

# GeoMICS:

## Global scale Microbial Interactions across Chemical Surveys



Jim Moffett, Eric Webb, Chris Suffrige, Sergio Senudo-Wilhemly, Jagruti Vedamati (USC), Ben Twining, Mike Sieraki, Ramunas Stepanauskas, Pete Countway, Sara Rauschenberg (Bigelow), A.J. Limardo, Alex Worden (MBARI), Randie Bundy, Kathy Barbeau (Scripps), Tim Mattes (U. Iowa), Alyssa Kent, Adam Martiny (UC Irvine), Curtis Deutsch (UW), Craig Carlson (UCSB), Bryn Durham, Mary Ann Moran (UGa), Bethany Jenkins, Dreux Chappel, Leanne Pritchard (URI), Ginger Armbrust, Anitra Ingalls, Bob Morris, Francois Ribalet, Gabrielle Rocap, Michael Carlson, Jaci Saunders, Rachel Horak, Katherine Neal, Gwenn Hennon, Helena van Tol, Jarred Swalwell, Sara Bender, Tony Bertagnolli, Wei Qin, Dave Stahl, Al Devol, David French, Laura Truxel, Bill Howe, Dan Halperin, Konstantin Wietz (UW), Ben van Mooy, Patrick Martin, Mak Saito, Liz Kujawinski, Winn Johnson (WHOI), Greg Cutter, Chris Powell (ODU), Simone Alin (NOAA PMEL), Jessica Green (UO), Adrian Marchetti, Kim Delong (UNC), Ann Pearson, Hilary Close, Sarah Hurley, Naomi Levine (Harvard), Karen Casciotti (Stanford), Carl Cerrano (SDS), Astrid Gaerdes (MPI) , Mick Follow (MIT)

## A brief history...

Nov, 2010: NSF OCB-sponsored workshop:

“The Molecular Biology of Biogeochemistry: Using Molecular Methods to Link Ocean Chemistry with Biological Activity”

Jim Moffett, Eric Webb

Establish a “stand-alone sectional survey program in microbial biogeography...[with] GEOTRACES [as] a good model ... inclusive process for designing [a] program and securing funding, as well as establishing an infrastructure for intercalibration and data management

Implement “pilot study linking high-resolution metagenomic sampling with high-resolution sampling for GEOTRACES core parameters across pronounced gradients”



## May, 2012: GeoMICS is launched

1 week cruise on the R/V Thompson along subset of Line P

- Identify interactions between changes in microbial diversity, community functions, and chemical features across a gradient
- Coordinate sampling protocols: inorganic geochemistry, organic geochemistry, and molecular biology



# Data from cruise (31 different labs)

## Physics/chemistry along transect

Model of surface water movement at time of transect based on ADCP, surface altimetry

Regional model of average water movement at time of year

[Chl], [O<sub>2</sub>], nutrients [NO<sub>3</sub>, NO<sub>2</sub>, NH<sub>4</sub><sup>+</sup>, PO<sub>4</sub>, Si], carbonate chemistry

TOC, DOC, POC

Temperature, salinity, chlorophyll fluorescence

Total dissolved Mn, Fe, Cu, Zn, Cd

Total refractory & labile Mn, Fe, Cu, Zn, P, Al, Cd, Mo, Co, Ti, V, Ni

## Diversity:

Underway and traditional flow cytometry for phytoplankton

16S and 18S diversity (tag sequences)

Diatom species counts

Distribution of *Thalassiosira* species (ARISA)

Distribution of *Pseudo-nitzschia* species (ARISA)

Quantitative counts (qPCR) of *Bathycoccus*, *Ostreococcus*, *Synechococcus* Clades I, IV

Viral counts (Sybr-stained)

Cell counts for DAPI-stained prokaryotes, FISH-based for bacteria/archaea,

GDCT concentrations and types (archaeal lipids)

Metagenomics of marine aerosols

Metagenomes (0.2-1.6)

# Data from cruise (31 different labs)

## Organismal readouts of chemical environment:

Photosynthetic efficiency of phytoplankton: Fv/Fm (FIRe)

Expression of diatom *Thalassiosira oceanica* flavodoxin as indicator of Fe limitation  
Fe, Cu ligand data

Total cellular Mn, Fe, Ni, Zn, S, C in different diatom taxa

Photoreactive siderophore gene abundances (*Marinobacter*, *Vibrio*, *Xanthomonads*)

μDOC

Intact polar diacylglycerolipids (9 classes)

*Synechococcus*-specific lipidomics

Glycolipid and phospholipid fatty acids  $\delta^{13}\text{C}$  values for different size classes.

Metatranscriptomics: prokaryotes (0.2-1.6); eukaryotes (1.6-53); eukaryotes (<1.6)

Metaproteomics: prokaryotes (0.2-1); eukaryotes (>1)

Targeted metabolomics (LCTSQ) prokaryotes (0.2-1.6 μm) and eukaryotes (>1.6 μm)

Growth rate and loss rate estimates for *Synechococcus*, pico-eukaryotes based on

SeaFlow data

amoA gene counts, diversity (t-rflp)

$\text{NH}_4^+$  uptake rates

$\text{NH}_4^+$  oxidation rates

Nitrate  $\delta^{15}\text{N}$

Feb, 2013: OCB-sponsored workshop to collate/merge data

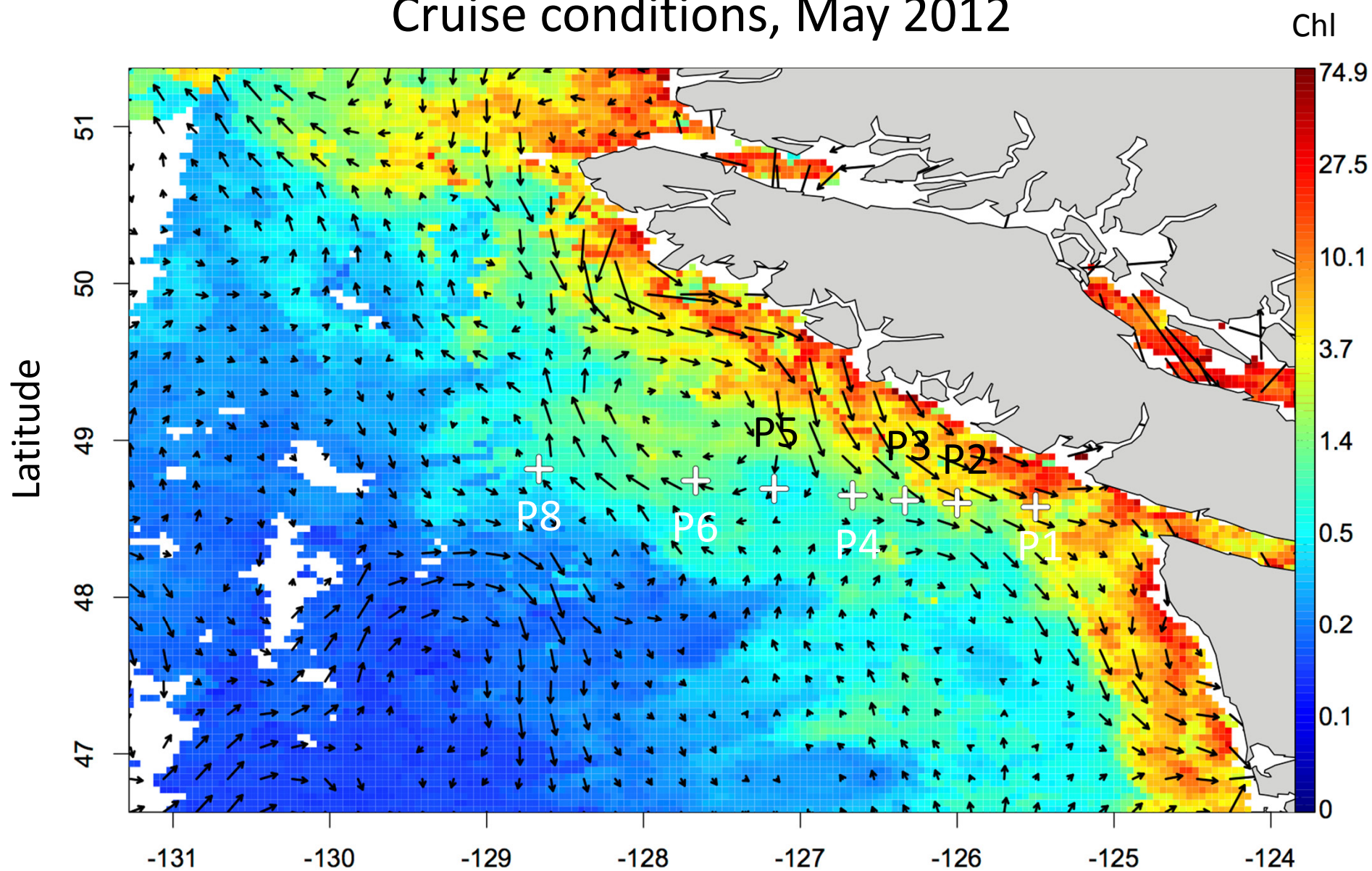
Coordinate analysis across 5 groups: inorganic geochemists, organic geochemists, molecular ecologists, modelers, computer scientists



Query across data sets in real-time – “not just faster...different!”  
UW eScience program



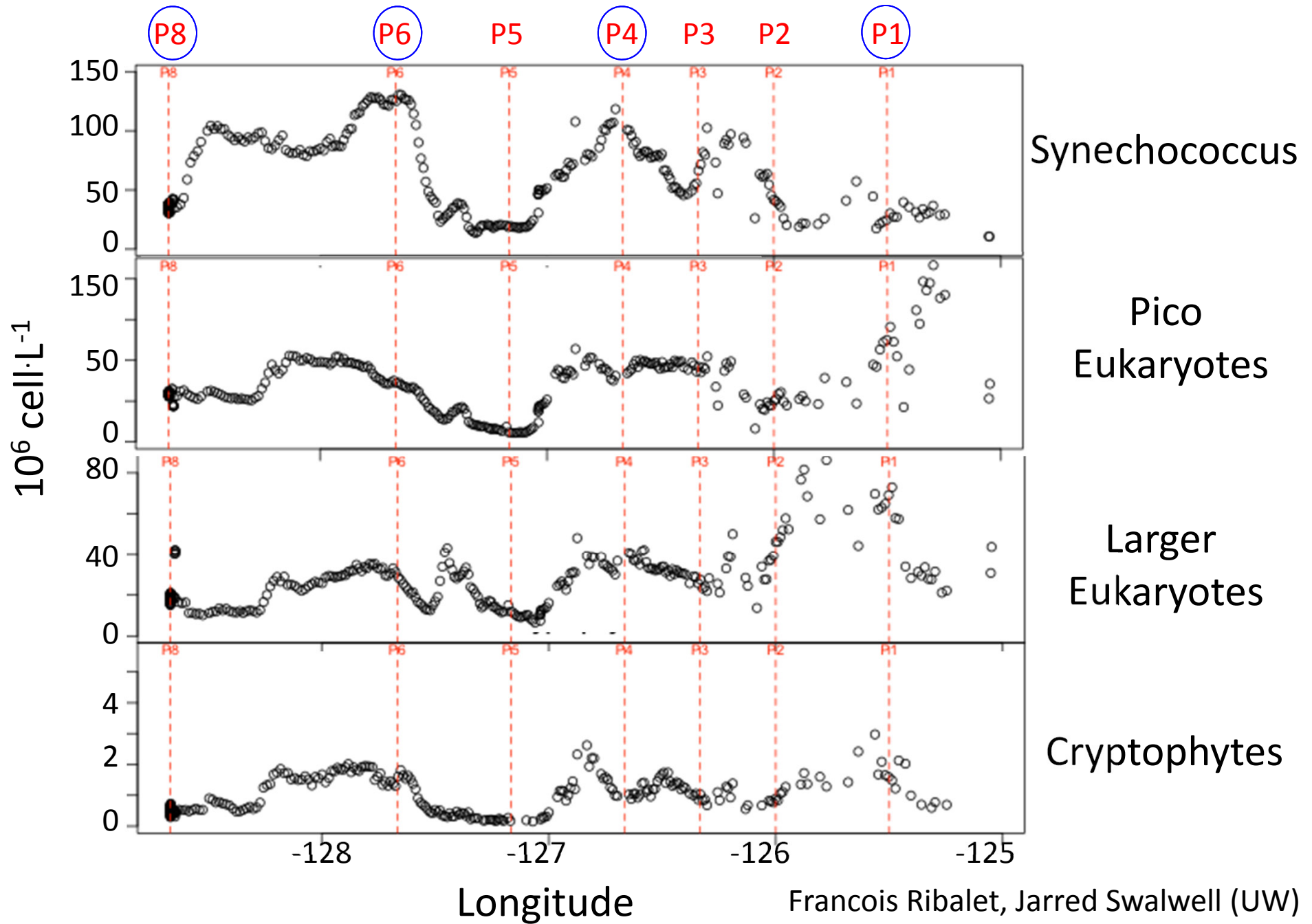
# Cruise conditions, May 2012



Francois Ribalet (UW)

