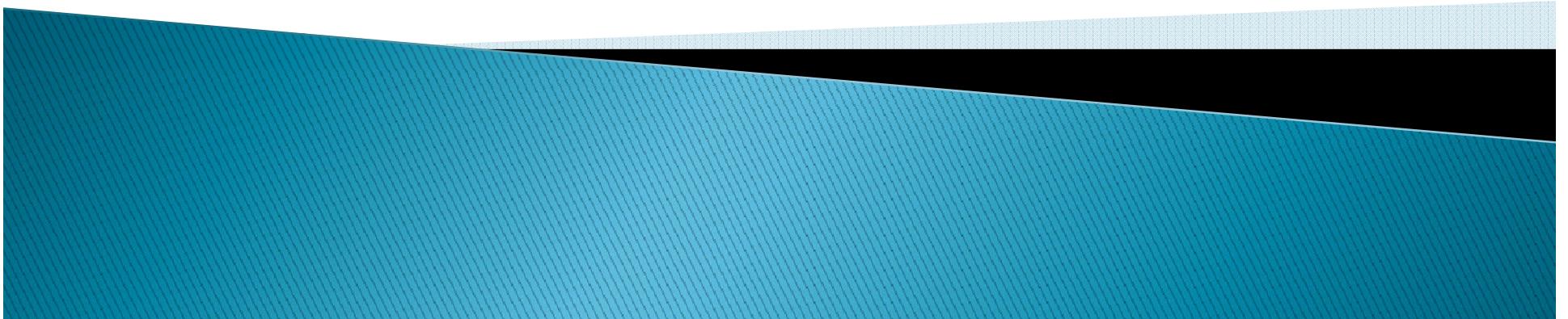
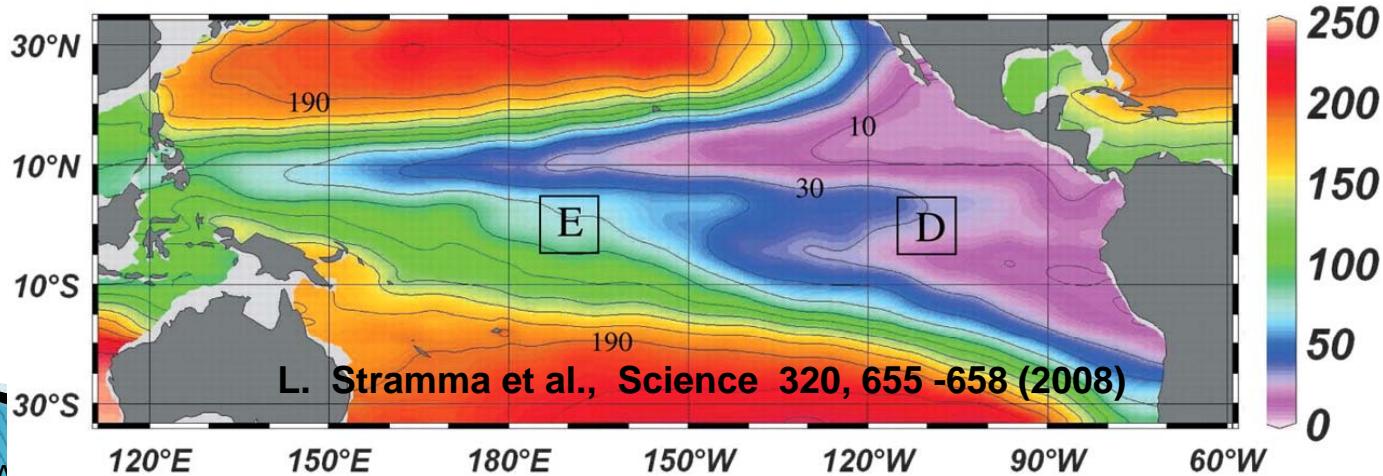
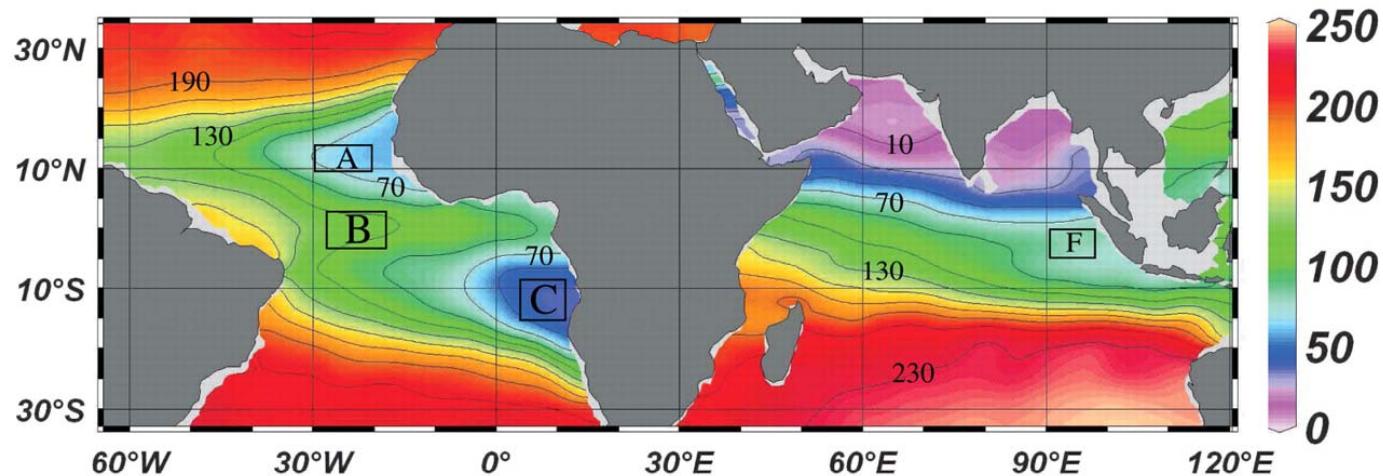


# **The evolving story of microbial nitrogen cycling processes in low oxygen zones**



# Oxygen minimum zones may be expanding

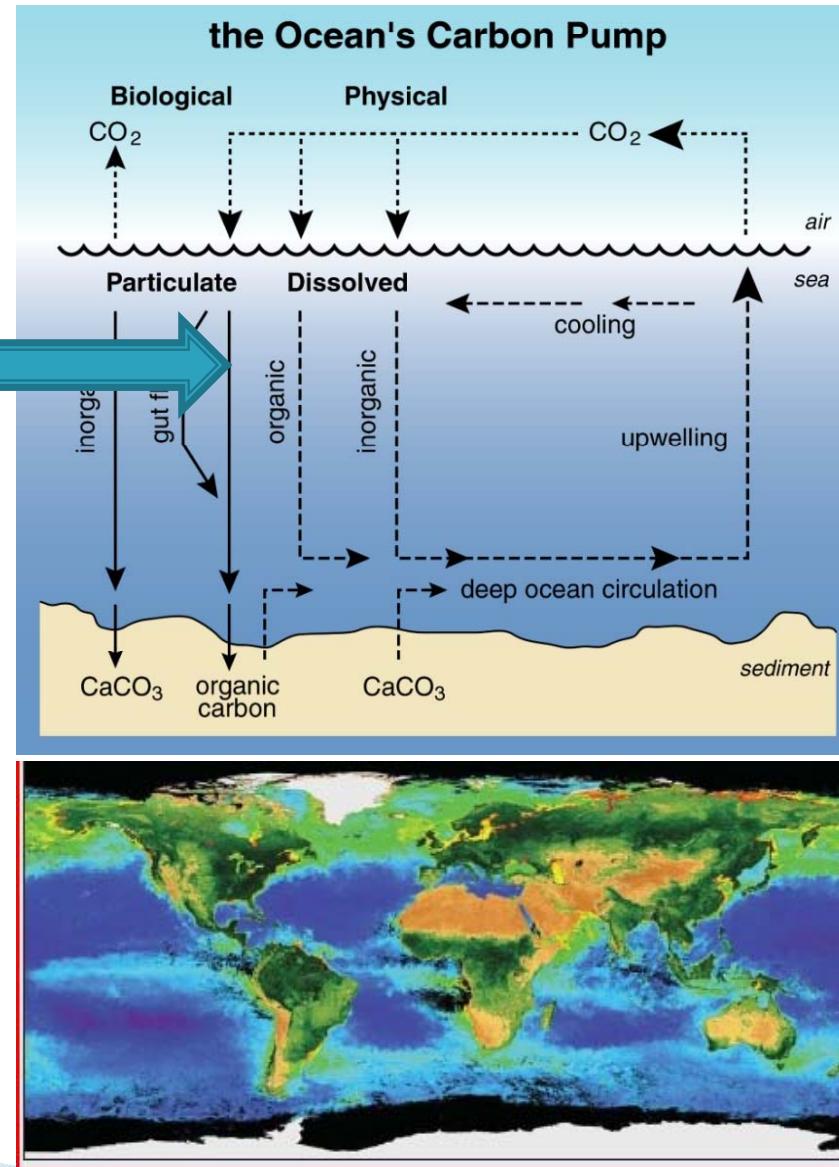
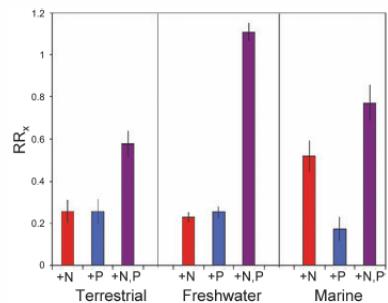
Local phenomenon with global consequences  
Global balances of nitrogen



# N important in global ocean carbon cycling

Nitrogen      Nitrogen fixation

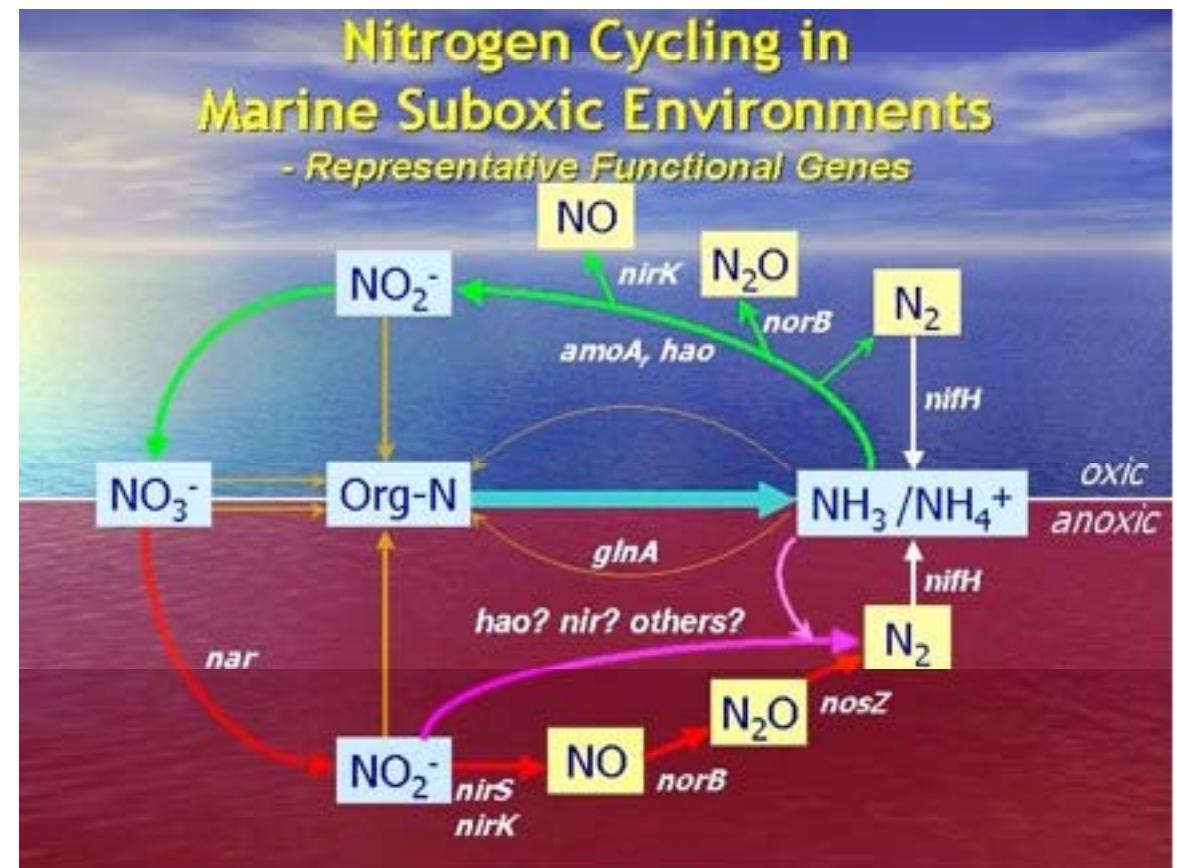
4 J. J. Elser et al.



# Low oxygen zones and the N cycle

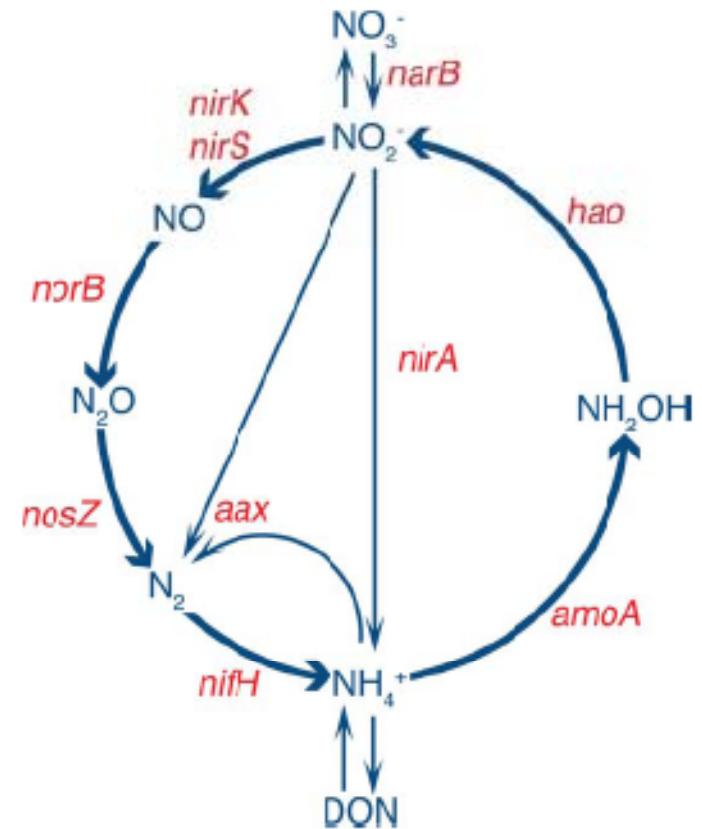
Link between  
oxygen depletion  
and nitrogen

Oxygen determines  
metabolic  
pathways  
involving N as  
electron acceptor  
or donor



# Microorganisms and genetic potential

- ▶ Identifying key genes
- ▶ Amo: responsible for deep water nitrate
- ▶ Annamox: important N removal process
- ▶ Nir: important N removal process
- ▶ Nrf: nitrate reduction to ammonium—important for recycling N in some environments
- ▶ Nar/Nas: important N uptake pathway for “new” production
- ▶ Nif: important N source



