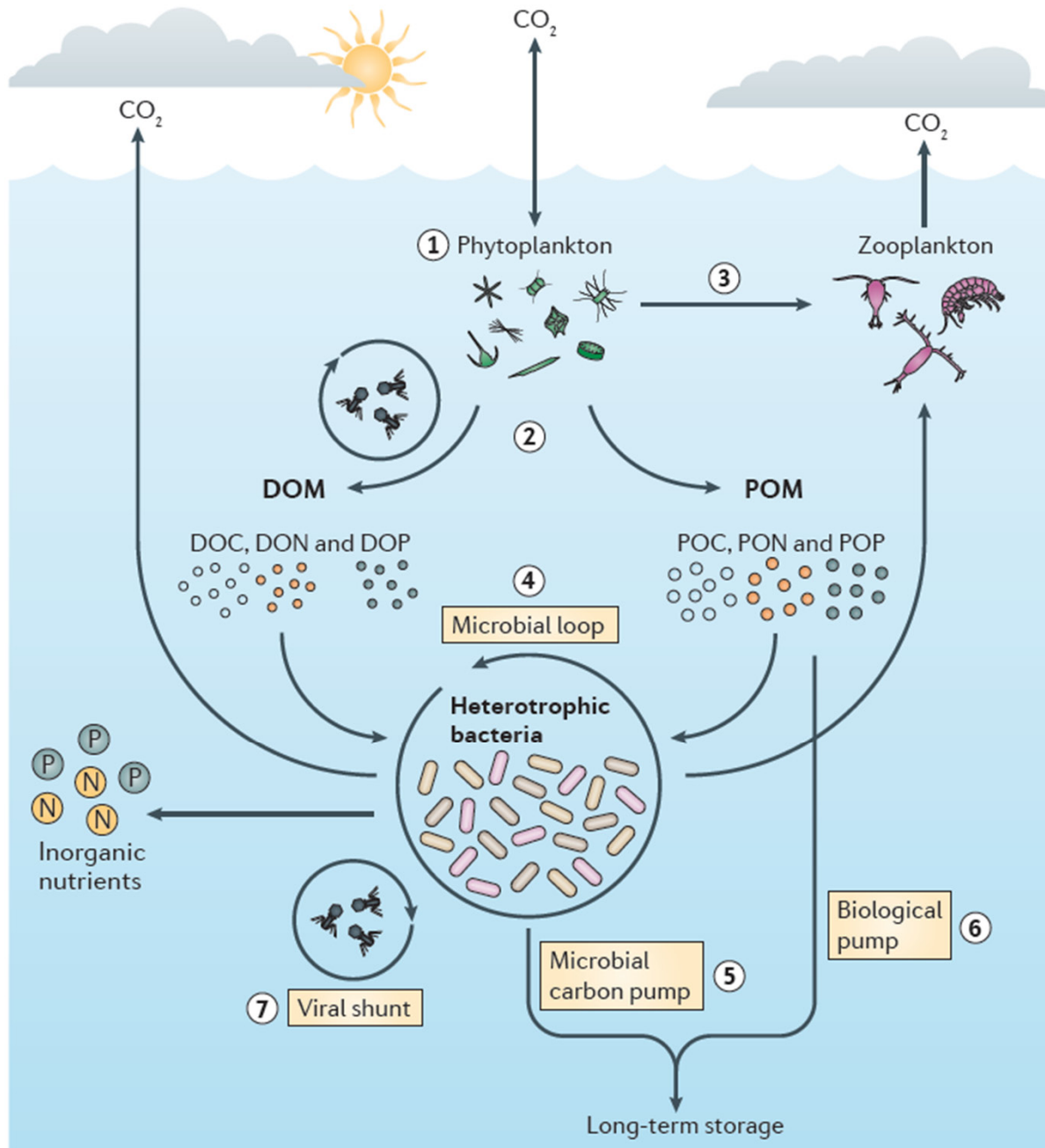
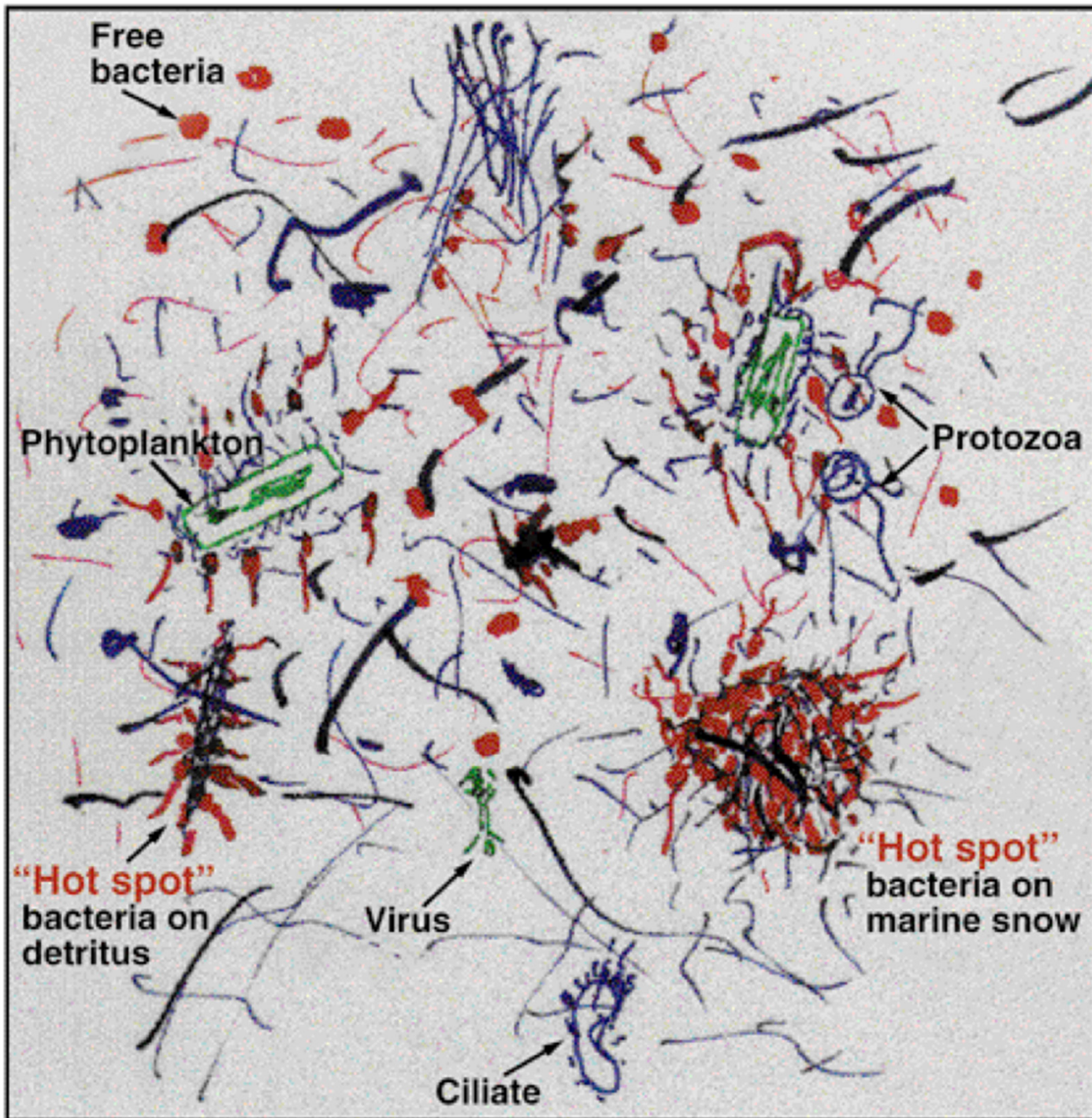


The bacterial response to phytoplankton blooms

Alison Buchan

Department of Microbiology





Generalized response

- Bacteria increase in abundance
- Secondary production increases
- Bacterial community composition changes in a successional fashion

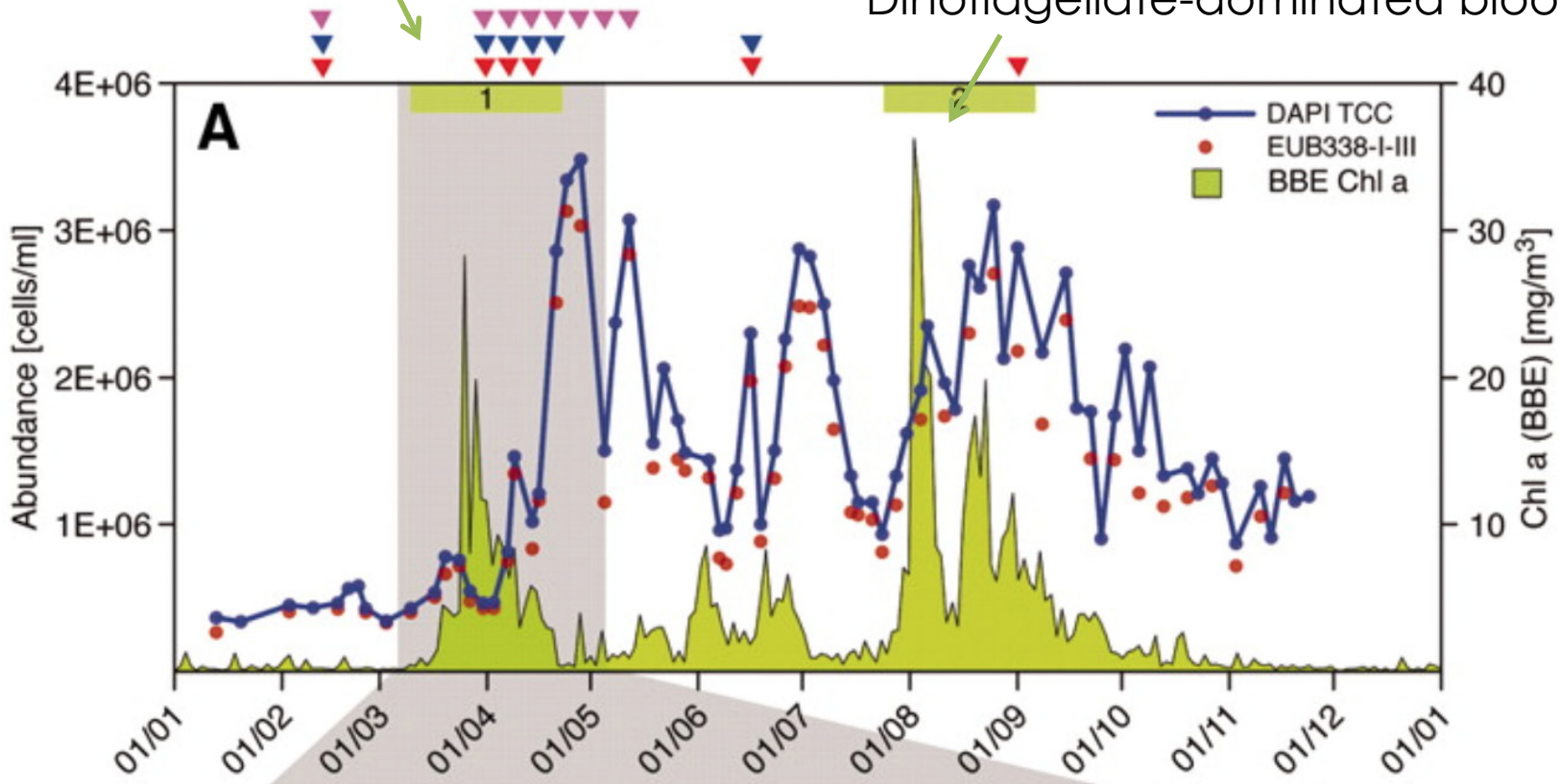
Substrate-Controlled Succession of Marine Bacterioplankton Populations Induced by a Phytoplankton Bloom