Longitude

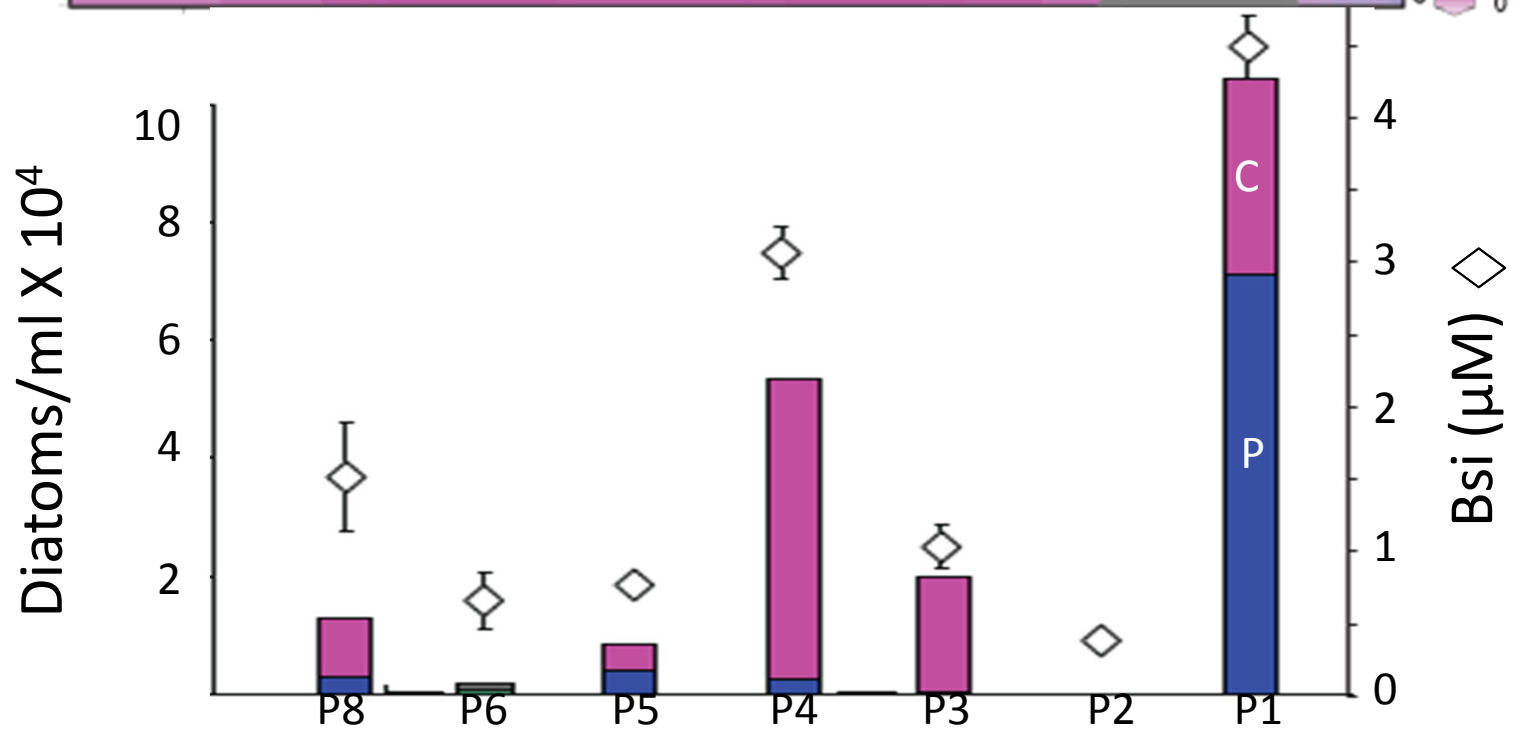
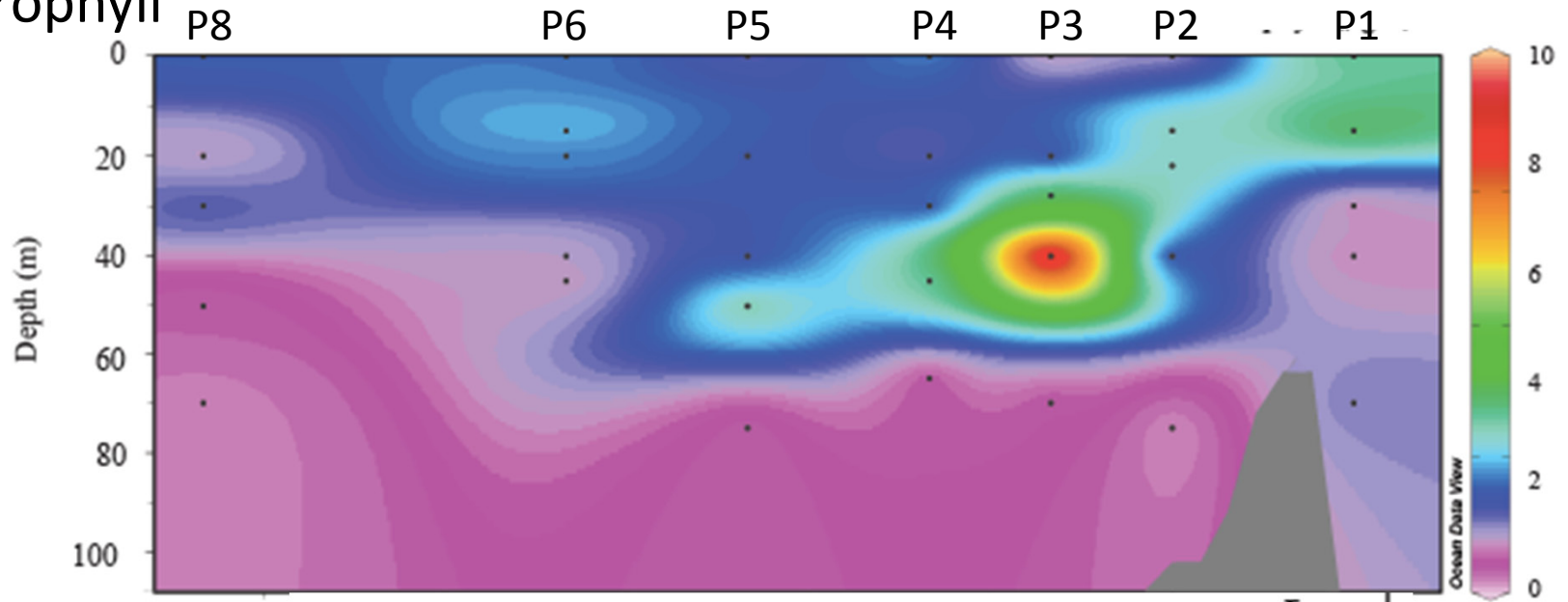
# Surface phytoplankton distributions defined sampling sites





