Past, present, and future Coccolithophores in a changing ocean.

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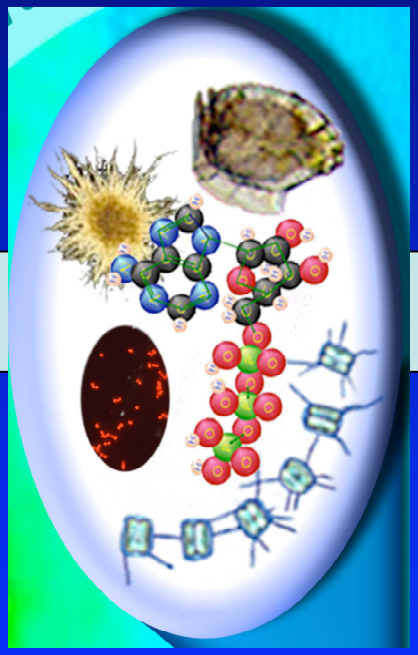
A changing ocean - predicting biological and biogeochemical responses

Warming
Inc CO_2
Dec pH
N and P?



Ecology
Biogeochemistry
Climate

The take home message…

- Coccolithophores are really cool - in part because the dynamics of this one group can dramatically influence biogeochemical cycling

- Of the coccolithophores, *Emiliania huxleyi* is emerging as increasingly important model for studies of …
  - *Paleo climate reconstruction*
  - *S cycling*
  - *Viral dynamics*
  - *Carbon cycling*

- Anatomy of a eukaryotic genome project "euks are challenging"

- Transcriptome profiling for aiding genome annotation and moving beyond "capacity"
  - *Introduction to SAGE*
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- What does the future hold? … The challenges of prediction in microbial oceanography
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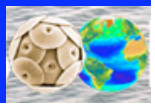
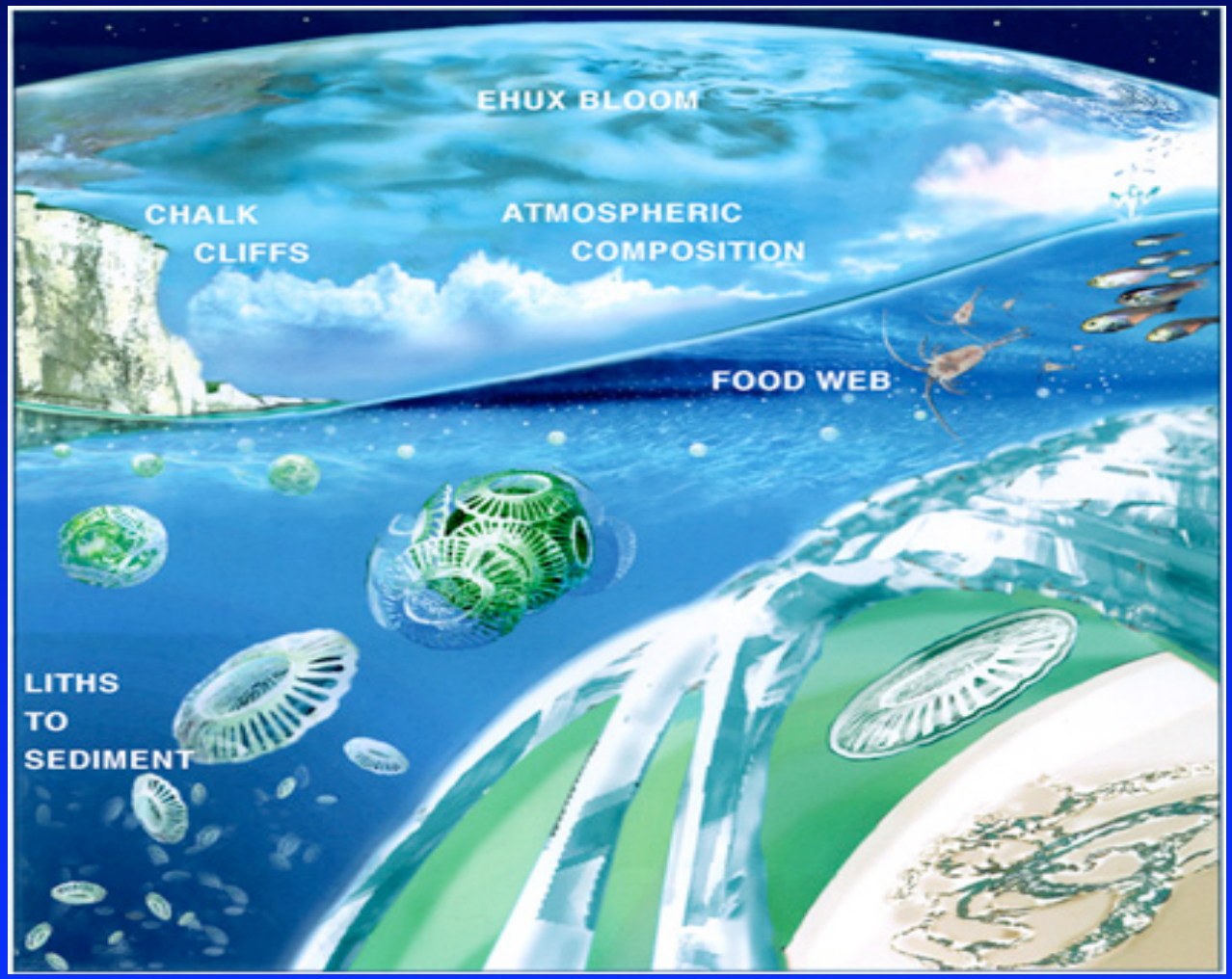
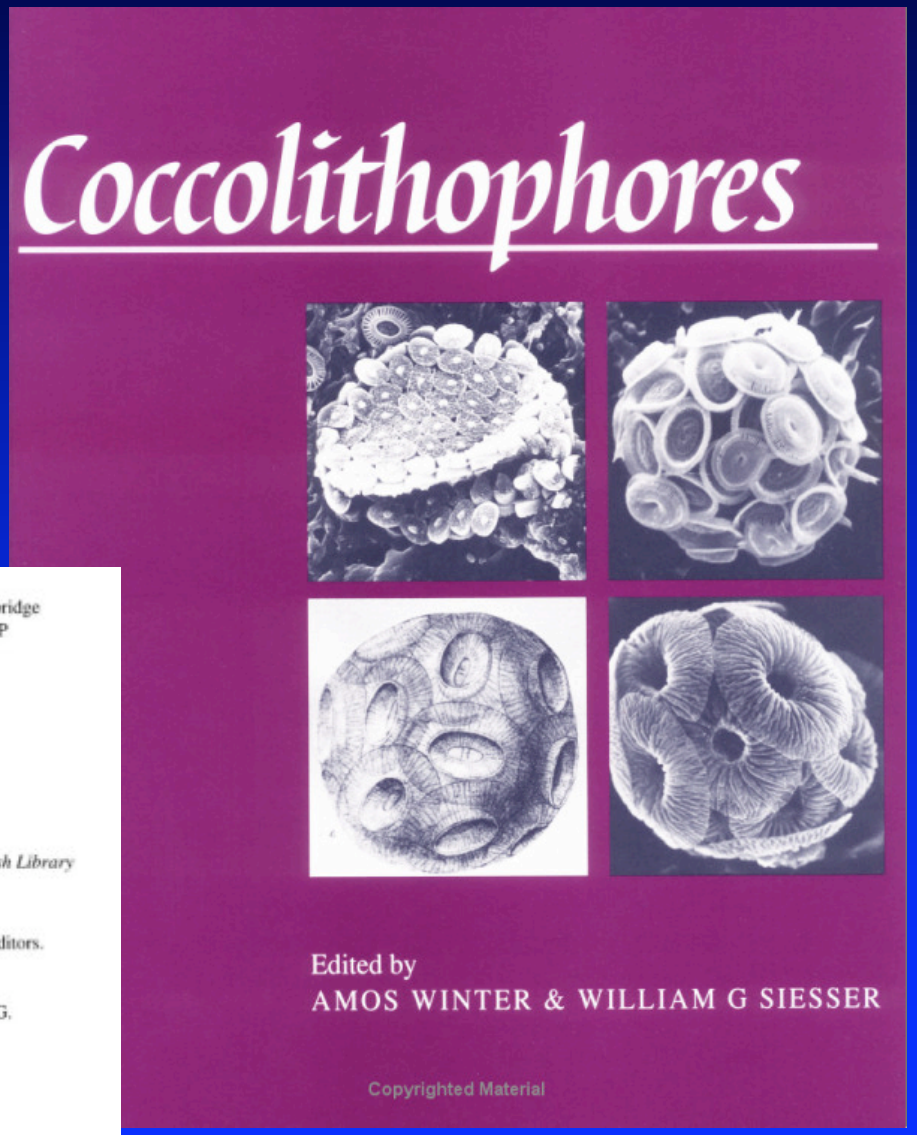


Coccolithophores are cool



Graphic: www.noc.soton.ac.uk

Cococlithophores - a rich natural history



Published by the Press Syndicate of the University of Cambridge
The Pitt Building, Trumpington Street, Cambridge CB2 1RP
40 West 20th Street, New York, NY 10011-4211, USA
10 Stamford Road, Oakleigh, Melbourne 3166, Australia

First published 1994

Printed in Great Britain at the University Press, Cambridge

A catalogue record for this book is available from the British Library

Library of Congress cataloguing in publication data

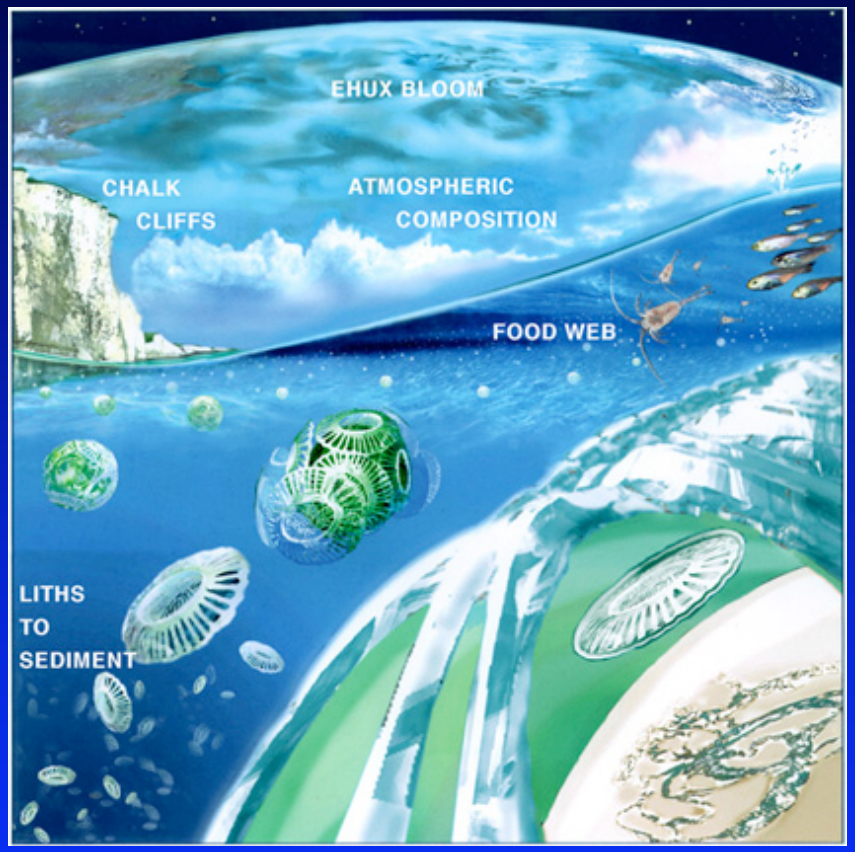
Coccolithophores / Amos Winter and William G. Siesser, editors.
p. cm.
ISBN 0-521-38050-2
1. Coccolithophores. I. Winter, Amos. II. Siesser, William G.
QK569.C63C63 1994
589.4'87–dc20 93-1777 CIP