German Bight, North Sea

Hanno Teeling,^{1*} Bernhard M. Fuchs,^{1*} Dörte Becher,^{2,5} Christine Klockow,^{1,3} Antje Gardebrecht,⁶ Christin M. Bennke,¹ Mariette Kassabgy,¹ Sixing Huang,¹ Alexander J. Mann,^{1,3} Jost Waldmann,^{1,2,3} Marc Weber,^{1,3} Anna Klindworth,^{1,3} Andreas Otto,⁵ Jana Lange,² Jörg Bernhardt,^{5,7} Christine Reinsch,² Michael Hecker,^{2,5} Jörg Peplies,⁸ Frank D. Bockelmann,⁹ Ulrich Callies,⁹ Gunnar Gerdts,⁴ Antje Wichels,⁴ Karen H. Wiltshire,⁴ Frank Oliver Glöckner,^{1,3} Thomas Schweder,^{2,6}† Rudolf Amann¹†

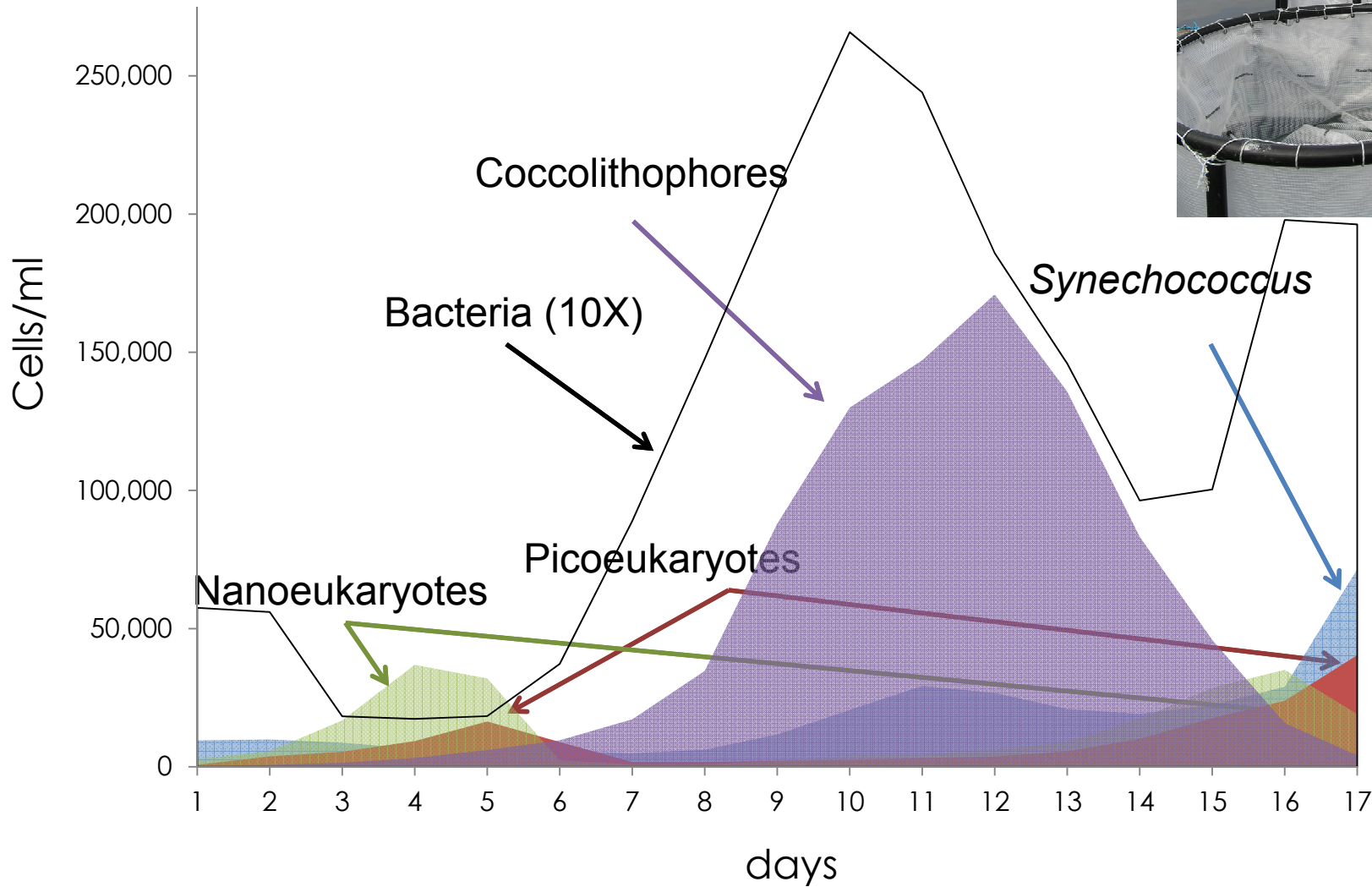
Diatom-dominated bloom

Dinoflagellate-dominated bloom



Mesocosm experiment: Raunefjorden, Espeland Norway

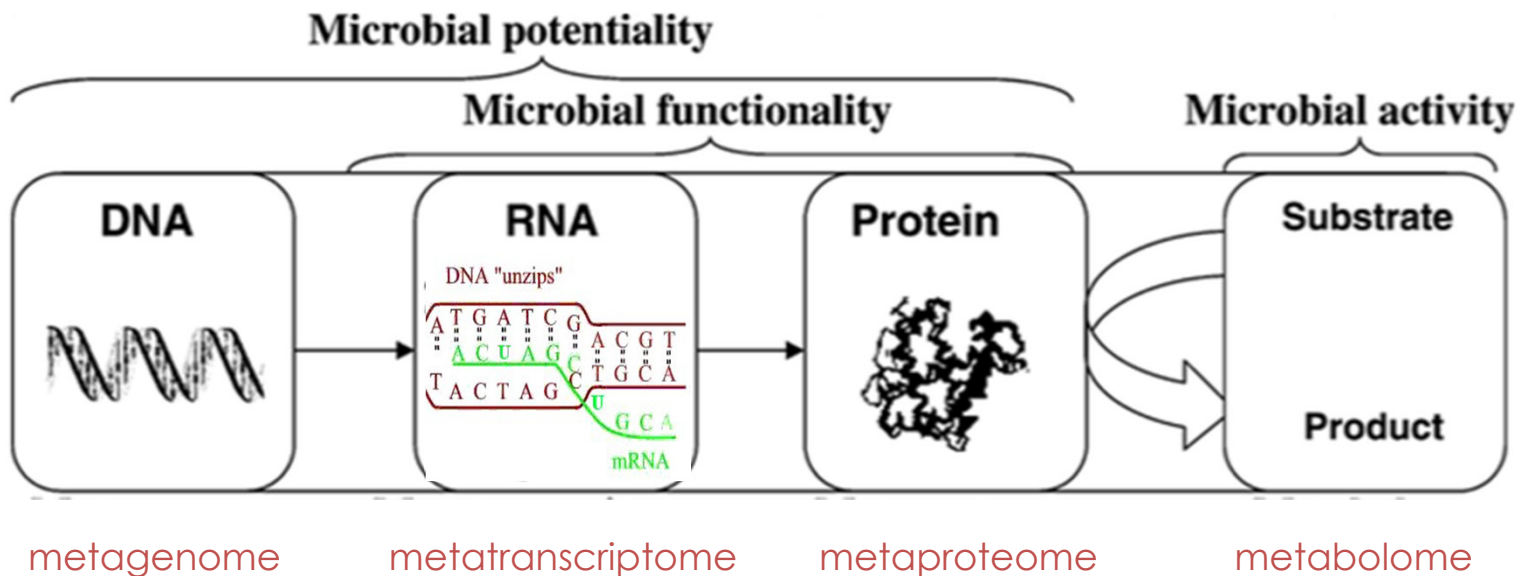
- Synechococcus
- Nanoeukaryotes
- Picoeukaryotes
- Coccolithophores



Data from Kimmance and Wilson

biomolecular signatures

- Amplicon sequencing of taxonomic (SSU rRNA) or functionally informative genes
- 'omics approaches



What do 16S rRNA gene surveys reveal about bacterial communities in blooms?

- They are diverse, but generally less so than non-bloom conditions
- Select lineages respond to bloom conditions
- They are dynamic
 - Successional changes from pre-bloom throughout bloom
 - Within broader phylogenetic groups, subgroups peak (“bloom”) at different times during the phytoplankton bloom

Changes in bacterioplankton composition under different phytoplankton regimens.

Pinhassi et al (2004) Appl Environ Microb

*“...majority of the bacterial phylotypes identified in our study belonged to the **Roseobacter** group or the **Bacteroidetes** phylum.”*

Differing growth responses of major phylogenetic groups of marine bacteria to natural phytoplankton blooms in the Western North Pacific Ocean

Tada et al (2011) Appl Environ Microb

*“**Roseobacter** bacteria remained widespread, active, and proliferating despite large fluctuations in organic matter and chlorophyll a concentrations. The relative contribution of **Bacteroidetes** to total bacterial production was consistently high.”*

Major differences of bacterial diversity and activity inside and outside of a natural iron-fertilized phytoplankton bloom in the Southern Ocean.

West et al (2008) Environ Microbiol

*“In the bloom, the dominant operational taxonomic units (OTUs) were the **Roseobacter NAC11-7** cluster, SAR92 and a Cytophaga-**Flavobacteria**-Bacteroides cluster related to the agg58 group, whereas in the HNLC region, SAR11, **Roseobacter RCA** and **Polaribacter** dominated.”*

Substrate-controlled succession of marine bacterioplankton populations induced by a phytoplankton bloom

Teeling et al (2012) Science

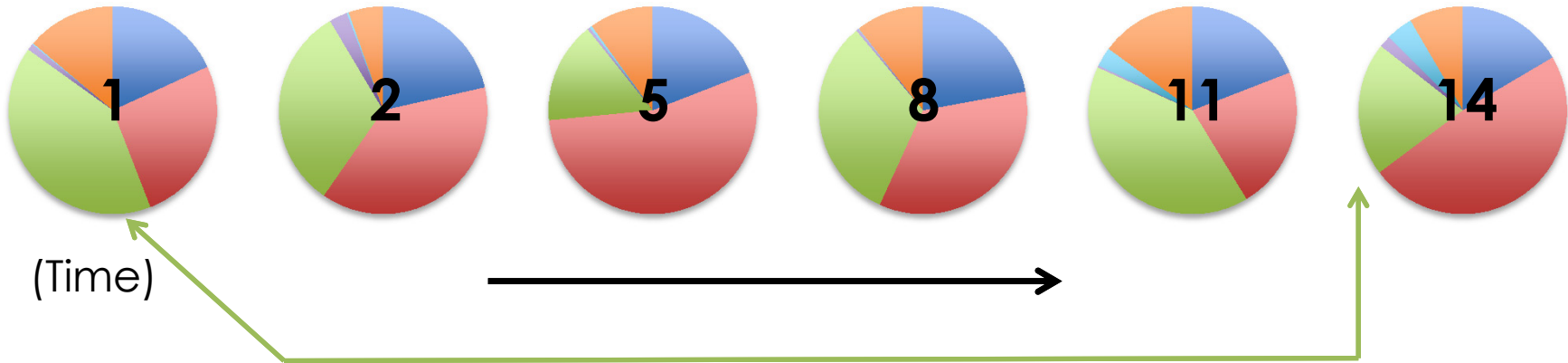
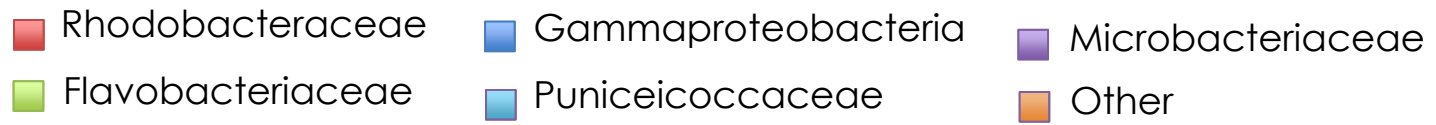
*“...distinct populations of **Bacteroidetes**, **Gammaproteobacteria**, and **Alphaproteobacteria** are specialized for successive decomposition of algal-derived organic matter.”*

“Roseobacter”