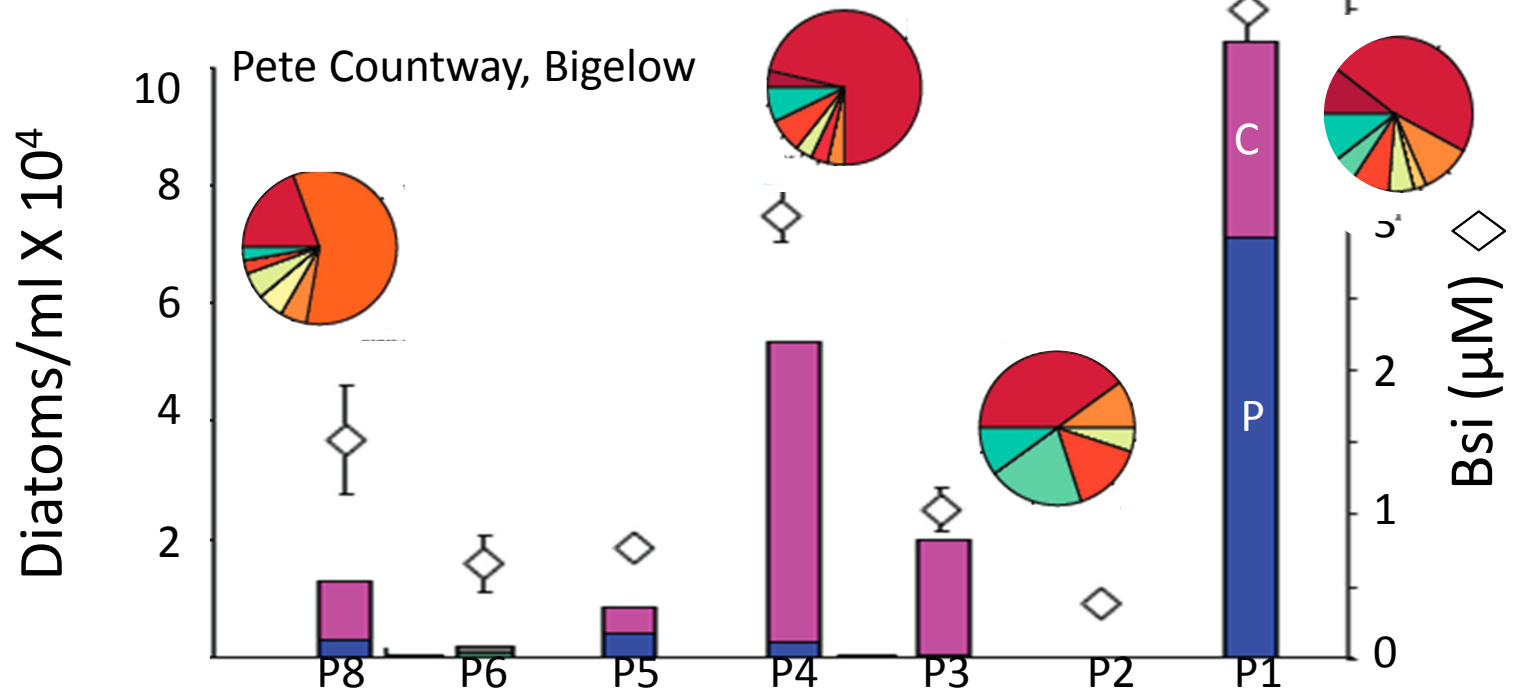
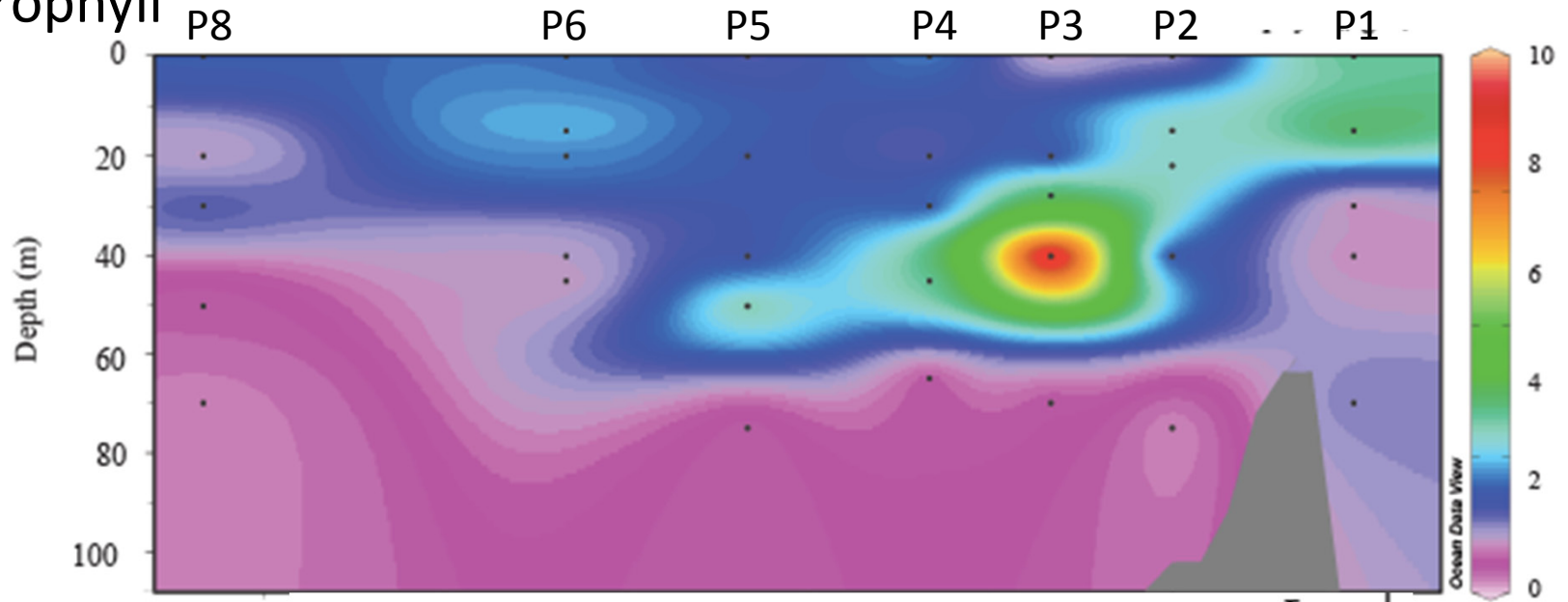
A diatom example...

