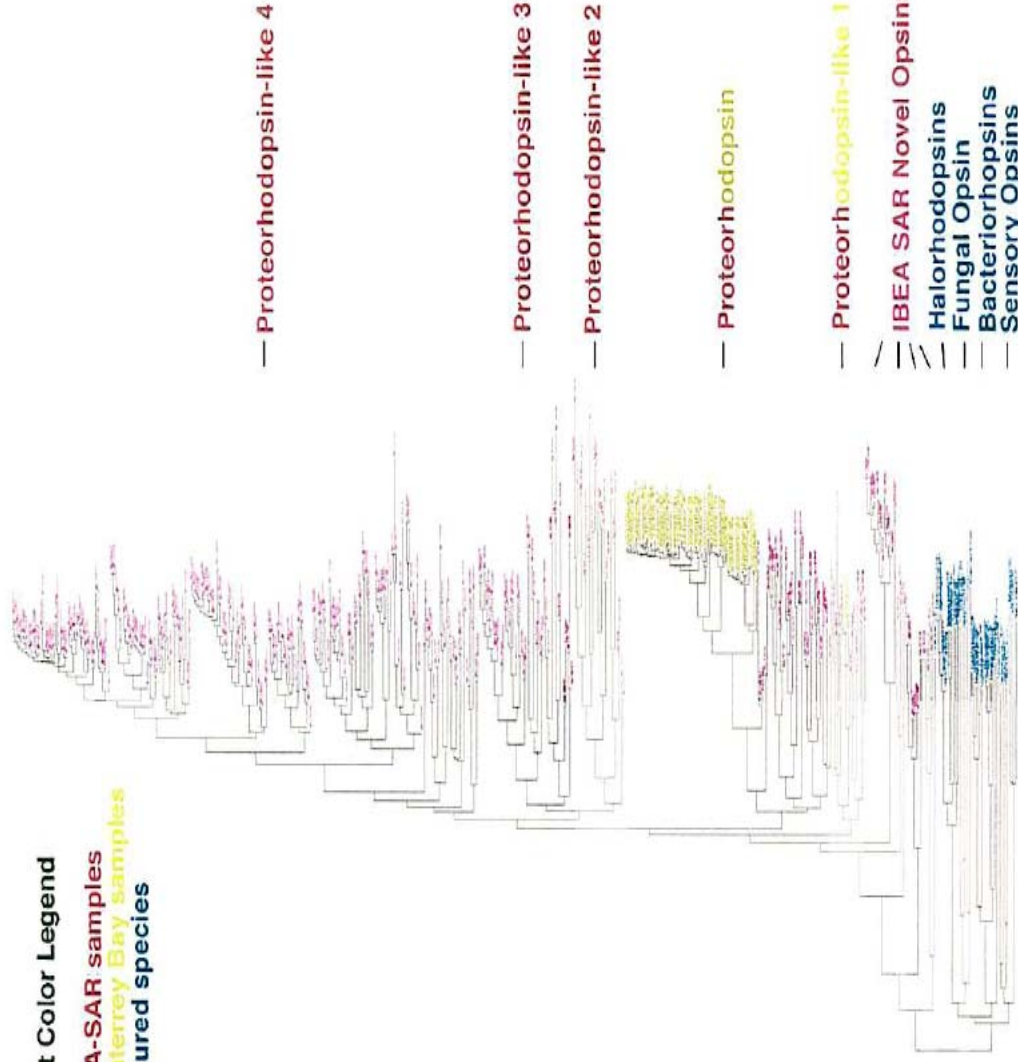


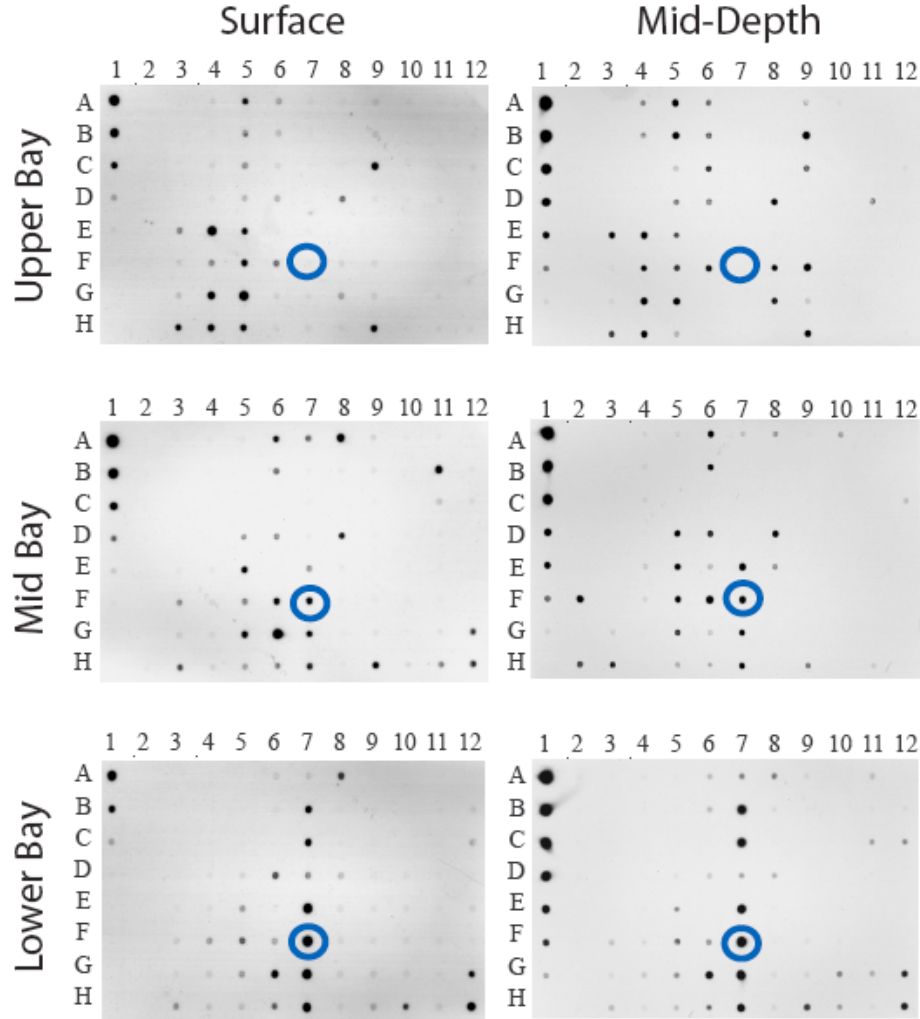
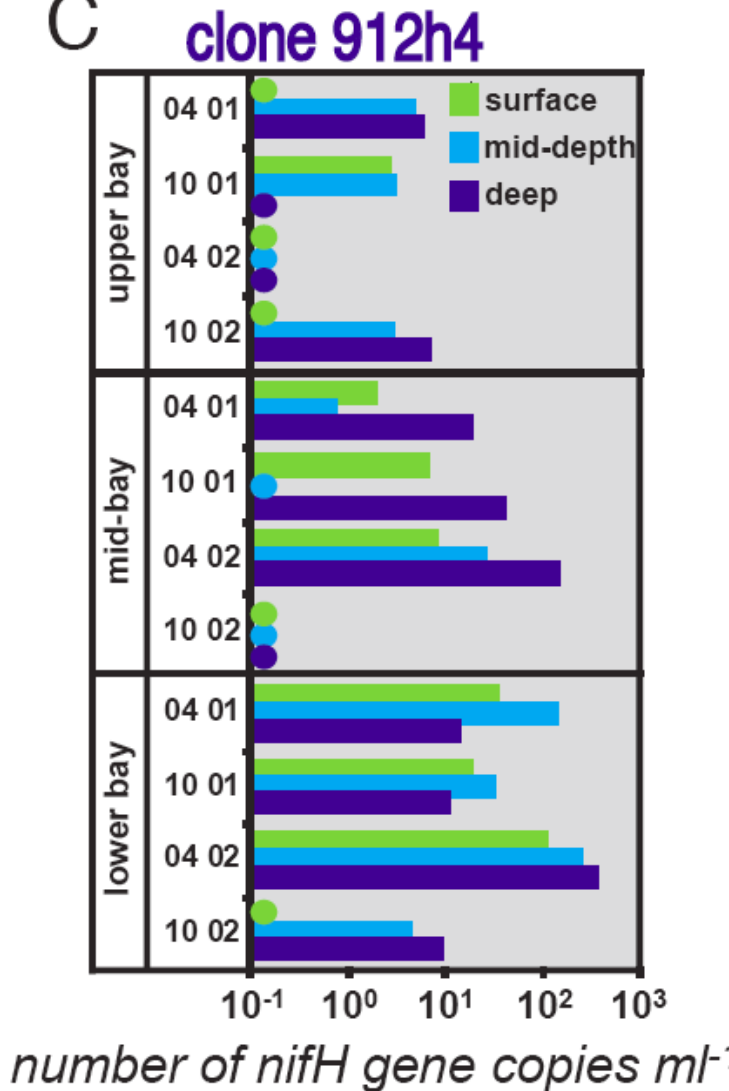
Font Color Legend