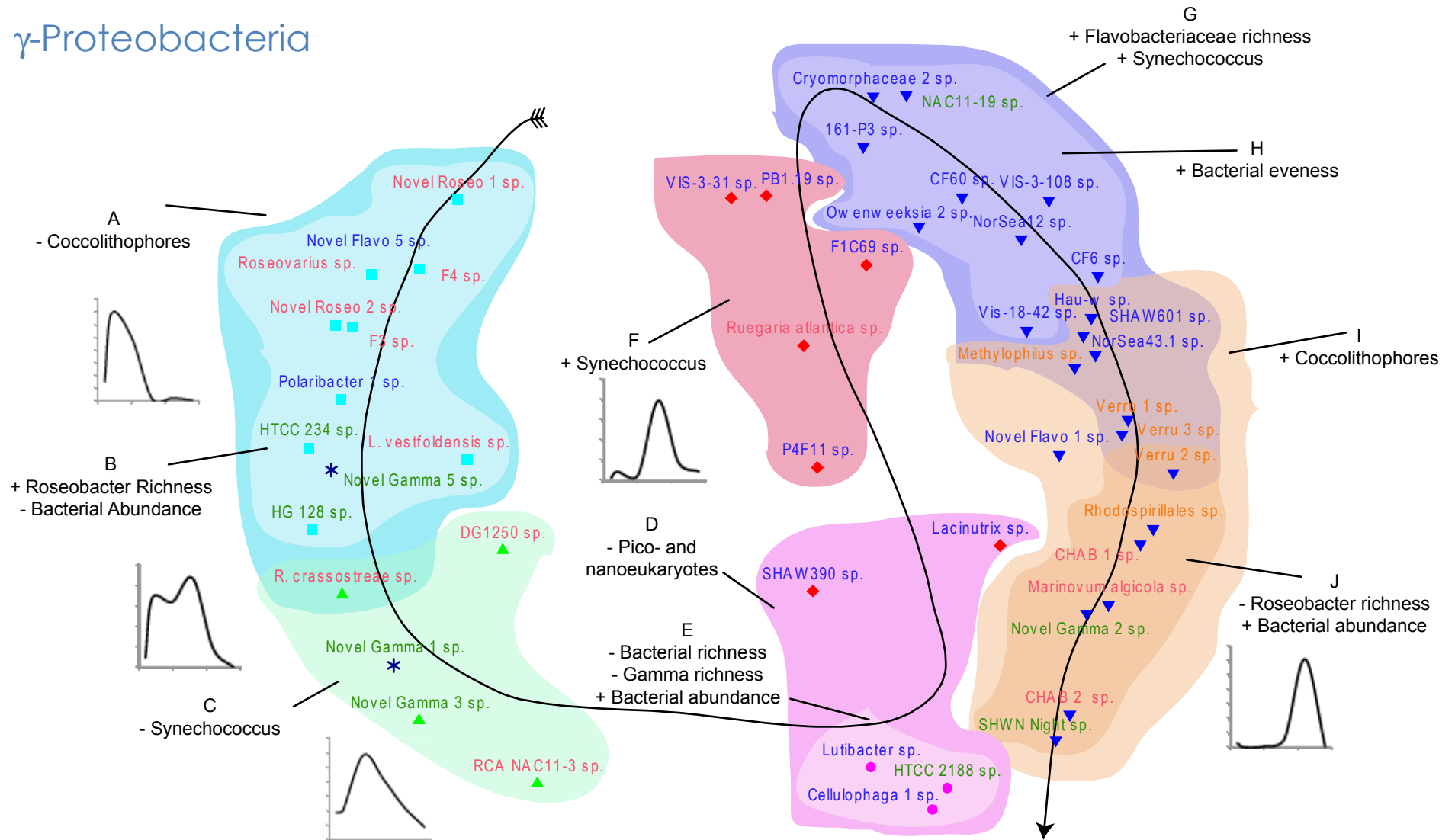
Domain: Bacteria
Phylum: Proteobacteria
Class: Alphaproteobacteria
Order: Rhodobacterales
Family: Rhodobacteraceae

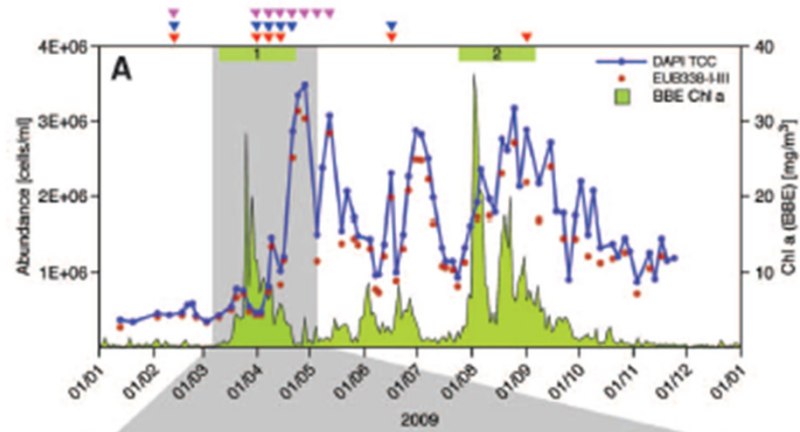
“Flavobacteria”

Bacteria
Bacteroidetes
Flavobacteriia
Flaviobacteriales
Flaviobacteriaceae

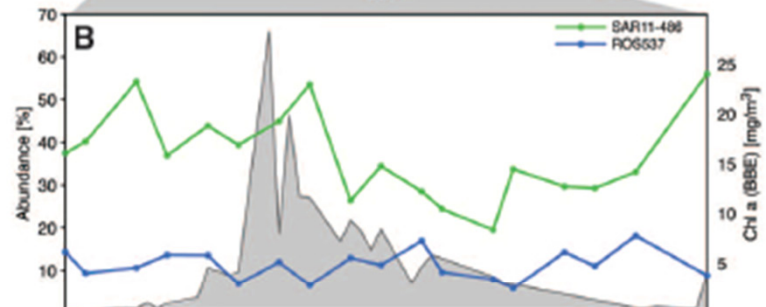


Rhodobacteraceae
 Flavobacteriaceae
 γ -Proteobacteria

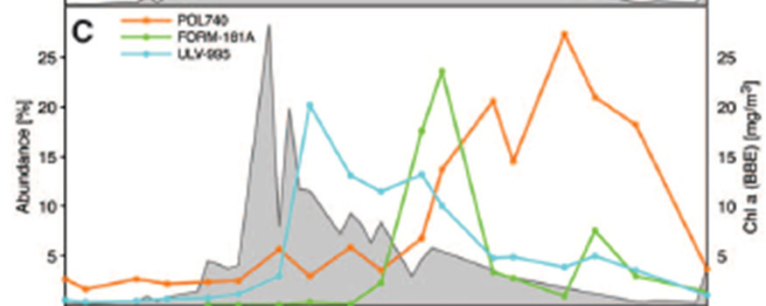




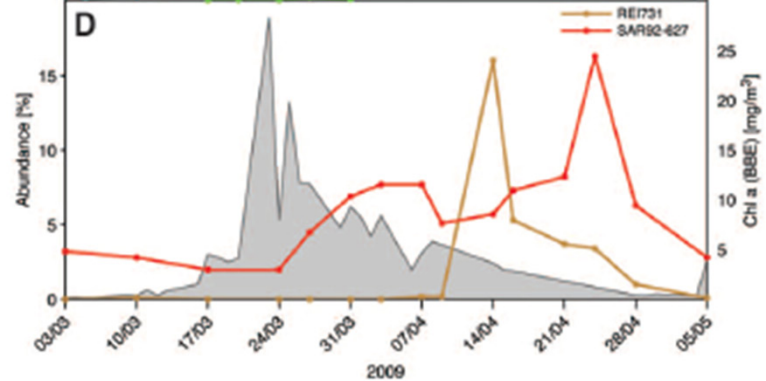
Red = metagenome
 Blue = metaproteome
 Magenta = 16S rRNA