# Chlorophyll



Sara Bender, Megan Schatz, UW

# Chlorophyll

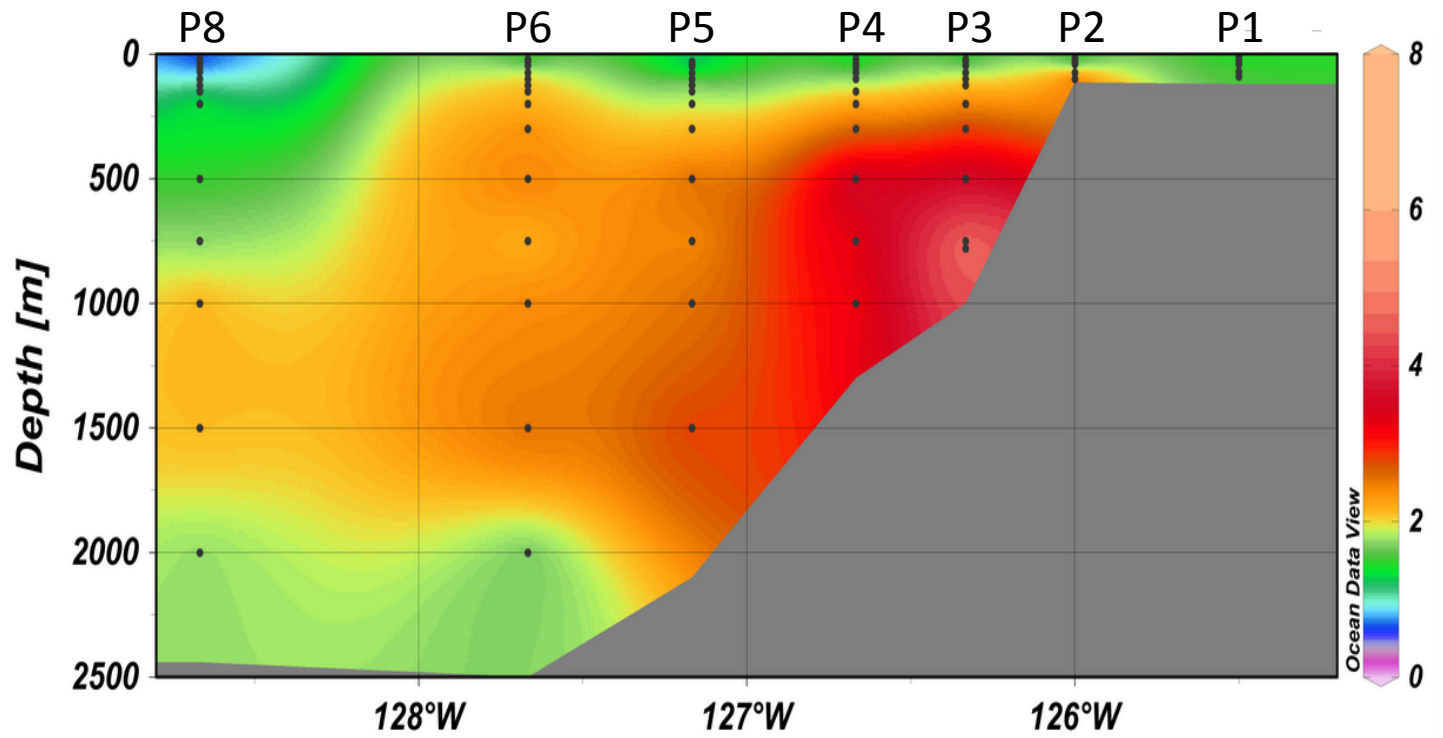


Sara Bender, Megan Schatz, UW

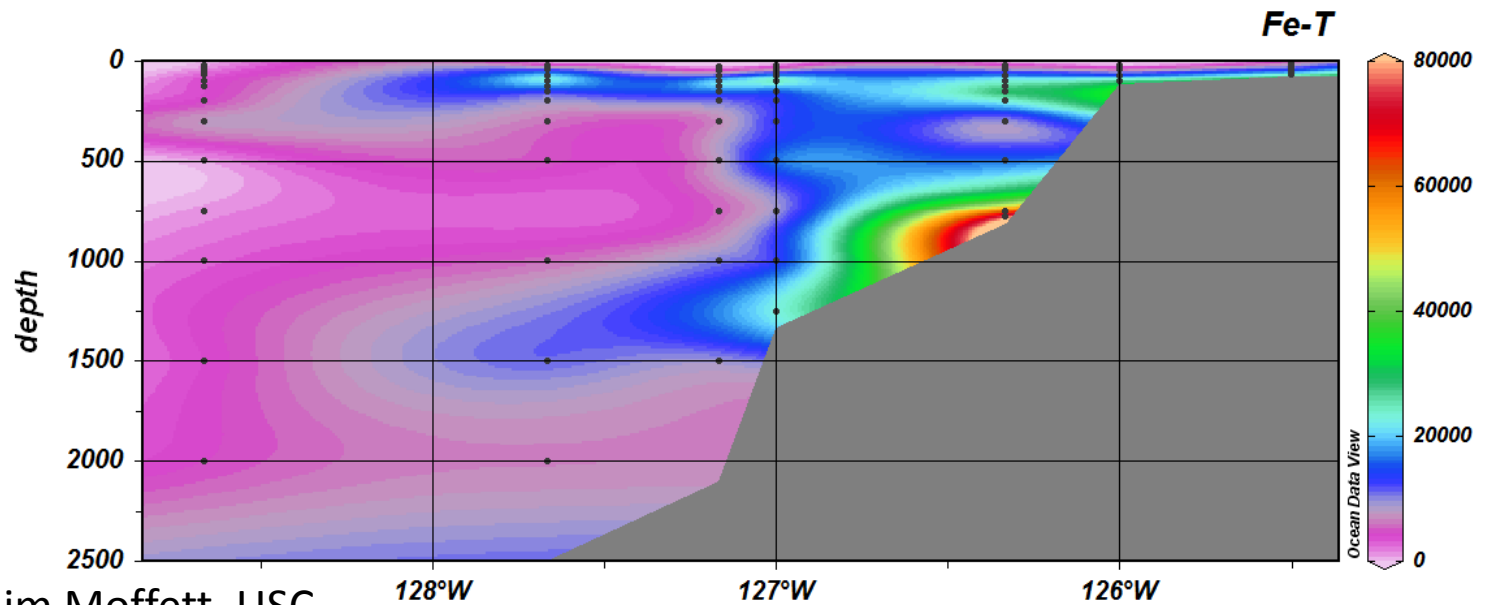


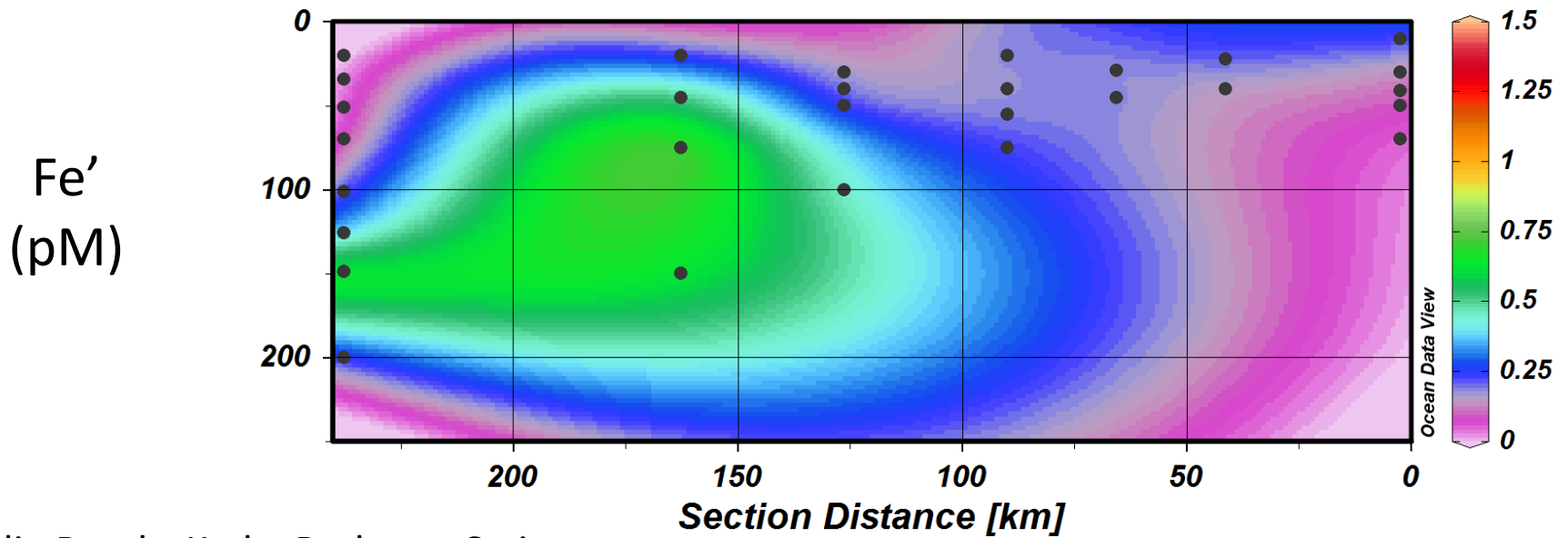
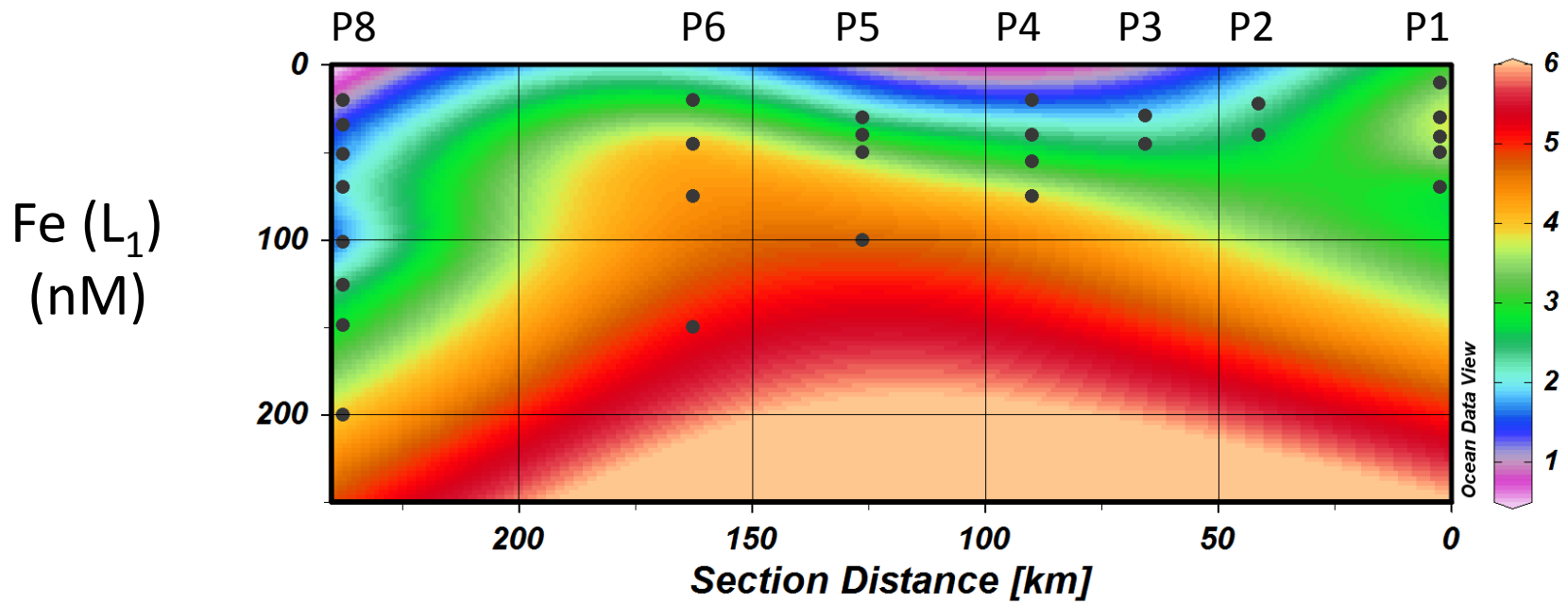
# Iron

Total dissolved  
(nM)