IBEA-SAR samples

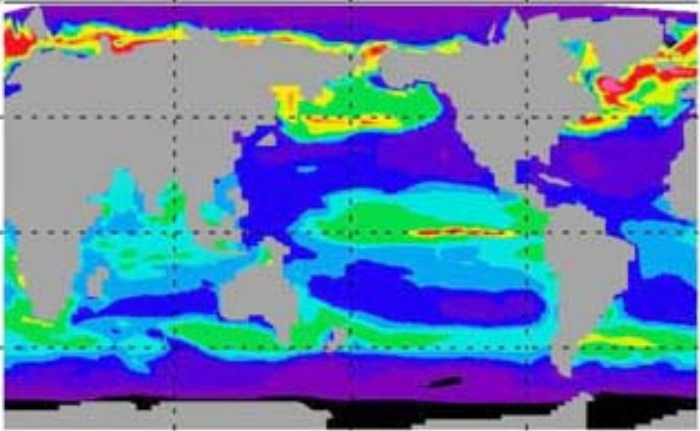
Monterrey Bay samples

Cultured species

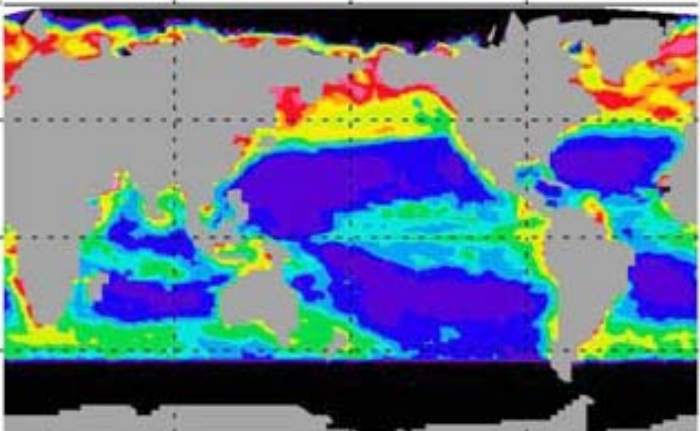


B**C**

A) BEC Model June



B) SeaWiFS June



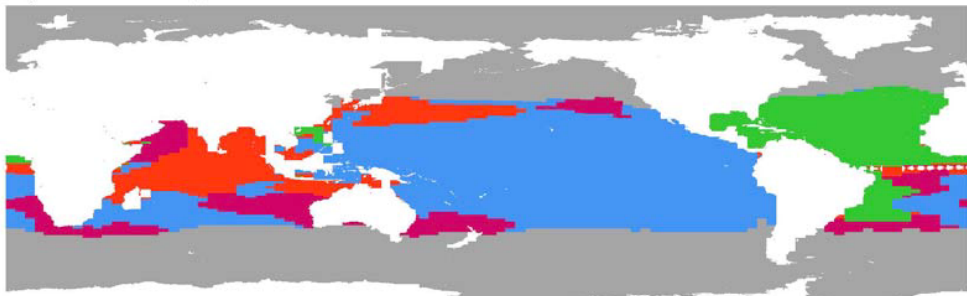
A) Diatom Growth Limitation



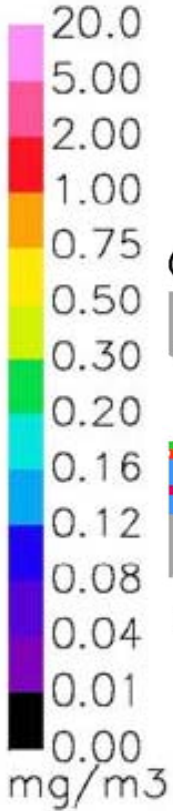
Nitrogen 58.35%, Iron 28.84%, Silica 10.08%, Phosphorus 0.467%
Light 2.148%, Replete 0.088%