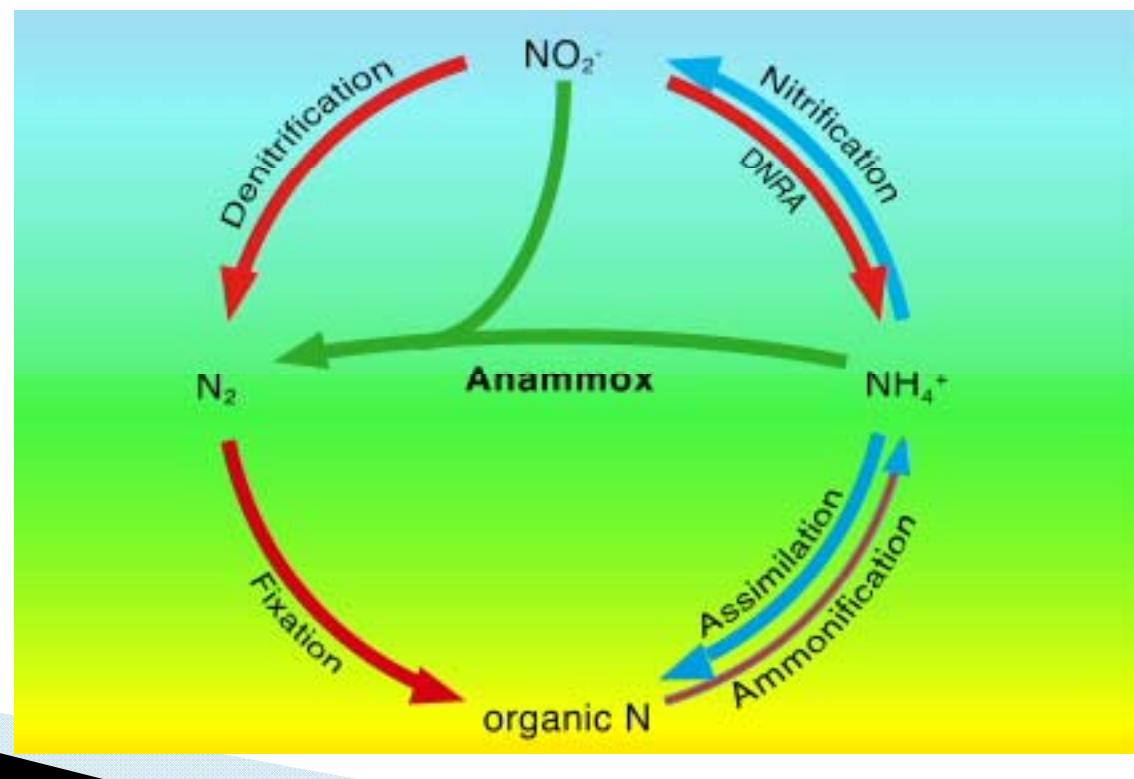
# Two controversies

- ▶ Denitrification vs anammox as major N loss pathways in oxygen depleted waters
- ▶ OMZs directly linked to nitrogen fixation



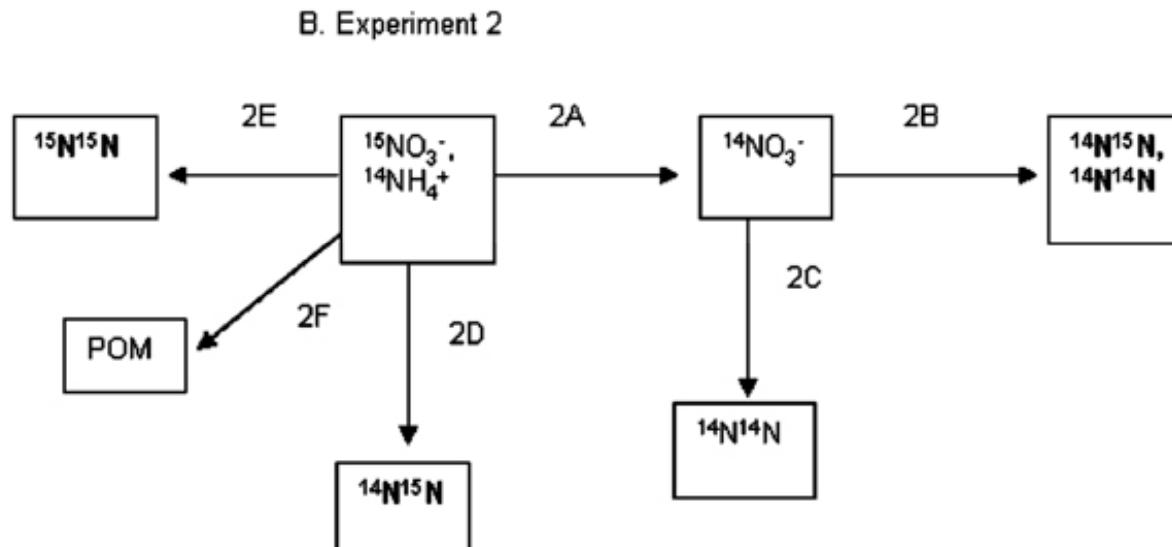
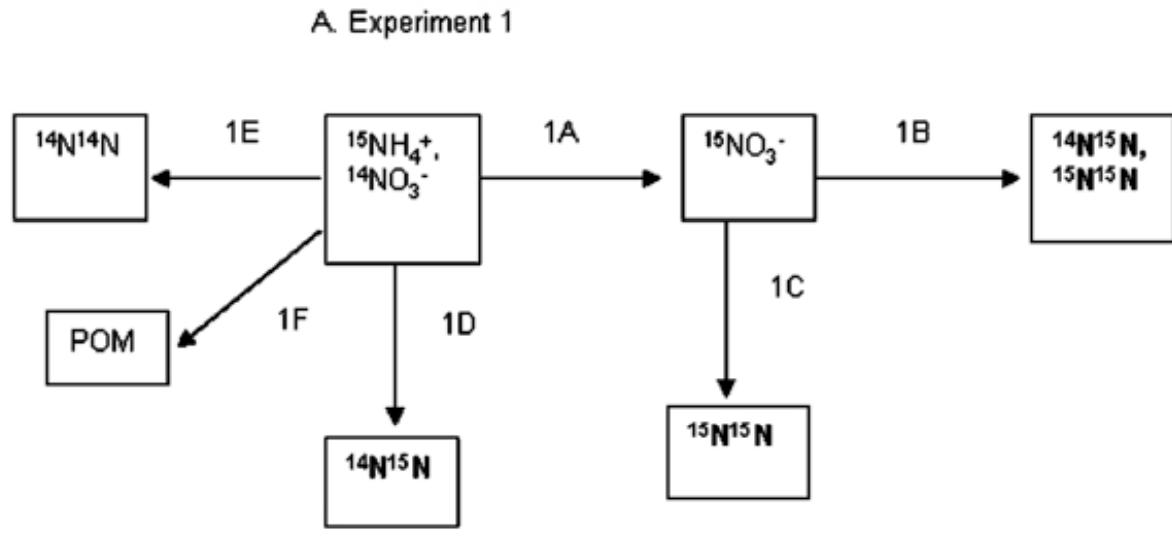
# Paradox of N loss pathways in low oxygen zones

- ▶ Anammox recently shown to be important
- ▶ Requires nitrite, ammonium and low oxygen
  - Explaining how anammox can be supported in OMZs major challenge



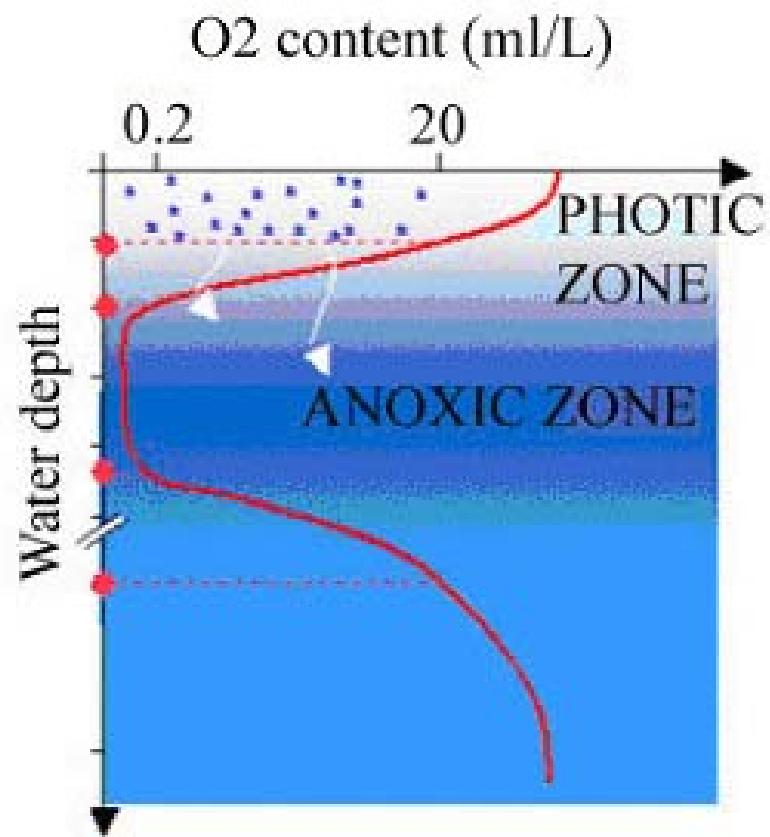
## Stable isotope methods: difficult to separate transformations

- ▶ Dalsgaard
- ▶ Thamdrup
- ▶ Kuypers



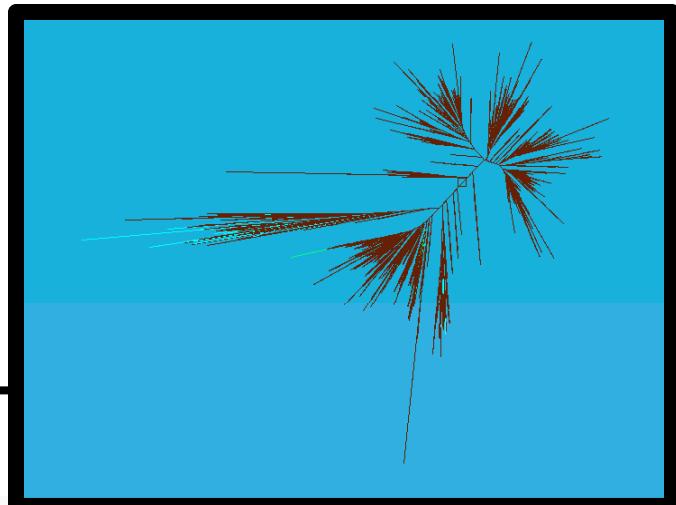
# Identification of N pathways with gene expression

- ▶ N loss in OMZs
- ▶ Denitrification
  - Nitrate  $\rightarrow$  N<sub>2</sub>
- ▶ Anaerobic ammonia oxidation
  - Nitrite + ammonium  $\rightarrow$  N<sub>2</sub>



# “Probes” from gene sequences

## Quantitative PCR



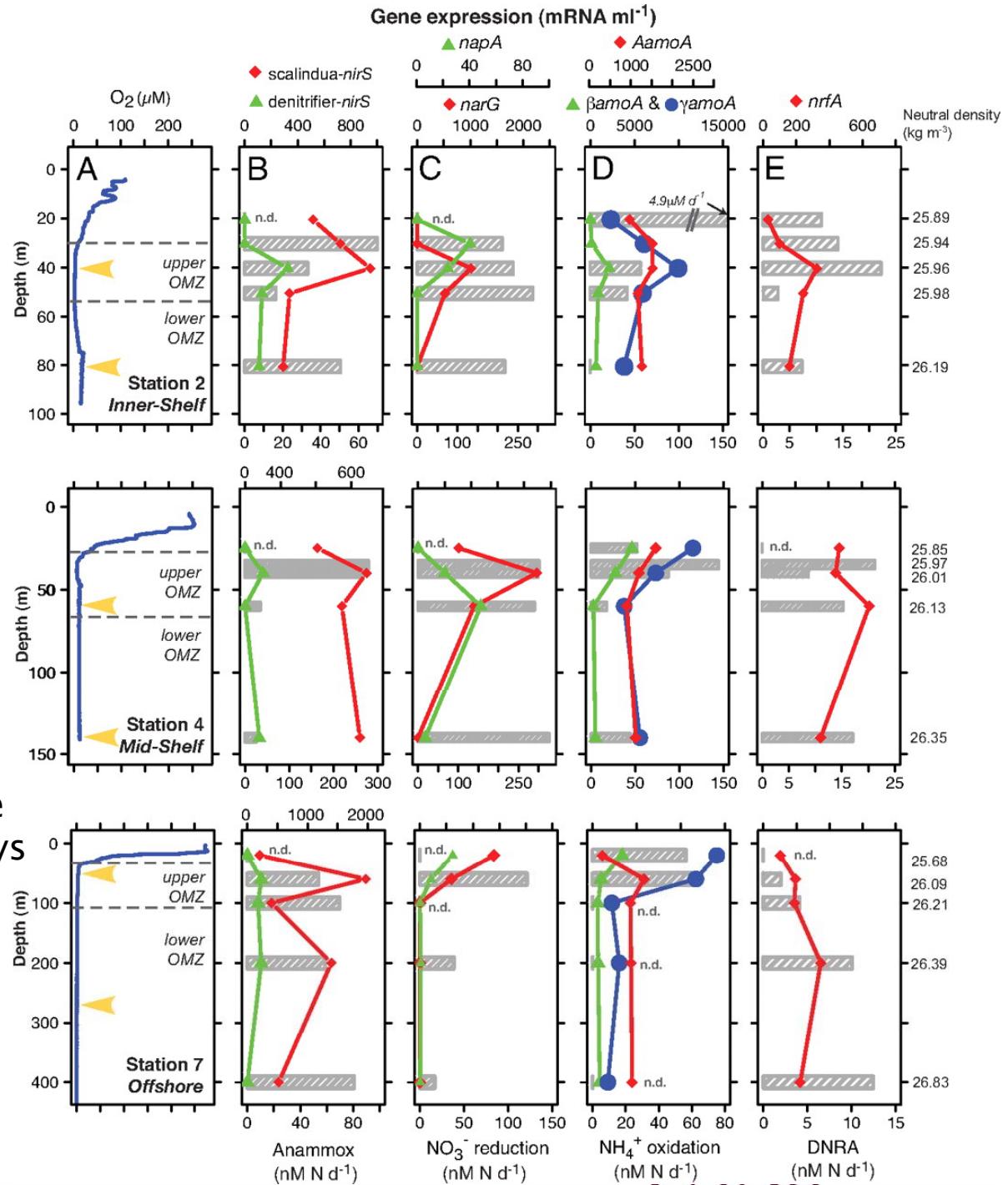
**Vertical distribution of oxygen (A) and the various measured  $^{15}\text{N}$  rates along with corresponding functional gene expression (B–E) at Stations 2 (inner shelf), 4 (mid-shelf), and 7 (offshore).**