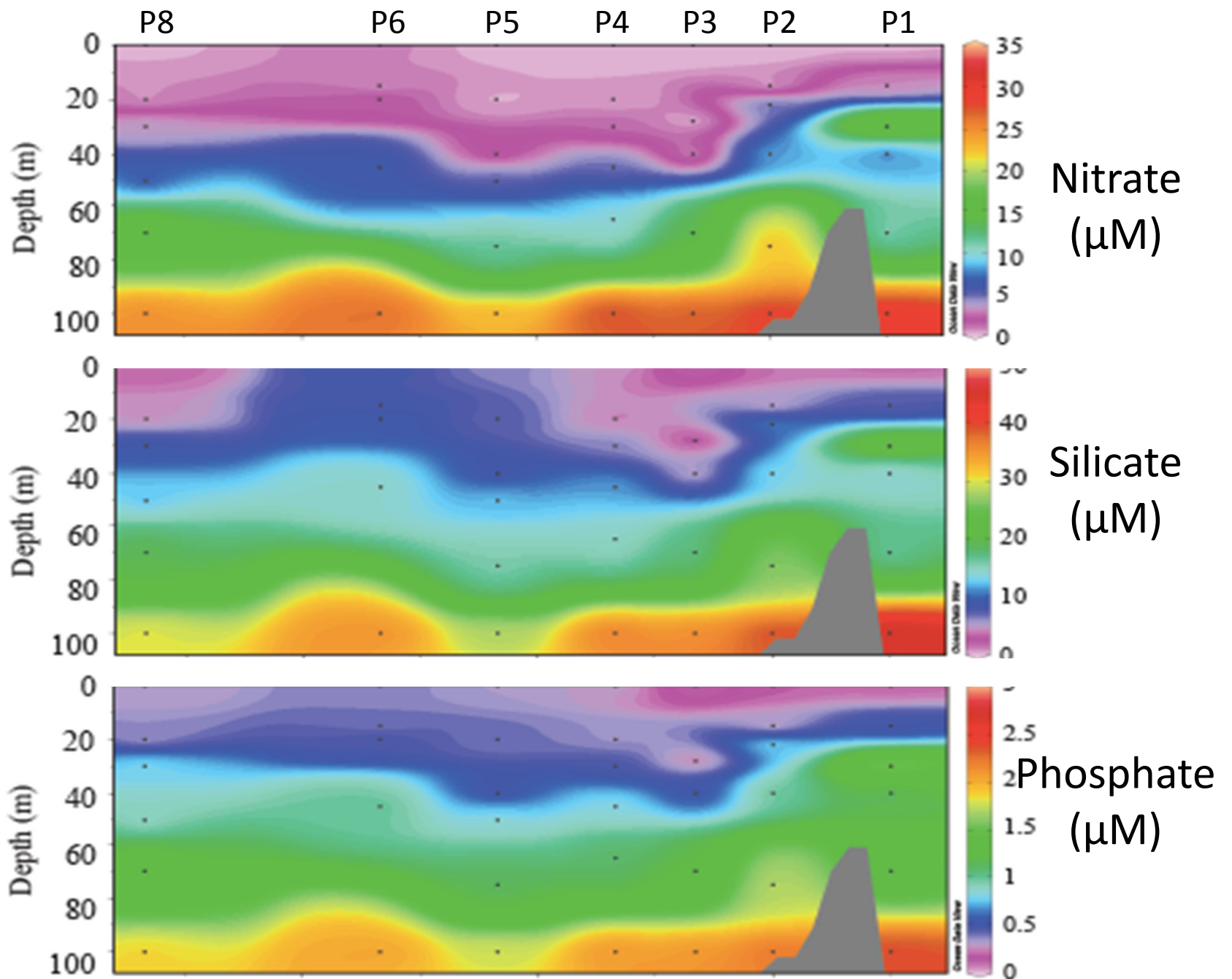


Total particula



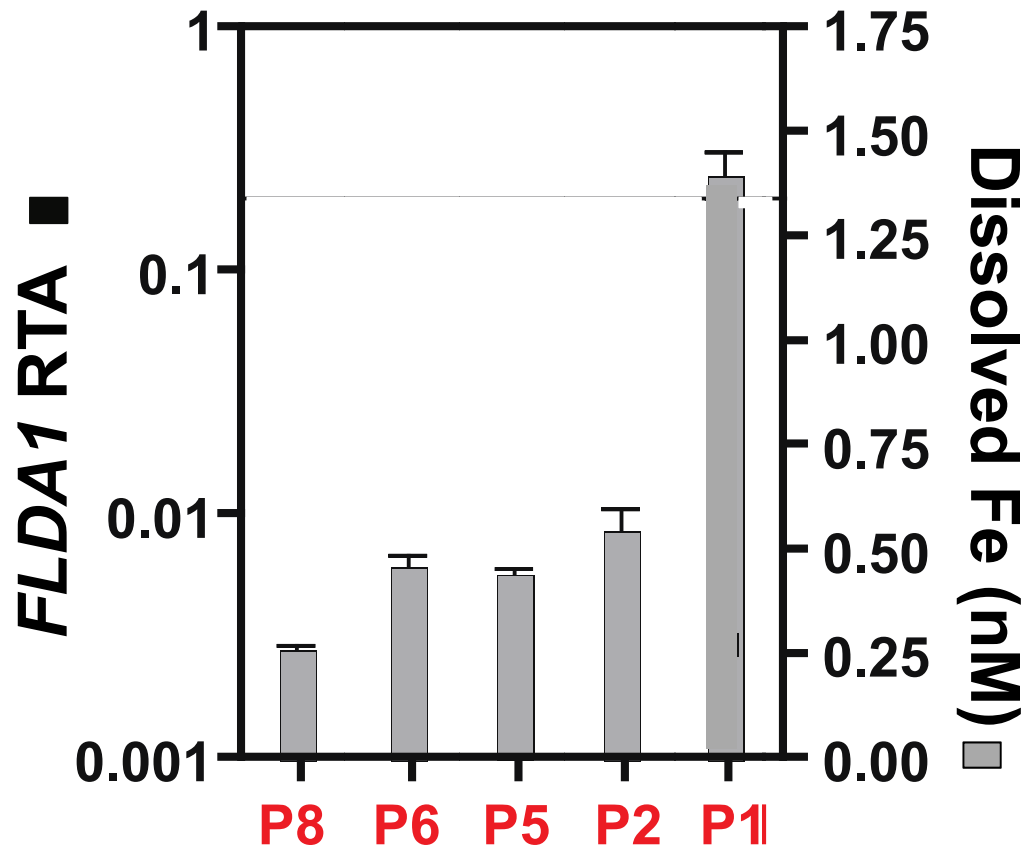


Randie Bundy, Kathy Barbeau, Scripps

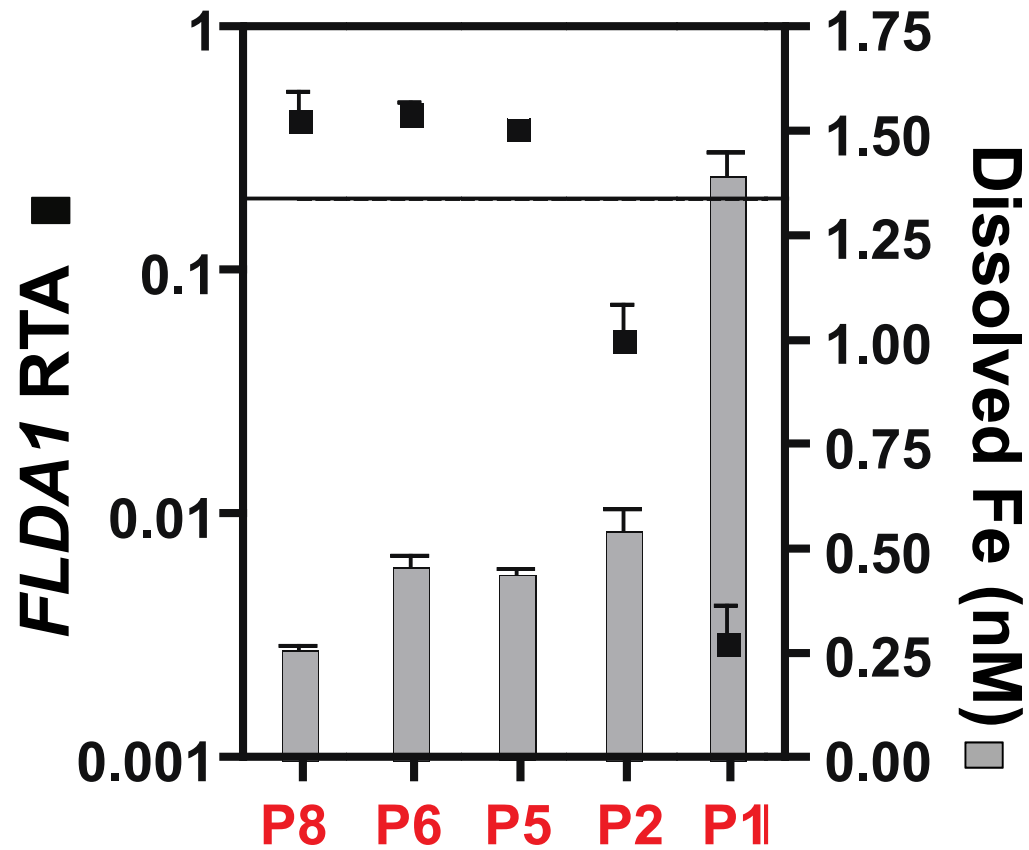




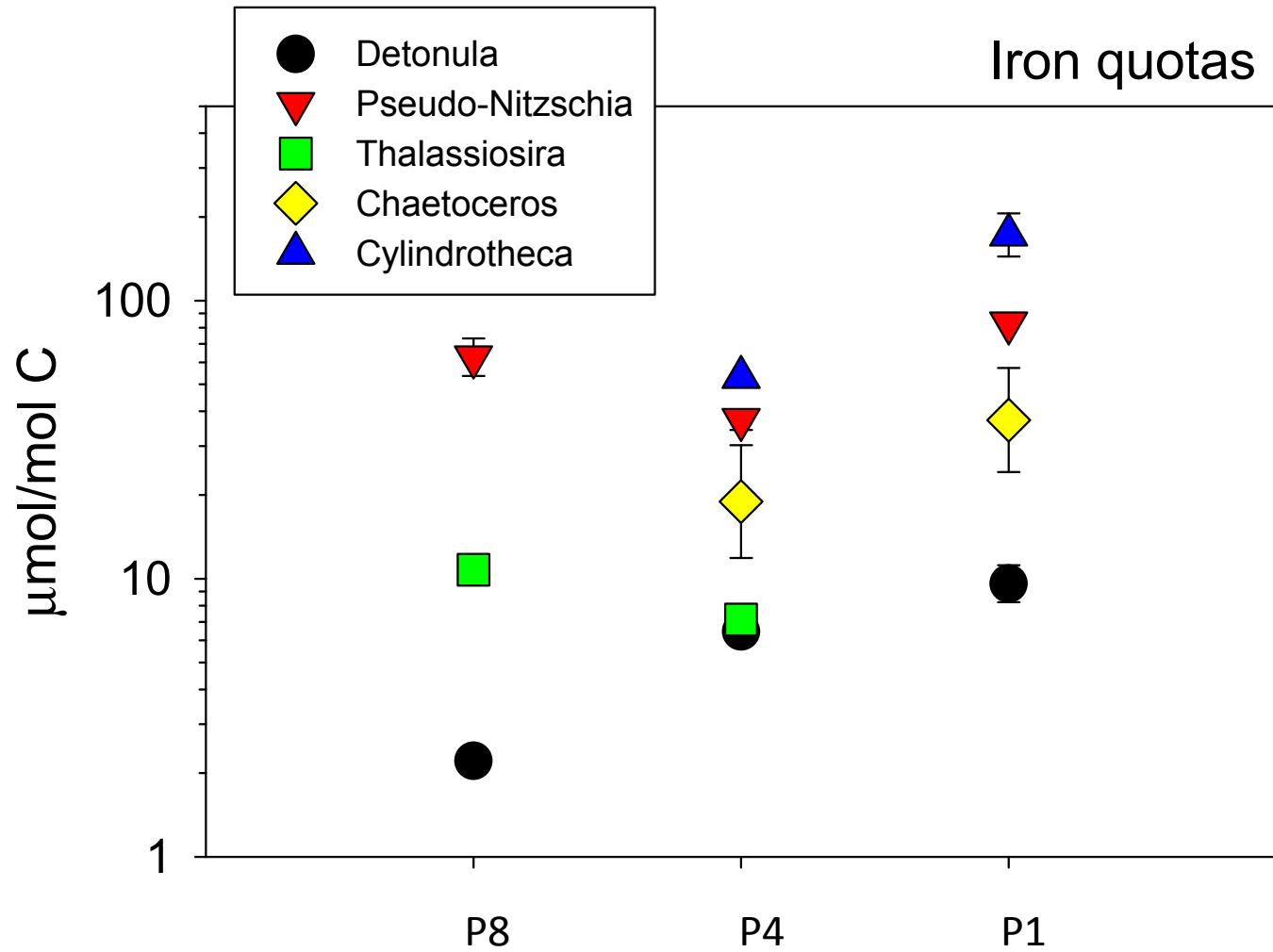
Flavodoxin transcription: indicator of iron limitation  
*Thalassiosira oceanica*



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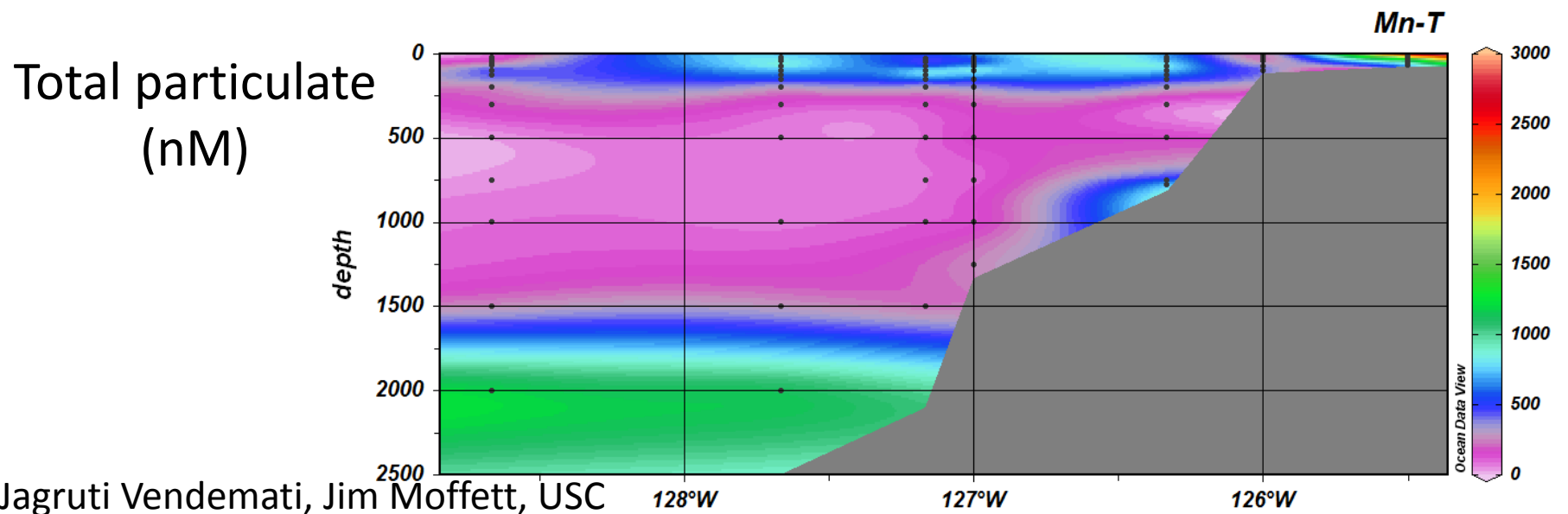
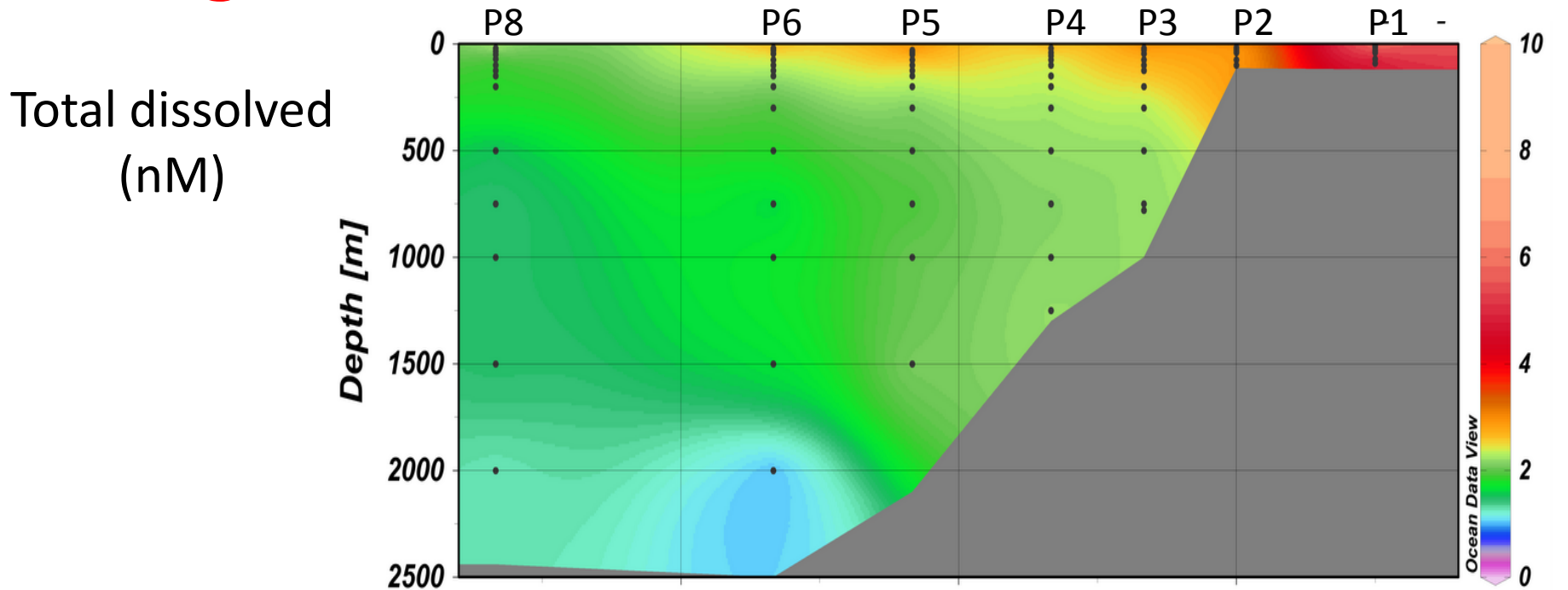