■ Nitrogen ■ Iron ■ Phosphorus ■ Silicon
■ Light ■ Temperature ■ Replete

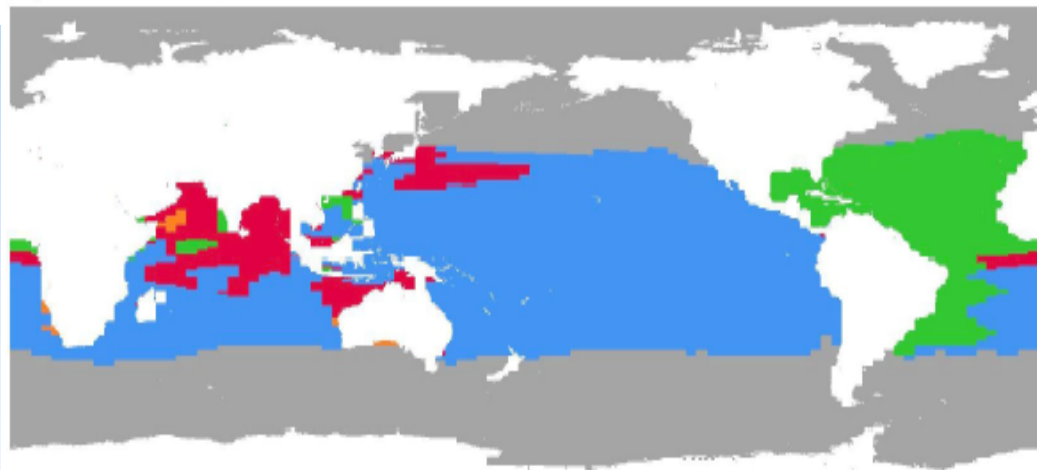
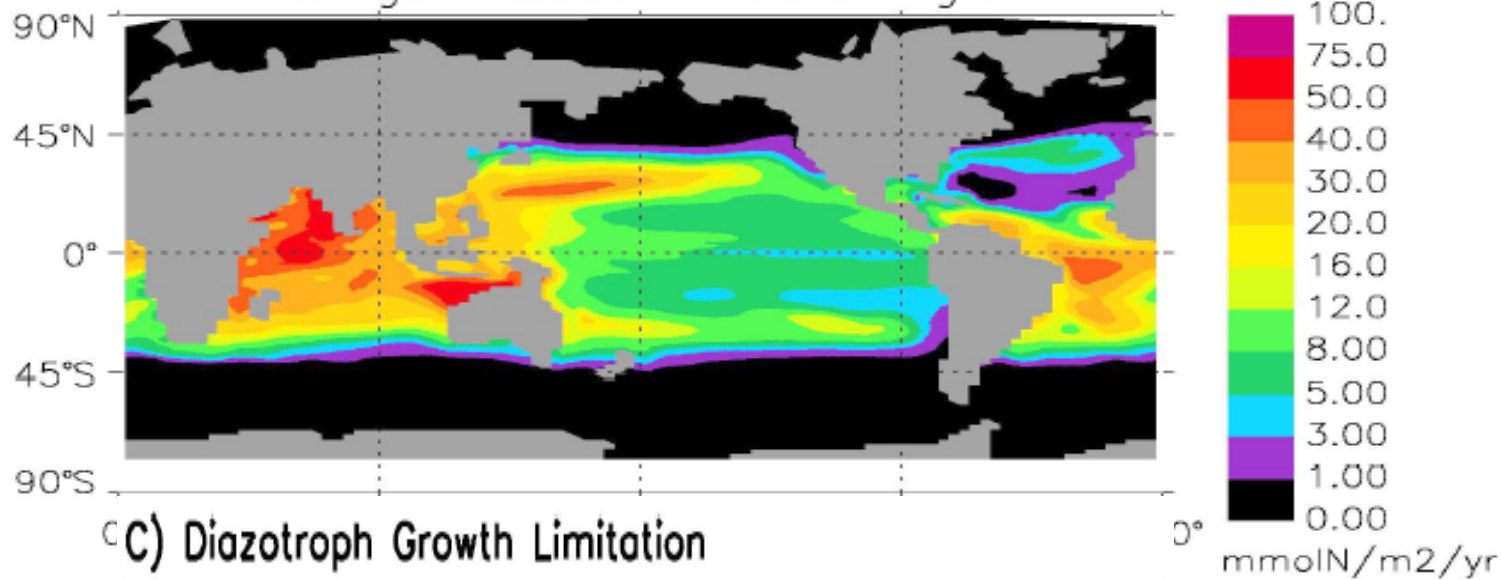
C) Diazotroph Growth Limitation



Nitrogen 0.000%, Iron 35.35%, Phosphorus 10.52%
Light 9.607%, Temperature 36.81%, Replete 7.702%



Nitrogen Fixation = 55.51 Tg N

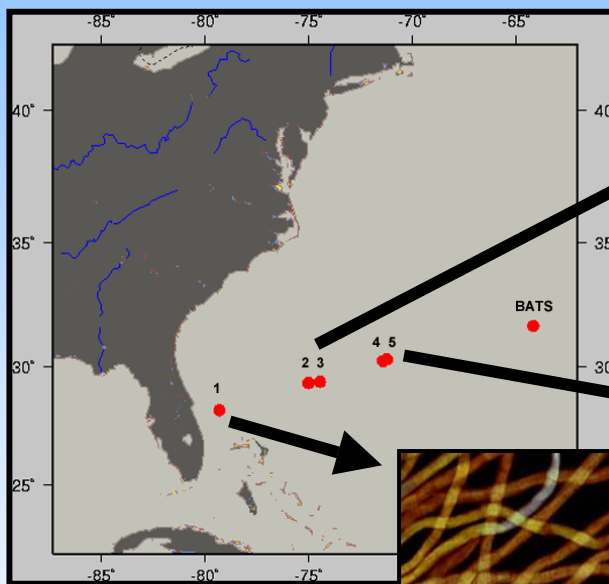
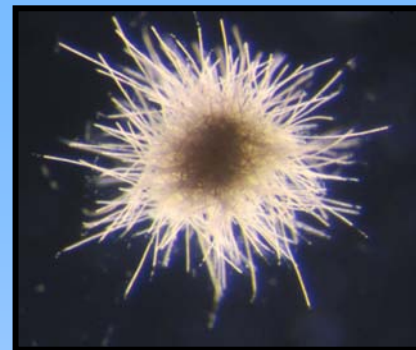
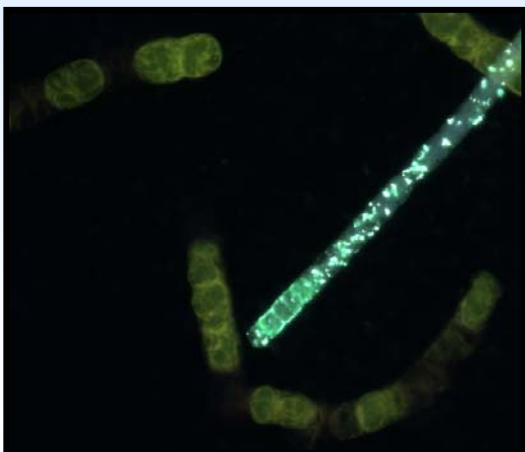
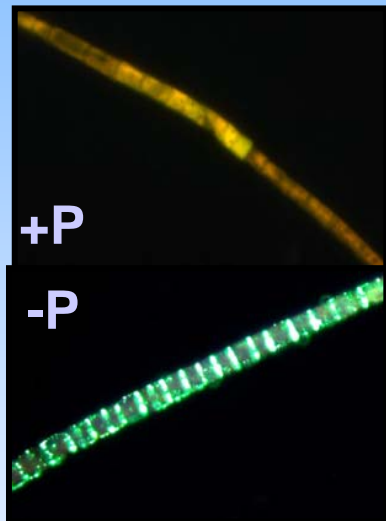