ISBN 0 521 38050 2 hardback

Cococlithophores - a rich natural history

- **Ehrenberg (1795-1876) “the Founder of Micropaleontology”**
  - ***First to discover and identify fossils of what would be called coccoliths***
  - ***1836 First “coccolith” observation in from chalk deposits from the Baltic***

- **Thomas Huxley, naturalist and “Darwin’s Bulldog”**
  - ***1857 coins the term coccolith “spherical stone” for the mineral bodies resembling coccoid cells which he observed in sediments***



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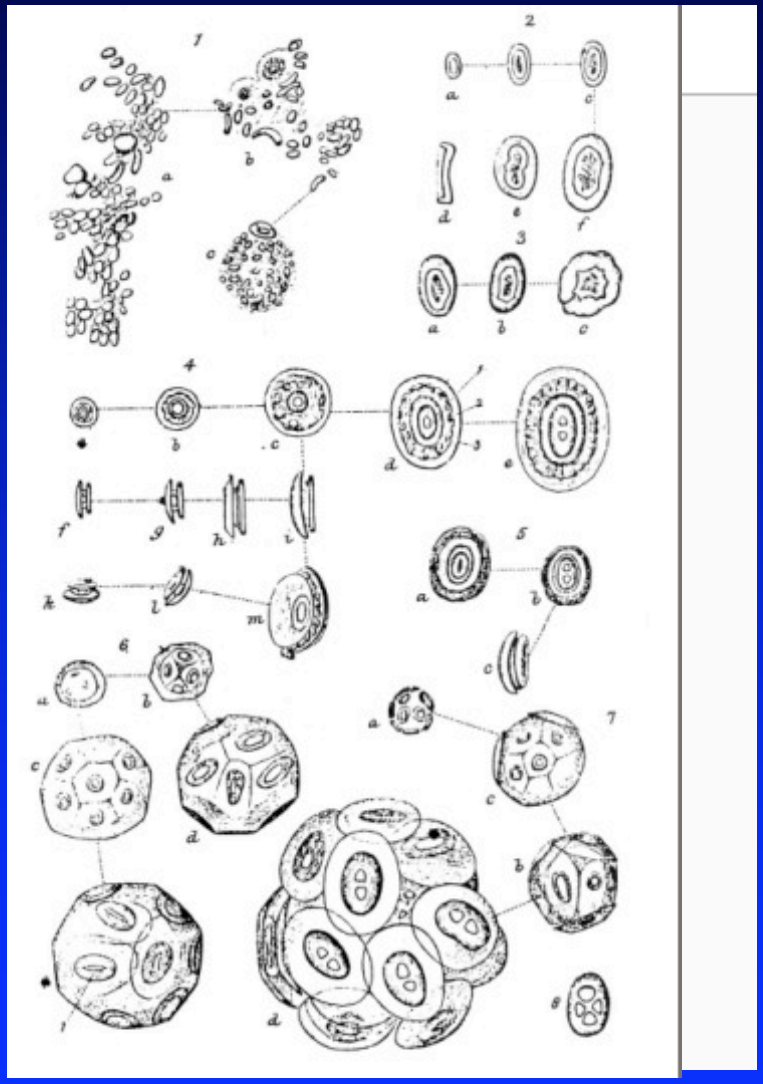
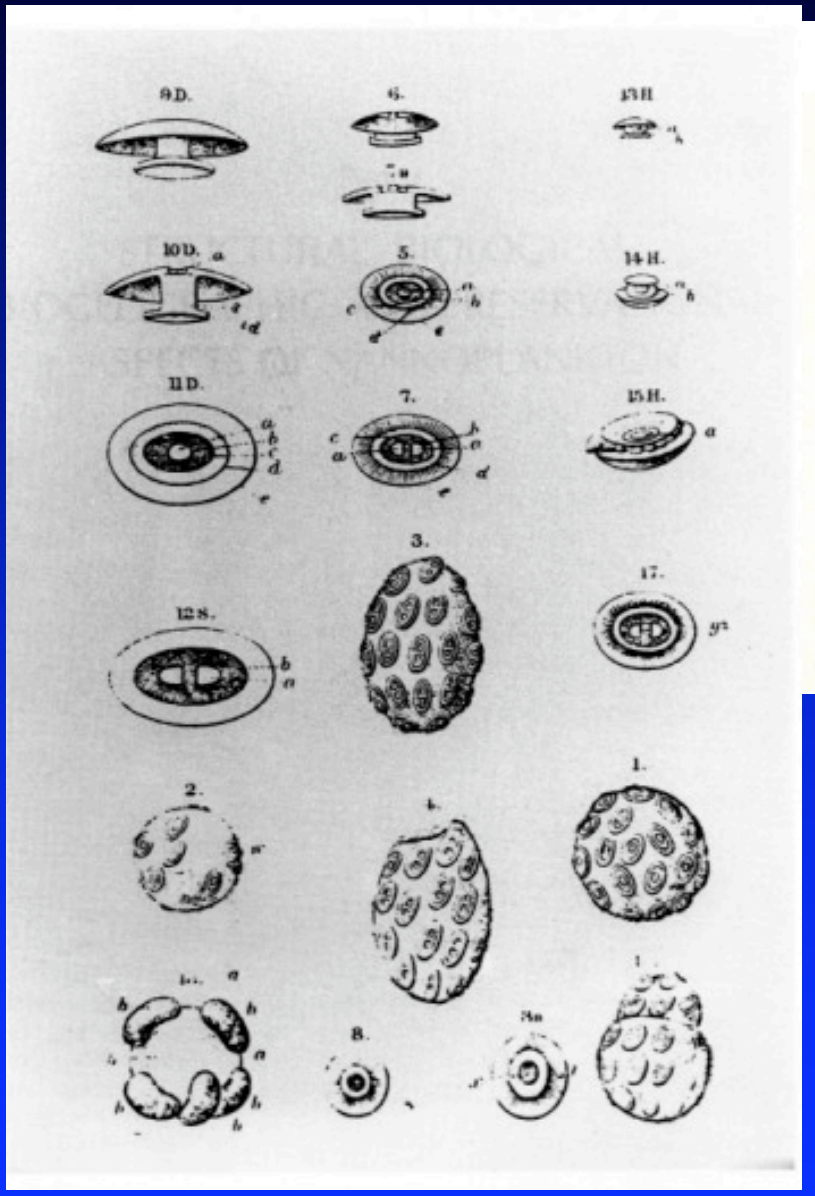


Fig. 2. Coccospheres and coccoliths from Huxley (1868). Coccospheres of the ‘compact’ type (Fig. 6) and the ‘loose’ type (Fig. 7) are shown. His Fig. 1 shows the gelatinous mass, *Bathybius*. Note the coccoliths enclosed in *Bathybius*.

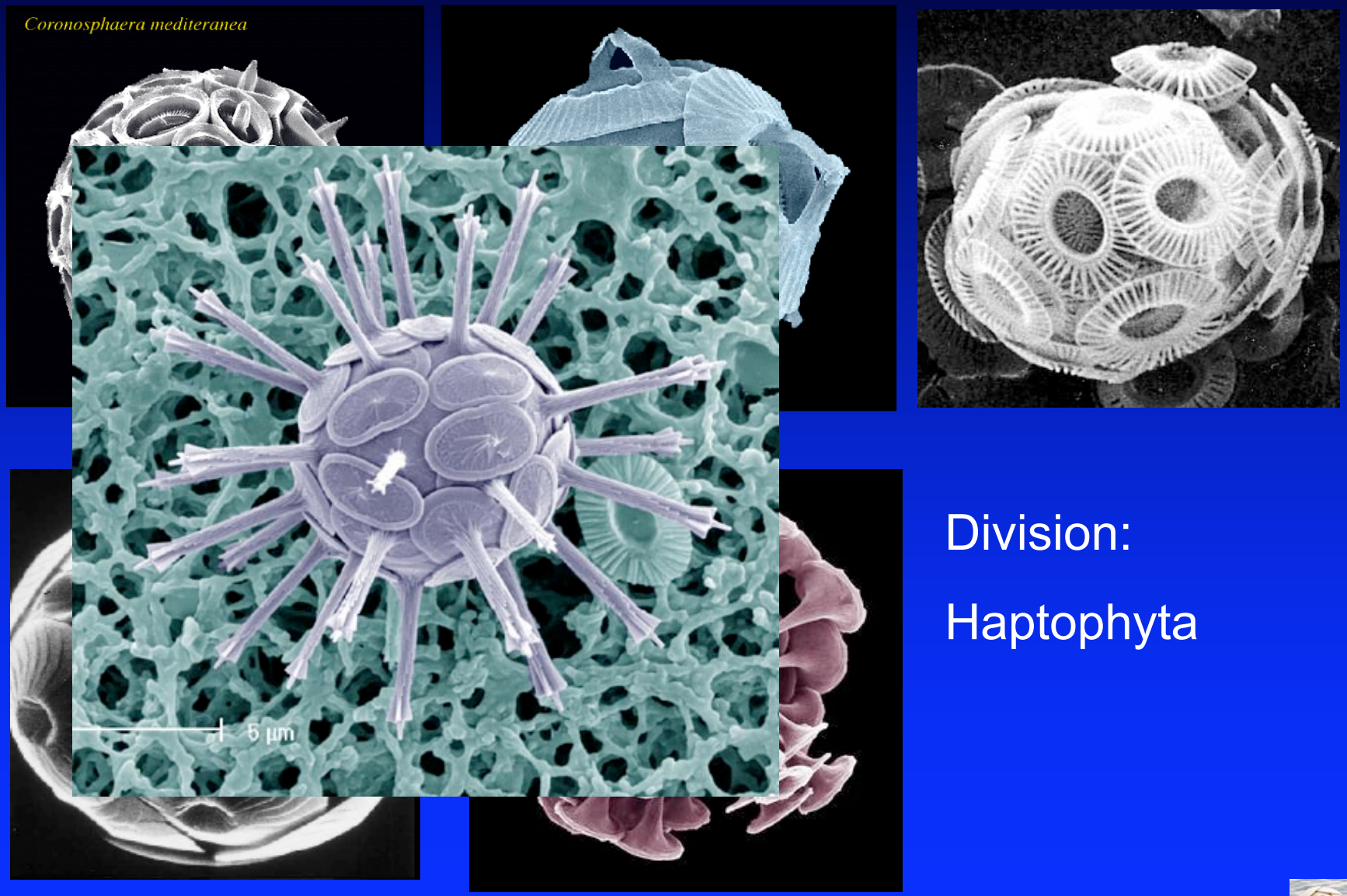
- **Wallich on HMS Challenger Expedition**
  - 1877 describes association of coccoliths with single spherical structures (cells) termed coccospheres

Fig. 4. Coccospheres and coccoliths of *Coccosphaera pelagica* and *Coccosphaera carterii* from Wallich (1877). *Coccosphaera pelagica* is shown as Figs. 1, 2, 5, 8, 9, 10, and 11. *Coccosphaera carterii* is shown as Figs. 3, 4, 6, and 7. Figure 18 is identified as a sporangium of a 'protophyte' from Bengal.