# Less iron per cell as move offshore





# Manganese



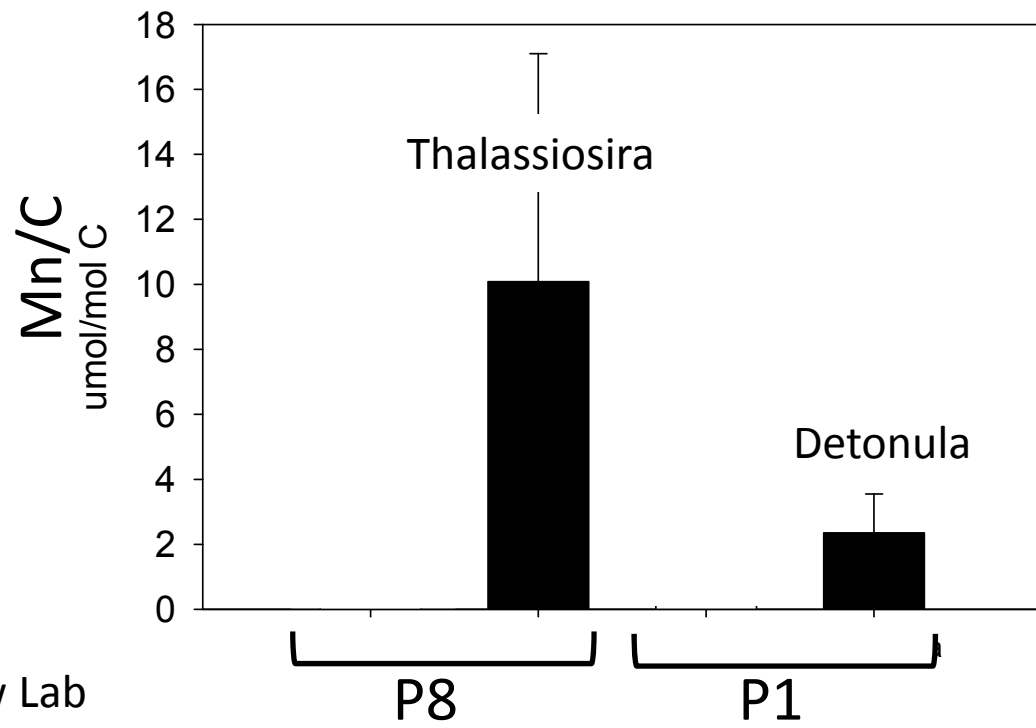
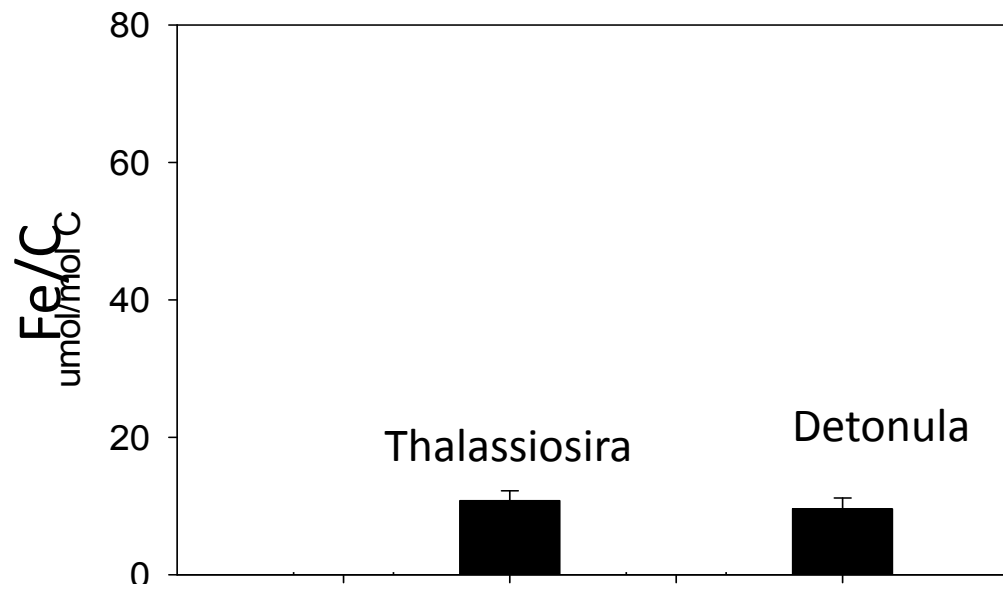
# A role for manganese in superoxide dismutases and growth of iron-deficient diatoms

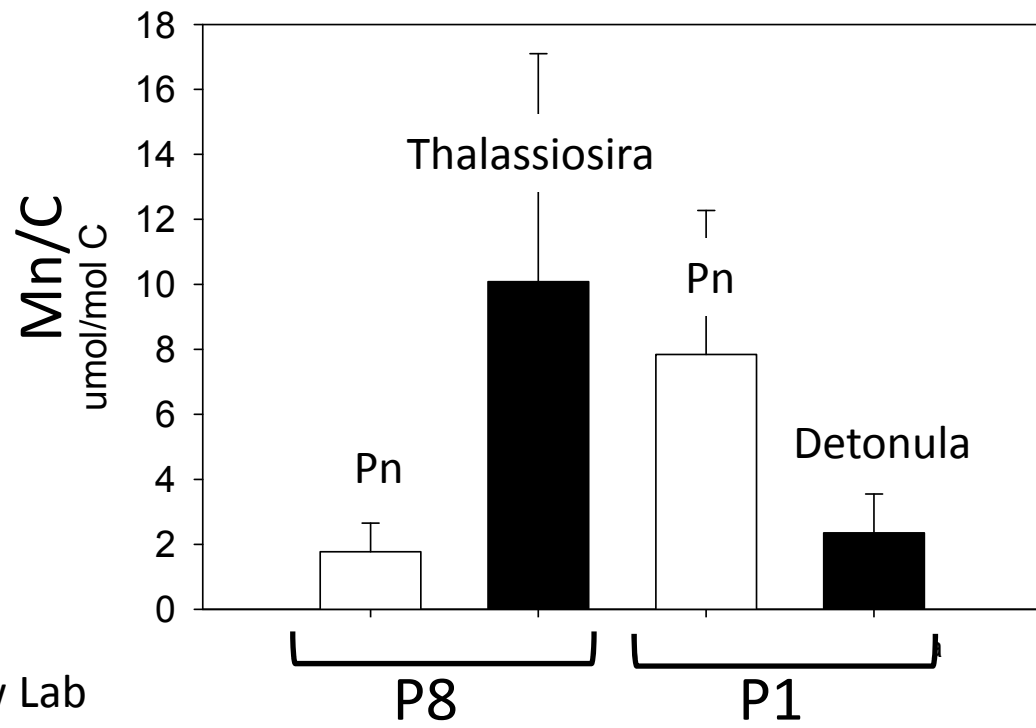
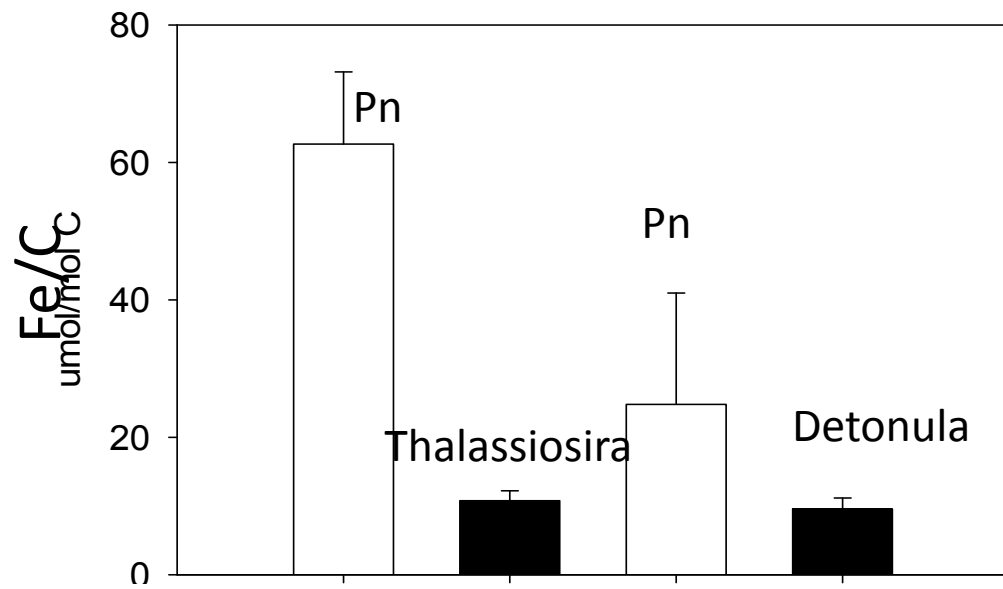
*Graham Peers<sup>1</sup> and Neil M. Price*

Department of Biology, McGill University, 1205 Avenue Dr. Penfield, Montreal, Quebec, H3A 1B1

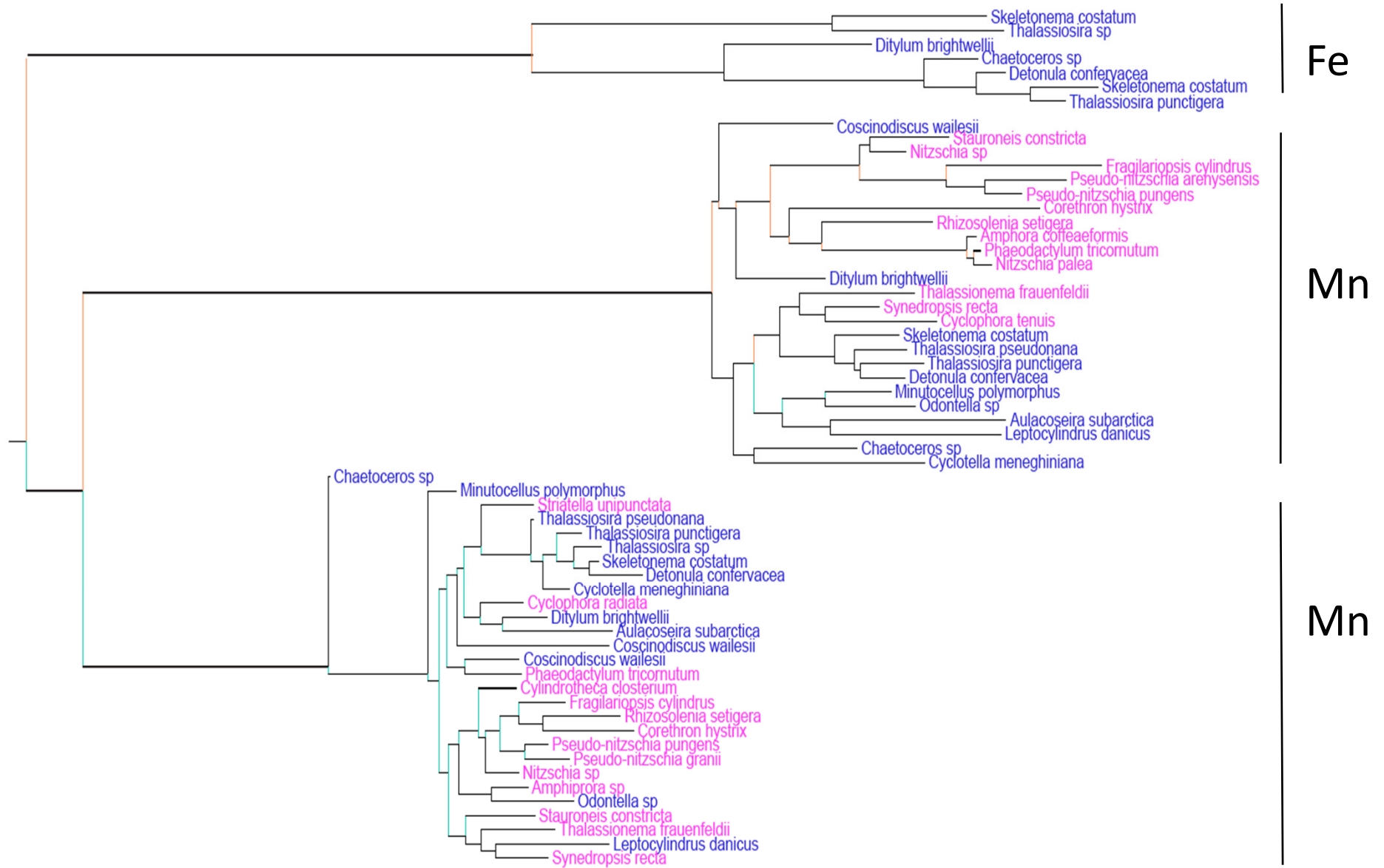
*Limnol. Oceanogr.*, 49(5), 2004, 1774–1783