Nitrogen 0.000%, Iron 44.06%, Phosphorus 11.66%
Light 7.072%, Temperature 36.81%, Replete 0.376%

■ Nitrogen ■ Iron ■ Phosphorus ■ Silicon
■ Light ■ Temperature ■ Replete

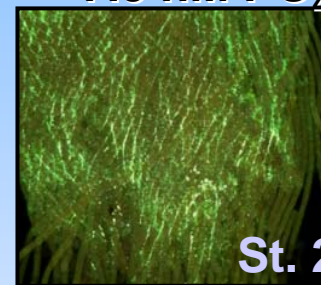
Molecular Detection of *Trichodesmium* Phosphorus Stress

Assay development:
Cultures grown with (+P) or without (-P) phosphorus.



12.1 nM PO_4^{3-}

7.5 nM PO_4^{3-}

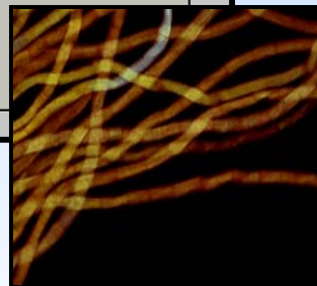


St. 2

7.5 nM PO_4^{3-}



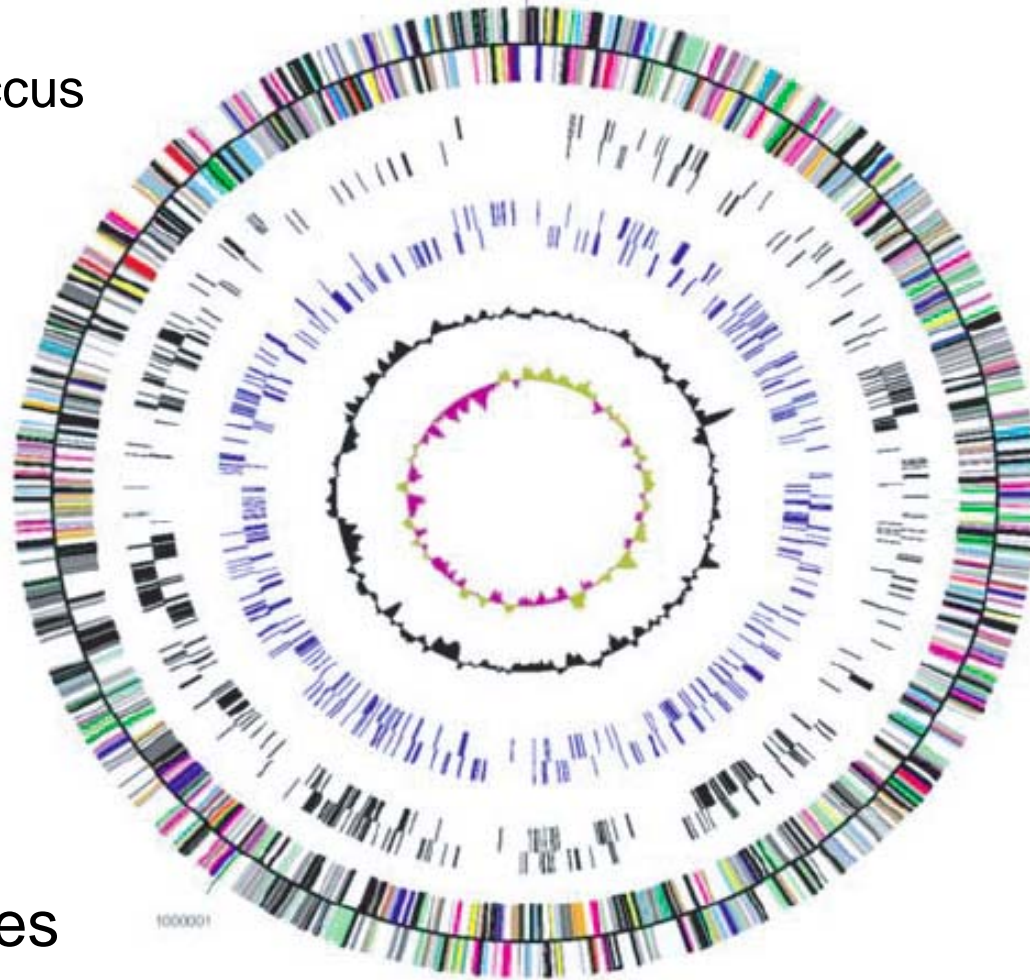
St. 5



Species Heterogeneity

Dyhrman et al. 2002

Prochlorococcus
genome
Rocap et al.
(2003)



- Energy Metabolism
- Photosynthesis
- DNA replication
- Fatty Acid
- Biosynthesis of Cofactors
- Cellular Processes
- Transport
- Translation
- Regulation
- Amino Acid Biosynthesis
- Cell Envelope
- Transcription
- Purines, pyrimidines
- Central Metabolism
- Other
- Conserved Hypothetical
- Hypothetical