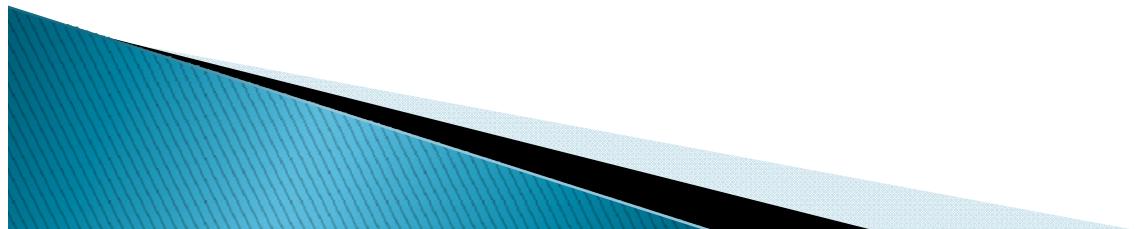
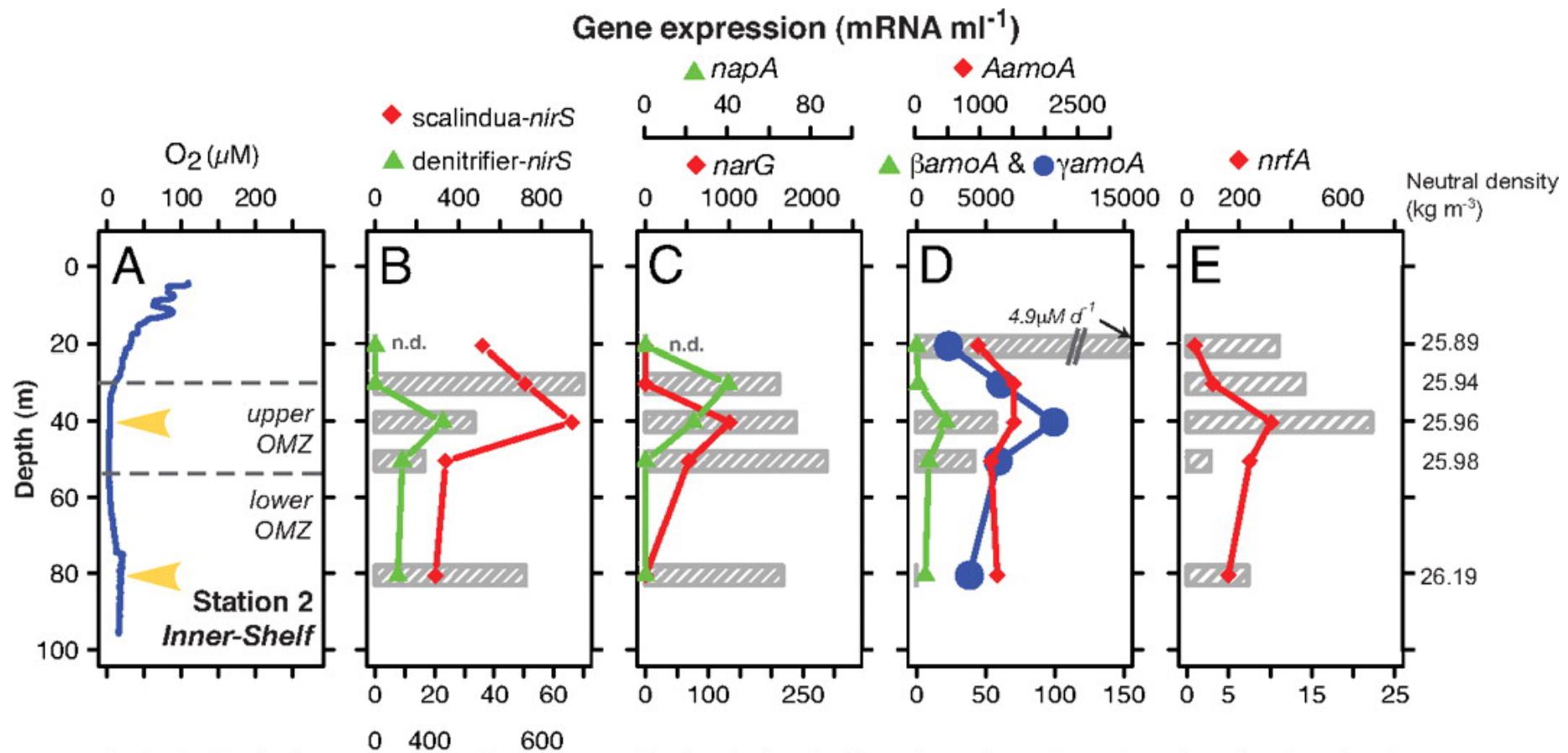
Genes

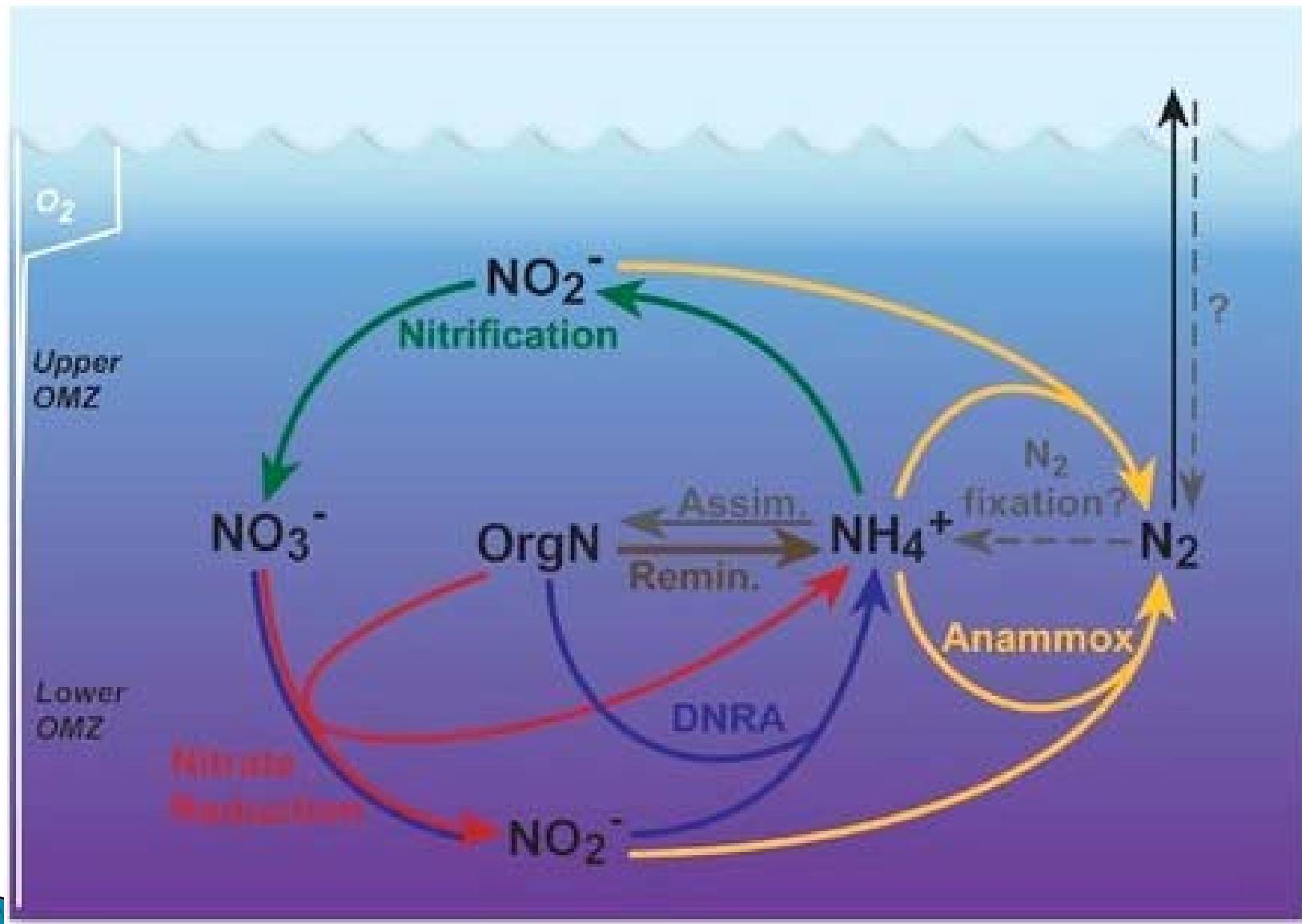
Nir  
Nar  
Amo  
Nrf

Gene expression suggests relative importance of different N pathways

Role of dissimilatory reduction of nitrate in providing ammonium



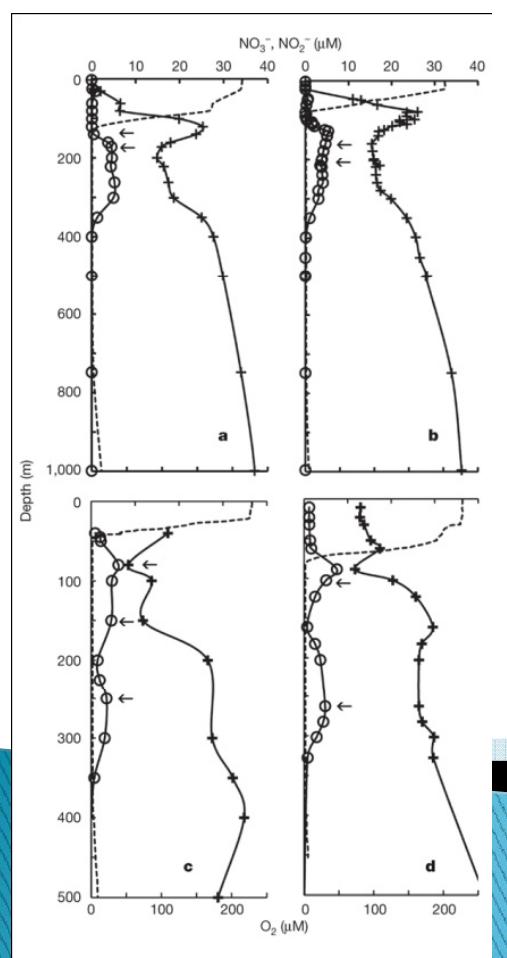




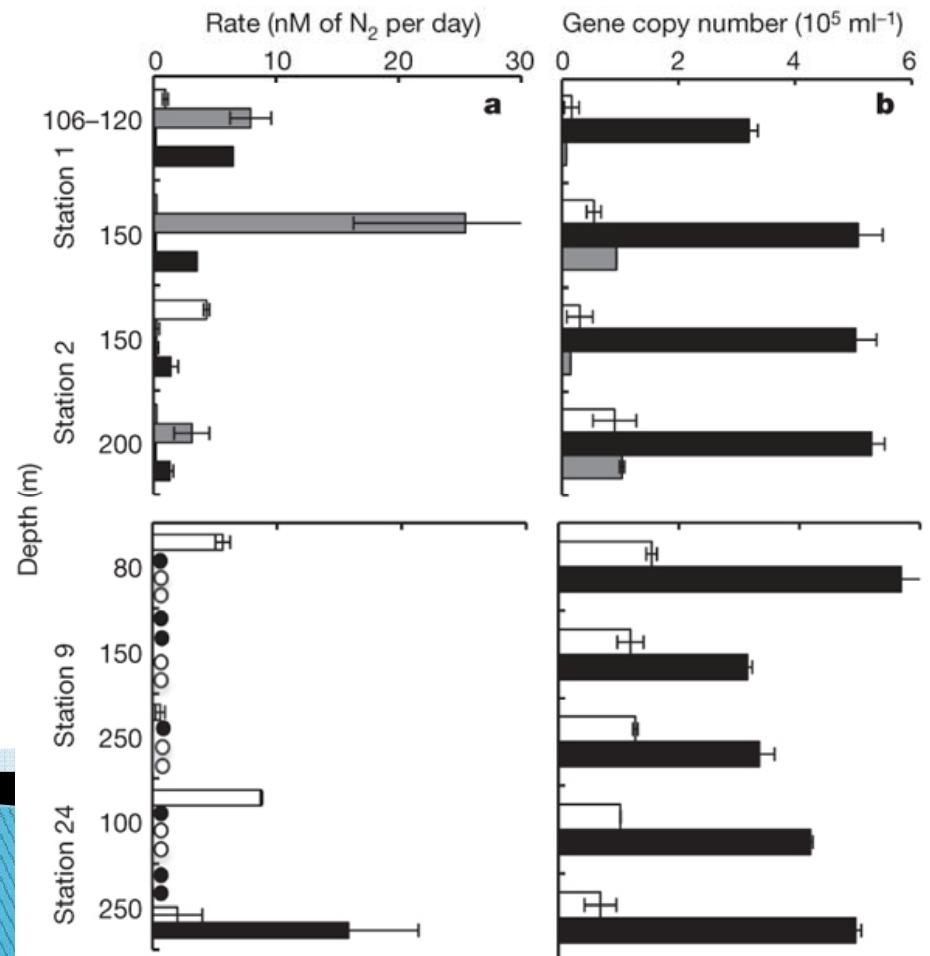
# Chemical profiles for experimental stations in the Arabian Sea and ETSP.