- **Lohmann**
  -1902 introduces the term… coccolithophore

Cococlithophores - Google image

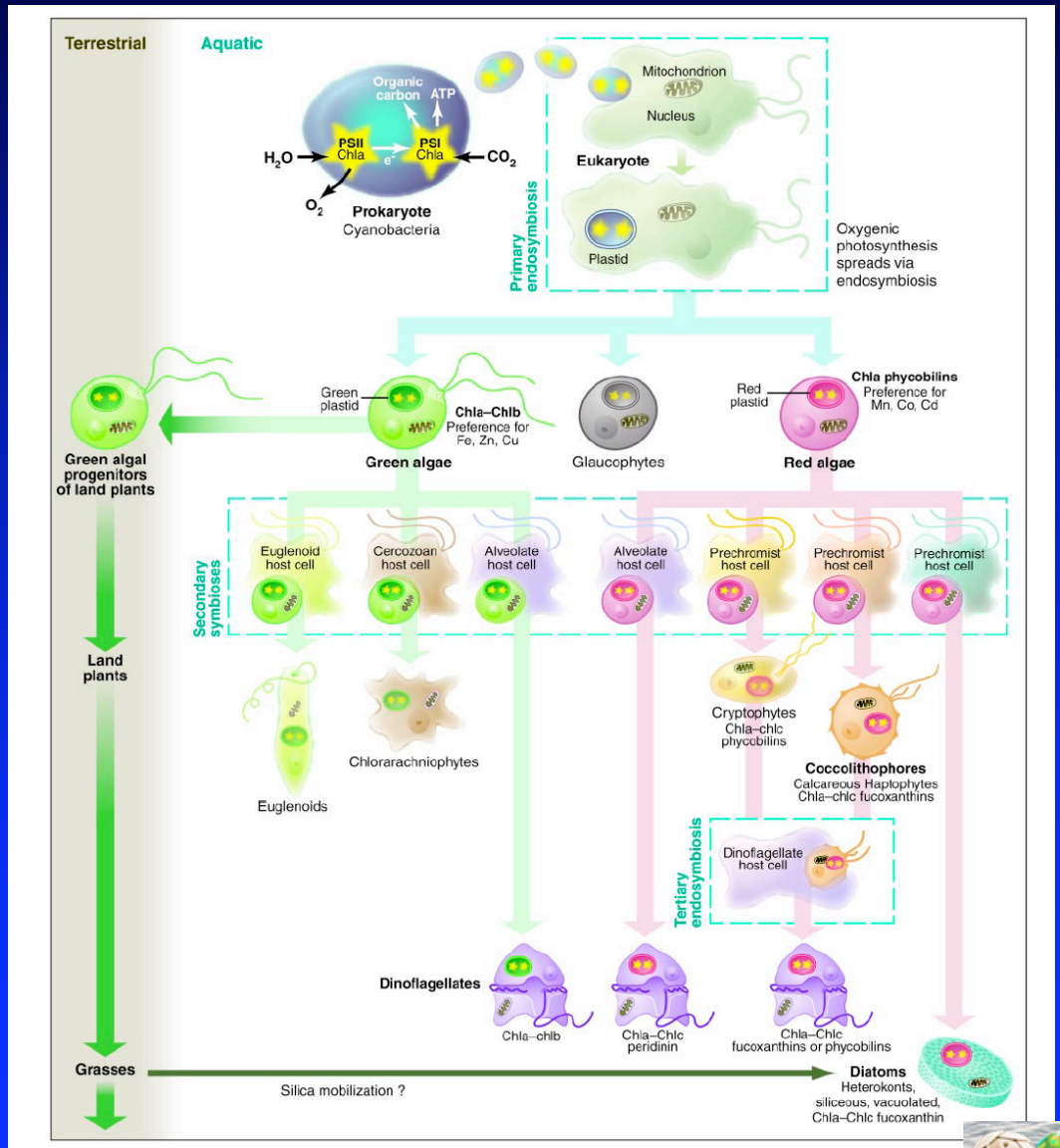


Division:

Haptophyta

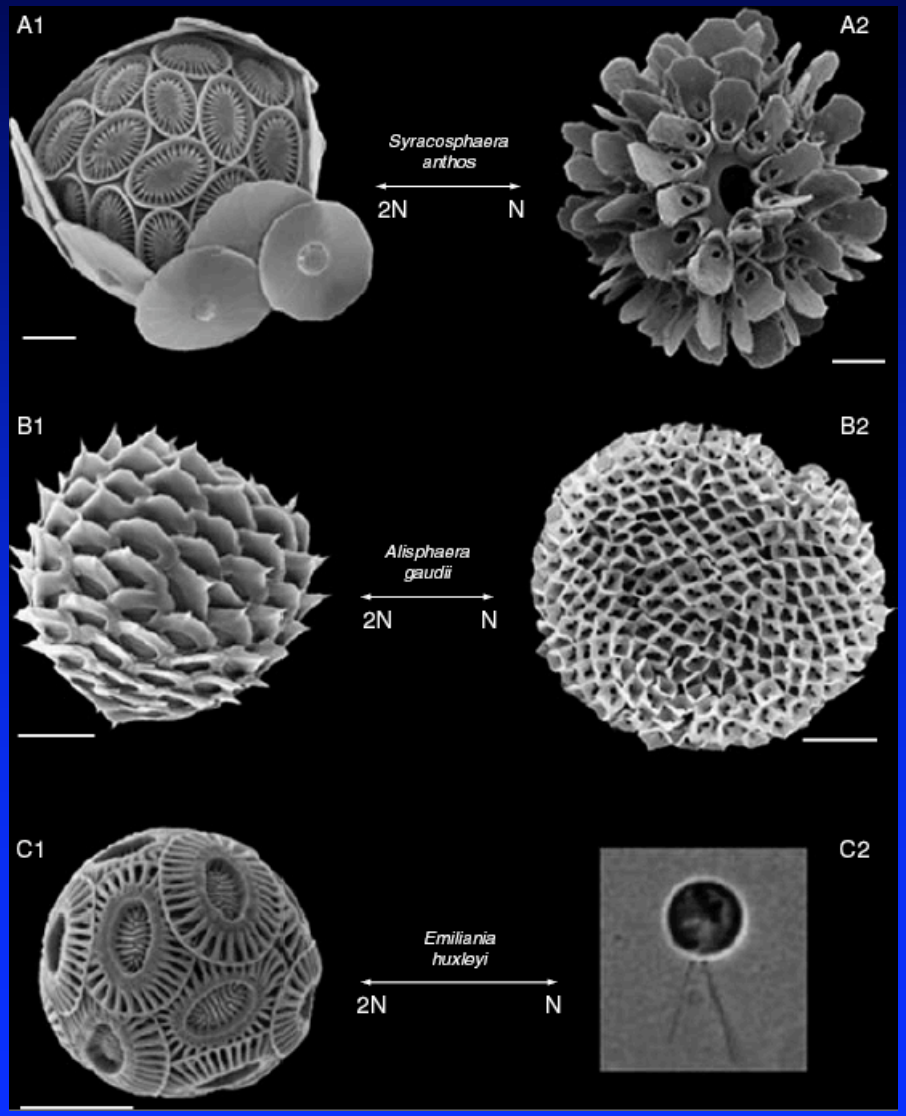
Haptophyte characteristics

- Molecular genetic data has shown that the Haptophytes are a discrete group from other algal protists
- Diverged during the Pre-Cambrian (>600Ma) protist radiation and acquired chloroplasts subsequently (possibly in the Late Palaeozoic, ca 300-400Ma) as result of secondary endosymbiosis
- Haptophytes are a+c chl containing of the red algal lineage



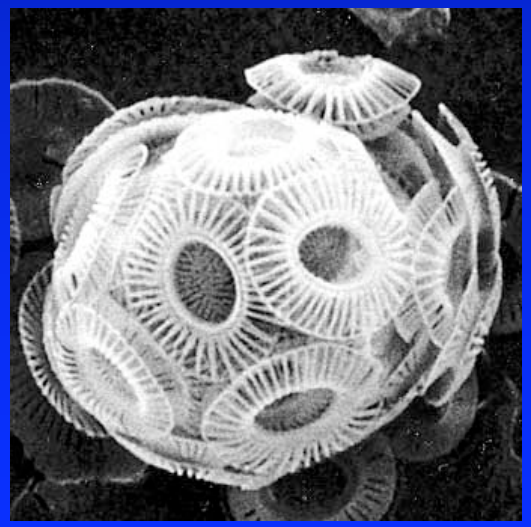
Haptophyte characteristics

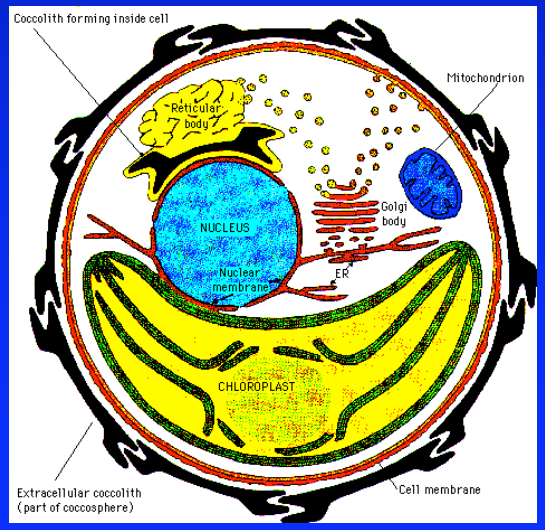
- Haplo-diploid life cycles where both haploid and diploid are capable of asexual reproduction (differs from diploid diatoms, haploid dinoflagellates)
- Morphological diversity between life-history stages



Haptophyte characteristics

- Emerging monophyletic identity of calcifying haptophytes has no formal name, but subclass calcihaptophycidae was proposed by DeVargas et al. (2006)
- Currently bout 280 morphologically distinct genera of calcifying haptophytes or… coccolithophores
- Calcification is the distinguishing feature, but the process is poorly understood