Genome
Sequences

-novel metabolic pathways

-

Environmental Controls on Plankton Species Distributions: An Example for Coccolithophores

Universal distribution => local selection

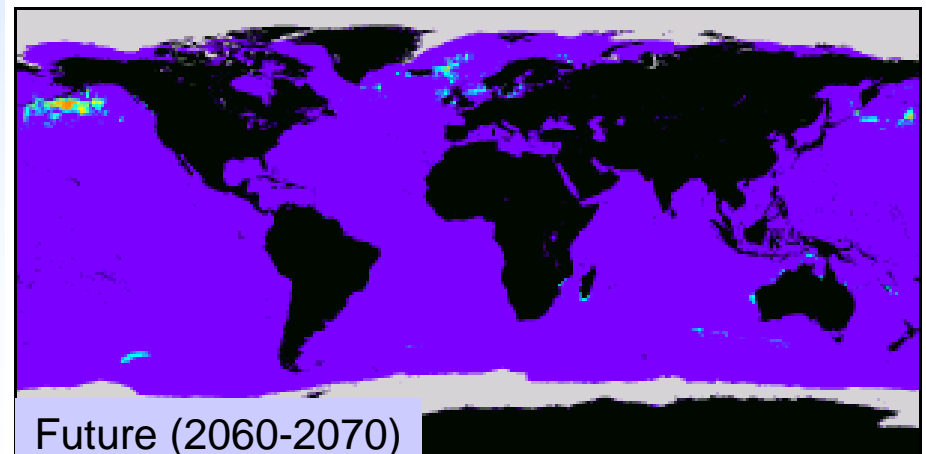
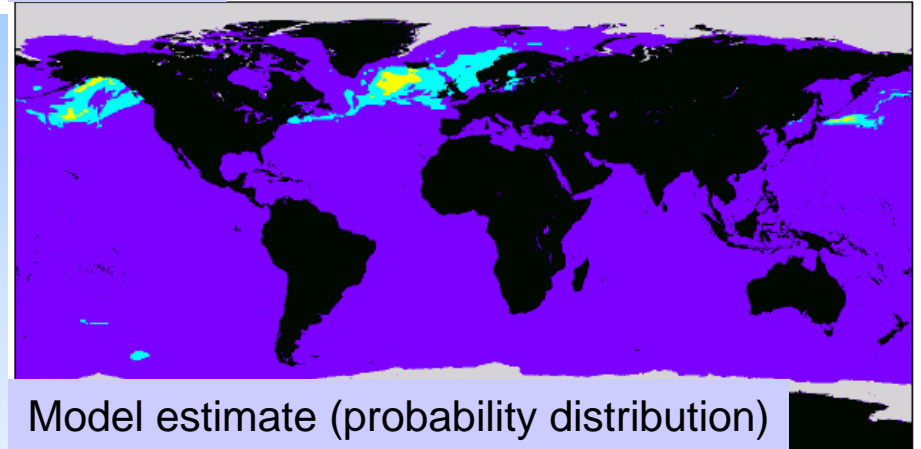
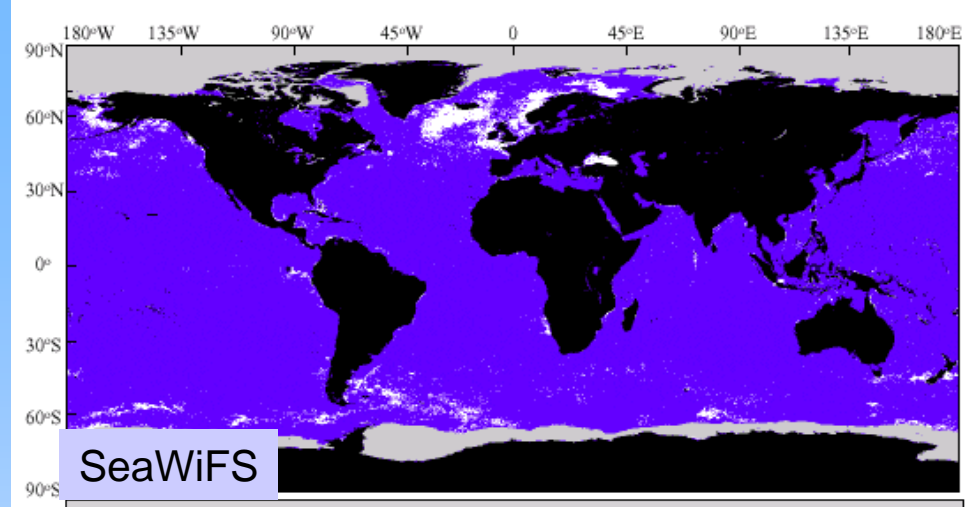
Step 1: Satellite mapping of coccolithophorid blooms

Step 2: Compare with modern physical variables (SST, nutrients, light, mixing depth)