coastal and oceanic diatoms require more manganese (Mn) to grow in iron (Fe)-deficient than in Fe-sufficient seawater. ...SODs [superoxide dismutase] contain Mn and may account for part of the observed increase in the Mn quota. Such an increased biochemical requirement may elevate the Mn content of low Fe diatoms...resulting in high Mn: Fe ratios in particulate matter in Fe-limited regions of the sea.





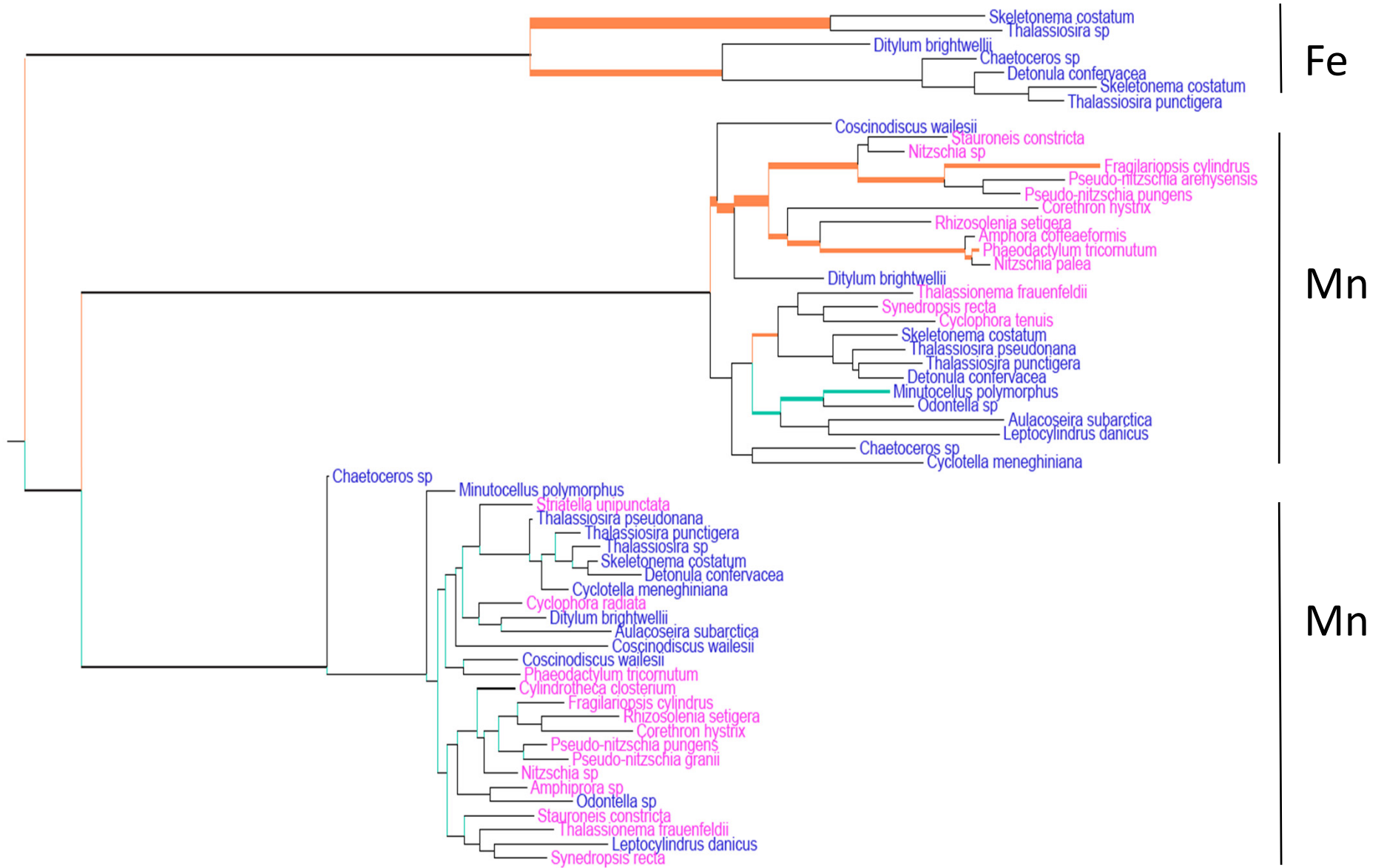
# Diatom super oxide dismutase



Ryan Groussman, Micaela Parker, Sara Bender, UW

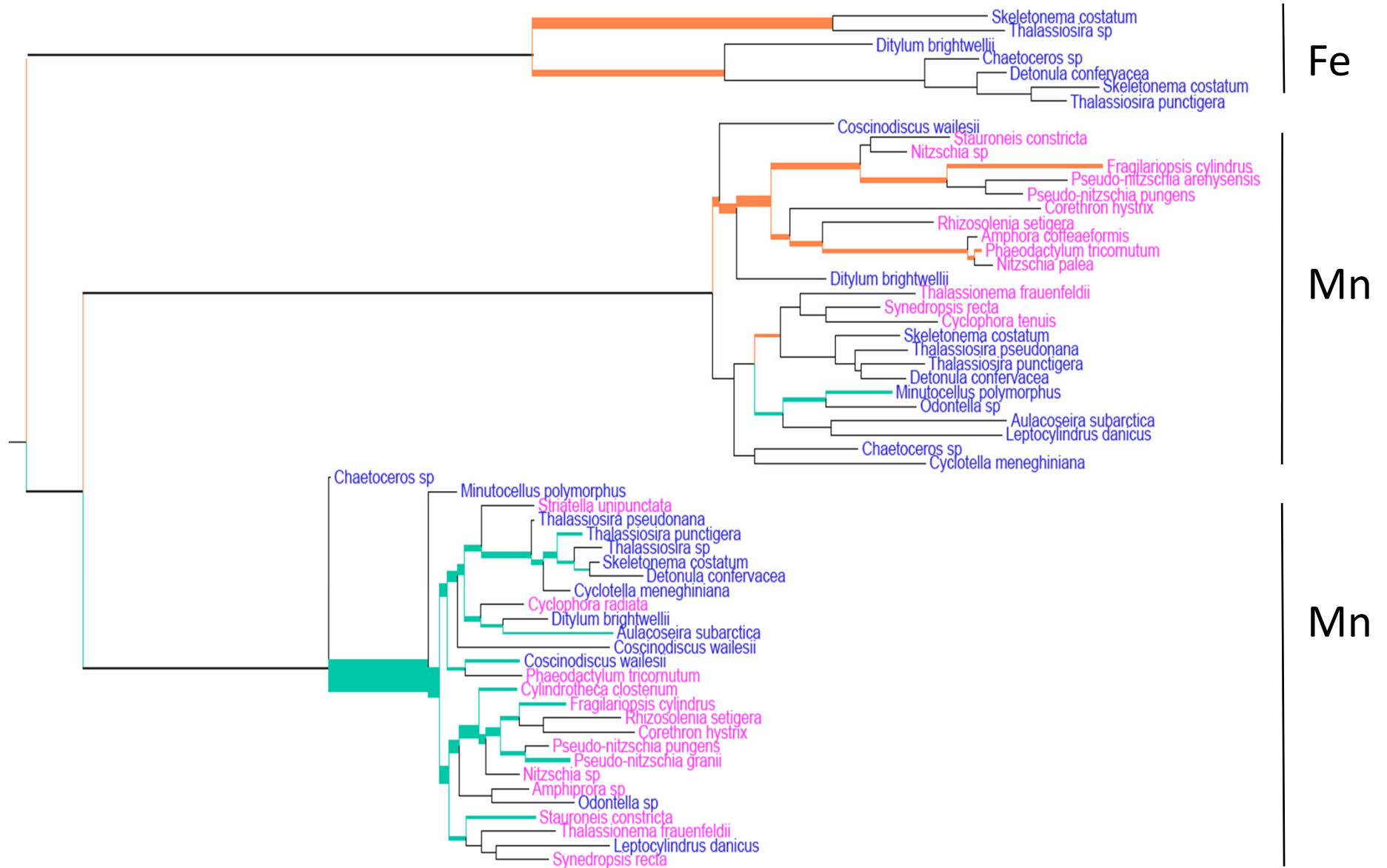


# Diatom super oxide dismutase



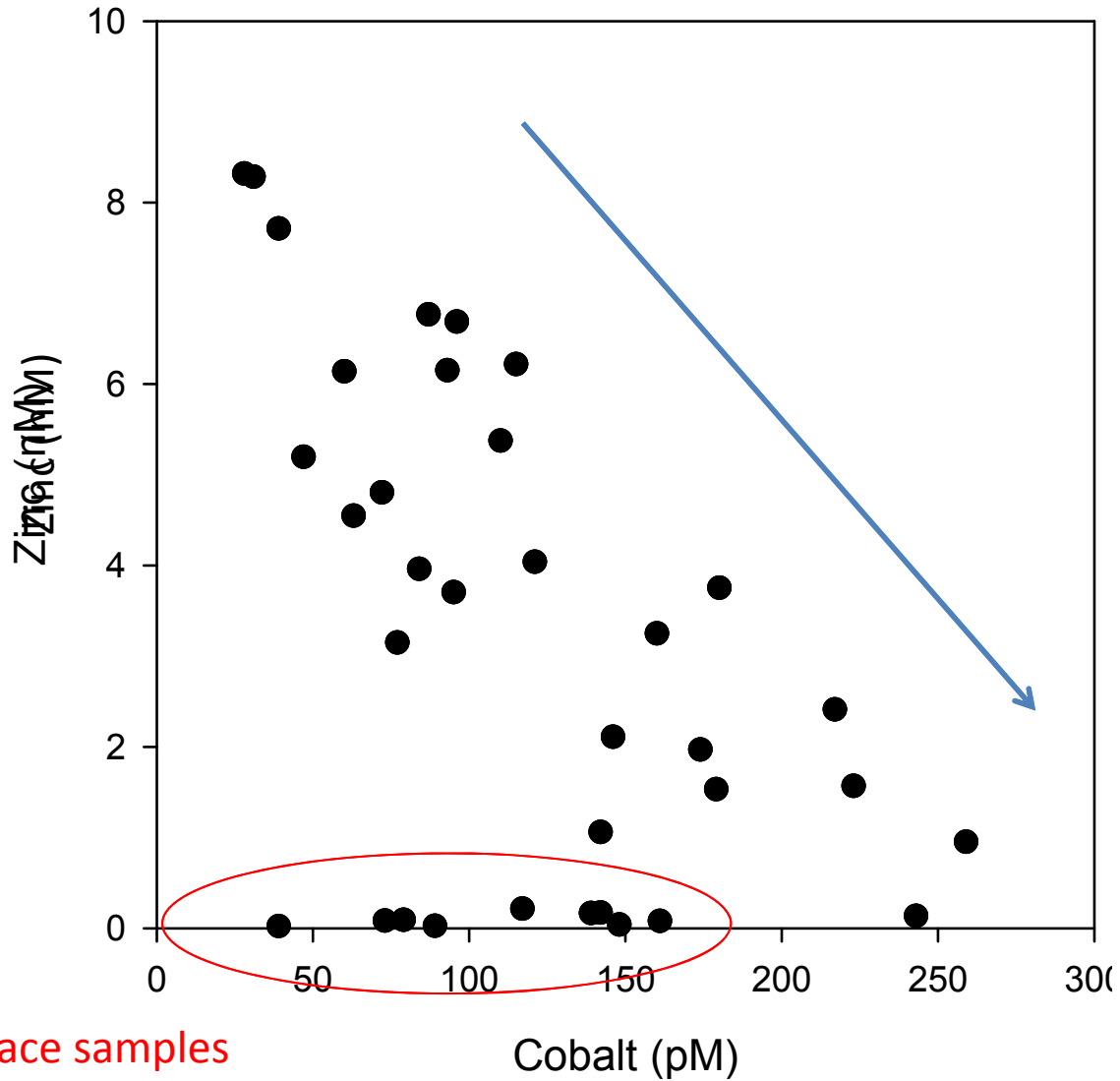
Ryan Groussman, Micaela Parker, Sara Bender, UW

# Diatom super oxide dismutase



Ryan Groussman, Micaela Parker, Sara Bender, UW

Substitution of Co for Zn?  
Diatom signature? (prefer Zn to Co)



Carbonic anhydrase  
Alkaline phosphatase