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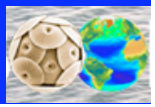
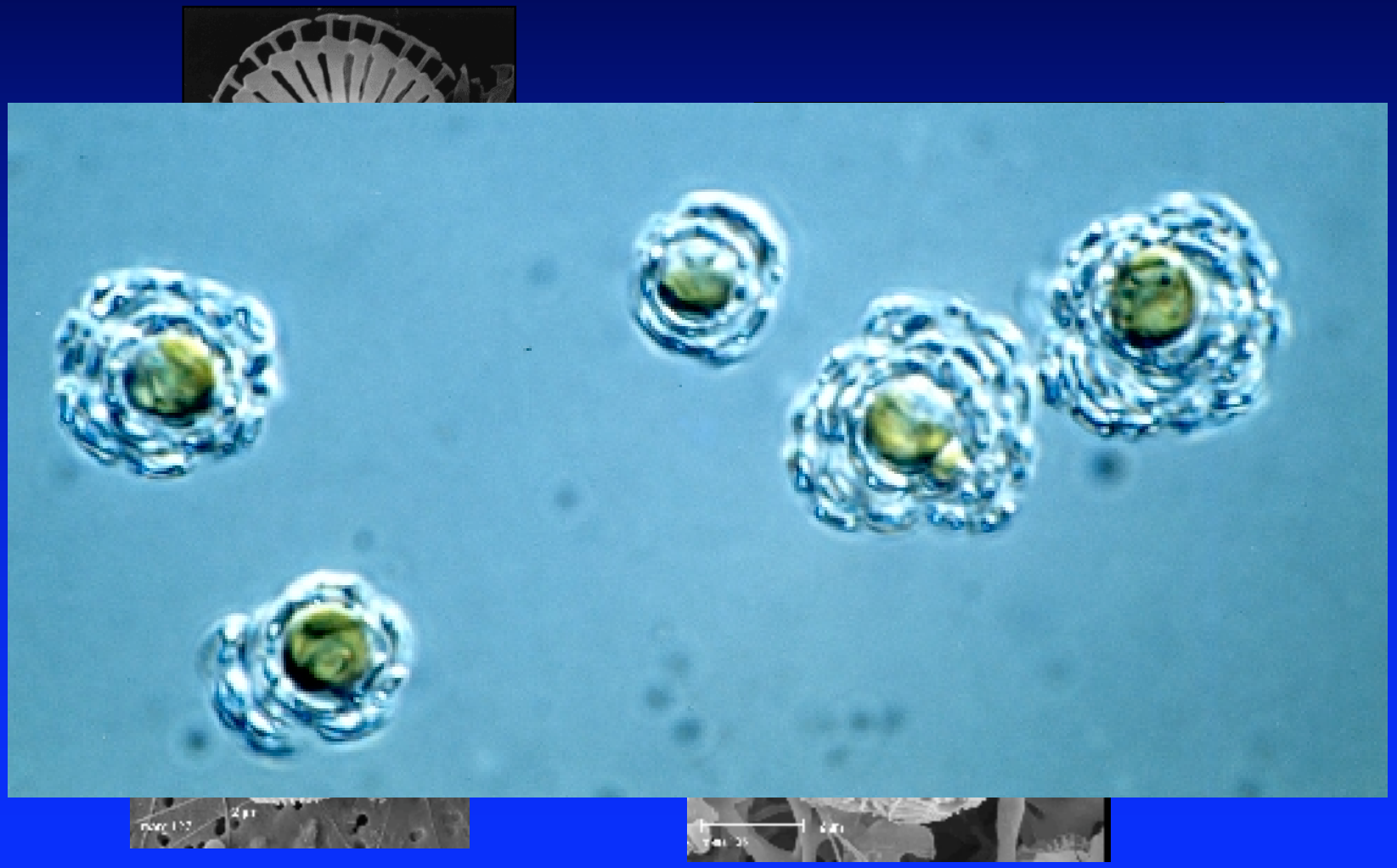
- **Currently bout 280 morphologically distinct genera of calcifying haptophytes or… coccolithophores**
- **Of those … *Emiliania huxleyi* is an important representative**
  - *E. huxleyi* is virtually ubiquitous in surface waters
  - Occurs at temperatures from near freezing to over 30°C
  - Distribution spans equatorial to arctic latitudes
  - Forms large blooms



Emiliania huxleyi



Photos: www.noc.soton.ac.uk

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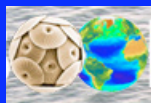

Paleoceanography

GEOCHEMISTRY, GEOPHYSICS, GEOSYSTEMS, VOL. 2, 2001
[Paper number 2000GC000052]

Effects of biosynthesis and physiology on relative abundances and isotopic compositions of alkenones

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Ulf Riebesell

Alfred Wegener-Institute for Polar and Marine Research, Bremerhaven, Germany

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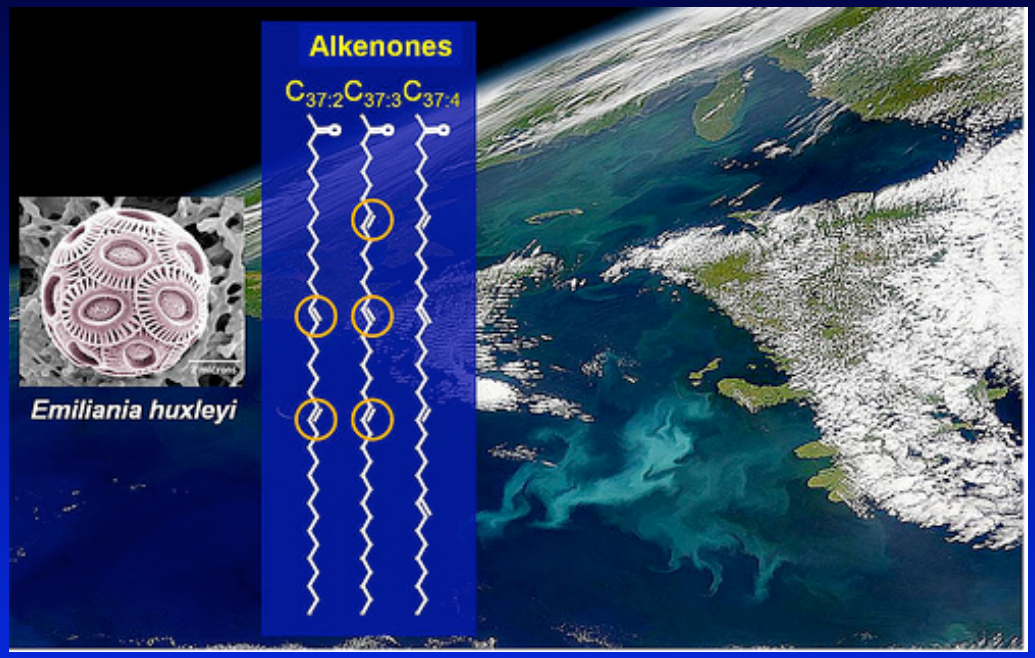
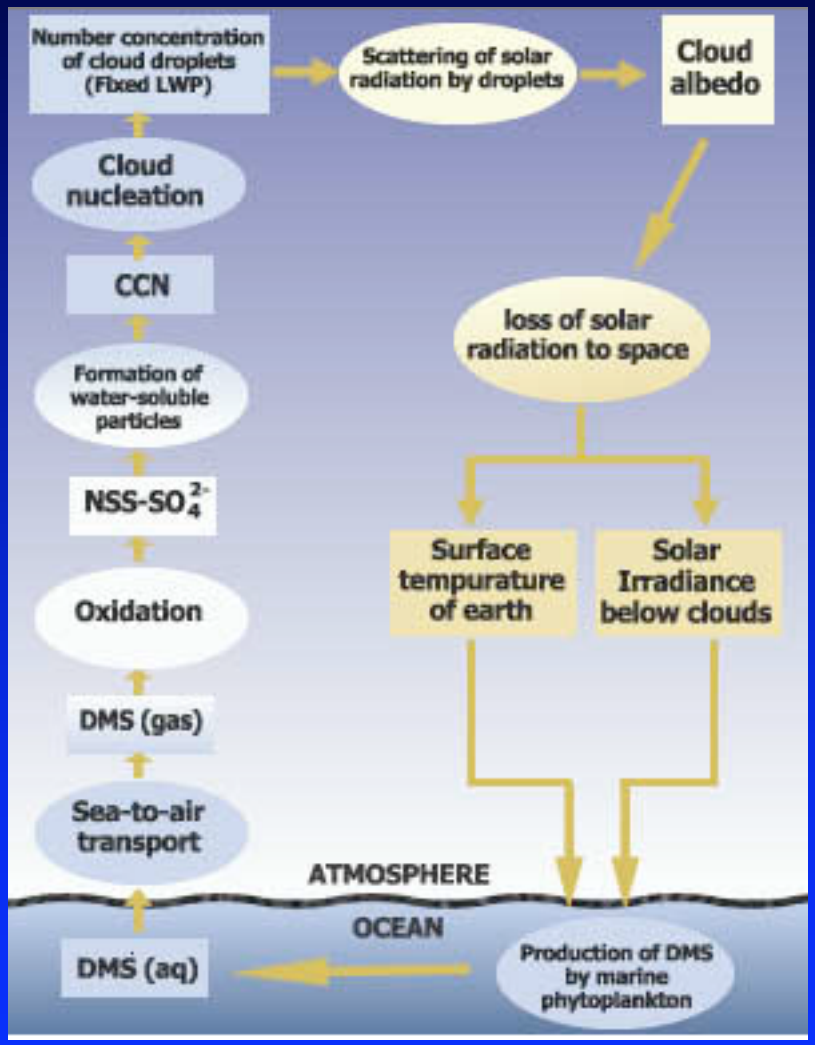


Graphic: http://farm3.static.flickr.com/2175/2070743773_7e05044bb8.jpg

- Synthesize long-chain lipids = Alkenones
- Degree of saturation is dependent on the ambient temperature at the time of synthesis
- Alkenones are well-preserved in sediments so fossil alkenones can be used as a “thermometer” for ancient sea surface temperature.
- Pathways of biosynthesis not known

Sulfur cycle



http://www.video.bluemicrobe.com/qt/56k/emilianiahuxleyi.mov

Emiliania huxleyi virus 86

The coccolithovirus microarray: an array of uses

Michael J. Allen and William H. Wilson

Corresponding author. Michael J. Allen, Plymouth Marine La
The Hoe, Plymouth, PL1 3DH, UK. E-mail: mija@pml.ac.uk

The *Coccolithoviridae* is a recently discovered famil
Here, we review the genomic and transcriptomic cha
family based on the results generated from a coccolit
The microarray has been used to aid the annotation c
investigate the infection process at the transcriptional
diversity in genomic content within the family.

Keywords: *Coccolithovirus, Coccolithoviridae, Mic*

Unreviewed, UniProtKB/TrEMBL **Q4A316** (Q4A316_9PHYC)

Last modified February 5, 2008. Version 12. History...

Clusters with 100%, 90%, 50% identity | Third-party data | Customize display TEXT XML

Names and origin · Ontologies · Sequence annotation (Features) · Sequences · References · Cross-references · Entry information

Names and origin

Protein names	**Putative phosphate permease** [Precursor] EMBL CAI65540.1
Gene names	ORF Names: EhV117 EMBL CAI65540.1
Organism	**Emiliania huxleyi virus 86** EMBL CAI65540.1
Taxonomic identifier	181082 [NCBI]
Taxonomic lineage	Viruses › dsDNA viruses, no RNA stage › Phycodnaviridae › Coccolithovirus
Protein existence	Inferred from homology.