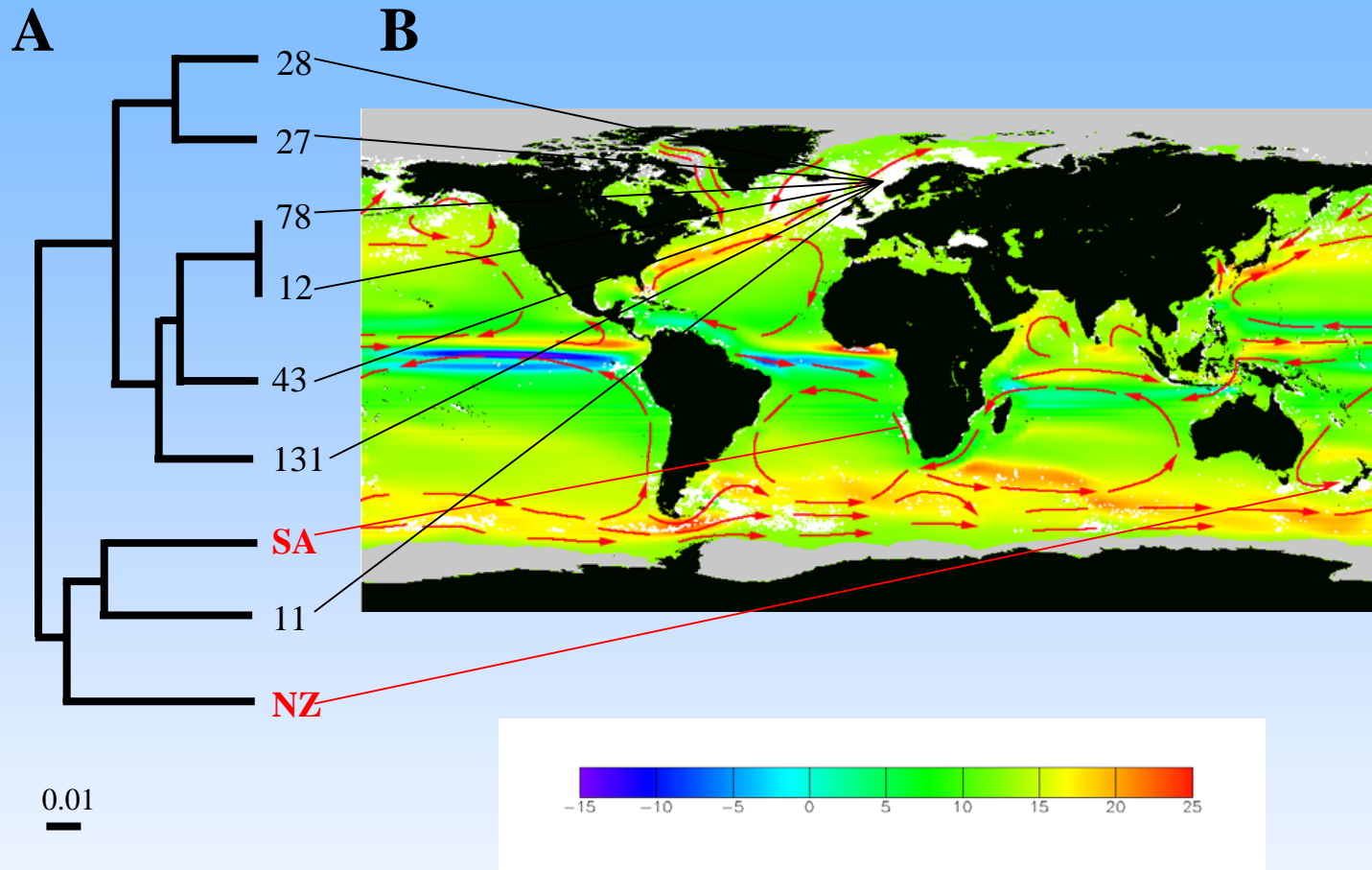
Step 3: Develop “conditional probability function”

Step 4: Project future using results of climate models

Iglesias-Rodreguiz (2002)



Amplified Fragment Length Polymorphism (AFLP)



Distinct genetic populations of *Emiliana huxleyia* in Northern and Southern Hemisphere blooms => different physiological responses to environmental forcing

Genes to Physiology



-Phylogeny (evolutionary relationships):
dominance of uncultured microbes
Archea (new Domain of life)

-Diversity

large number species/taxa, many unidentified
relative number of organisms

-Metabolic pathways

new functions or unexpected capabilities
deeper genetic “potential” (genotype)

Genes to Physiology



- Gene expression
- Responses to environmental forcing (physical, chemical, biological)

Brief Genomic Tutorial



-Diversity
(DNA, rRNA)
-Metabolic
pathways
-Genetic
potential
“genotype”

-Gene Expression
-Response to
environmental
forcing

-Proteomics
-Physiological
Rates
-“Phenotype”

Molecular/genomic data

- validation
- new metabolism
- why are some pathways turned on
- improved

Current generation models

- many aspects empirically based
- aggregate trophic levels
- geochemical functional groups