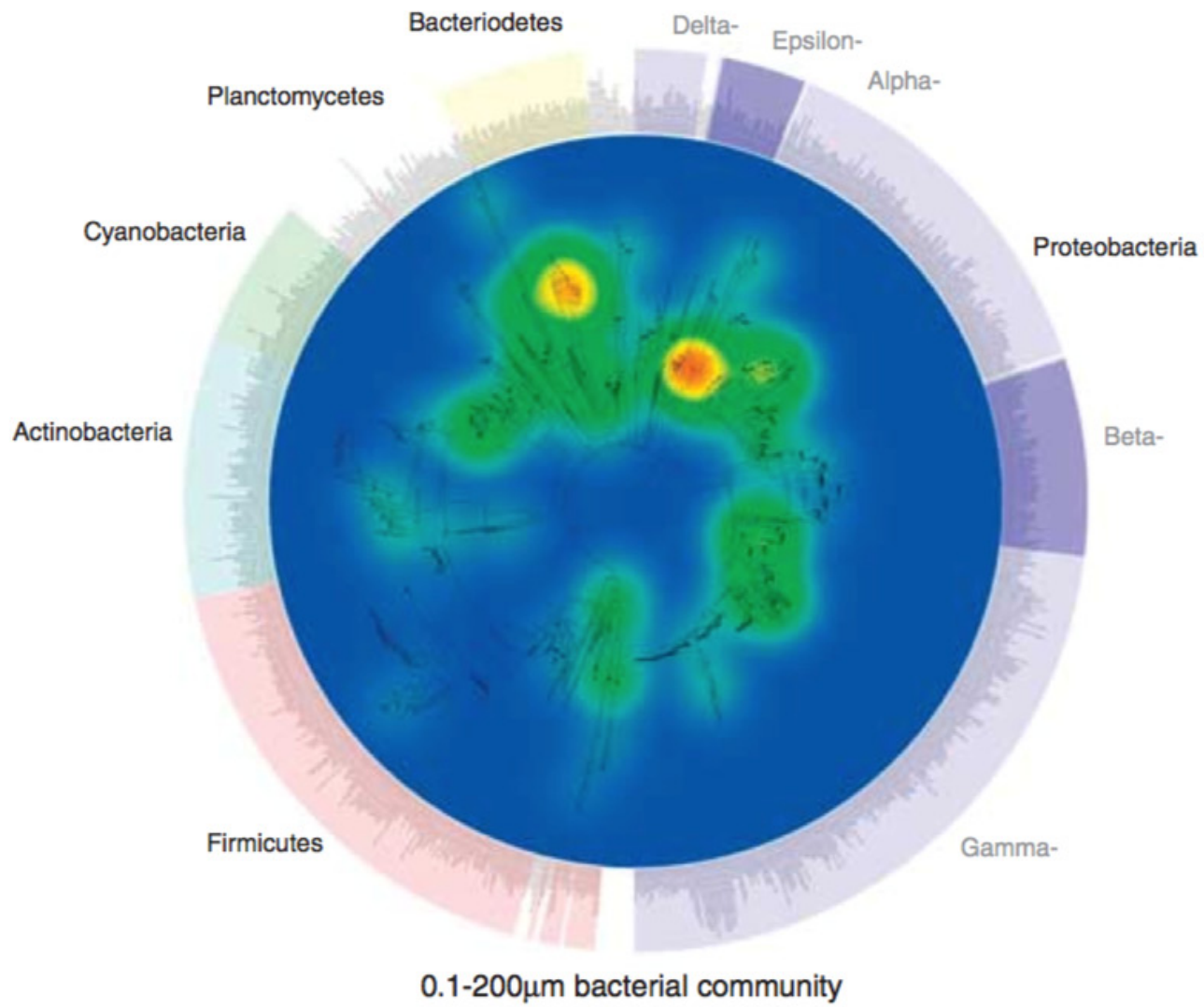
Alphaproteobacteria



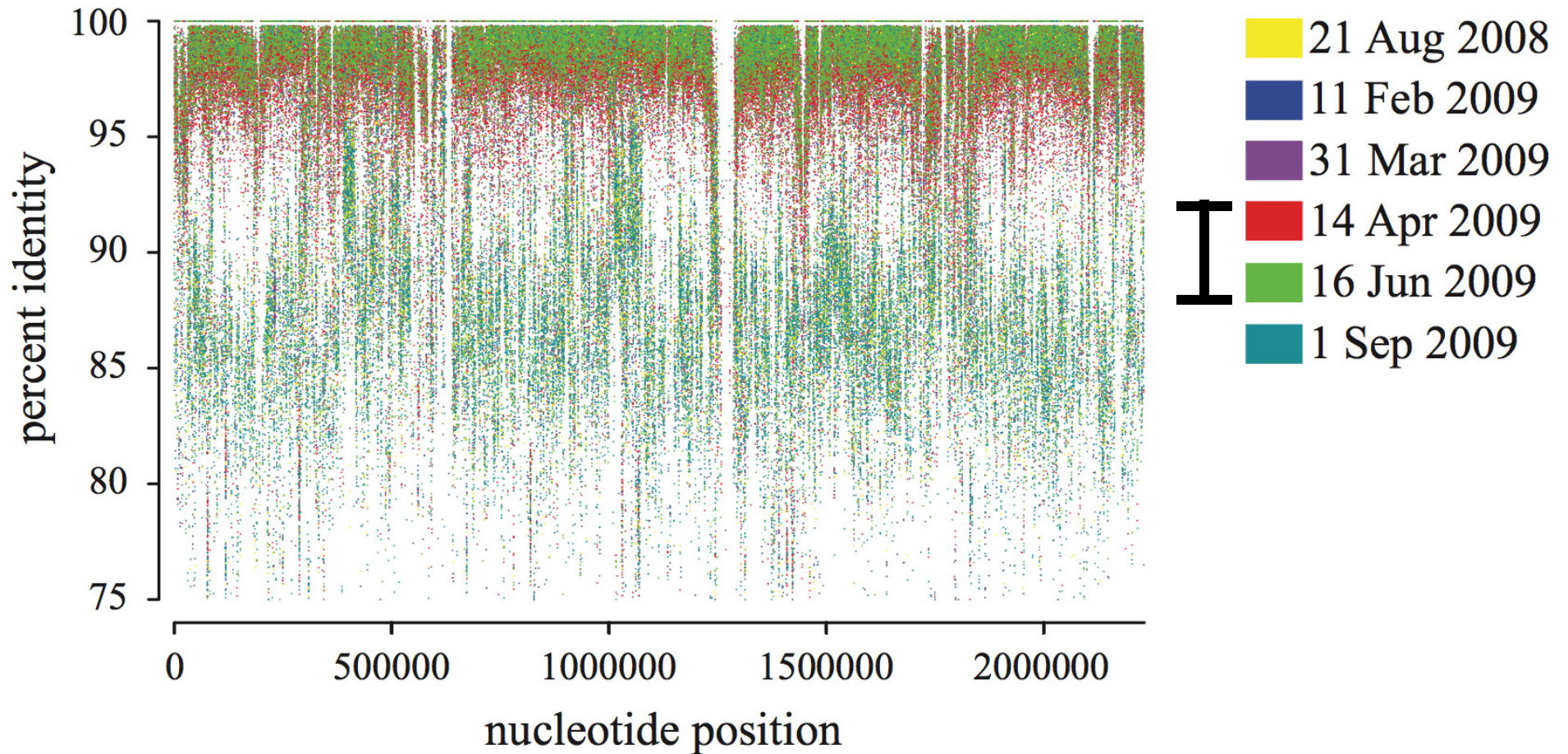
Flavobacteria



Gammaproteobacteria

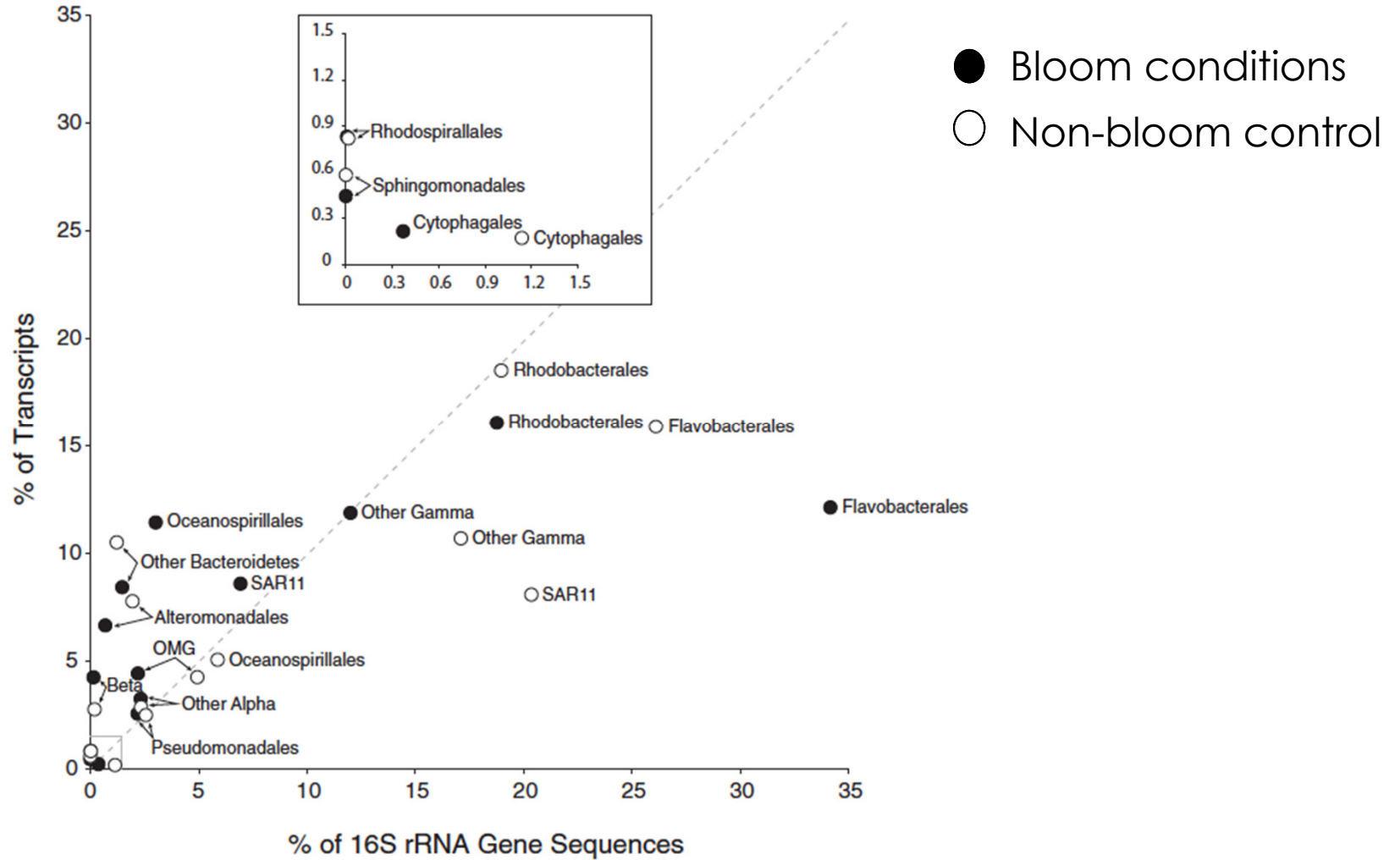


Recruitment of Teeling data to Roseobacter genome HTCC 2150

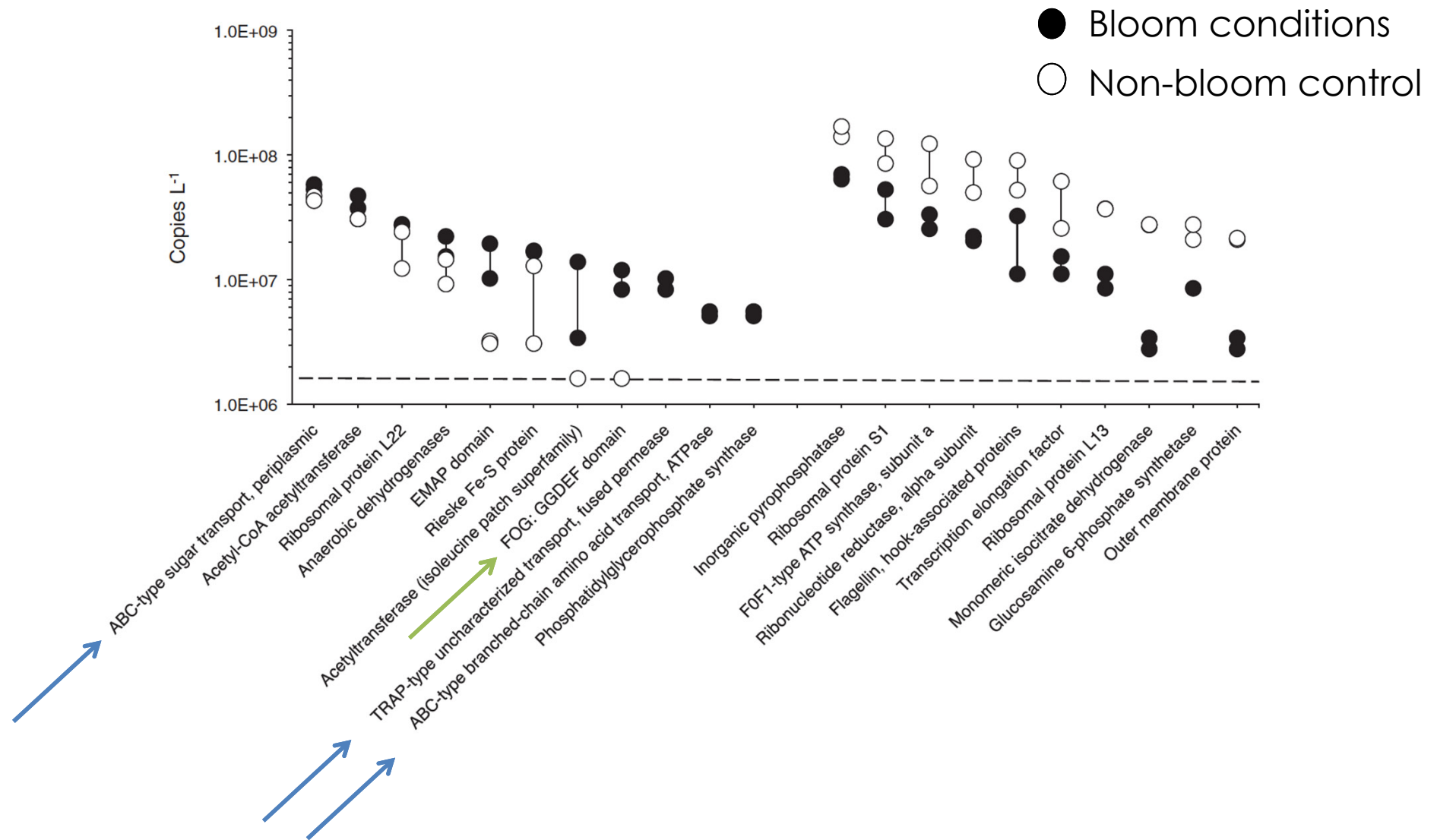


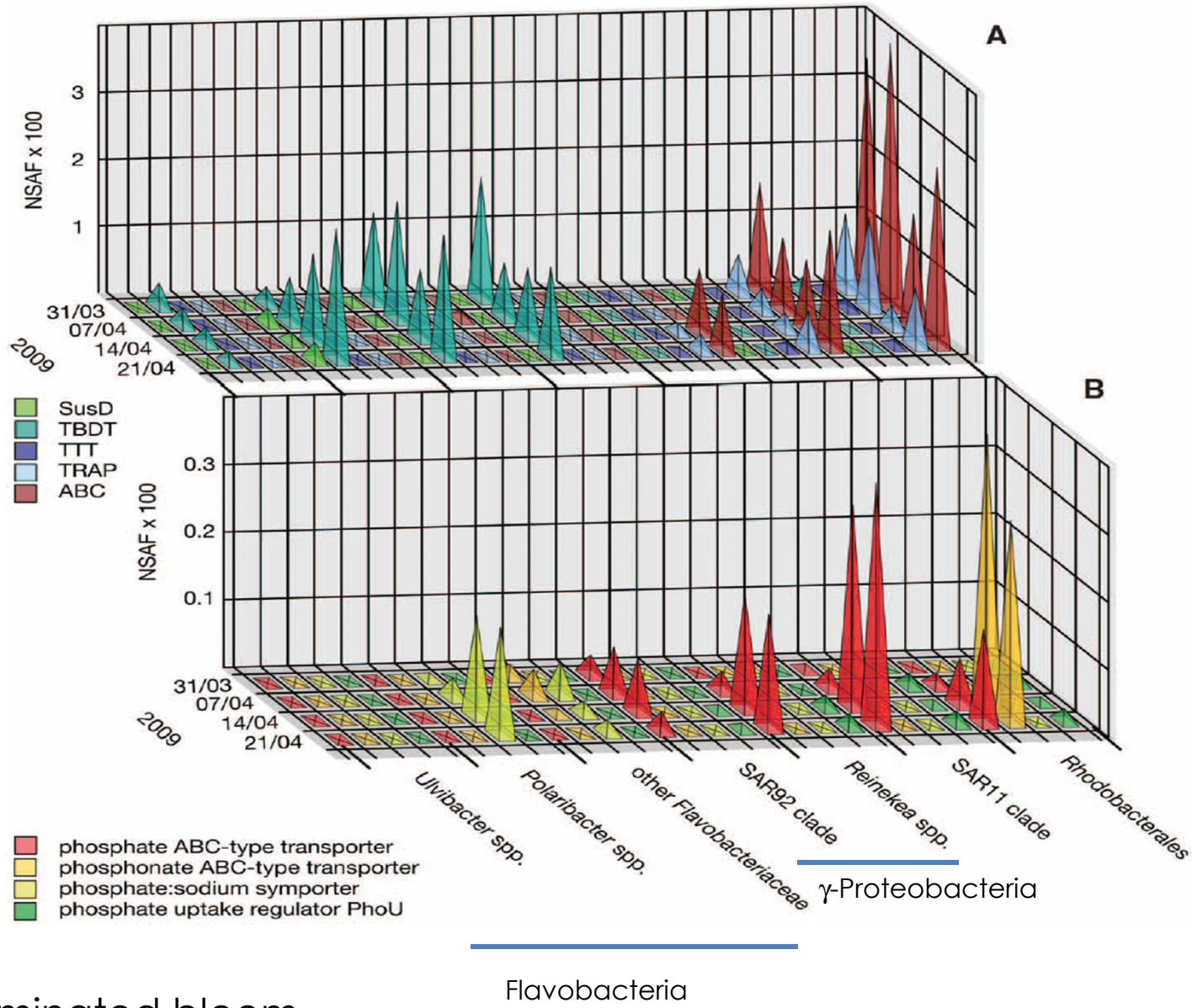
April/June is diatom-dominated summer bloom

Gulf of Mexico mesocosm bloom

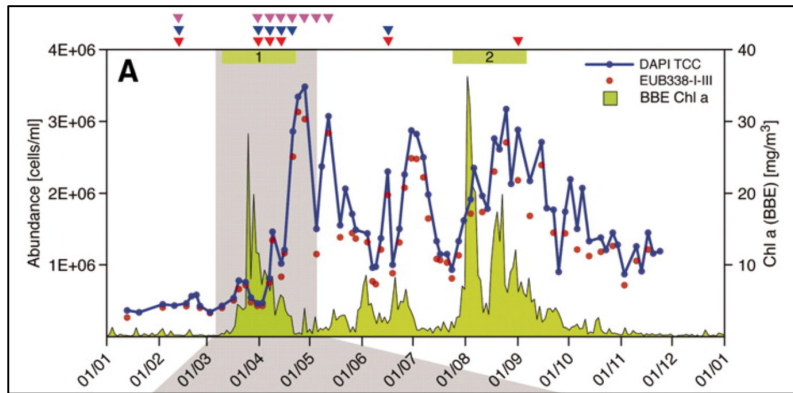
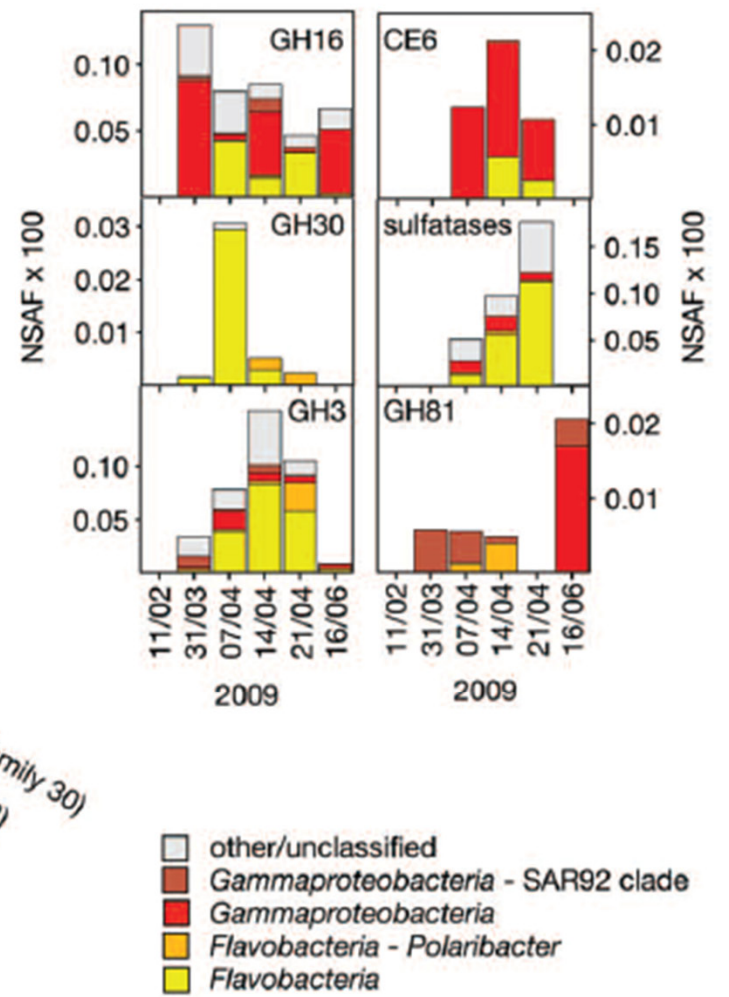
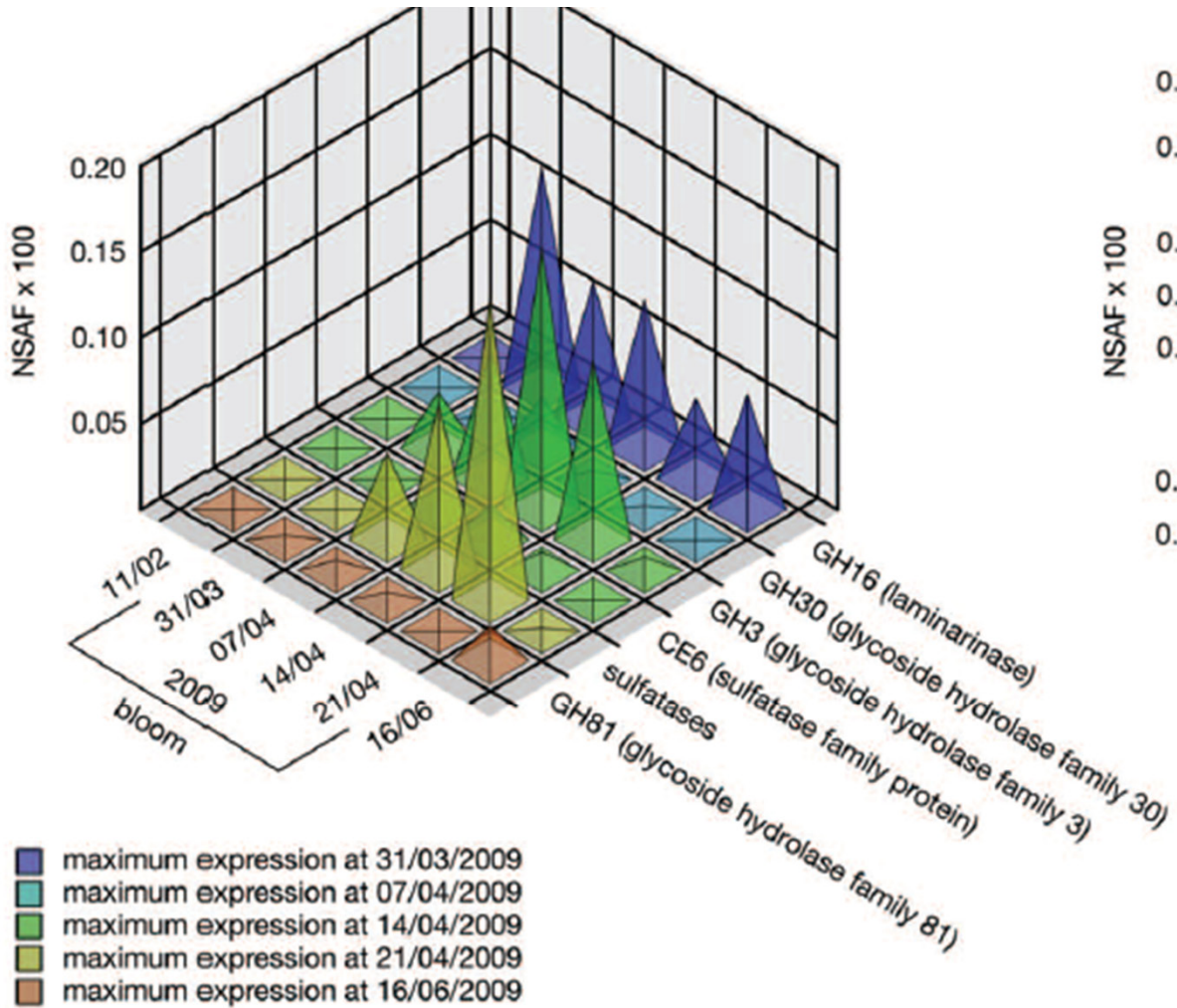