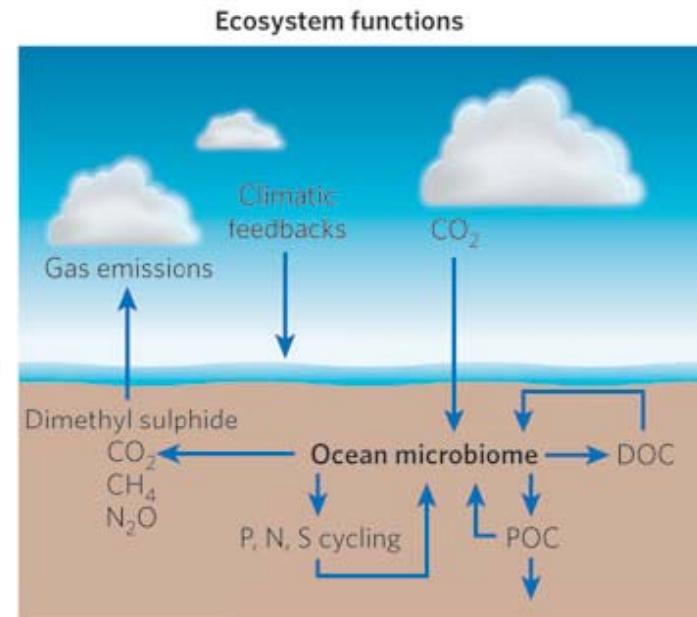
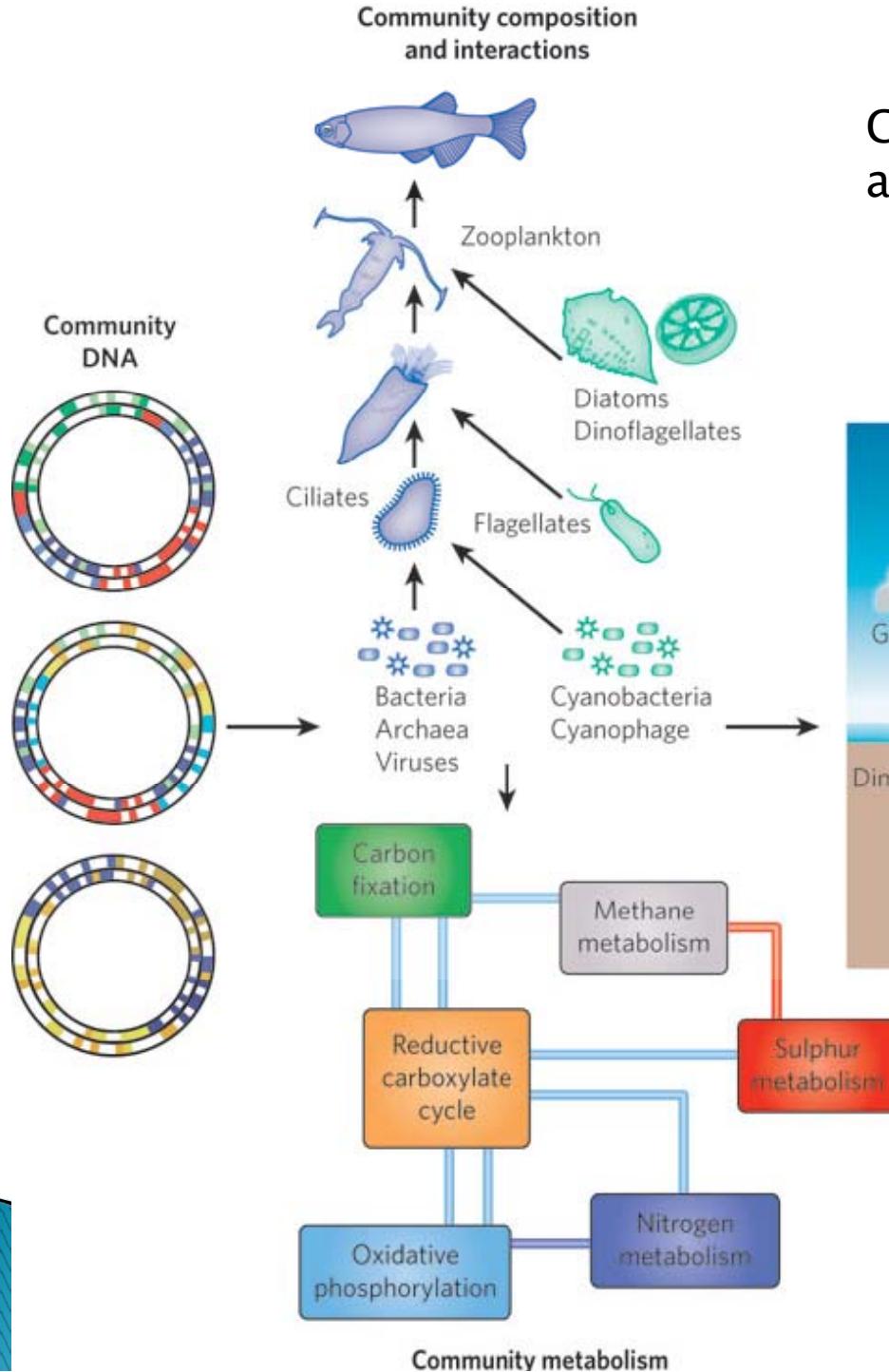
**nature**



## Conflicting results of

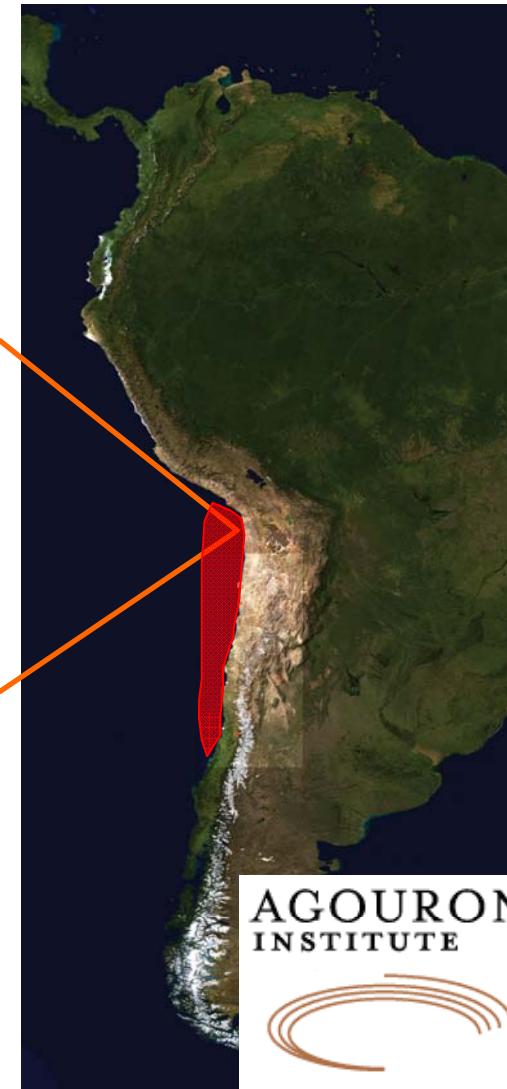
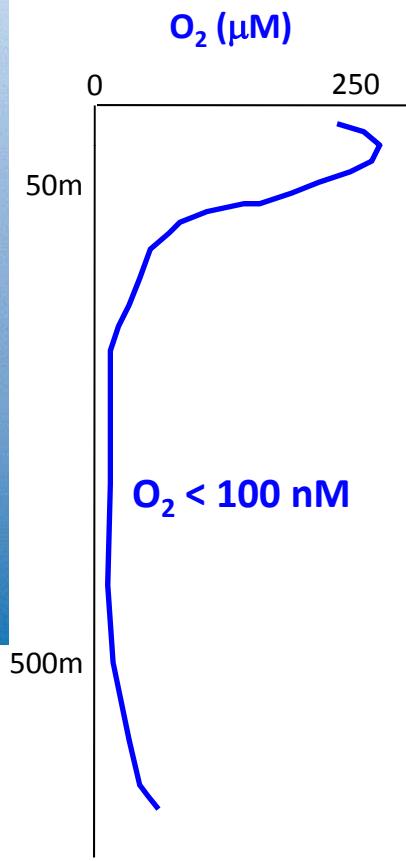
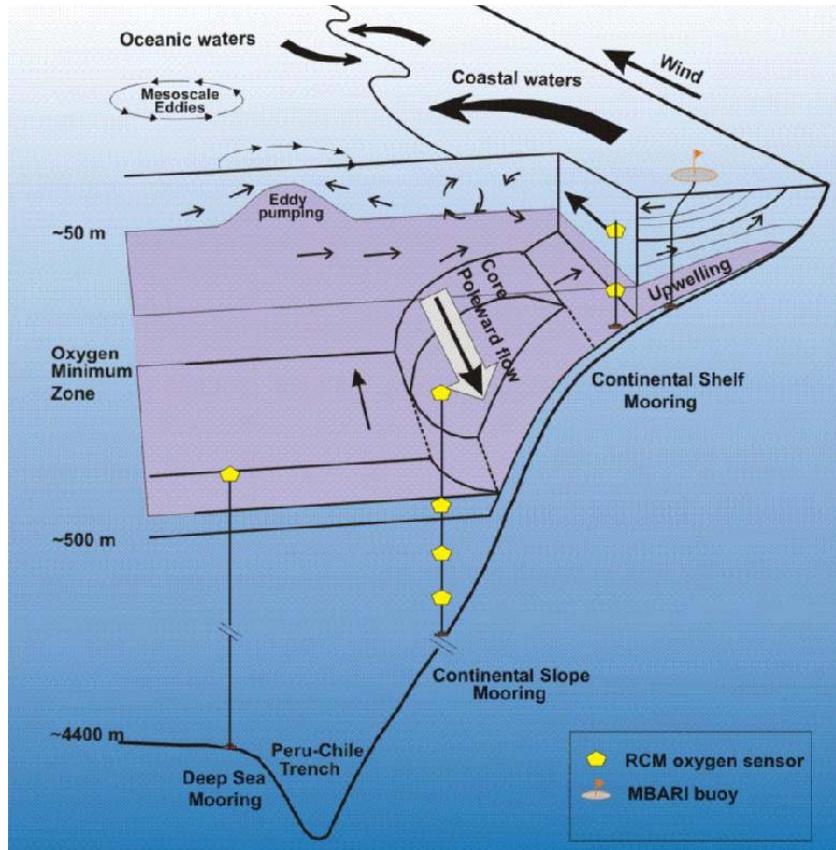