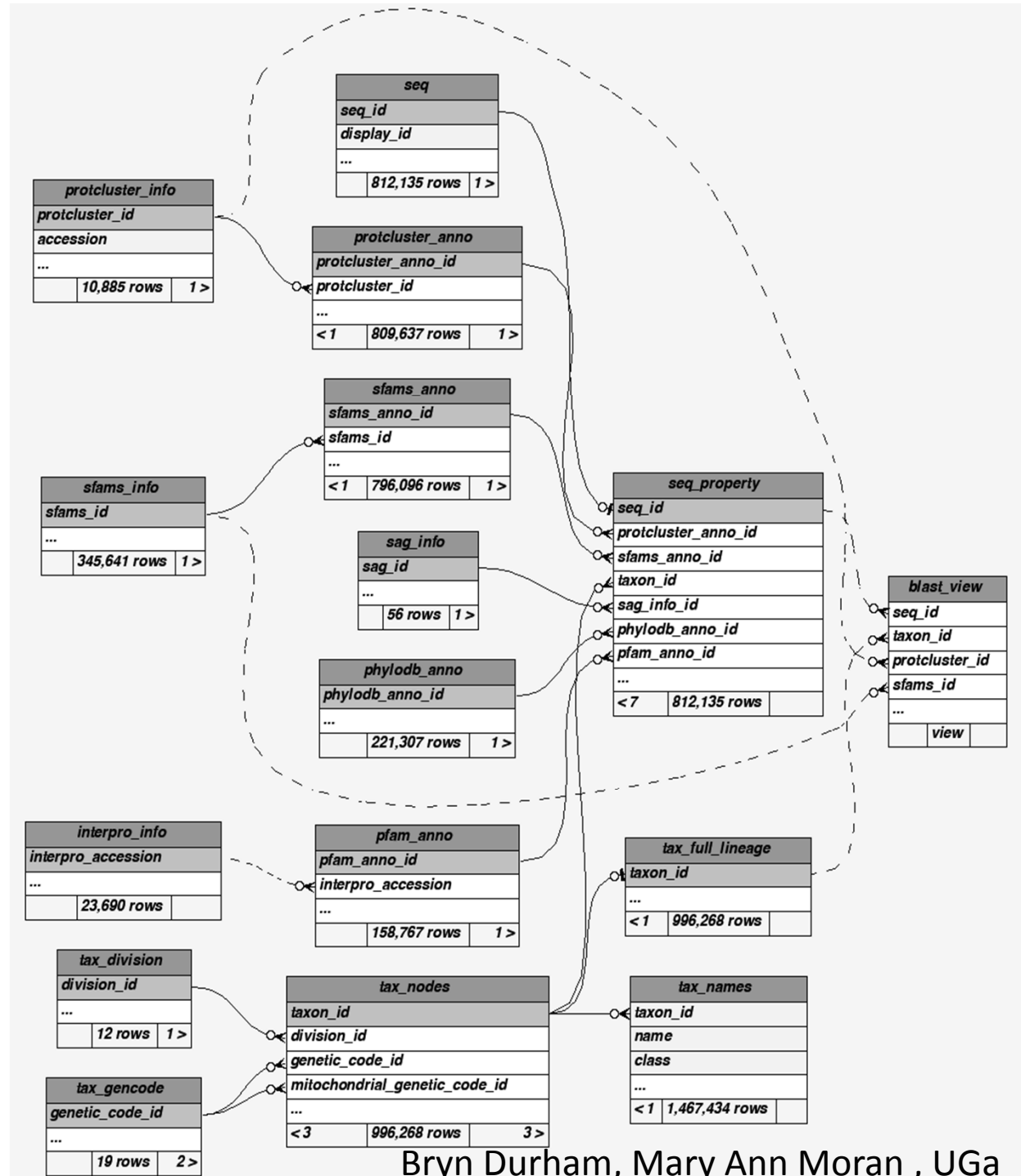
# GeoMICS In-House Database Schema

SQL database

- Sfams (Sharpton et al. 2012)
- ProtClustDB (NCBI)

812,135 proteins and growing

Public prokaryote genomes	108
Single amplified prokaryote genomes	63
Moore Marine Microeukaryote EST datasets	15/85
Public eukaryotic genomes	29
Public EST datasets	10



Bryn Durham, Mary Ann Moran, UGa

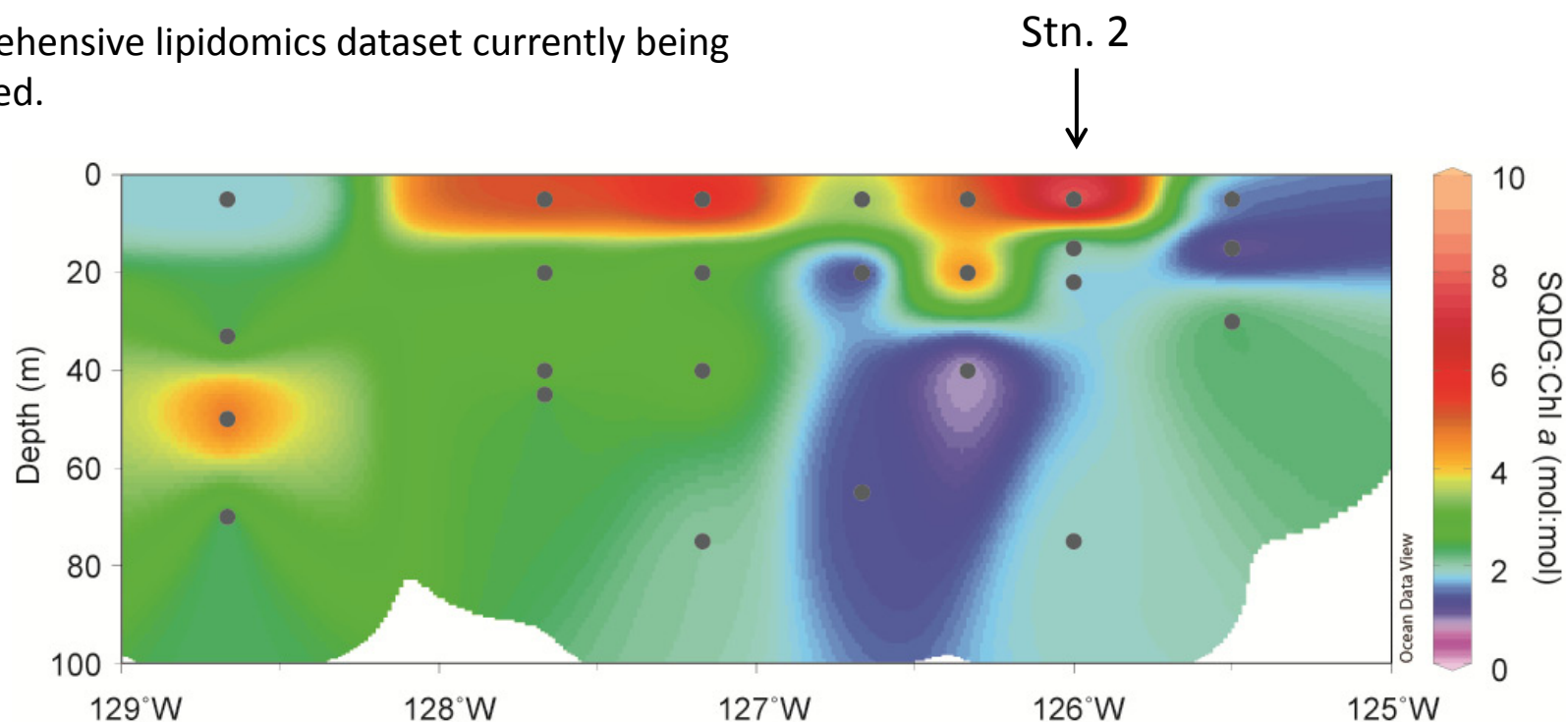
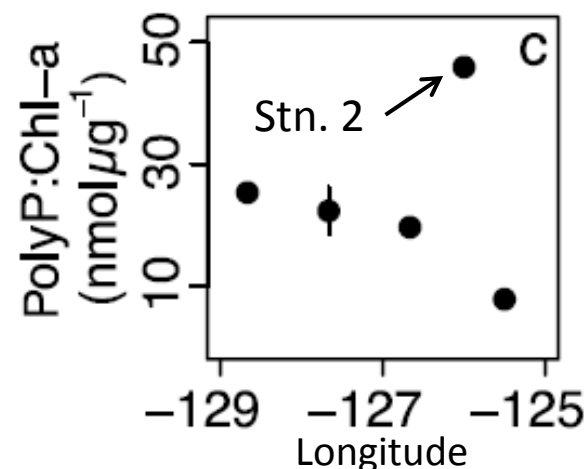
Concentrations of IP-DAGs (100+ different molecules) were determined across the transect.

Polyphosphate quantified in surface samples only.

Two of the clearest signals are at Station 2.

- High SQDG/Chl-*a*
- High Poly-P/Chl-*a*
- Both signals are indicative of nutrient stress and characteristic of oligotrophic gyre communities.

Comprehensive lipidomics dataset currently being collected.





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