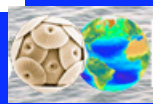
Ontologies

Keywords

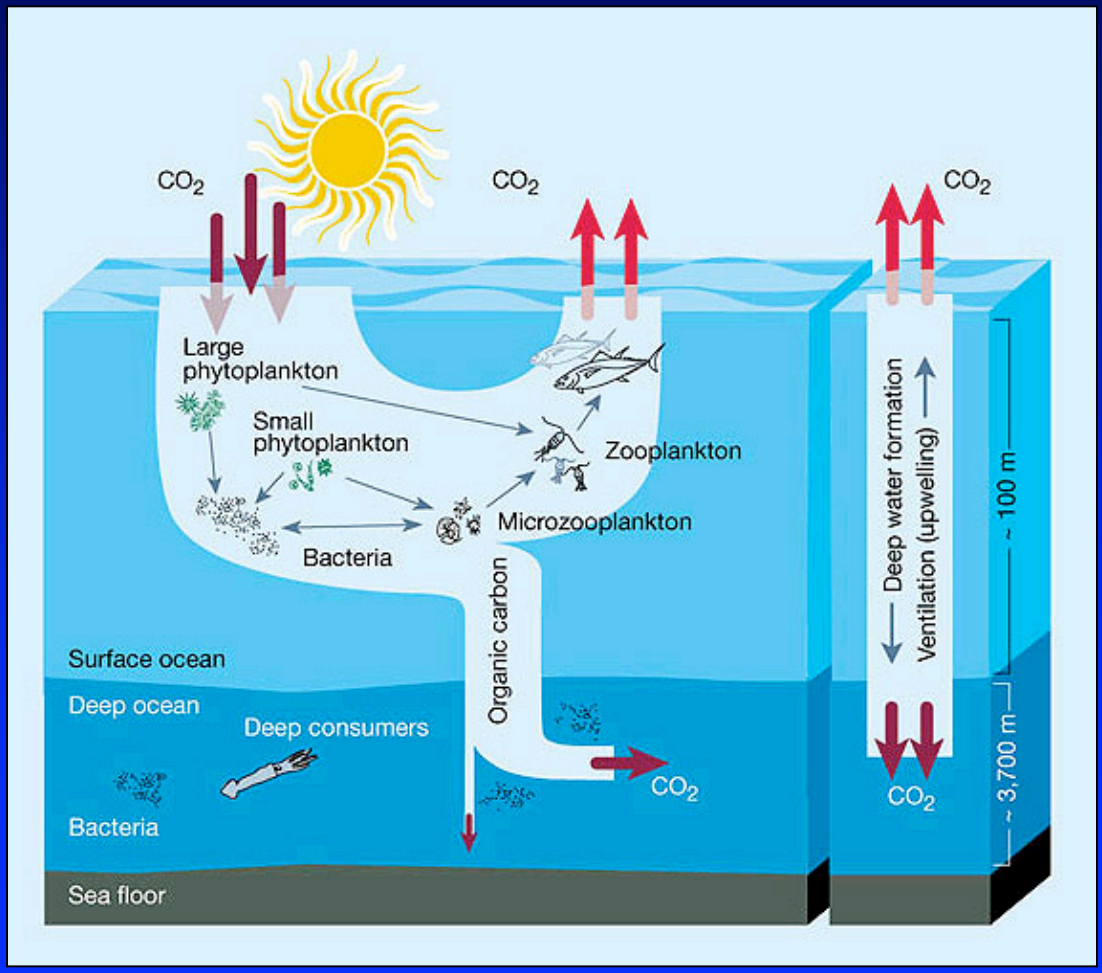
Domain	Signal

Gene Ontology (GO)

Biological process	phosphate transport Inferred from electronic annotation. Source: InterPro
Cellular component	membrane Inferred from electronic annotation. Source: InterPro
Molecular function	inorganic phosphate transmembrane transporter activity Inferred from electronic annotation. Source: InterPro

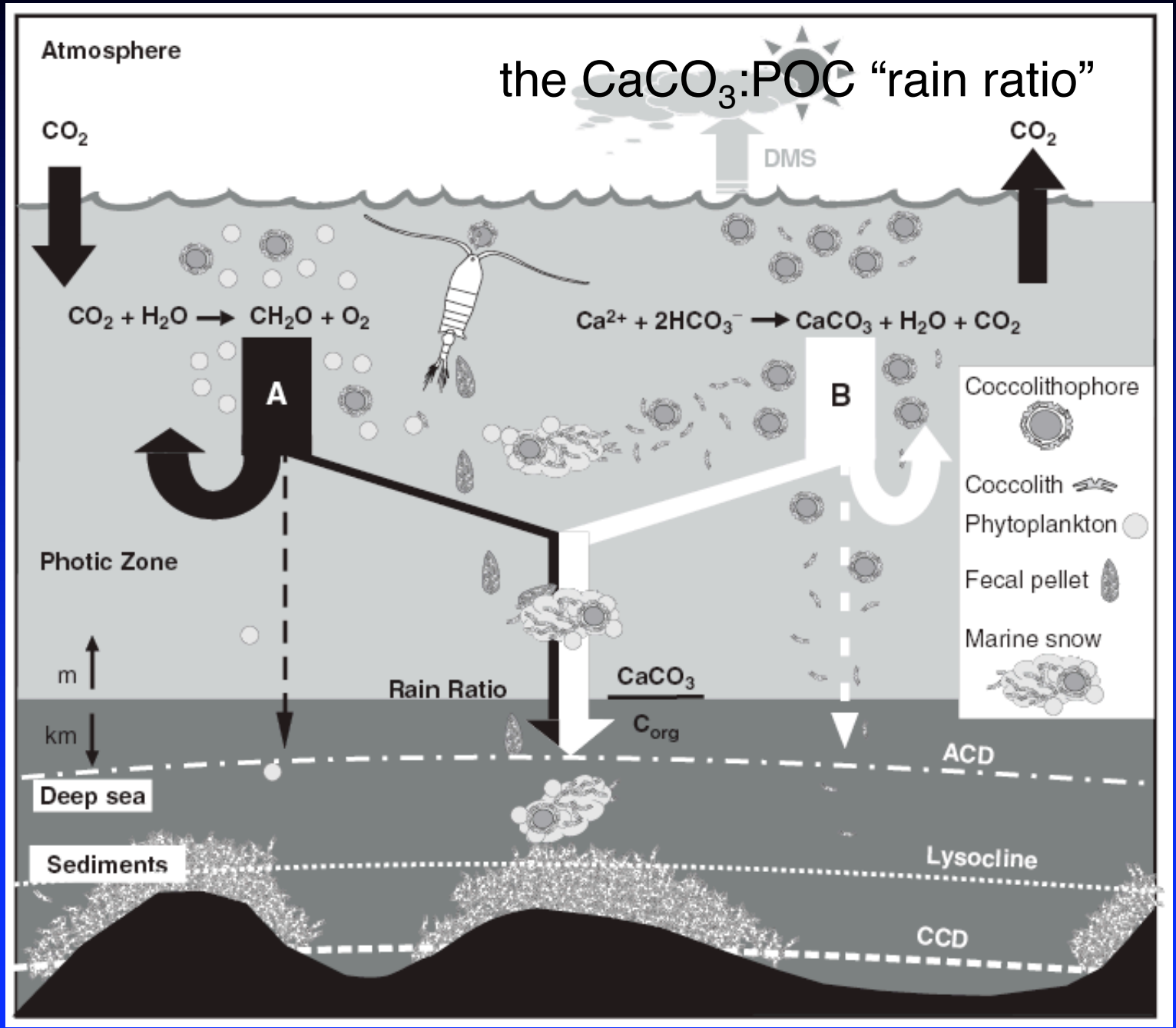


Carbon cycle



Chisholm 2000

the $CaCO_3$:POC "rain ratio"



Large blooms…

Daily Mail, Friday, July 30, 1999 Page 33

Vegetable soup that's the size of Cornwall

A CLOUD of plankton so big that it can be seen from space is causing the sea around the South West of England to turn turquoise.

The spectacular bloom, which sailors thought at first might be pollution, is estimated to be the size of Cornwall.

Scientists believe the vegetable plankton, Emiliania huxleyi, has reproduced at such a staggering rate due to long spells of sunshine. The colouring effect is produced by chalky protective outer layers, which the plankton shed.

The sea off part of the Cornish coast turned red earlier this week. The cloud, which has been visible to sailors for several days, appears from space as a white mass (right) stretching from South Devon to the Scilly Isles. It is moving west.

Scientists say the bloom, which gives the sea a milky texture, is completely harmless to humans.

Plankton are so small they are barely visible under a microscope, but in their millions they provide a rich soup of nutrients that sustain the ecology of the oceans. They are the favourite food of whales.

A spokesman for Brixham Coastguard in Devon, which received calls from fisherman, said: "It was a very strange sight as the water looked almost blood-coloured. It is a perfectly natural phenomenon despite looking like a large slick, but in the twilight it can seem very eerie."