# Community Metagenomics and Metatranscriptomics



DeLong Nature

# Eastern Tropical South Pacific OMZ



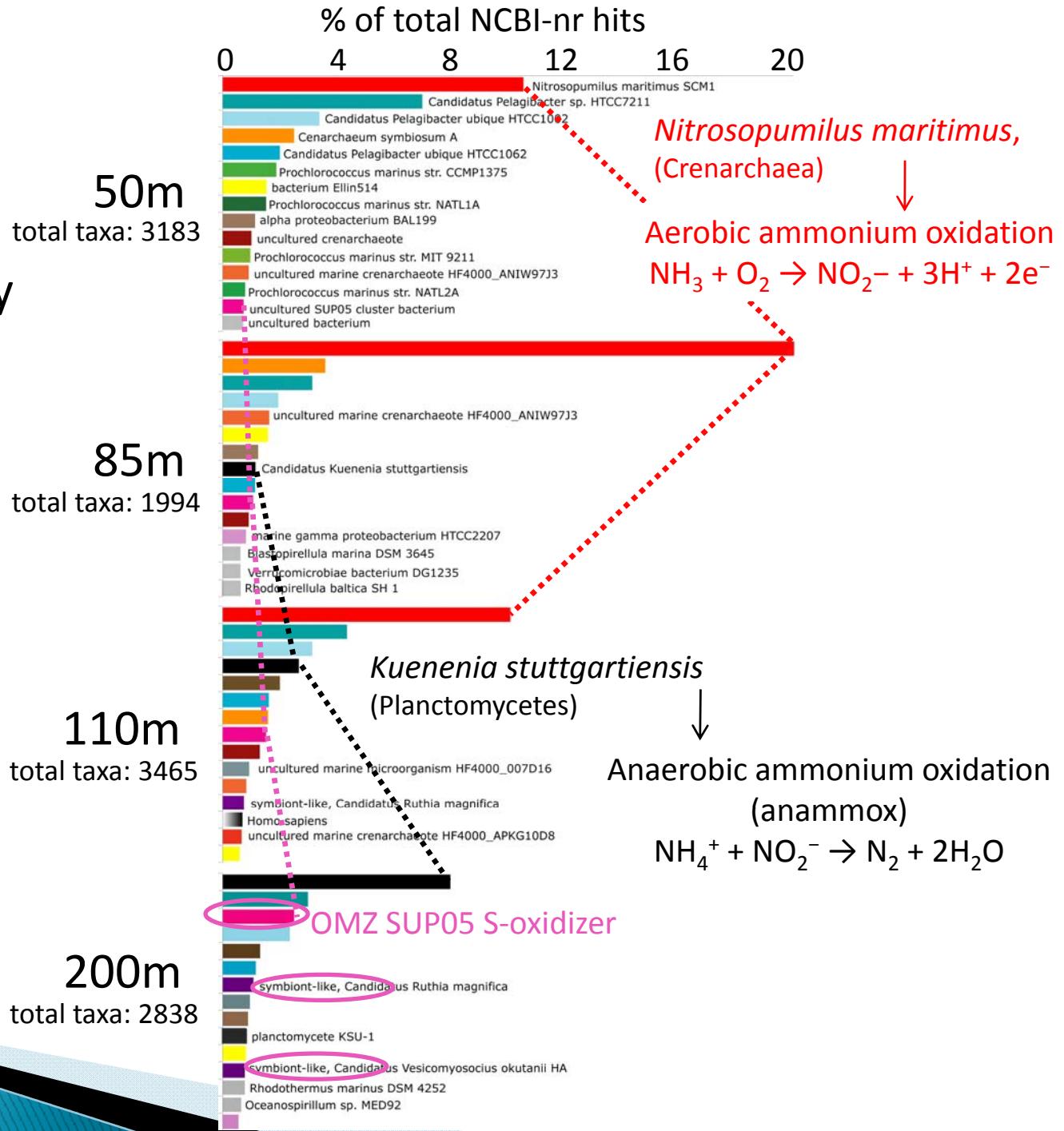
AGOURON  
INSTITUTE

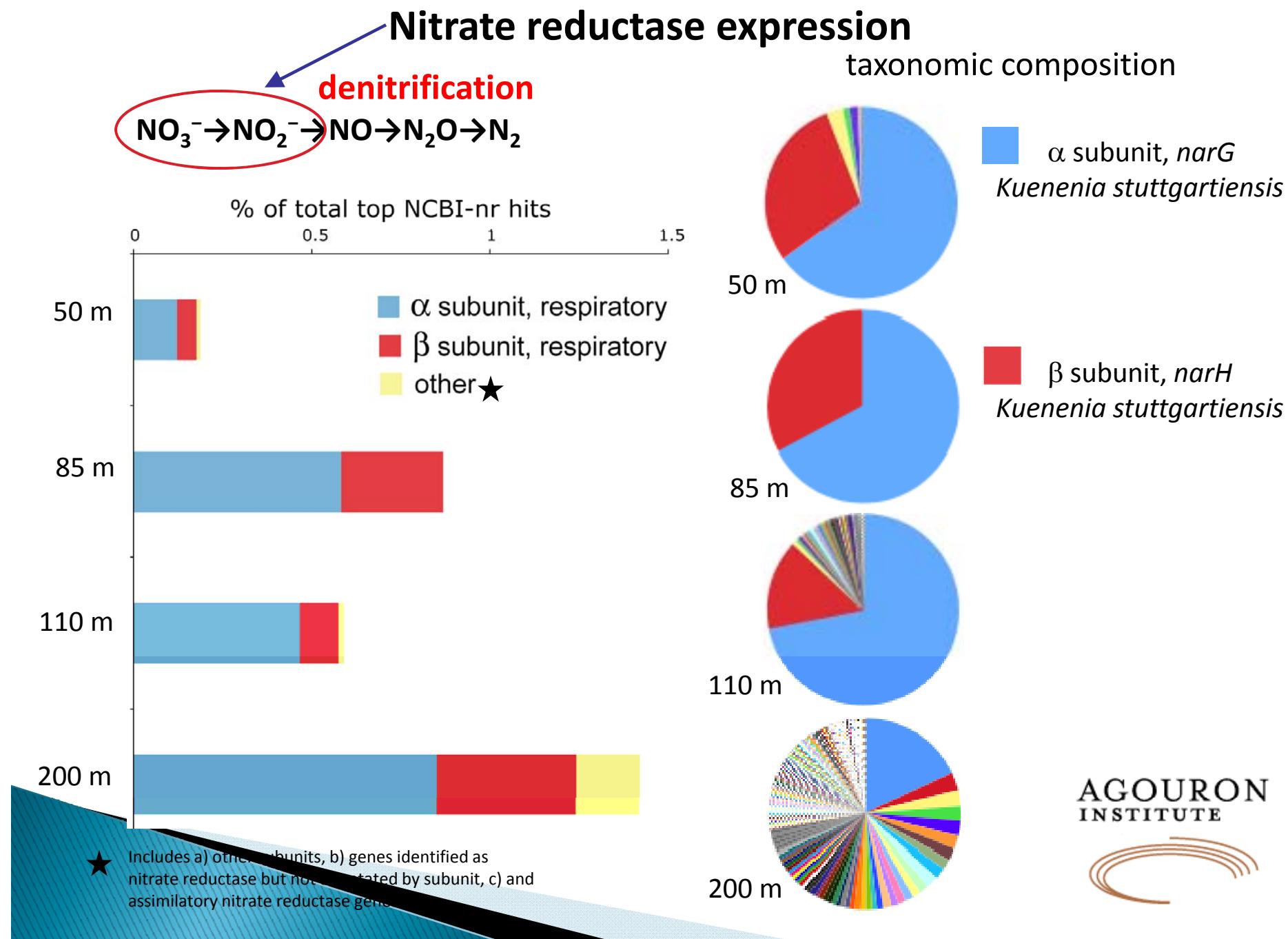


- Perennial
- Strong nutrient-rich upwelling
- Adjacent to productive fisheries

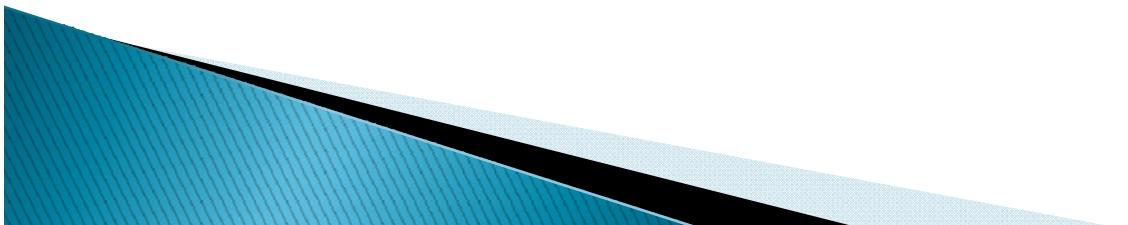
# Who's there?

Annotations of protein-coding cDNA reads informs taxonomy





- ▶ Limitations in interpretation of molecular techniques
  - Gene abundance—representation of cell abundance?
  - Gene expression—representation of enzyme activity?
- ▶ Temporally dynamic populations may influence relative importance
- ▶ May be cross feeding between microorganisms
  - Difficulty in integrating across time and space



- ▶ OMZs directly linked to nitrogen fixation
  - Due to effect of oxygen
- ▶ Global balance between  $N_2$  fixation and denitrification hard to determine
- ▶ Limited measurements in space and time
- ▶ Nitrogen fixation: Biogeochemical inference

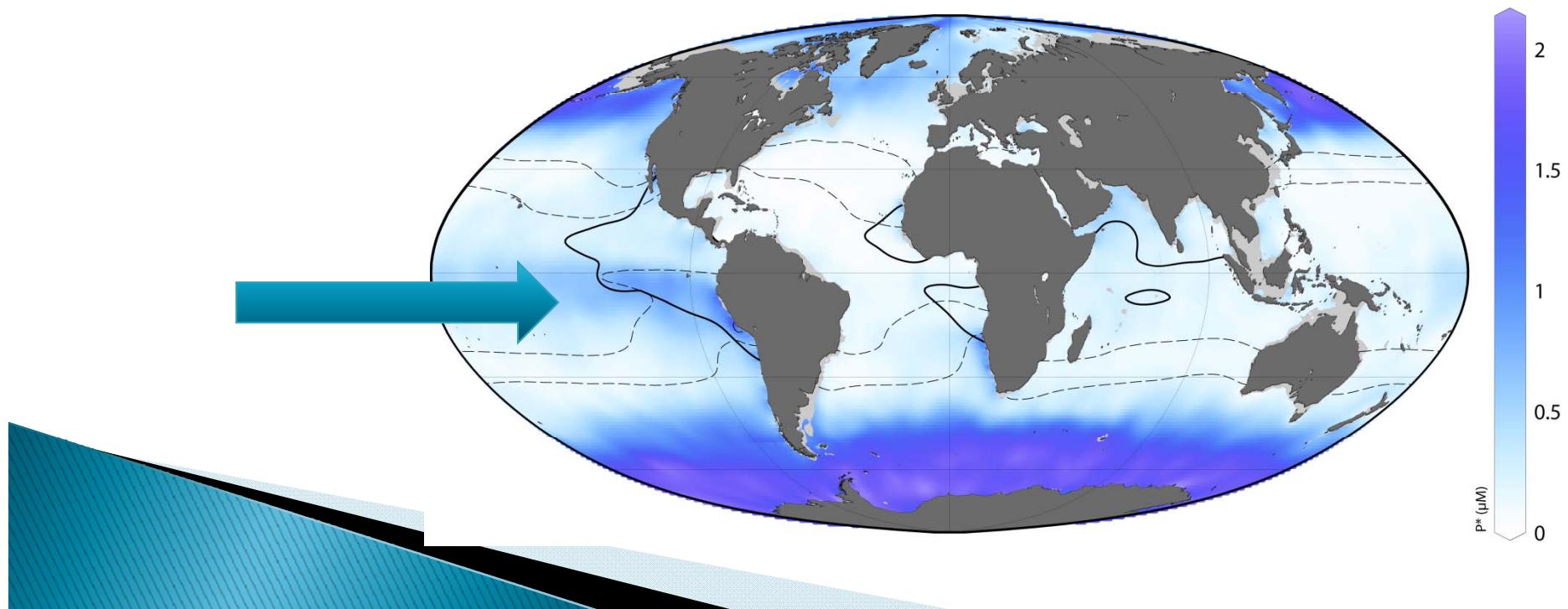
# Nitrogen fixation enhanced in OMZ due to removal of N (denitrification)

$$P^* = PO_4^{3-} NO_3^- / r_n,$$

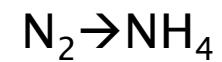
Biogeochemically inferred processes

$P^*$  → regions selecting for  $N_2$  fixation

" $N_2$  fixation will be revealed as a reduction in  $P^*$  along the transport path of a surface water mass, and its rate can be estimated by combining the observed distributions of nutrients with information about the rate of ocean circulation and mixing."



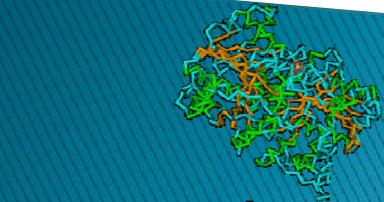
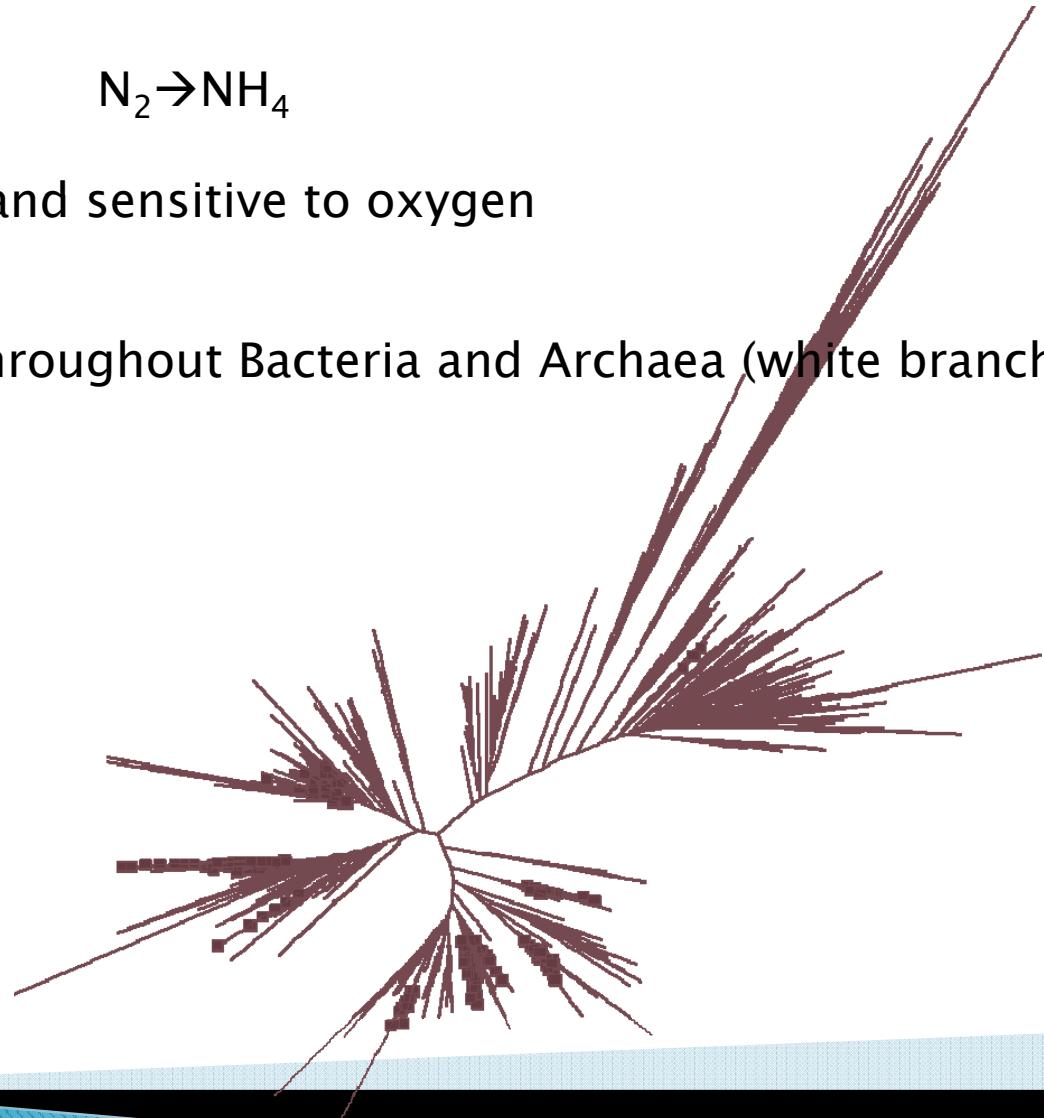
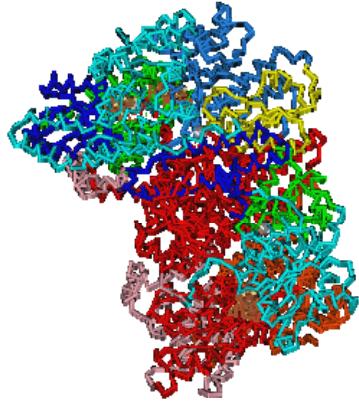
Biological nitrogen fixation



Energetically expensive and sensitive to oxygen

*nif* genes widely distributed throughout Bacteria and Archaea (white branches)

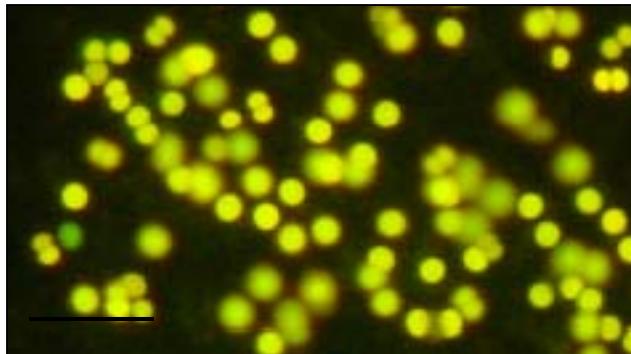
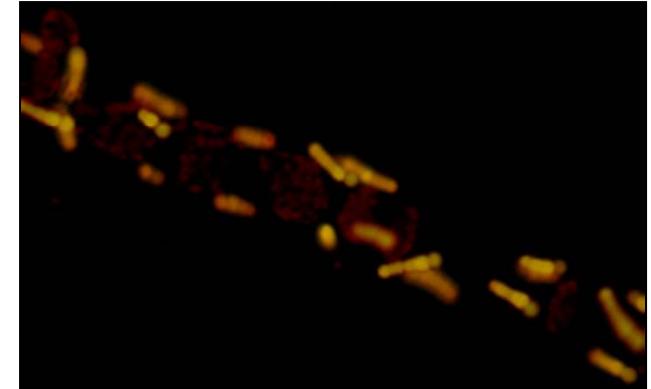
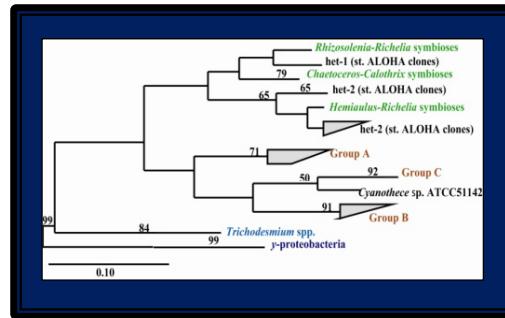
### MoFe protein



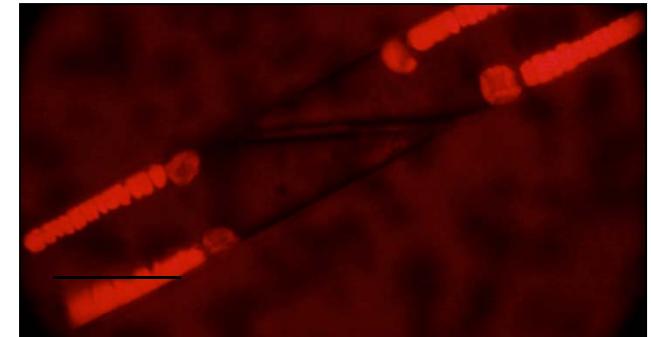
### Fe protein

>15,500 nitrogenase (*nifH*) genes sequenced

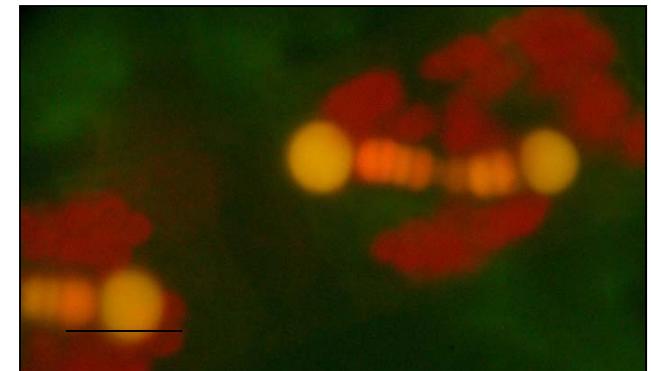
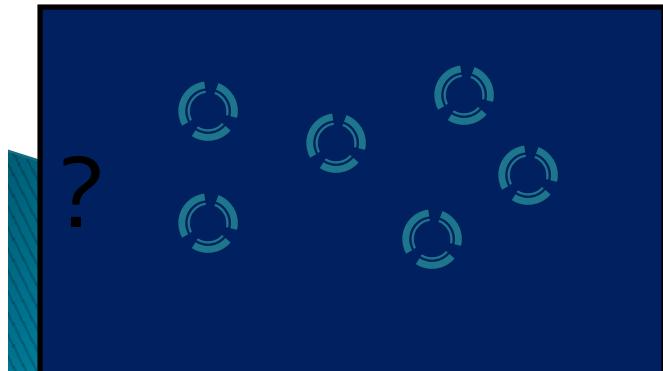
# Open ocean N<sub>2</sub>-fixing cyanobacteria: microscopy and gene amplification (PCR)