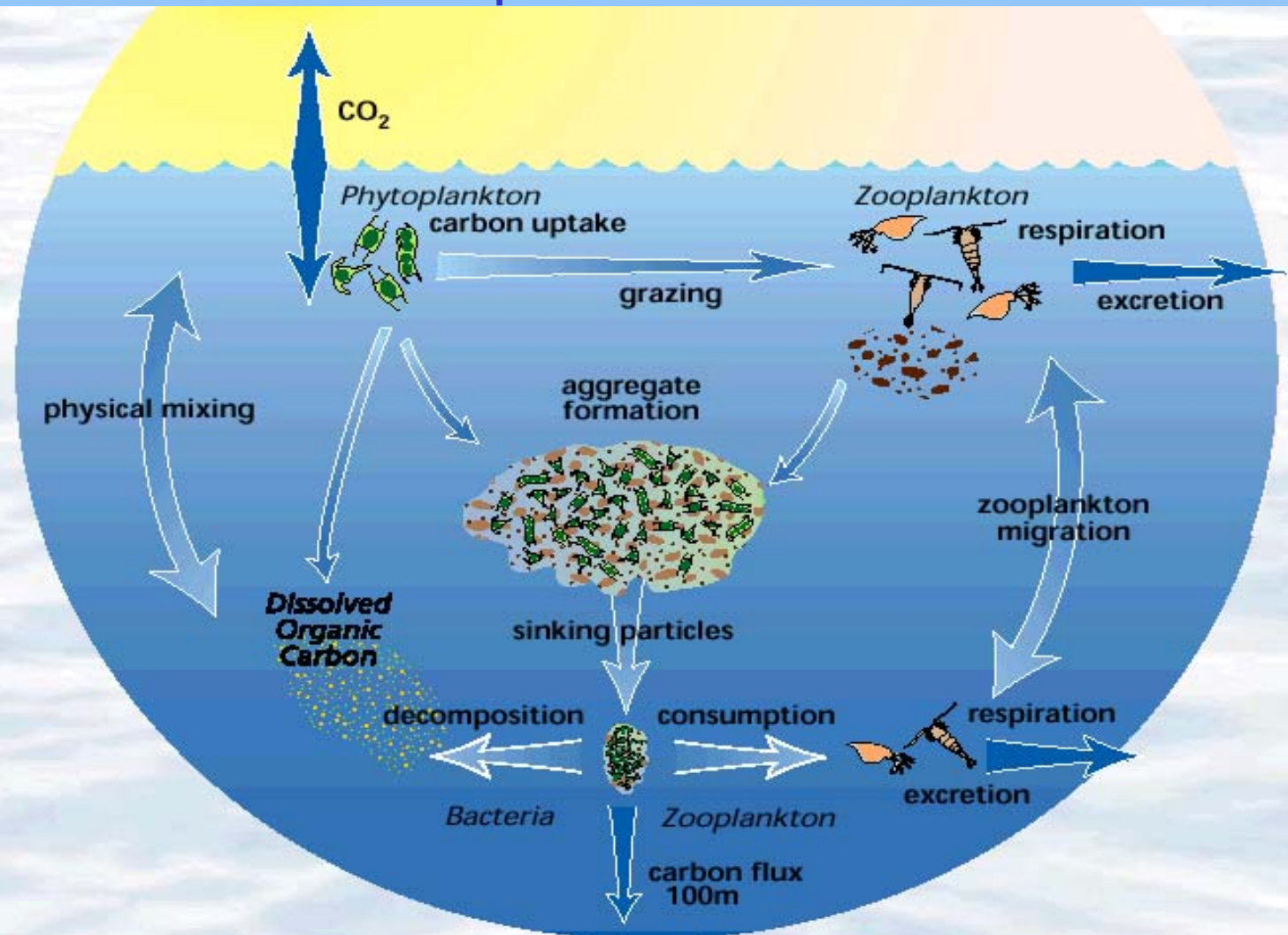
Increased biological complexity

- biological “sub-grid-scale” parameterization

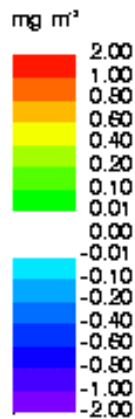
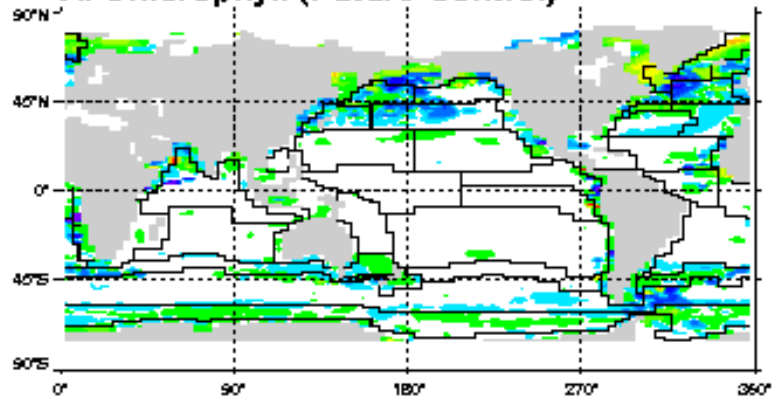
Molecular/genomic data

- validation
- new metabolism
- why are some pathways turned on
- improved

- Microbes dominate marine ecology/biogeochem.
- Regulation of atm. CO_2 & other radiative gases
- Responses & feedbacks to warming, dust, ...
- Predictions require mechanistic understanding

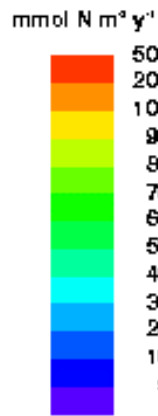
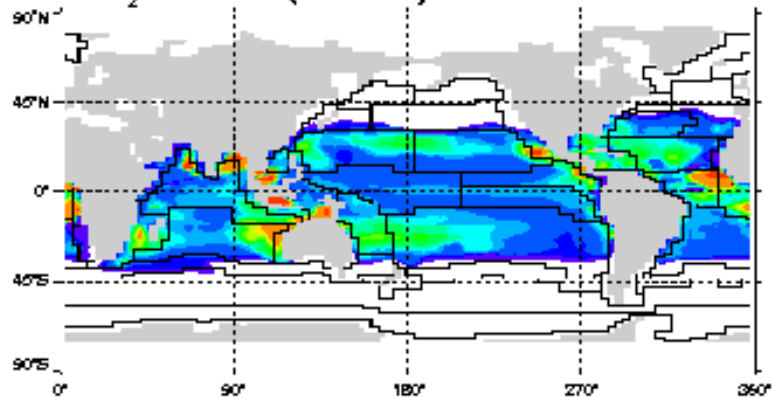


A. Chlorophyll (Future-Control)



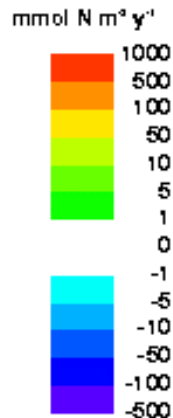
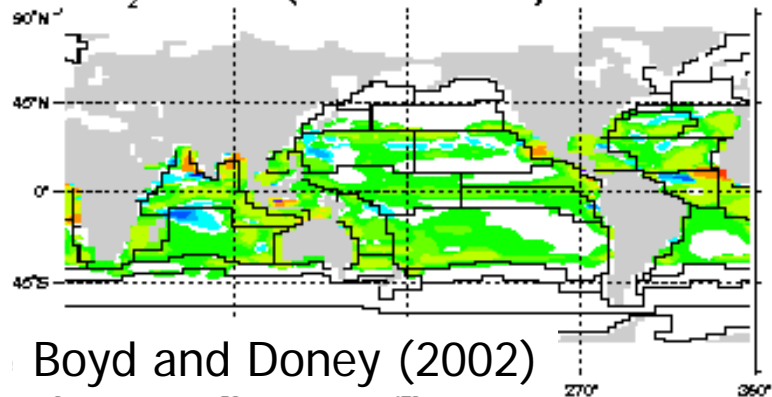
Regional changes in ecosystem boundaries, productivity & **community structure**

B. N₂ Fixation (Control)



Warming & stratification
⇒ Increased N₂ fixation

C. N₂ Fixation (Future-Control)



Reduced dust??
⇒ Increased N₂ fixation

Boyd and Doney (2002)

ECO-C3 Marine Ecosystem Component

Phytoplankton

Picoplankton /
Coccolithophores
(C, Chl, Fe, CaCO₃)

Diazotrophs
(C, Chl, Fe)

Diatoms
(C, Chl, Fe, Si)

Fixed C/N/P, Variable Fe/C, Chl/C, Si/C

Dissolved Organic Material
(C, N, P, Fe)

Sinking Particulate Material
(C, (N, P), Fe, Si, CaCO₃, Dust)

Zooplankton
(C)