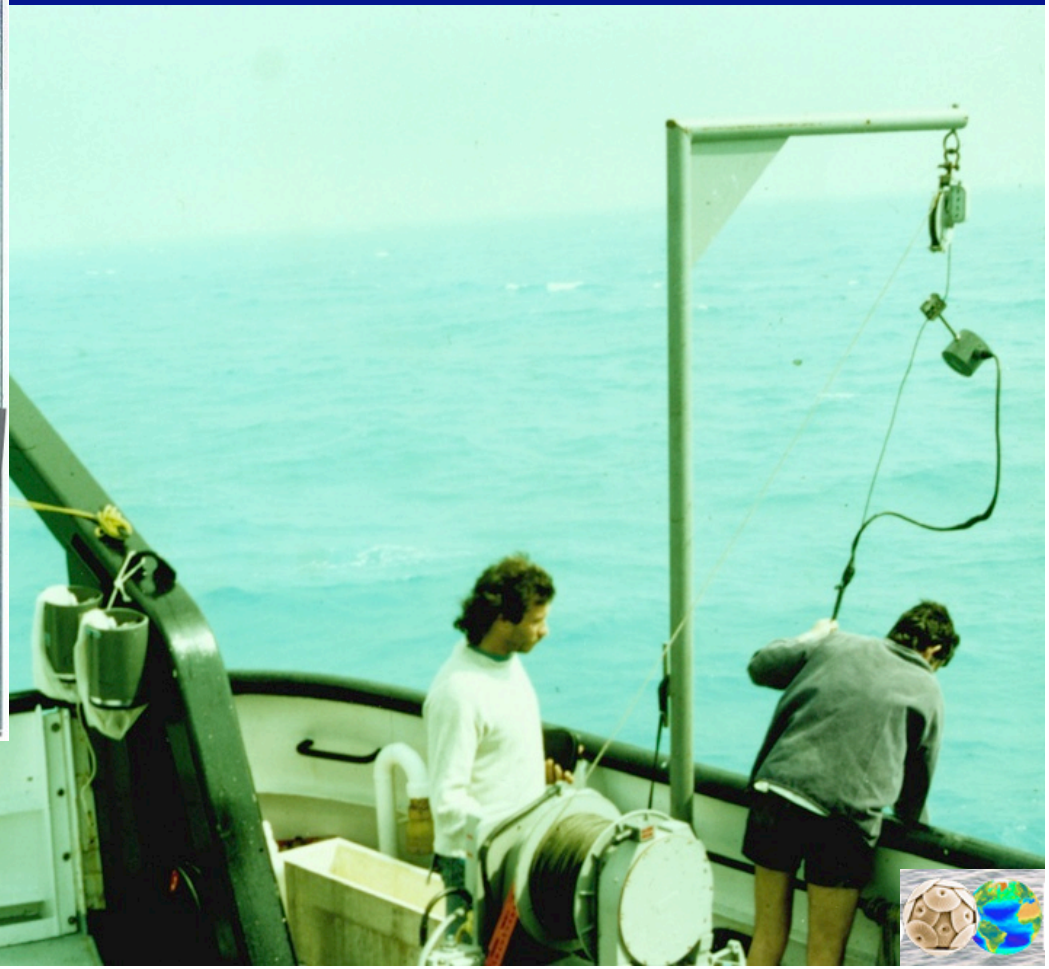
Satellite picture: NASA

CORNWALL

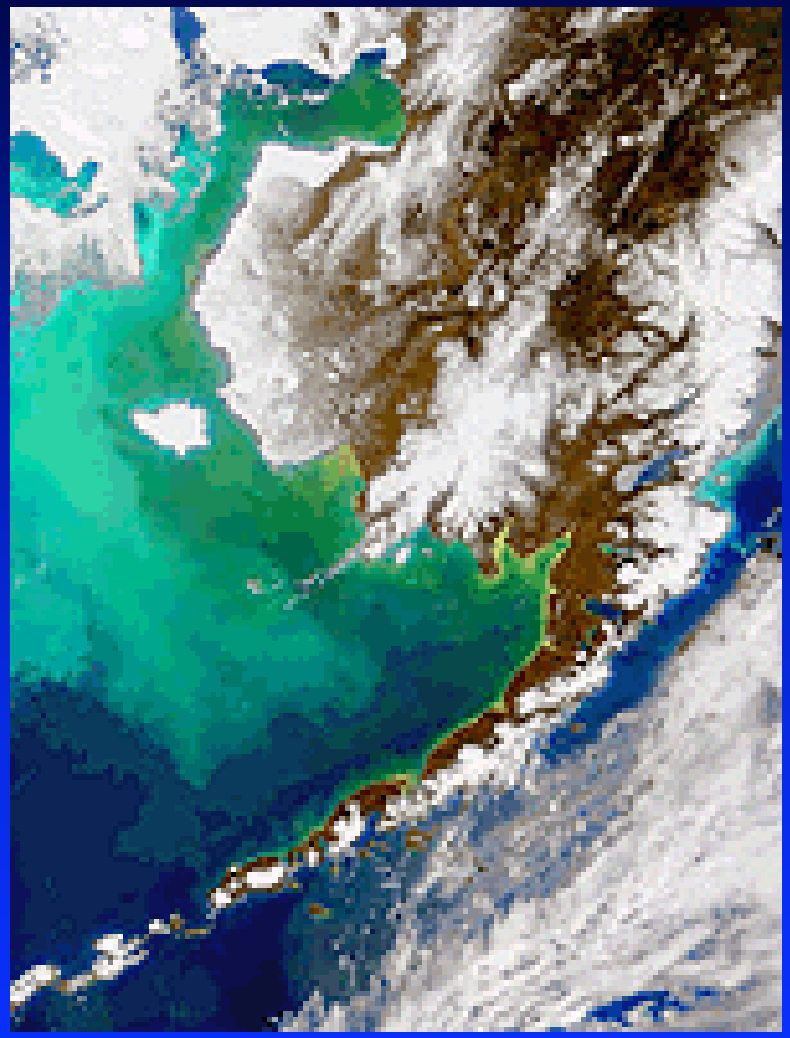
ENGLISH CHANNEL

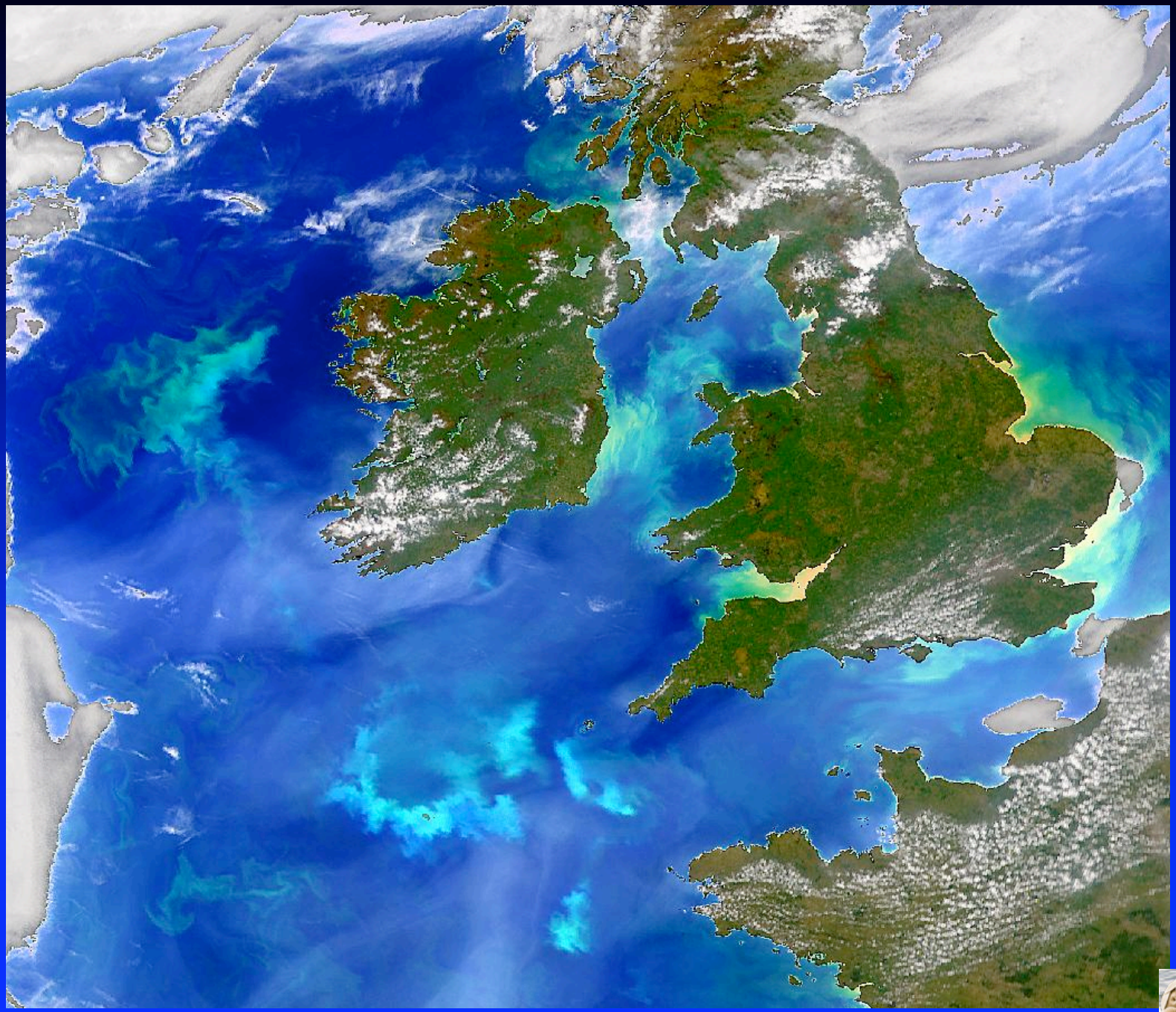
Plankton bloom

FRANCE



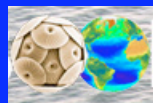
Large blooms…remotely sensed





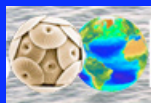
Biomes to genomes

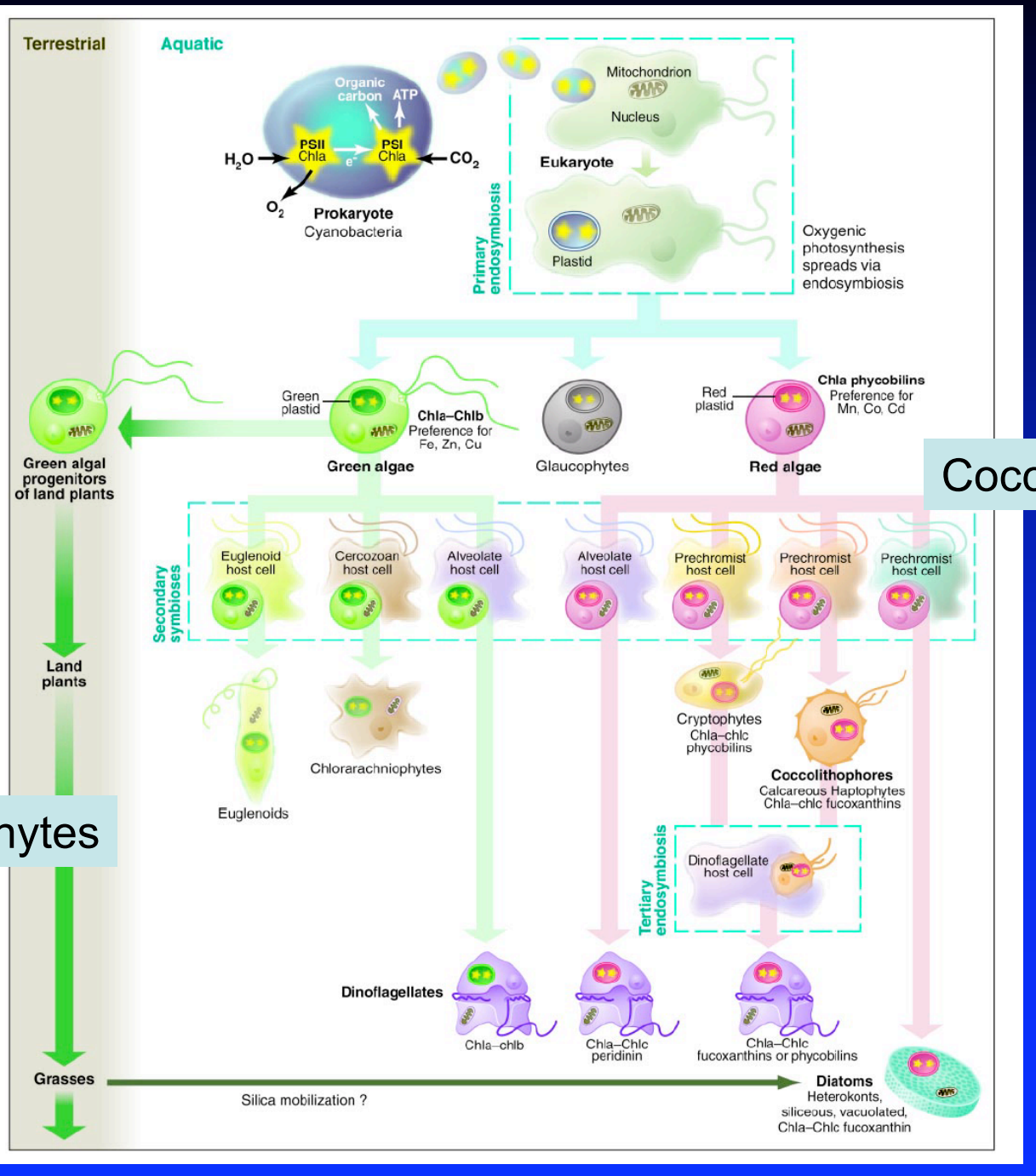
- Despite a growing and broad understanding of coccolithophore evolution, biogeochemistry and ecology, many basic questions remain.
- *What are metabolic pathways and preferred sources of N, P and C?*
- *Biosynthesis and stability of alkenones?*
- *Influence of virus infection on loss terms and the cycling of S, C, N, P ?*
- *How and why to they calcify?*
- *How will all of these processes influence their distribution and activity in a future ocean?*
- These questions and more were used to rationalize the sequencing of a coccolithophore genome sequence.