Crocospaera  
-cultivated



“Group A”  
-uncultivated



# $N_2$ -fixers highly variable in space and time

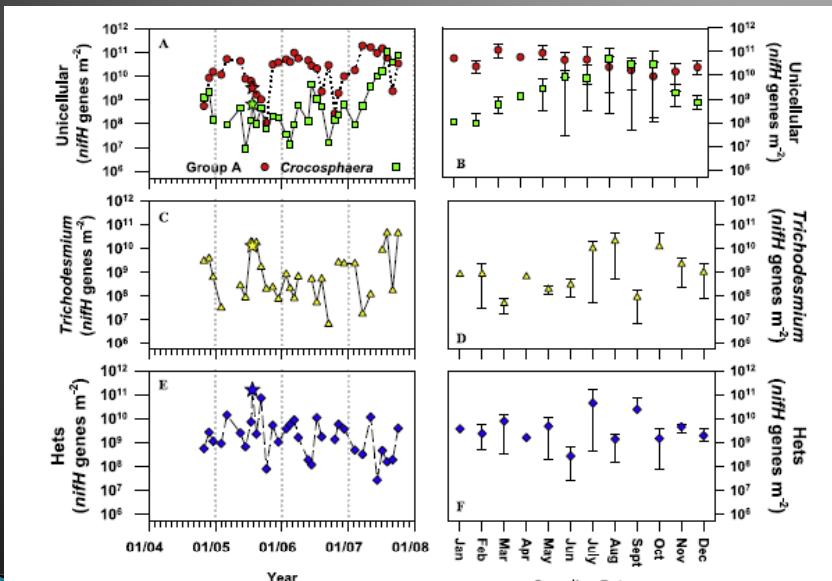
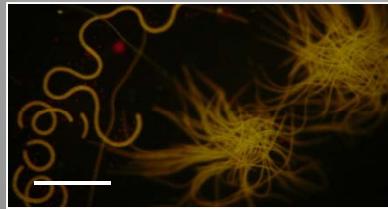
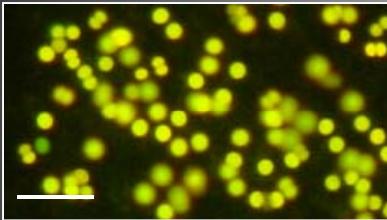
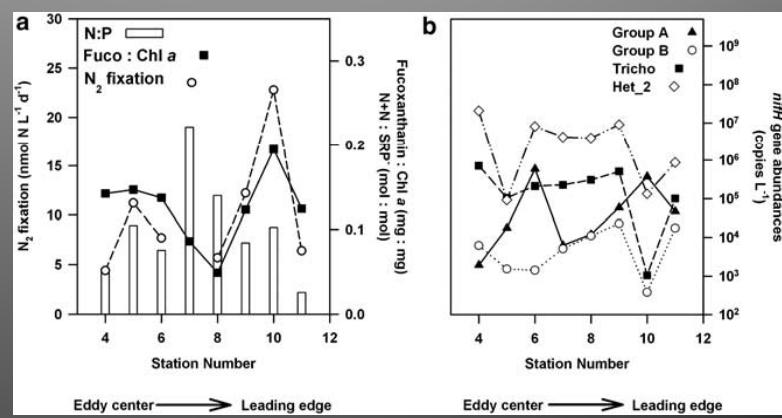
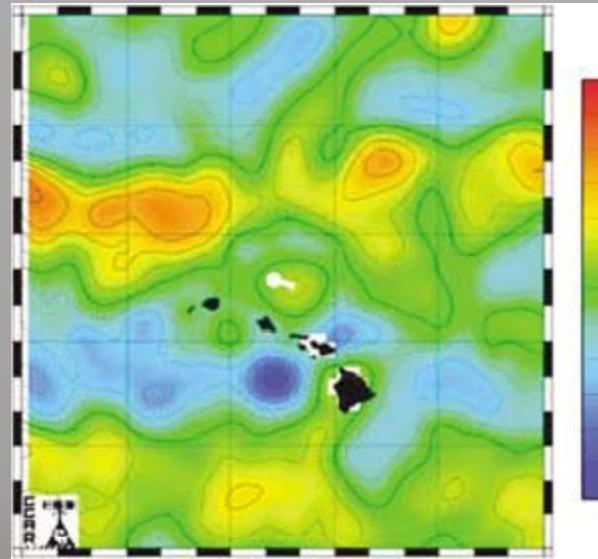


Figure 7. Time series of depth-integrated ( $0\text{--}100\text{ m}$ )  $nifH$  gene abundances at Station ALOHA.

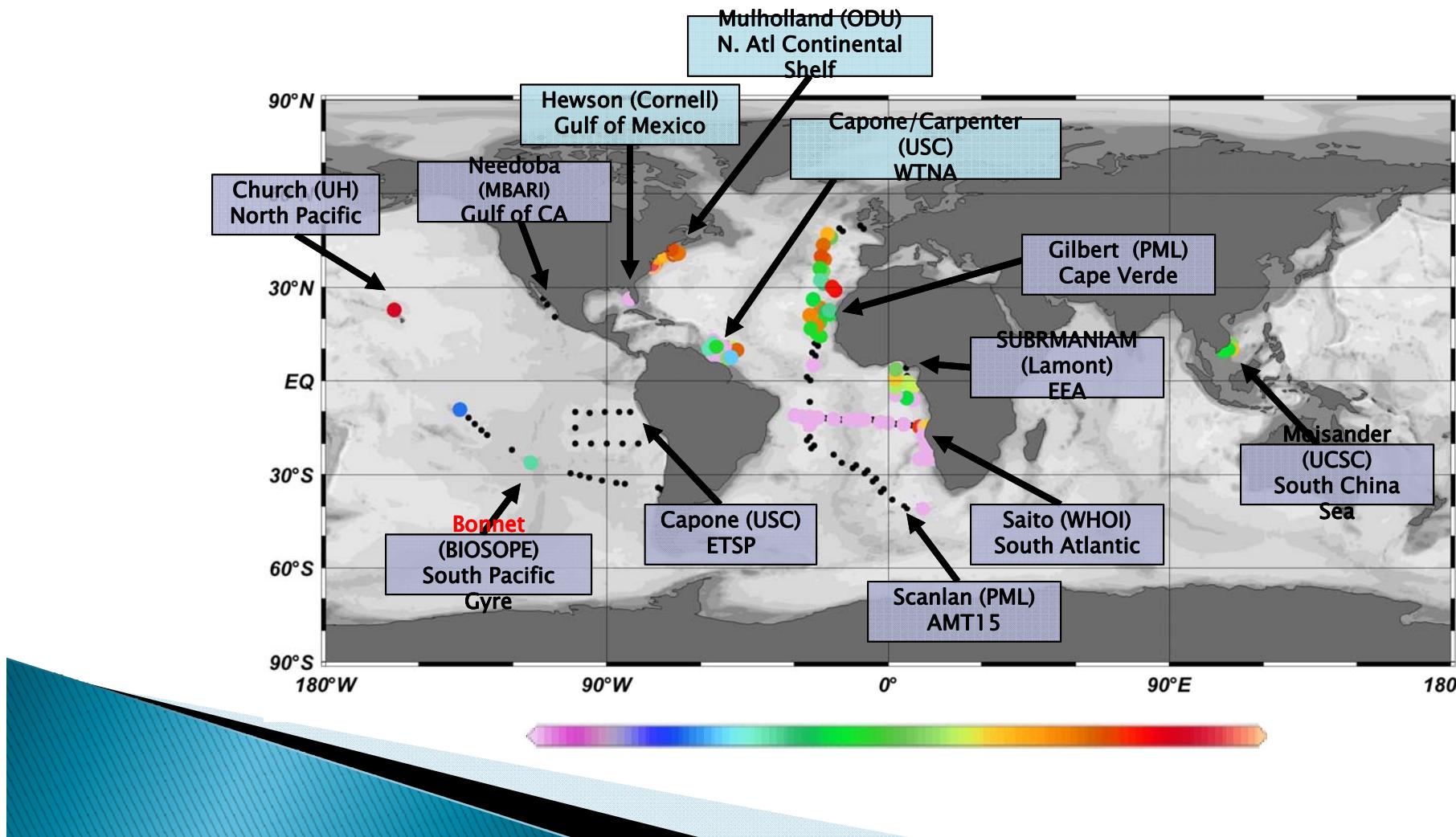


Church et al. 2009 GBC

Fong et al. 2008 ISME Journal

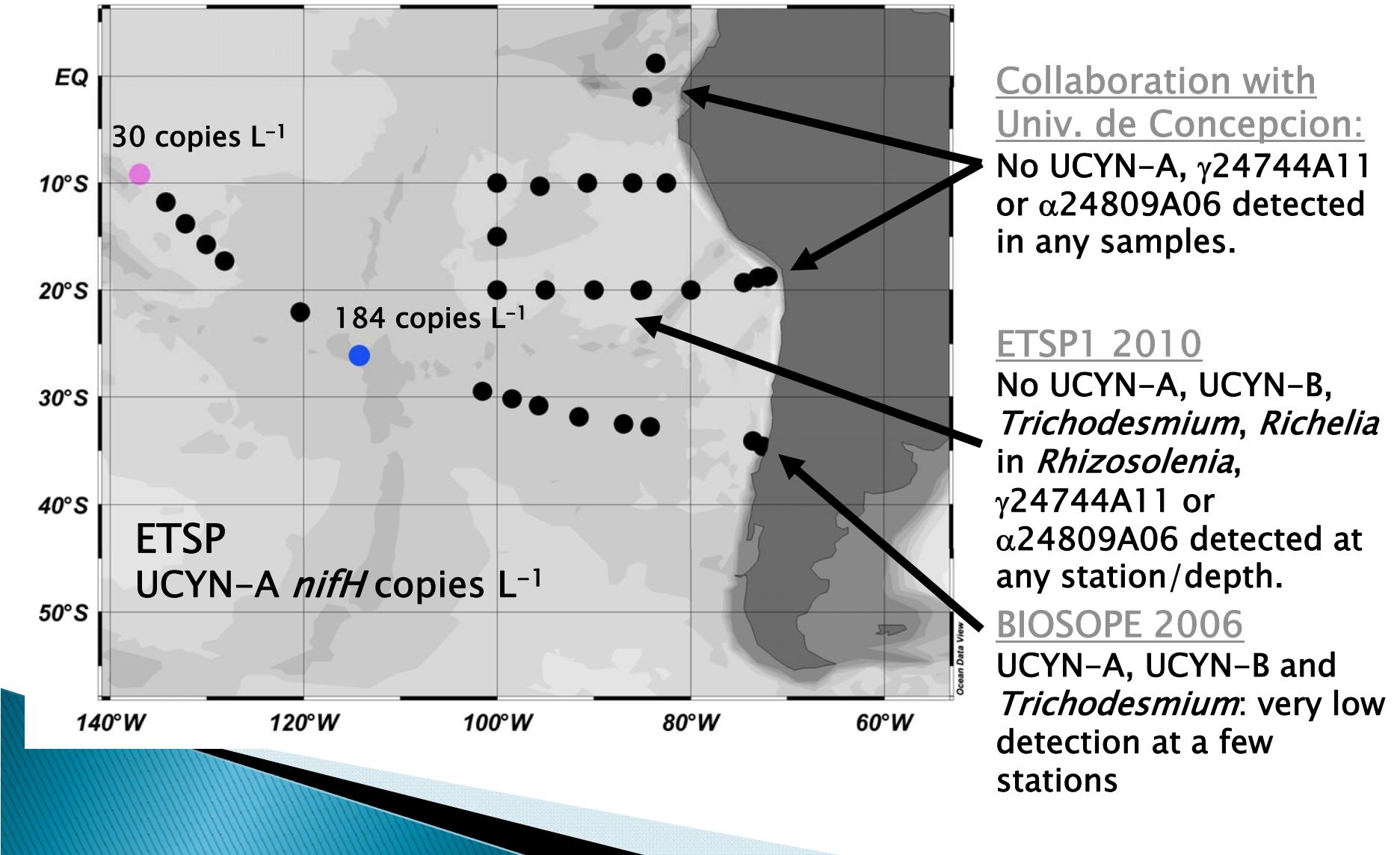
# From genomes to ecosystems

Global collaborative efforts



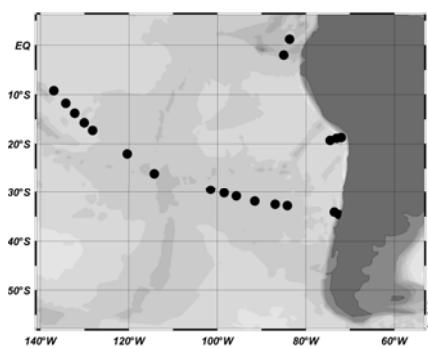
# Eastern Tropical South Pacific

## Very few diazotrophs detected using qPCR assays on DNA extracts



# Eastern Tropical South Pacific

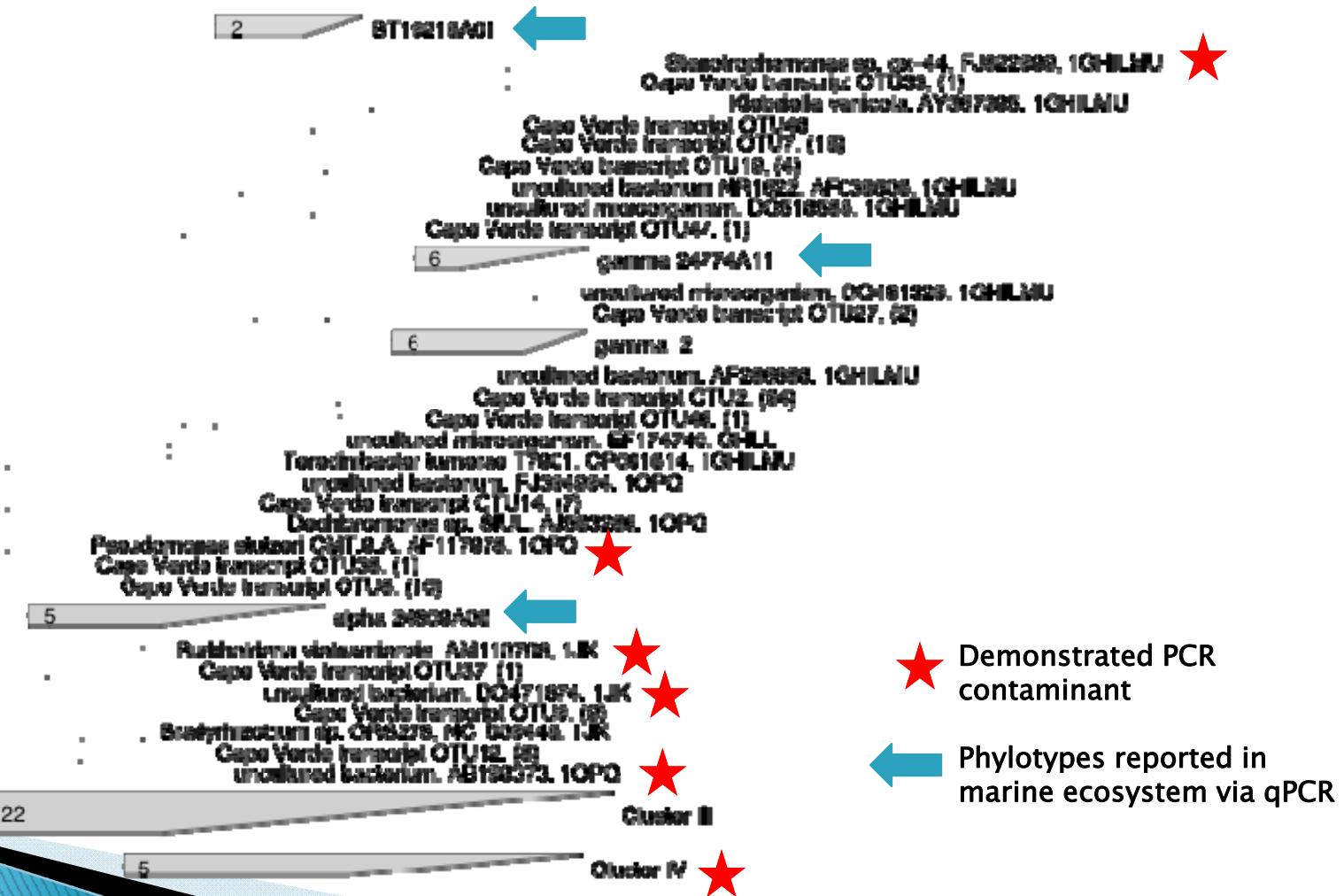
## All *nifH* sequences characterized are proteobacterial