Transcripts of specific functional gene families are more (or less) abundant during blooms





Diatom-dominated bloom



Teeling et al (2012) Science

Moving forward with 'omics

- Missing low abundance functional traits
- Making sense of hypothetical genes/proteins
- Making sense of annotated genes/proteins
 - Deciphering the underlying interactions that give rise to system-level response
- Relating data to system level C fluxes

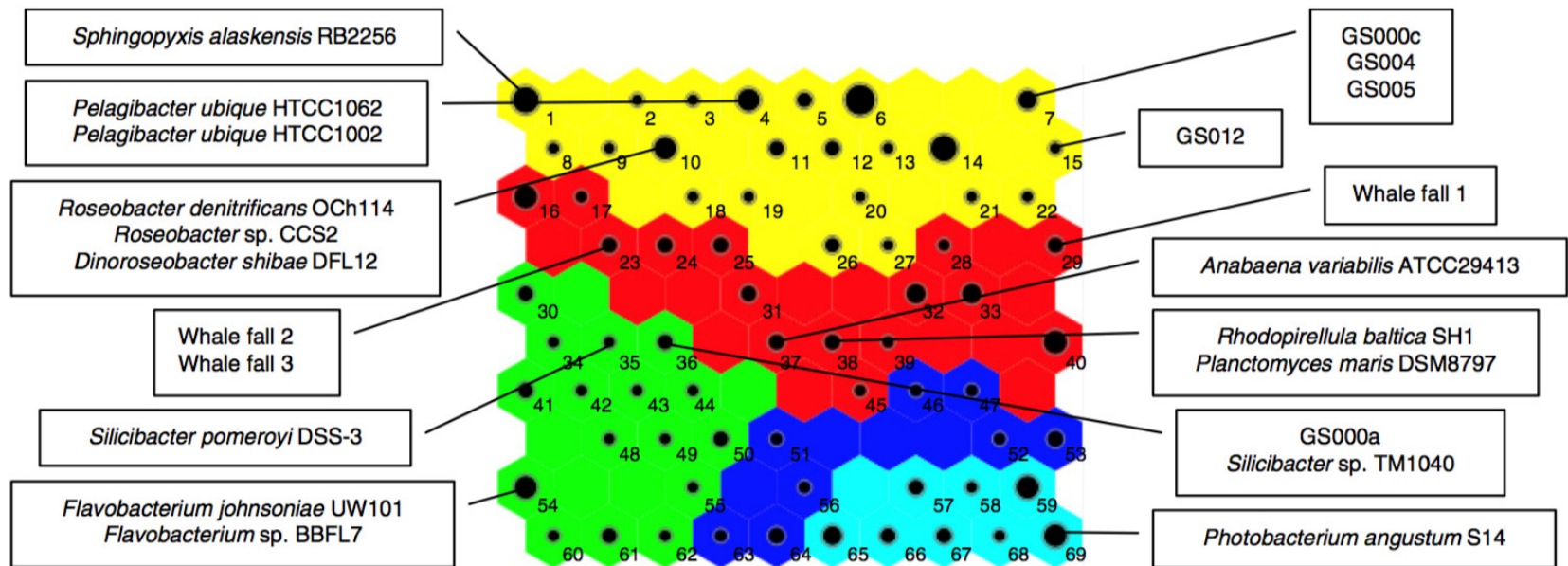
General features of bloom response bacteria