Selected sequencing efforts with marine eukaryotic phytoplankton

- Diatom: *Thalassiosira* (genome, EST) Armbrust et al. 2004
- Prasinophyte: *Ostreococcus* (genomes) Palenik et al. 2007
- Dinoflagellate:
  - *Karenia* (EST)
  - *Alexandrium* (EST)
- Haptophyte: *Emiliania* (genome, EST) Read and Wahlund
- Pelagophyte: *Aureococcus* (genome, EST) Gobler and Wilhelm
- *Limited genomic infrastructure relative to marine cyanobacteria*



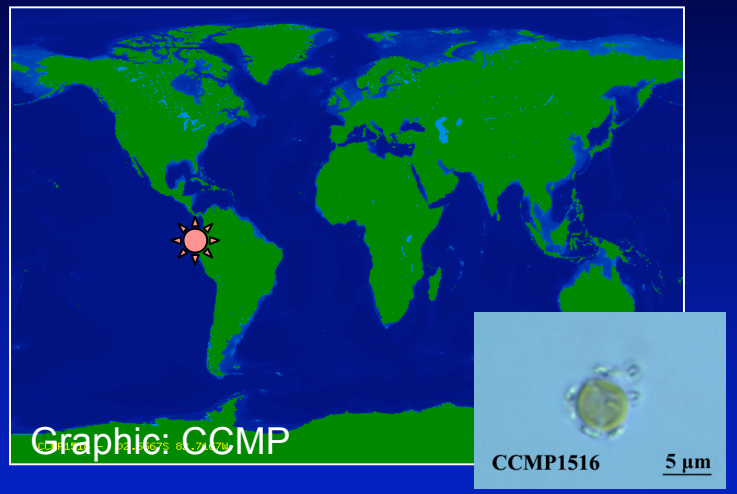


Coccolithophores

Prasinophytes

E. huxleyi strain 1516 genome

- Isolated in 1992 from the South Pacific
- Calcifying in f/50
- Relatively slow growth rate



- DOE/JGI has sequenced 80,000 ESTs (e.g. Wahlund et al. 2004) and a draft of the genome (B. Read and T. Wahlund PIs)
- Assembly presented a an unexpectedly huge challenge for the JGI. We were told *E. huxleyi* is the most difficult genome JGI has ever tried to assemble!
- The genome size is ~168 MB with a GC content of 66%. The assembly resulted in 7,809 scaffolds with 94% sequence completeness at 10X coverage

E. huxleyi strain 1516 genome

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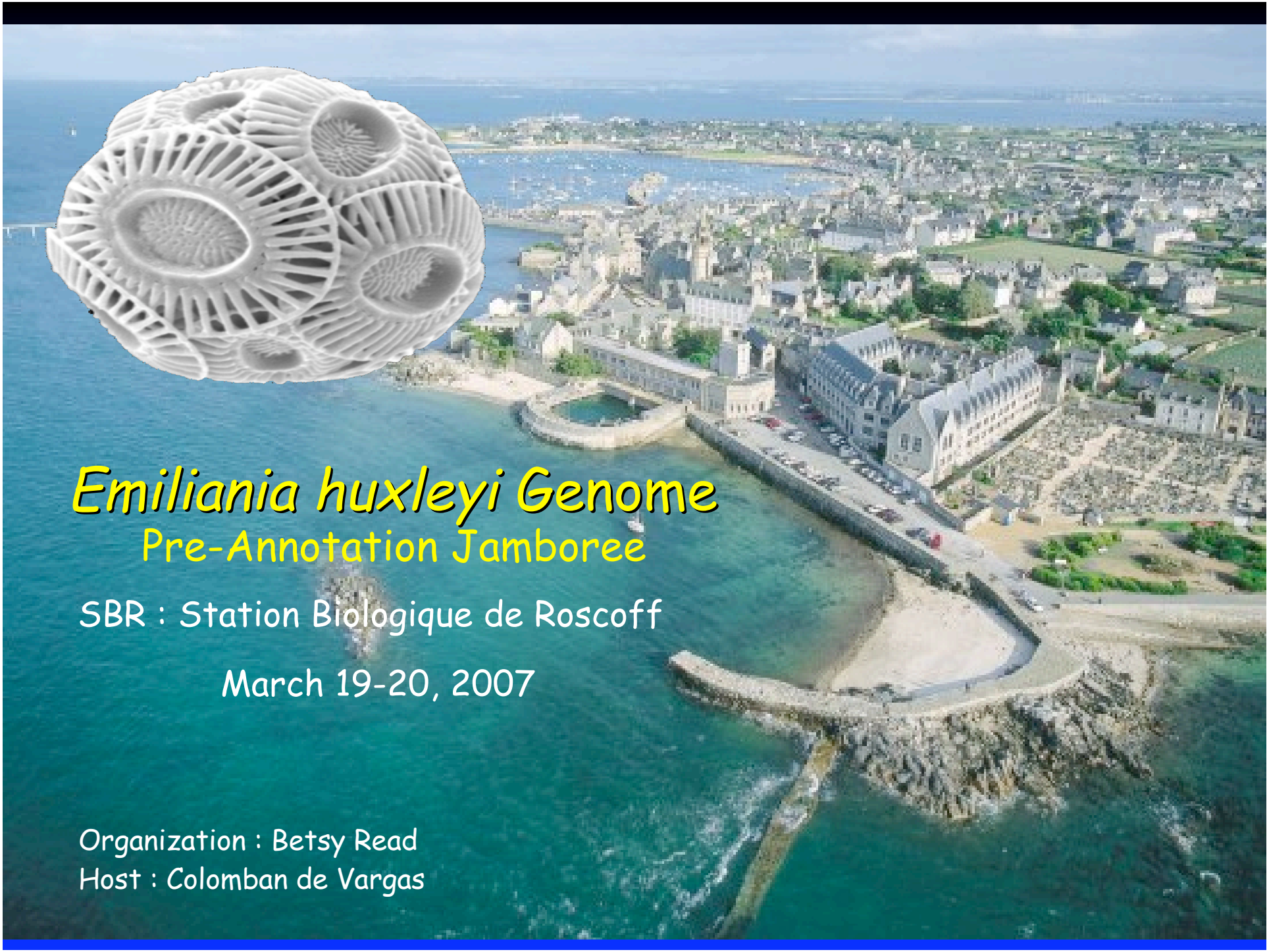
EMILIANIA HUXLEYI GENOME PROJECT

General Features	
Genome Size	168 Mb
Scaffold Number	7809
Coverage	10X
Number of Predicted Genes	39126

Average Properties	
Gene Length	1718.78 nt
Transcript Length	1112.13 nt
Protein Length	340.70 aa
Exon Frequency	3.60 exon/gene
Exon Length	307.27 nt
Intron Length	237.27 nt
Gene Density	233.31 genes/Mb


Emiliania huxleyi Genome
Pre-Annotation Jamboree
SBR : Station Biologique de Roscoff
March 19-20, 2007
Organization : Betsy Read
Host : Colomban de Vargas

E. huxleyi strain 1516 genome

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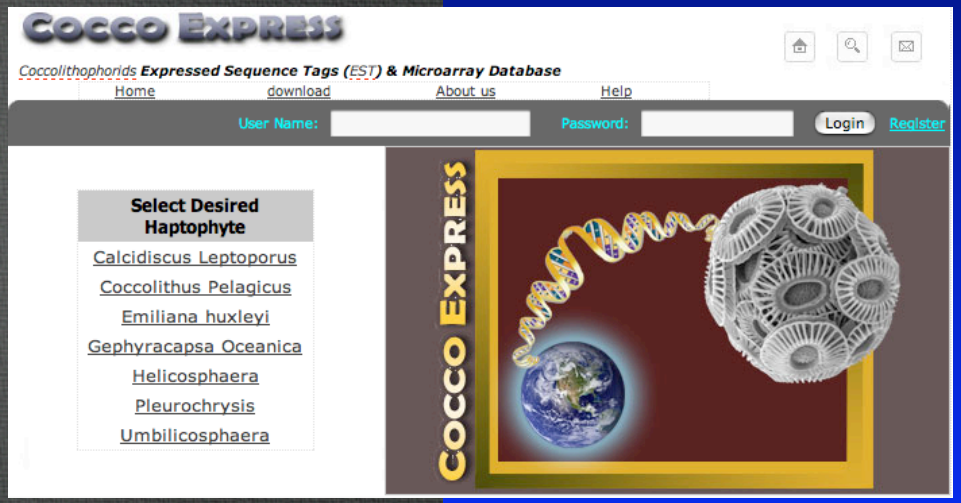


THE GENOME ANNOTATION TEAM

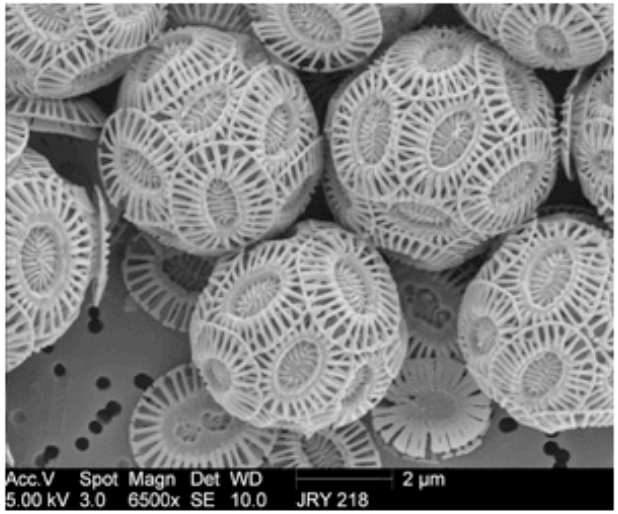
As a genome-savvy community representing a variety of biological disciplines we intend to promote *E. huxleyi* as a new model species. Our immediate goals are to: 1) improve the computational gene models and interpret genomic data for this model phytoplankton in comparative research, and 2) develop *E. huxleyi* as an important resource for environmental/climatology, biomedical, and material science investigations.

Manual annotation is underway

JGI

Emiliania huxleyi CCMP1516 v1.0

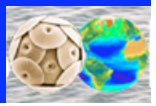
Search | BLAST | Browse | GO | KEGG | KOG | AdvancedSearch | Download | Info | Home | HELP!



Coccolithophores are marine haptophytes that derive their name from the calcium carbonate coccoliths that blanket the cell. They extend deep into the tree of life and represent the third most abundant group of phytoplankton in today's oceans with some 300 different species. The morphological diversity of their coccoliths is preserved in a continuous and complete fossil record spanning the last 200 Myr, and represents an important tool for dating and correlating strata, reconstructing past climate and oceanic conditions, and dissecting patterns of macroevolution.