- 72 **Vibrio clausonae** – 1GHILMU (7 ETSP sequences) ← ~50% sequence S
  - ETSP 33-chile60
  - ETSP 49-chile63
  - uncultured microorganism. DQ481270
  - Pseudomonas stutzeri. AJ297529
  - ETSP MH 248
- 11 **ETSP**
- 5 **proto 2 (Feng)** – 1GHILMU (2 ETSP sequences) ← Phylotype also observed in N. and S. Pacific, N. Atlantic, Arabian Sea and South China Sea
  - 3 **gamma247411** – 1GHILMU (1 ETSP sequence) ←
    - uncultured proteobacterium. EU181882
- 4 **ETSP**
  - uncultured nitrogen-fixing bacterium. DQ462834
  - ETSP 09-chile1
  - ETSP 13-chile1
  - uncultured bacterium. FJ398907
- uncultured bacterium. AY457323
  - ETSP 88-chile1
  - Azotobacter chroococcum. AY381872
  - uncultured microorganism. EP169435
  - Cape Verde transect OTU35
- 13 **gamma P (Langlois)** – 1OPQ (12 ETSP sequences) ← Phylotype also observed in N. Atlantic
  - ETSP 04-chile65
    - ETSP 18738a2
    - ETSP 18646a1
    - ETSP 18738a7
    - Aspergillus Indigoferae. U97114
    - ETSP 18738a4
    - unidentified bacterium. D83108
    - ETSP 18738a8
    - Ochrobactrum aromaticum RC8. CP000088.1
    - uncultured bacterium. FJ808193
  - ETSP 18738a9
  - uncultured microorganism. 1..321 EF174709
- 3 **Bultholdia** – 1JK (2 ETSP sequences)
  - ETSP 18646a2
  - Cupriavidus luteoruber. AY782062
- ETSP 18738a5
- uncultured bacterium. 1..324 EU181887
- Cyanothebaena** – 18 (no ETSP sequences) ← No Cyanobacterial diazotrophs

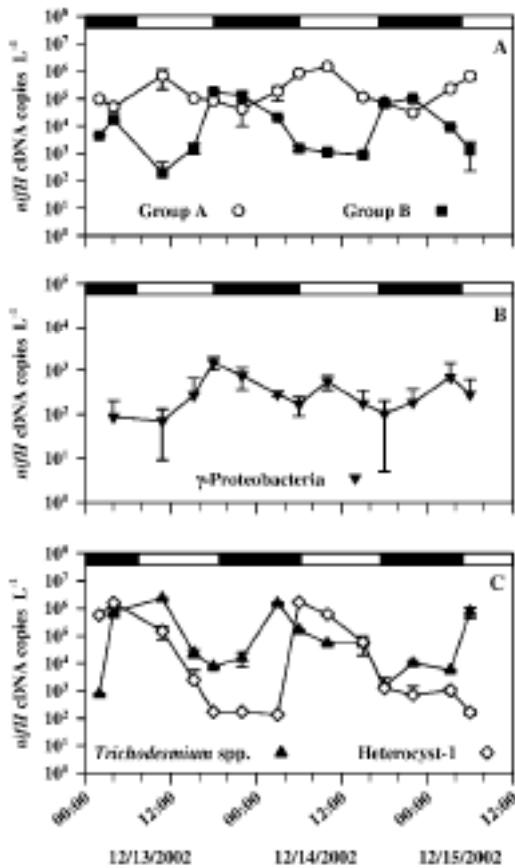
# Open ocean N<sub>2</sub>-fixing heterotrophs: gene amplification (PCR & qPCR)

Understanding heterotrophic diazotrophs contribution to N cycle is complicated due to prevalence of contaminants



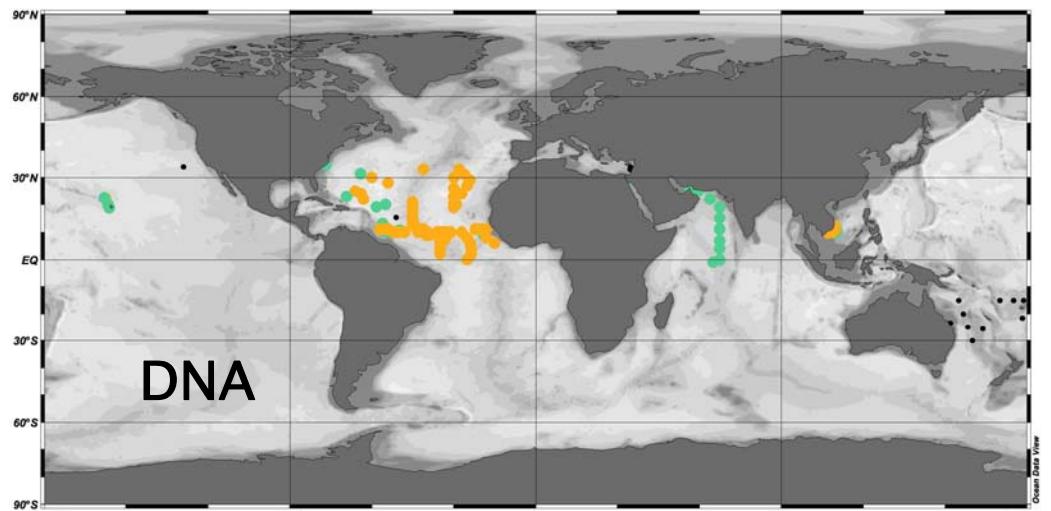
# Open ocean N<sub>2</sub>-fixing heterotrophs: gene amplification (PCR & qPCR)

Some heterotrophic diazotrophs have widespread distributions but low abundances – implications for global N cycle are unclear.

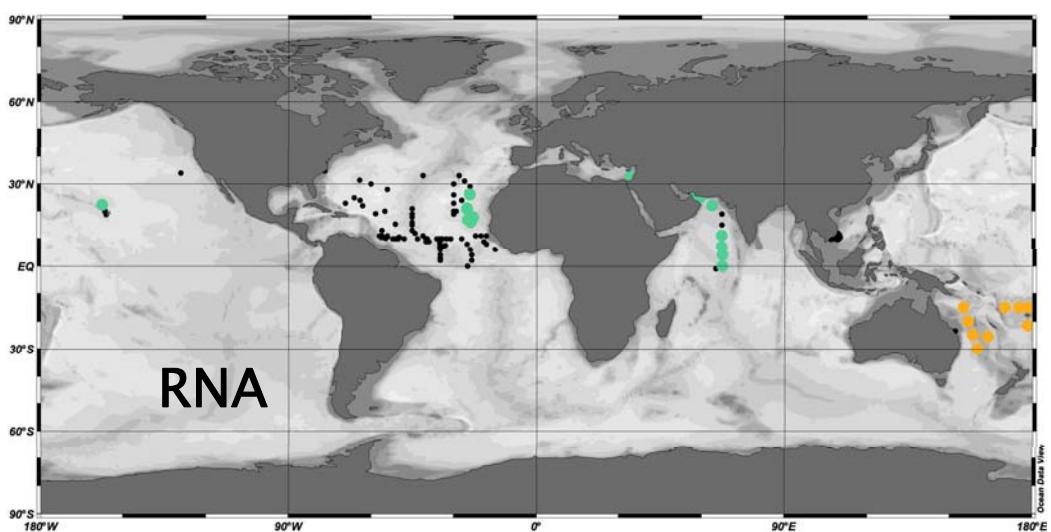


From Church et al, 2005

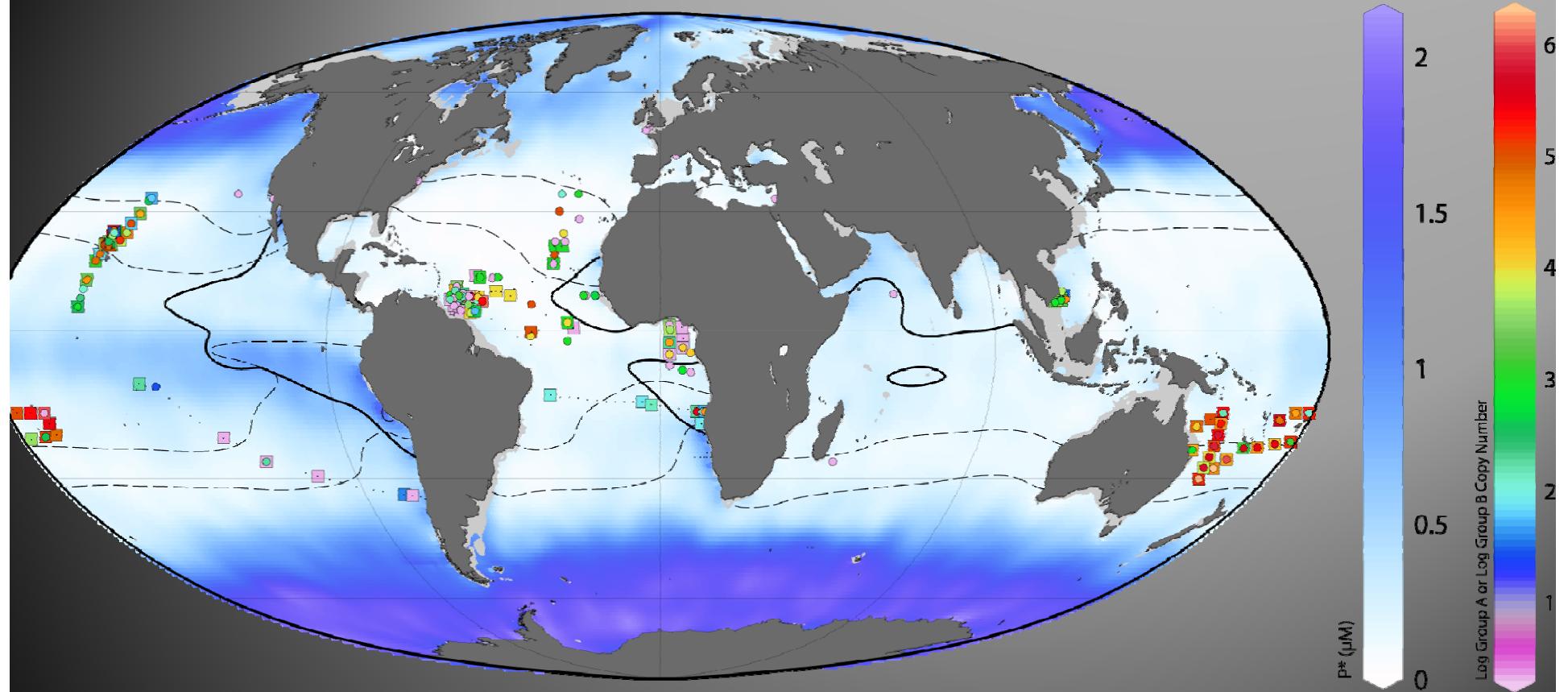
Global distribution of  $\gamma$ -proteobacteria 24774A11



● reported in clone libraries      ● detected in qPCR assays



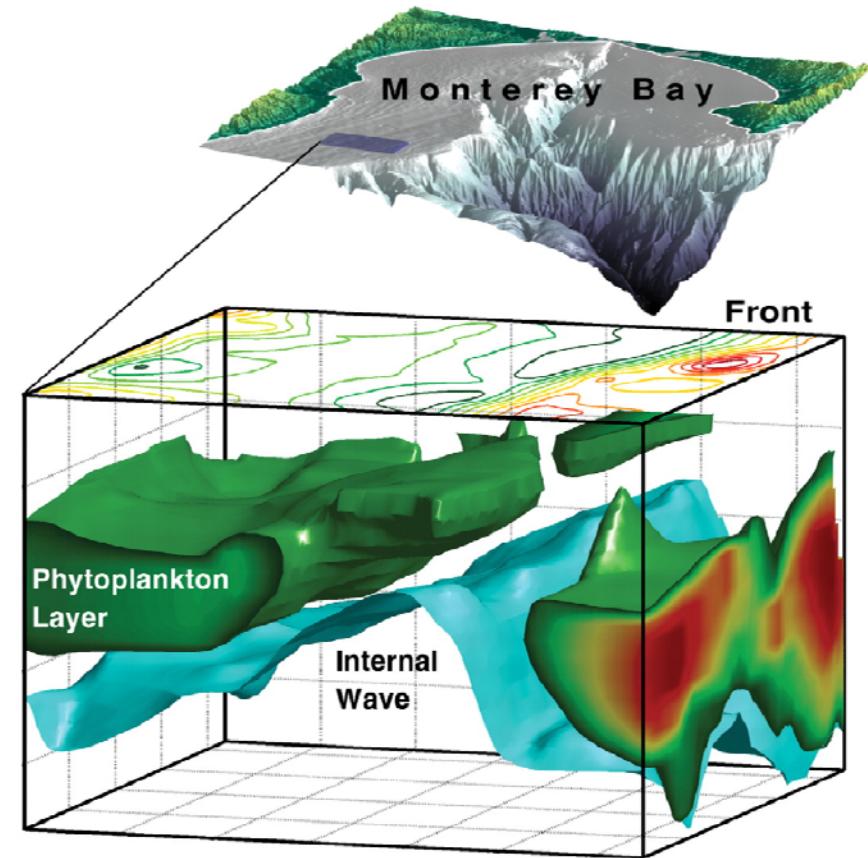
# Global map- $P^*$ with $N_2$ fixer distributions