Table 1. Physiological characteristics of the model copiotroph *P. angustum* S14 and oligotroph *S. alaskensis* RB2256

Physiological characteristic	<i>P. angustum</i> S14	<i>S. alaskensis</i> RB2256
Trophic strategy	Copiotroph	Oligotroph
Growth strategy	Feast and famine	Equilibrium
Cell size	Large (>1 μm^3)	Small (<0.1 μm^3)
Maximum growth rate	>1 h^{-1}	<0.2 h^{-1}
Growth rate dependence on media richness	Yes	No
Starvation cross-protection to high levels of other stress inducing agents	Yes	No
Growing cells inherently resistant to stress inducing agents	No	Yes
Lag phase after starvation	Yes	No
<i>rpoS</i> -dependent reductive cell division	Yes	No
Consistent cell yield during nutrient limited growth	No	Yes

Inferring trophic status from genome sequences

oligotroph

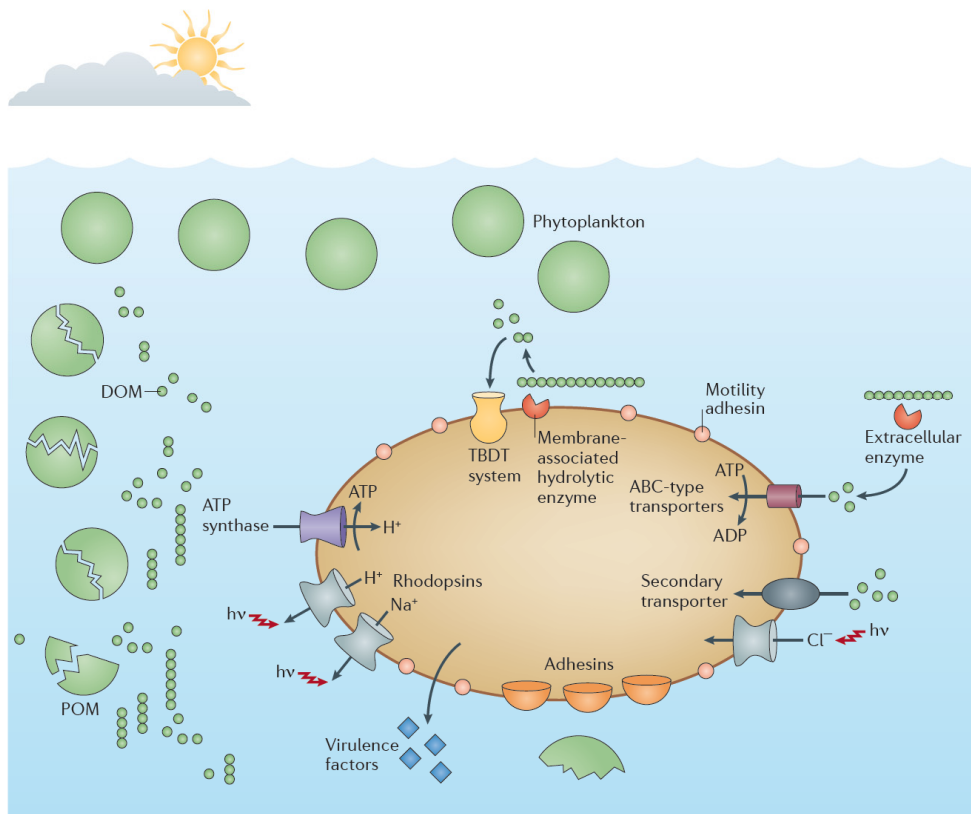


copiotroph

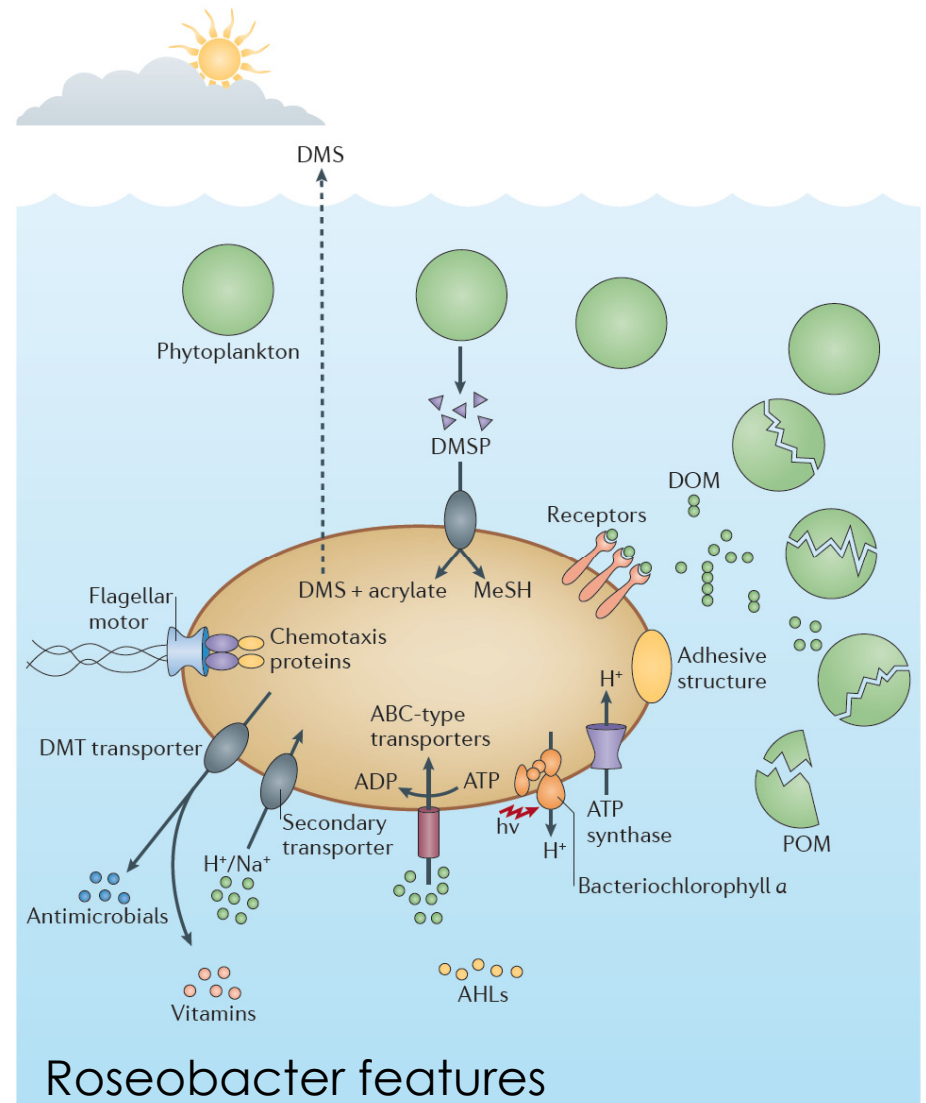
Genomic features of copiotrophs

- Large genome sizes (>4Mb)
- More transporters, high specificity
- More sensory mechanisms (e.g. chemotaxis)
- Motility & adhesion
- Secondary metabolite production, excretion and detoxification
- Complex and numerous regulatory networks
- Chemical signaling

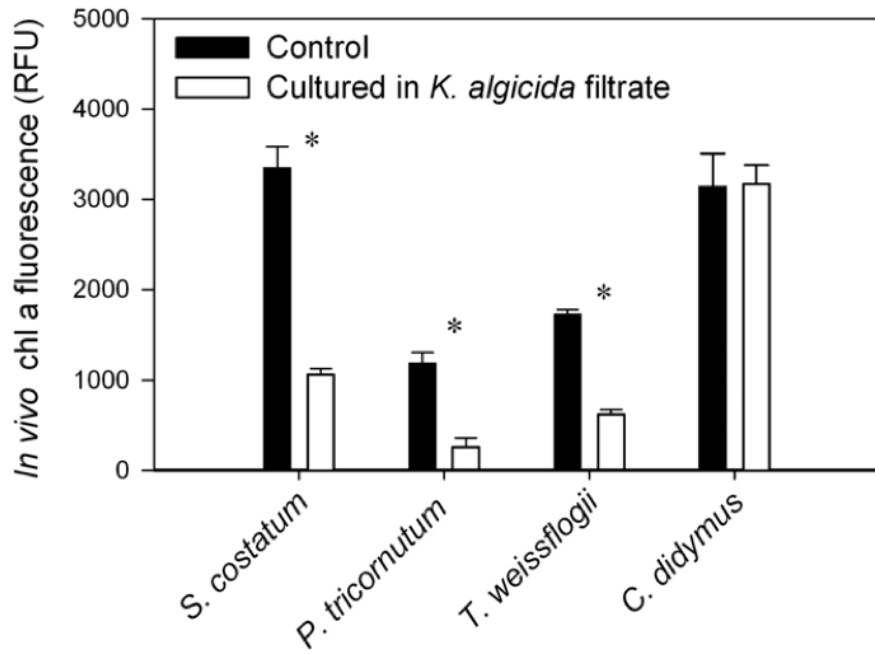
What can we learn from model systems?