Nutrients

Ammonium

Nitrate

Phosphate

Silicate

Iron

Ecosystem Modeling

Small Phytoplankton
C, Chl, Fe, CaCO₃

Diatoms
C, Chl, Fe, Si

Diazotrophs
C, Chl, Fe

Zooplankton
C

Nitrate

Ammonium

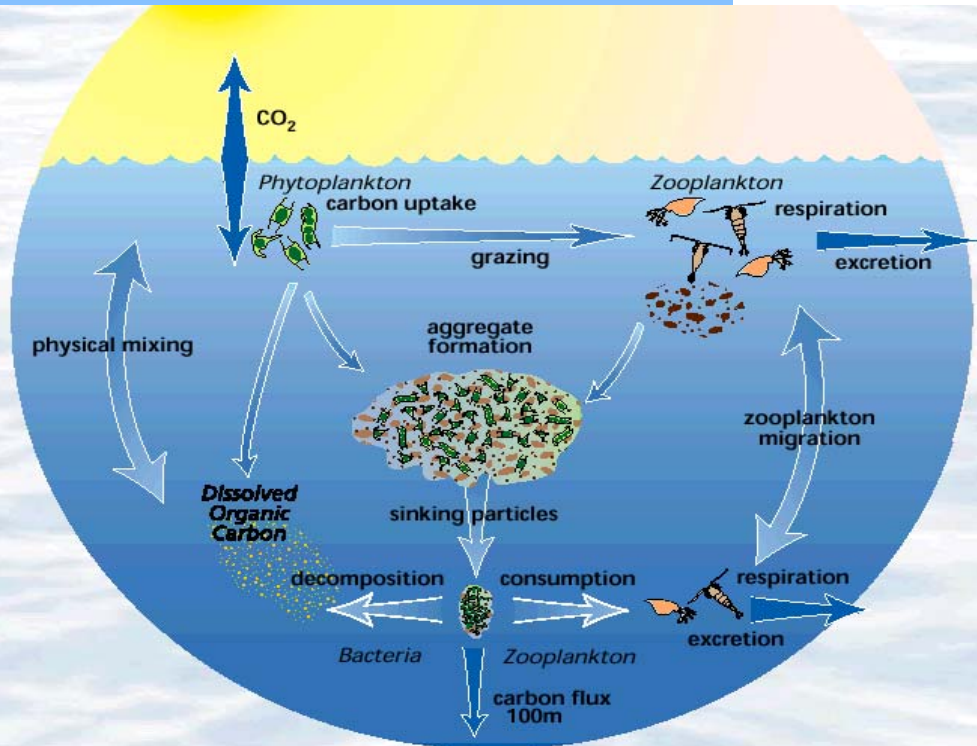
Dissolved Organic Material
C, N, P, Fe

Iron

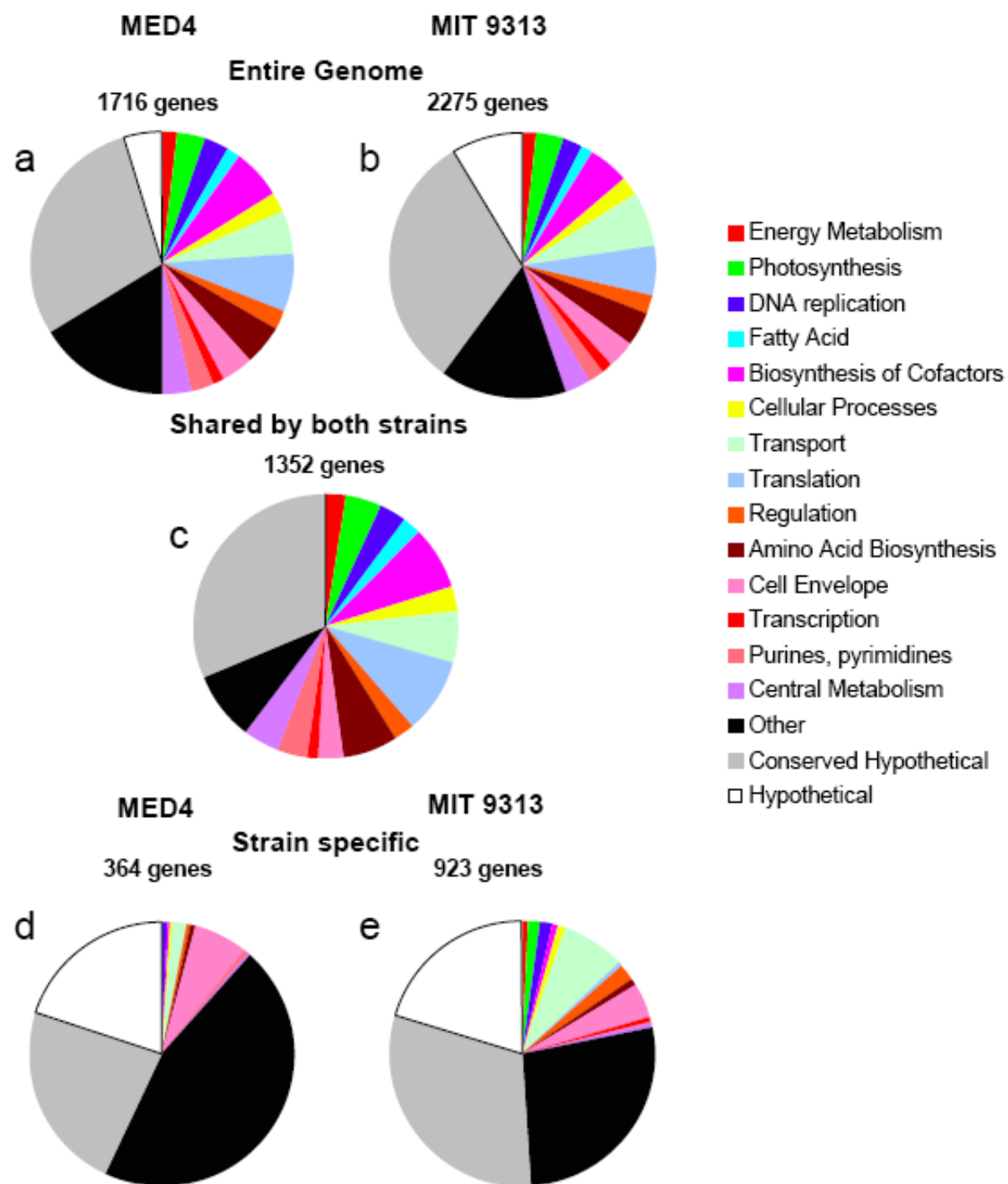
Sinking Particulate Material
C, Fe, Si, CaCO₃, Dust

Phosphate

Silicate



- Population dynamics based
- Multiple limiting nutrients
- Plankton community structure (size, geochemical functionality)
- Embed in full global 3-D physics model



Brief Genomic Tutorial



-Diversity
(DNA, rRNA)
-Metabolic
pathways
-Genetic
potential
“genotype”

-Gene Expression
-Response to
environmental
forcing

-Proteomics
-Physiological
Rates
-“Phenotype”