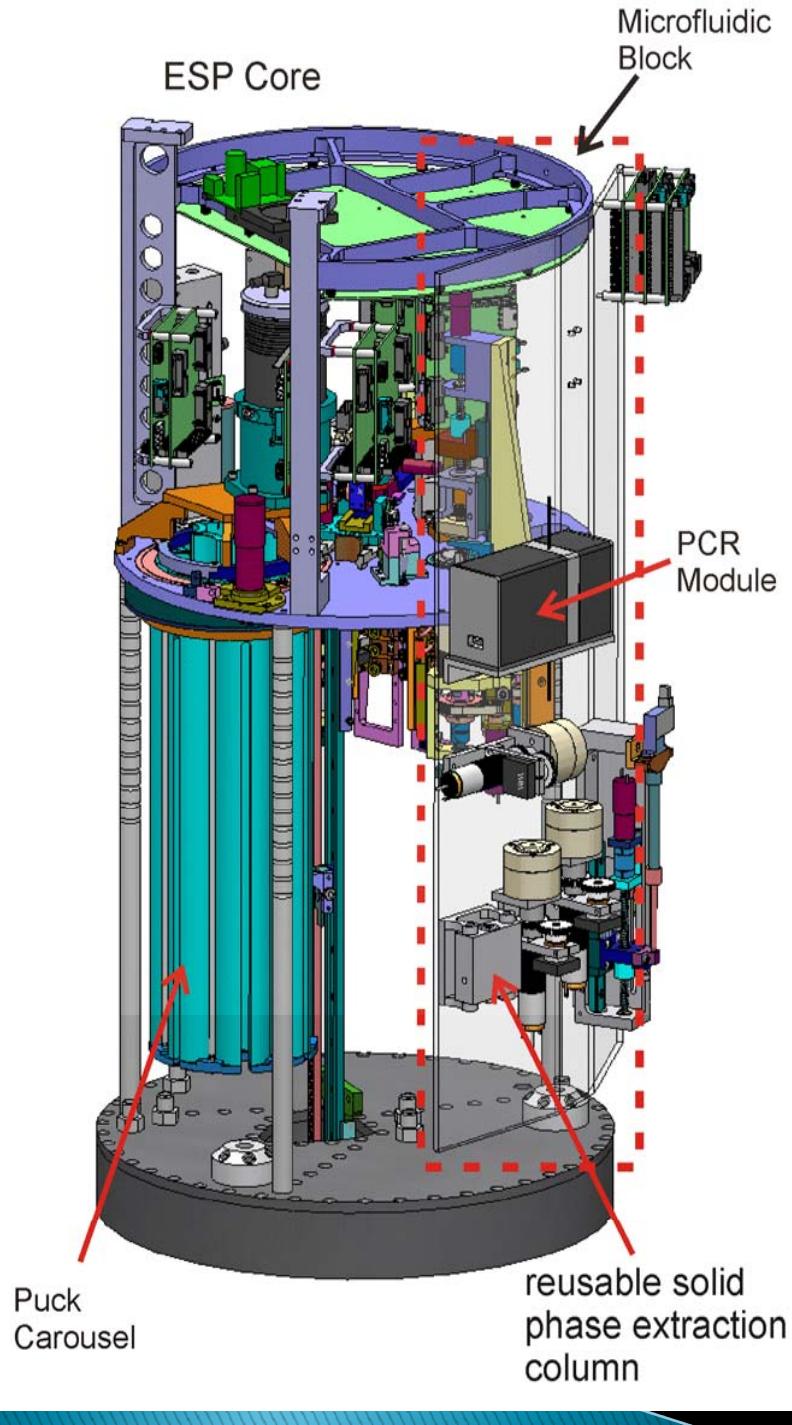
$N_2$  fixer distributions are not correlated with  $P^*$

# Molecular tools provide information on potential for N cycle processes, and whether they are active

- ▶ Understanding dynamics of N cycles in time and space requires higher resolution data
- ▶ Remote instrumentation increases sampling resolution
- ▶ Detection of microorganisms by genes, mRNA, etc.
- ▶ Environmental Sample Processor (ESP)–Chris Scholin/Chris Preston (MBARI), Julie Robidart (UCSC-MBARI)



John Ryan



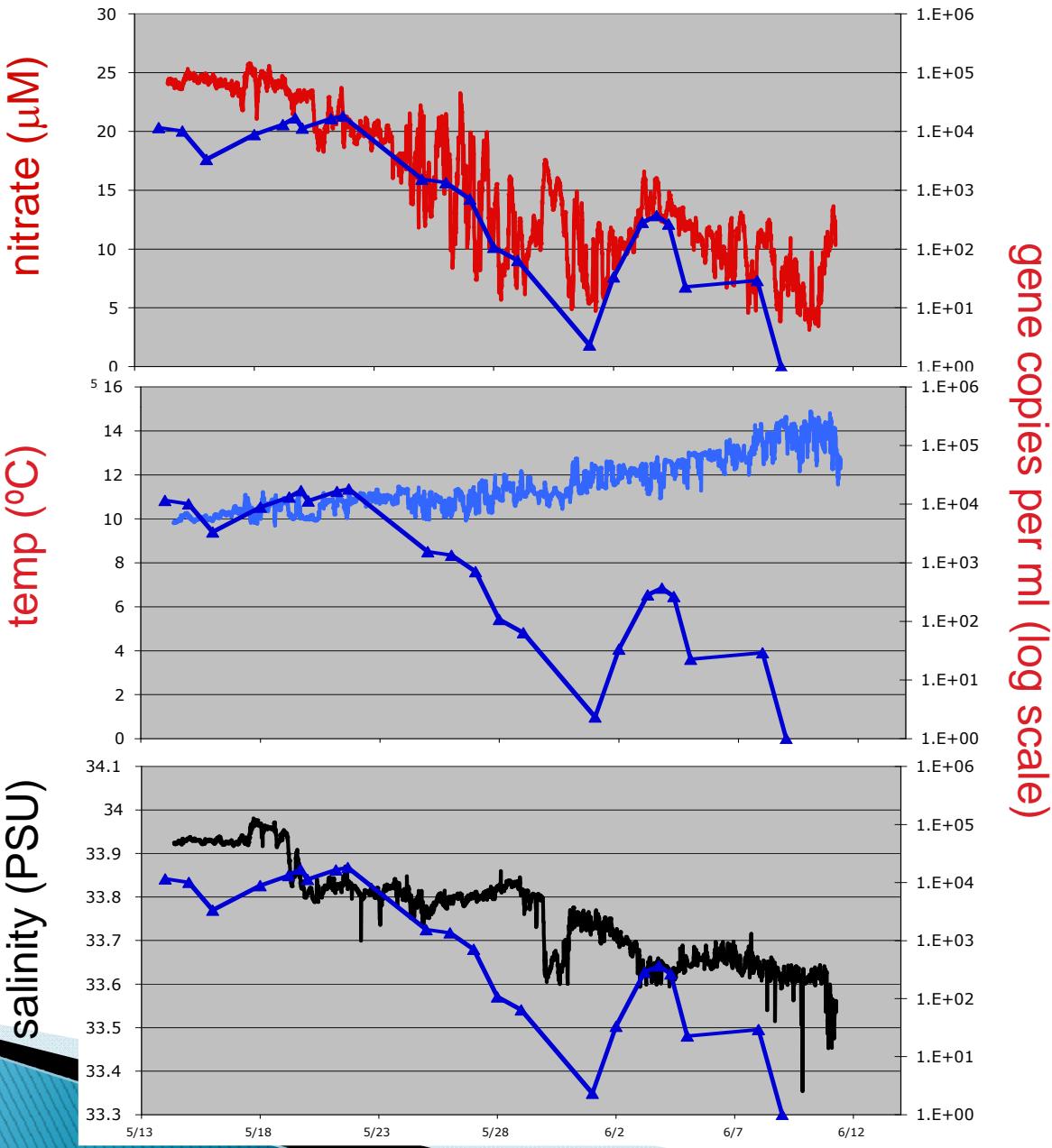
Remote instrumentation that can perform molecular biological measurements

Few molecular biological samplers-  
ESP and AMG

Can enumerate strains from genes-  
subspecies/ecotypes

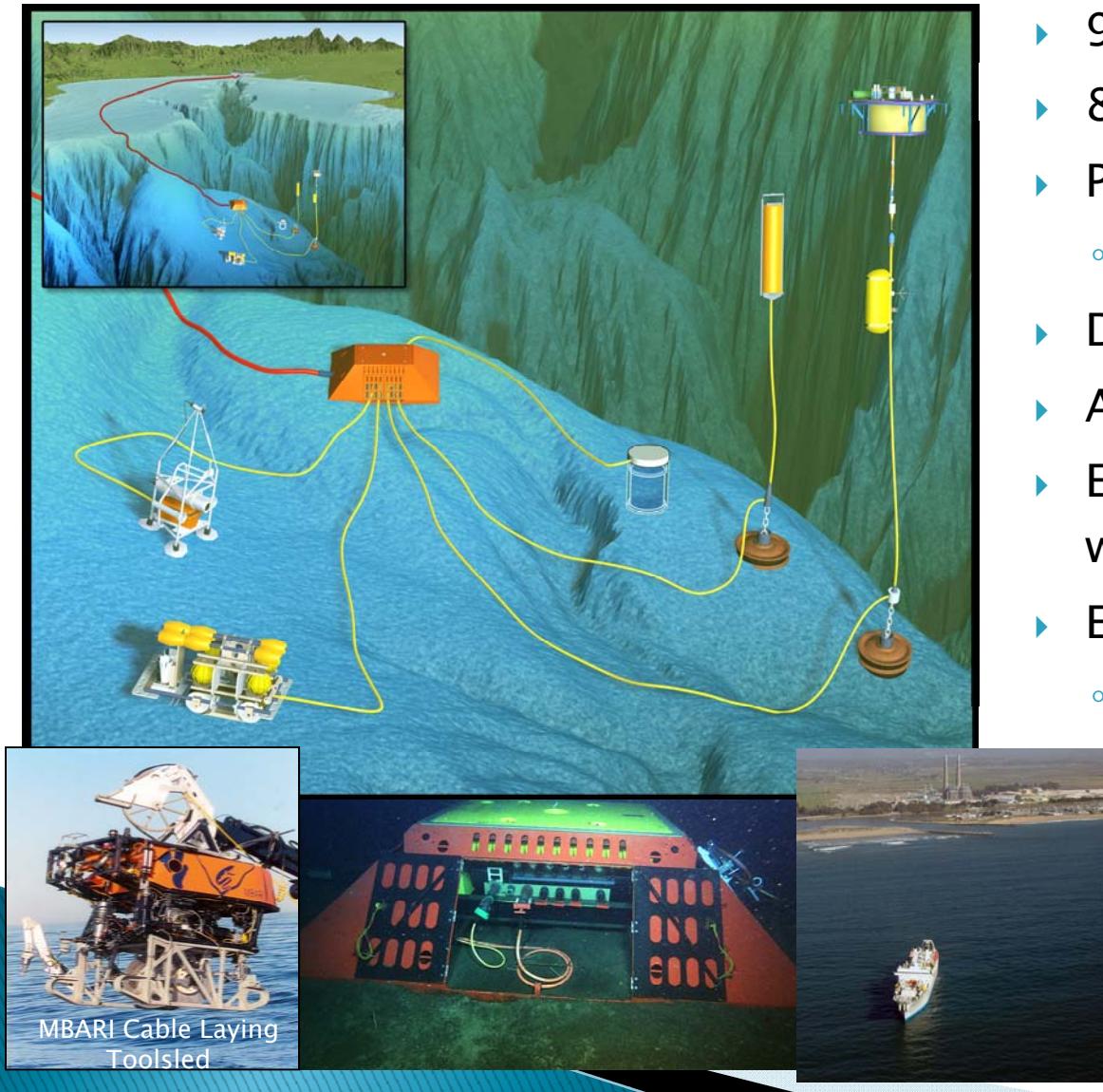
## Spring ESP Deployment

### *Crenarchaeota* vs. nitrate, temp, salinity



C. Preston

# The Monterey Accelerated Research System (MARS)

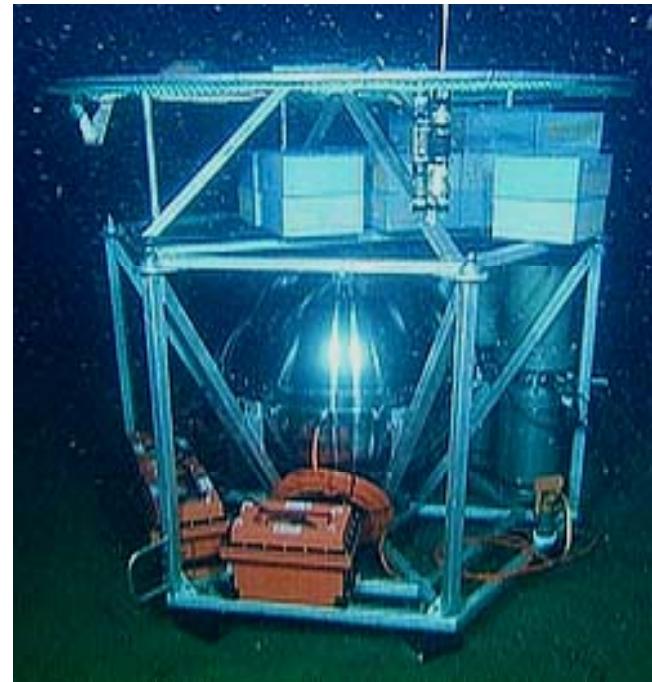


- ▶ 9 kW of power for science
- ▶ 8X 100 Mbit/sec Ethernet ports
- ▶ Precision time distribution
  - ~5 uSec
- ▶ Deep water – 890 meters
- ▶ Accessible – 2 hrs from MBARI
- ▶ Extended geographic coverage with extension cables
- ▶ Extensive shoreside support
  - Staging, ships, ROVs, expertise

<http://www.mbari.org/mars>

# D-ESP Deployment on MARS

Scholin et al. MBARI



900 m

# Summary

- ▶ Molecular biology needed for disentangling the N cycle
- ▶ Higher resolution data needed
- ▶ Need integration of models, remote instrumentation and molecular biology

# Acknowledgments

- Rachel Foster, Ian Hewson, Pia Moisander, Tuo Shi, Irina Ilikchyan
- Technical Support: Kendra Turk, Mary Hogan, Tracy Cote
- Grad students: Shellie Bench, Jason Hilton
- ◆ Dave Karl , C-MORE, HOT, Joe Montoya, Ed DeLong, John Waterbury, Mary Ann Moran and Rachel Poretsky, Ginger Armbrust, Robin Kodner, Jason Affourtit (454)



Gordon and Betty

**MOORE**  
FOUNDATION



454, A Roche Company