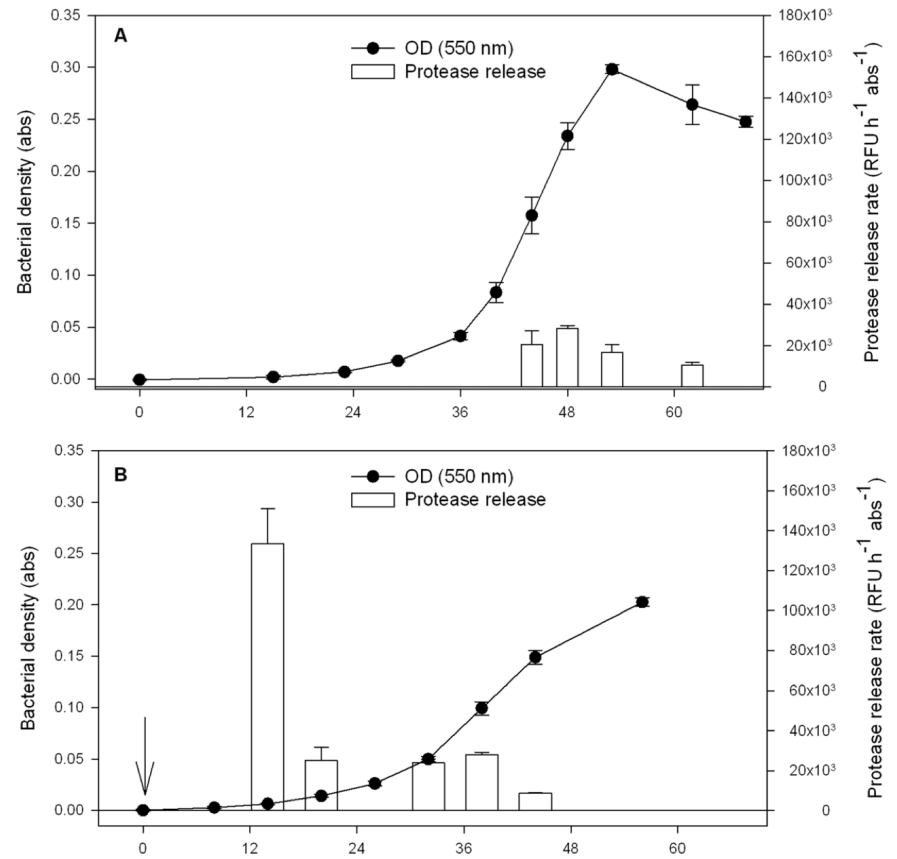
Flavobacteria features



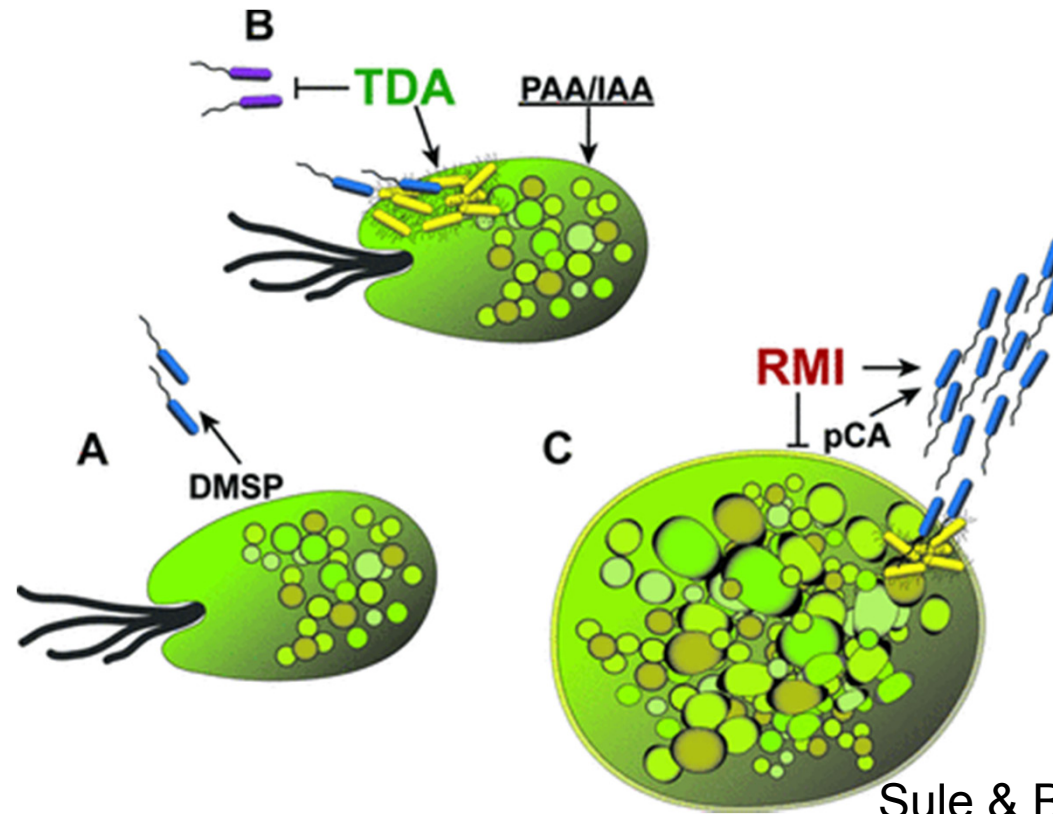
Roseobacter features



Flavobacteria strain produces protease active against diatoms



The “Jekyll & Hyde” nature of roseobacter-phytoplankton relationships

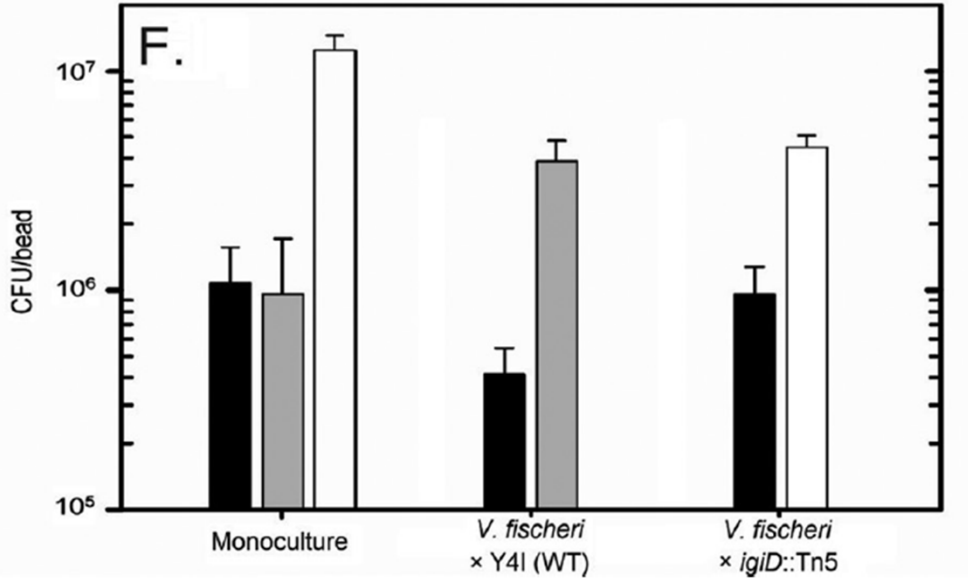


Sule & Belas 2012 (J Bact)

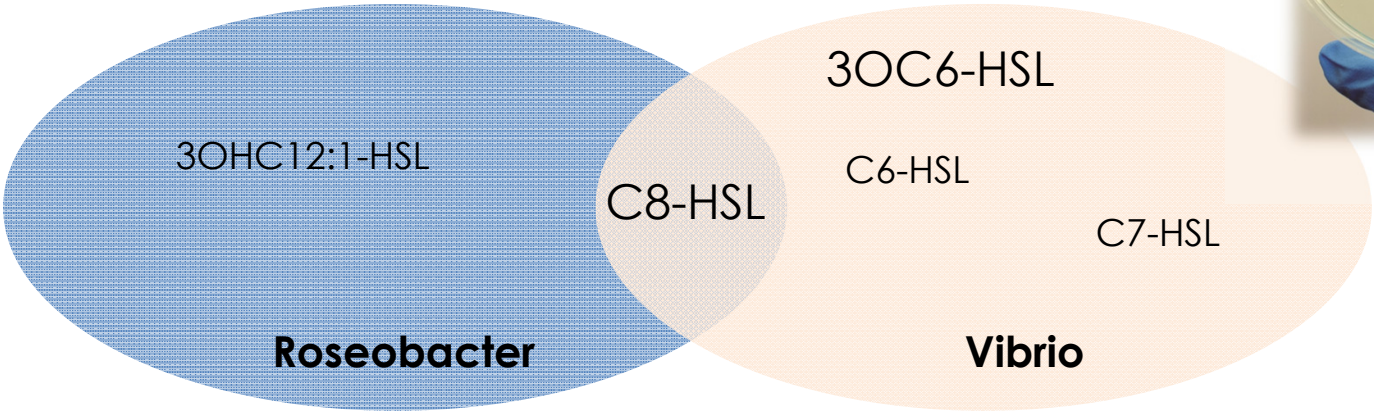
Reugeria sp.
Phaeobacter sp.
Dinoroseobacter shibae

Seyedsayamdost et al (2011) Nat Chem Bio
Wang et al (2014) (Frontiers)

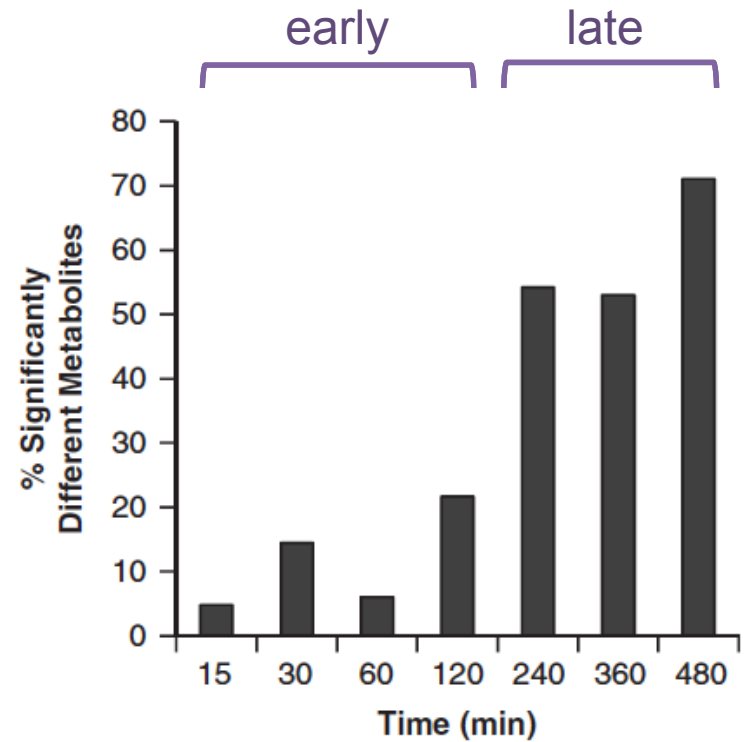
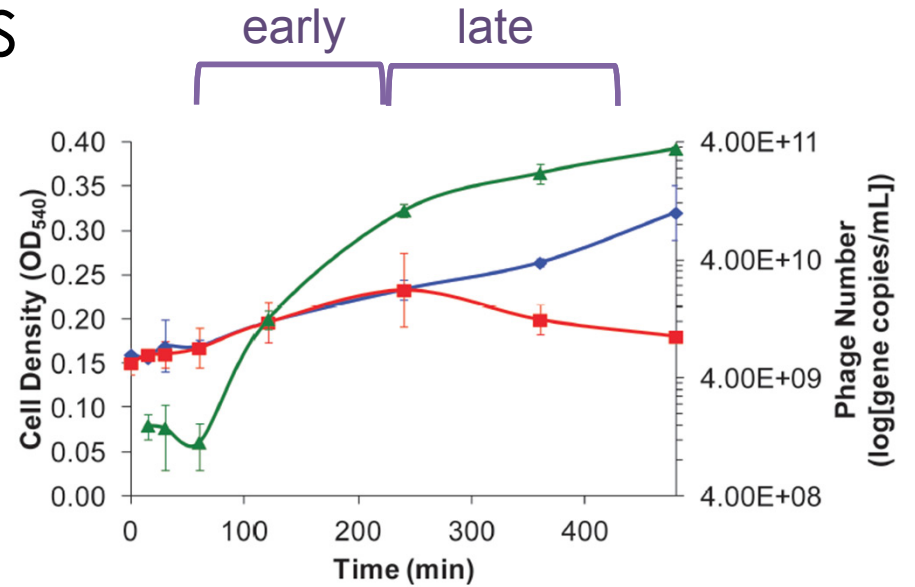
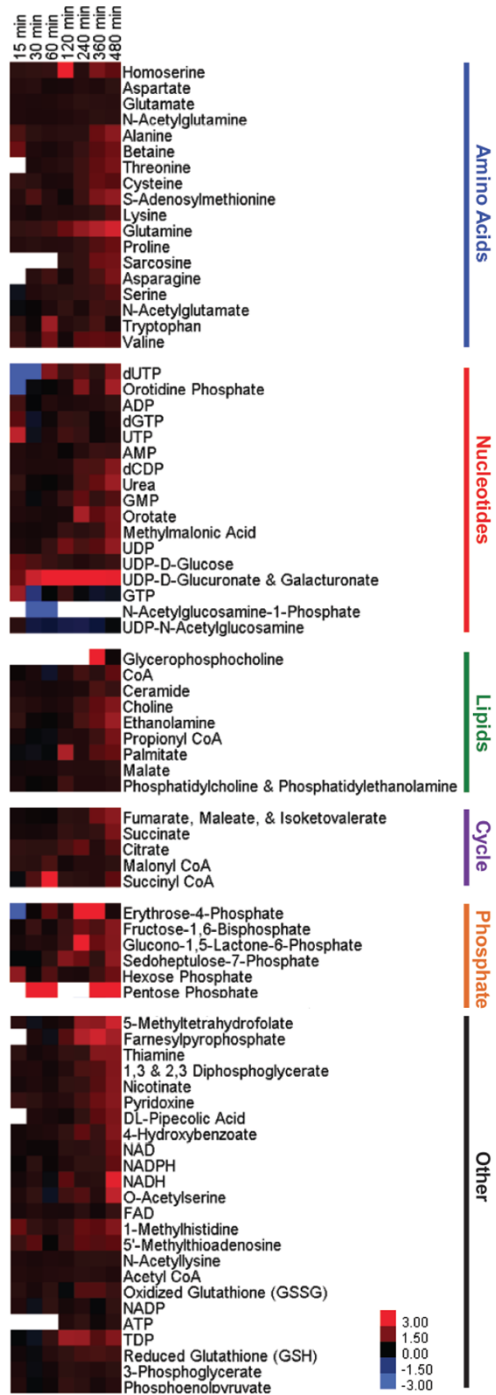
Interactions with other bacteria



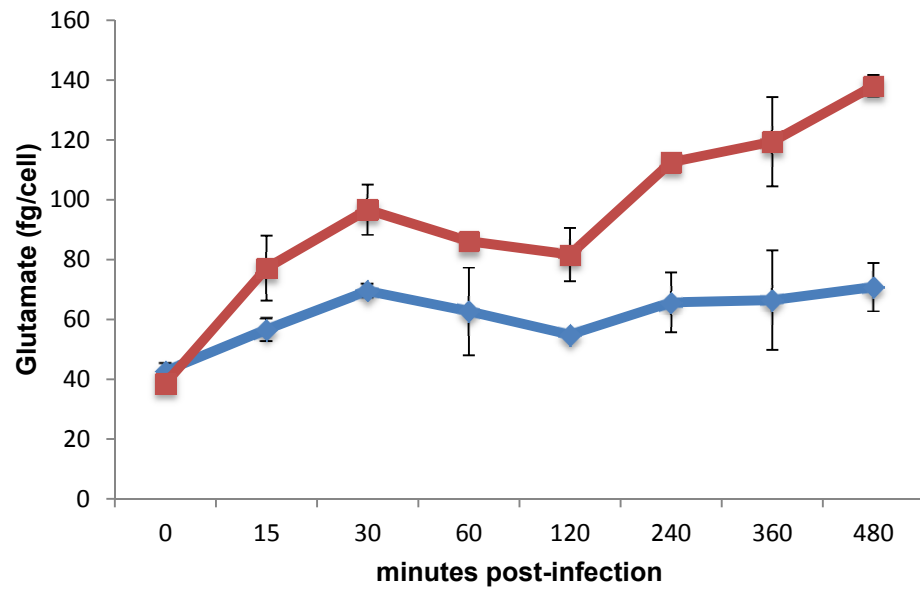
AHLs



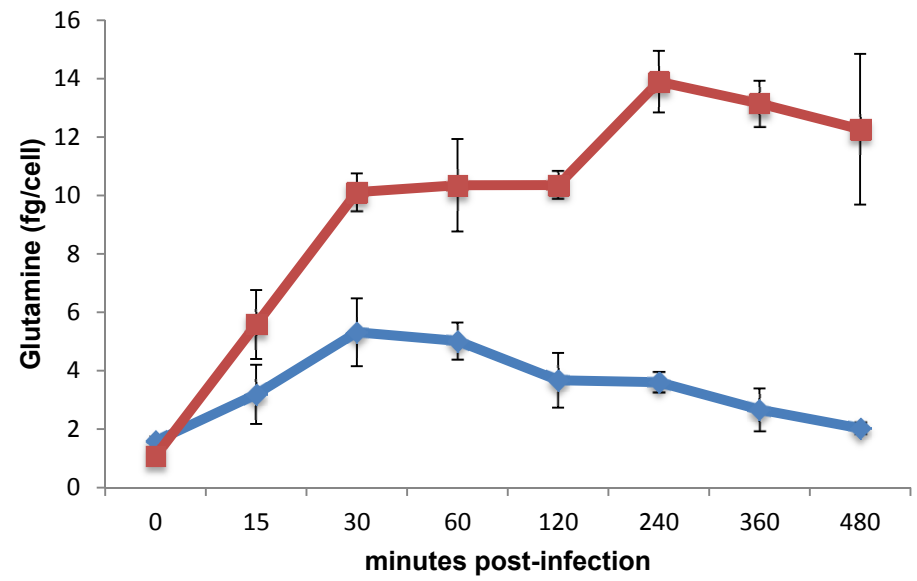
Interactions with viruses

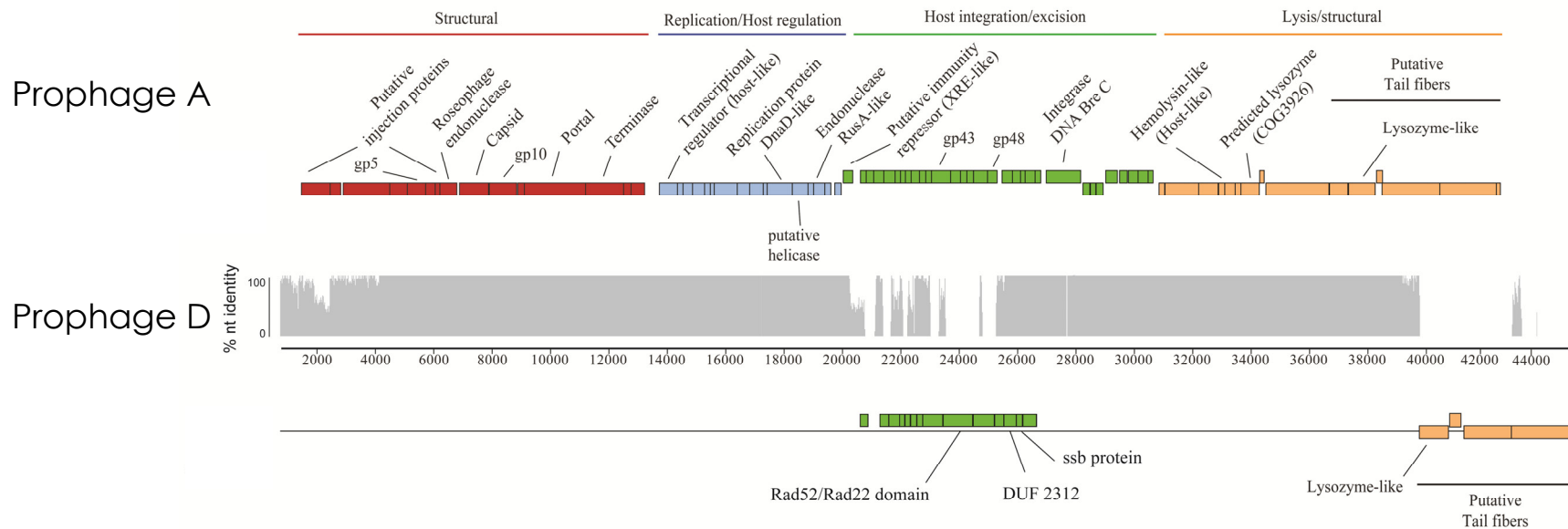


GLUTAMATE

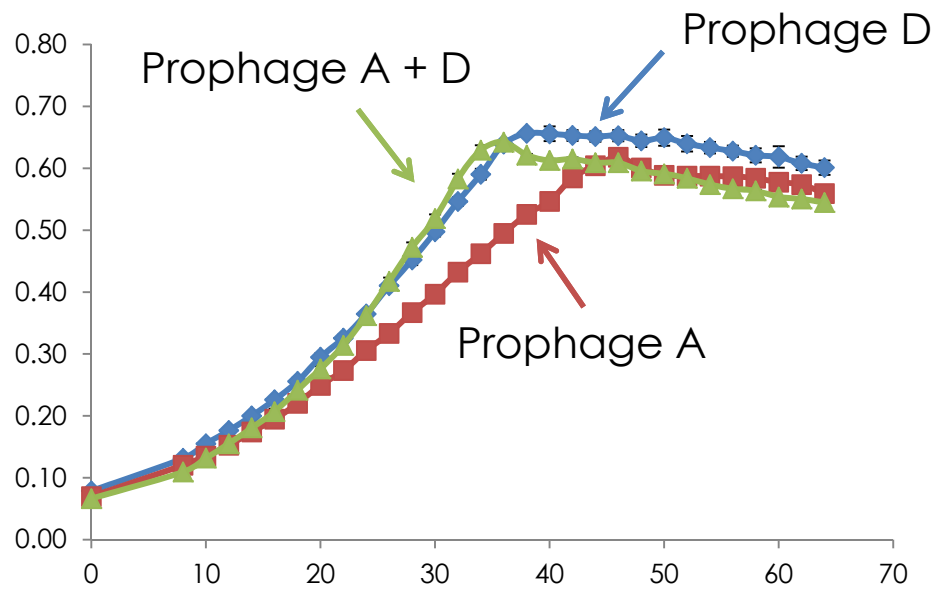


GLUTAMINE





Growth rates of different lysogens

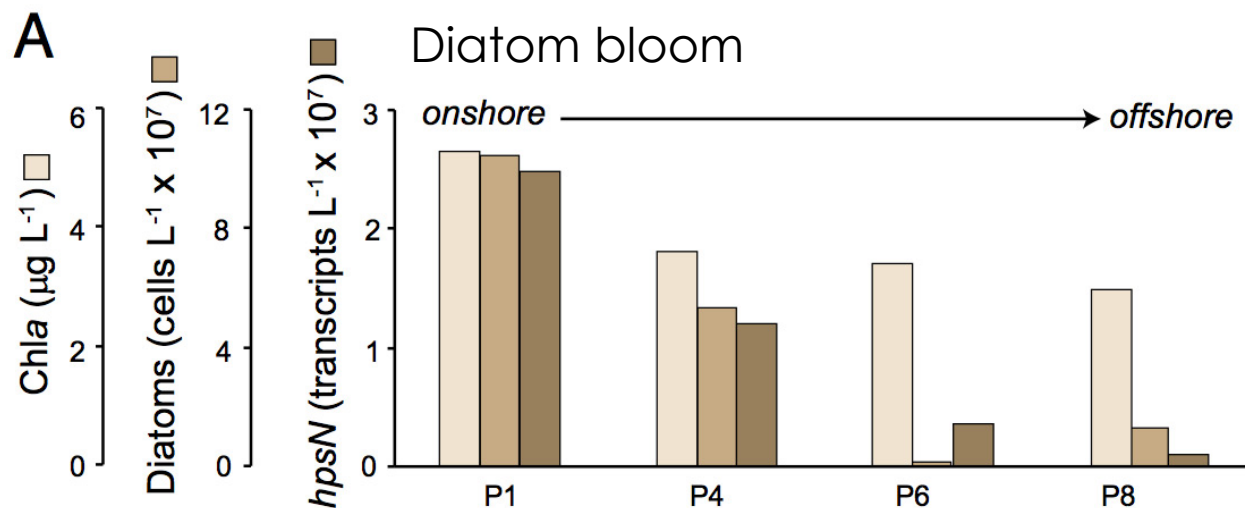


Interaction and signalling between a cosmopolitan phytoplankton and associated bacteria

S. A. Amin^{1,2}, L. R. Hmelo³, H. M. van Tol¹, B. P. Durham⁴, L. T. Carlson¹, K. R. Heal¹, R. L. Morales¹, C. T. Berthiaume¹,
M. S. Parker¹, B. Djunaedi¹, A. E. Ingalls¹, M. R. Parsek³, M. A. Moran⁵ & E. V. Armbrust¹ (2015) Nature

Cryptic carbon and sulfur cycling between surface ocean plankton

Bryndan P. Durham^a, Shalabh Sharma^b, Haiwei Luo^b, Christa B. Smith^b, Shady A. Amin^c, Sara J. Bender^d,
Stephen P. Dearth^e, Benjamin A. S. Van Mooy^d, Shawn R. Campagna^e, Elizabeth B. Kujawinski^d, E. Virginia Armbrust^c,
and Mary Ann Moran^{b,1} (2015) PNAS



Conclusions

- Specific lineages of marine bacteria respond positively to phytoplankton blooms
- “Omics field data provides evidence for niche specialization
- Lab experiments provide evidence for highly specific interactions between bacteria and phytoplankton
- Reconciling ‘omics data with system level measurements

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(University of La Laguna)



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