Emiliania huxleyi (*E. huxleyi*) is the most prominent coccolithophore and has attracted the attention of scientists from fields as diverse as geology, biogeography, paleoclimatology, ecophysiology, material science, and medicine. *E. huxleyi* is distributed throughout the world's oceans and is linked to the chemical balance between the atmosphere, hydrosphere, and geosphere. Massive blooms of the algae can cover 100,000s of square kilometers and can be detected via satellite imagery due to the reflective properties of its coccoliths. Because of its ecological success and its ability to fix inorganic carbon into both photosynthetic and biomineralized product, *E. huxleyi* has significantly impacted the biogeochemistry of the earth directing carbonate chemistry in surface oceans and exporting large amounts of C to deep water sediments. In addition to playing an important role in global carbon cycling, *E. huxleyi* also contributes to global sulfur cycling. During grazing *E. huxleyi* produces the climatically active trace gas dimethyl sulfide; emissions of which may contribute to marine cloud formation and climate regulation.

E. huxleyi is also of interest to those in biotechnology. A group of secondary metabolites known as polyketides that *E. huxleyi* synthesizes possess a wealth of pharmacologically important activities, including antimicrobial, antifungal, antiparasitic, antitumor and agrochemical properties. The ultrastructure and optical features of the coccoliths, on the other hand, are being targeted for applications in nanotechnology relating to biomedical, telecommunications and optoelectronic devices and/or materials.

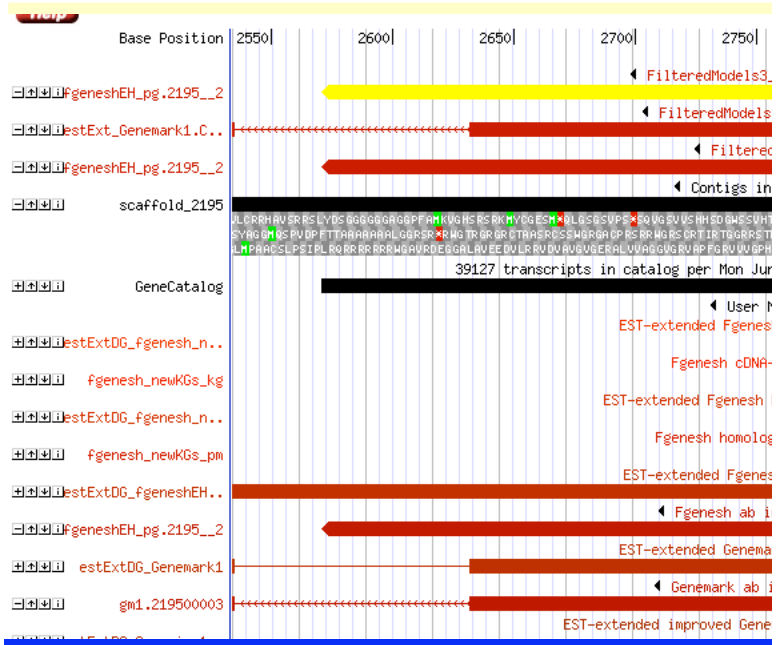


E. huxleyi strain 1516 annotation

JGI *Emiliania huxleyi CCMP1516 v1.0*

Search | BLAST | Browse | GO | KEGG | KOG | AdvancedSearch | Download | Info | Home | HELP!

Name:	fgeneshEH_pg.2195__2
Protein ID:	123369
Location:	Emihu1/scaffold_2195:2571-2945
Description:	
Best Hit:	gi|27462209|gb|AAO15381.1|AF334403_1 phos|
total hits(shown)	18 (10)



JGI *Emiliania huxleyi CCMP1516 v1.0*

Search | BLAST | Browse | GO | KEGG | KOG | AdvancedSearch | Download | Info | Home | HELP!

Annotator Account: Edit Account | Logout

TRANSCRIPT ANNOTATION

Emihu1/scaffold_2195:2571-2945 fgeneshEH_pg.2195__2 Hide

Attribute	Value	Creator	Action
Name			add
Description			add
Model Notes			add
Defline			add
Disposition	Catalog	AUTOMATIC	add edit
Literature			add

Assessment	? Note	Creator	Action
EST evidence			add
Needs GO			add

Evidence	Type	Creator	Action
			add

FUNCTIONAL (PROTEIN) ANNOTATION

User-Assigned Ontology add

ASPECT	DETAILS
function	
process	
component	
enzyme	
kog	

Automatic Ontology and Best Protein Alignments for transcript 123369

Automatic Ontology

ASPECT	GO/EC	SUPPORT	Action

High Scoring Alignments Change Hit Filter

gi|27462209|gb|AAO15381.1|AF334403_1
phosphate repressible phosphate permease [Emiliania huxleyi]
402 514

JGI

Emiliania huxleyi CCMP1516 v1.0

Search | BLAST | Browse | GO | KEGG | KOG | **AdvancedSearch** | Download | Info | Home | ***HELP!***

GENE/TRANSCRIPT/PROTEIN SEARCH

Search Terms

alkaline phosphatase

Search | Clear

Options

Method

- (•) Find directly
- ( ) Find by homology to related proteins with

E-Value less than 1.0e-20

Databases

- Emiliania huxleyi CCMP1516
- F. rubripes v3.0
- Generic tutorial
- H. robusta v1.0
- H. sapiens Chr. 16
- H. sapiens Chr. 19 (b34)
- H. sapiens Chr. 5
- L. gigantea v1.0
- Laccaria bicolor
- M. brevicollis v1.0

Download FASTA file of Protein

Found

Check All — Displaying results 1 to

	Relevance	Organism	Assigned Name		
	1.0	Emihu1	PHO1		
	1.0	Emihu1	GM1.15500120		
	0.88	Emihu1	GM1.16200121		
	0.88	Emihu1	GM1.1038000001		
	0.88	Emihu1	ESTEXTDG_GENEMARK1.C_91460001		
	0.88	Emihu1	ESTEXTDG_GENEMARK1.C_2850035		
	0.71	Emihu1	ESTEXTDG_FGENESH_NEWKGS_KG.C_160033	Alkaline phosphatase,	P T G
	0.71	Emihu1	FGENESH_NEWKGS_KG.373__4__EST_ALL.FASTA.CONTIG11950	Alkaline phosphatase, NULL,	P T G
	0.62	Emihu1	AP1	Alkaline phosphatase	P T G

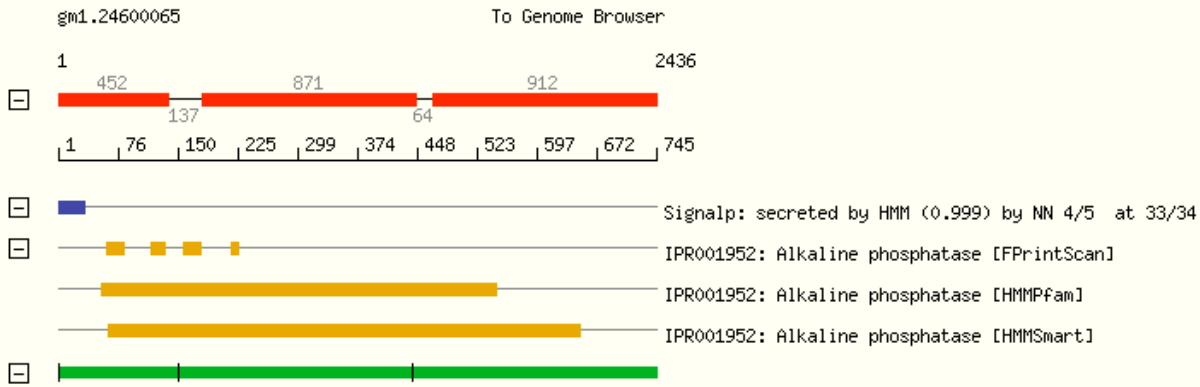
USER ANNOTATIONS

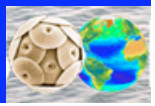
User	Name	Description	DefLine
Louie Wurch	PHO1	DOP metabolism	Putative alkaline phosphatase

View/modify manual annotation

View nucleotide and 3-frame translation To Genome Browser

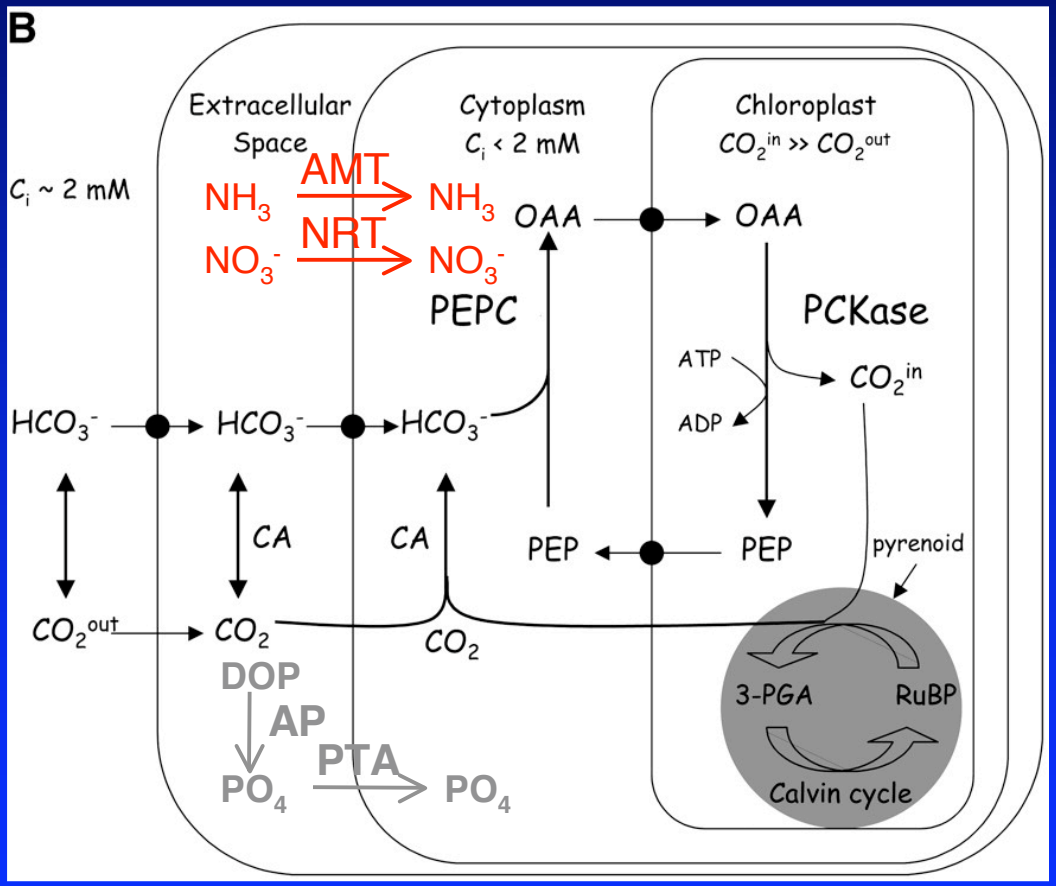
NCBI blastp Predicted number of transmembrane domains: 1





E. huxleyi strain 1516 gene annotation

Current model of CCM function in marine diatoms



C metabolism:
CA
PEPC
PCKase
RuBP

N metabolism:
AMT
NRT

P metabolism:
AP
PTA

Comparative genomics

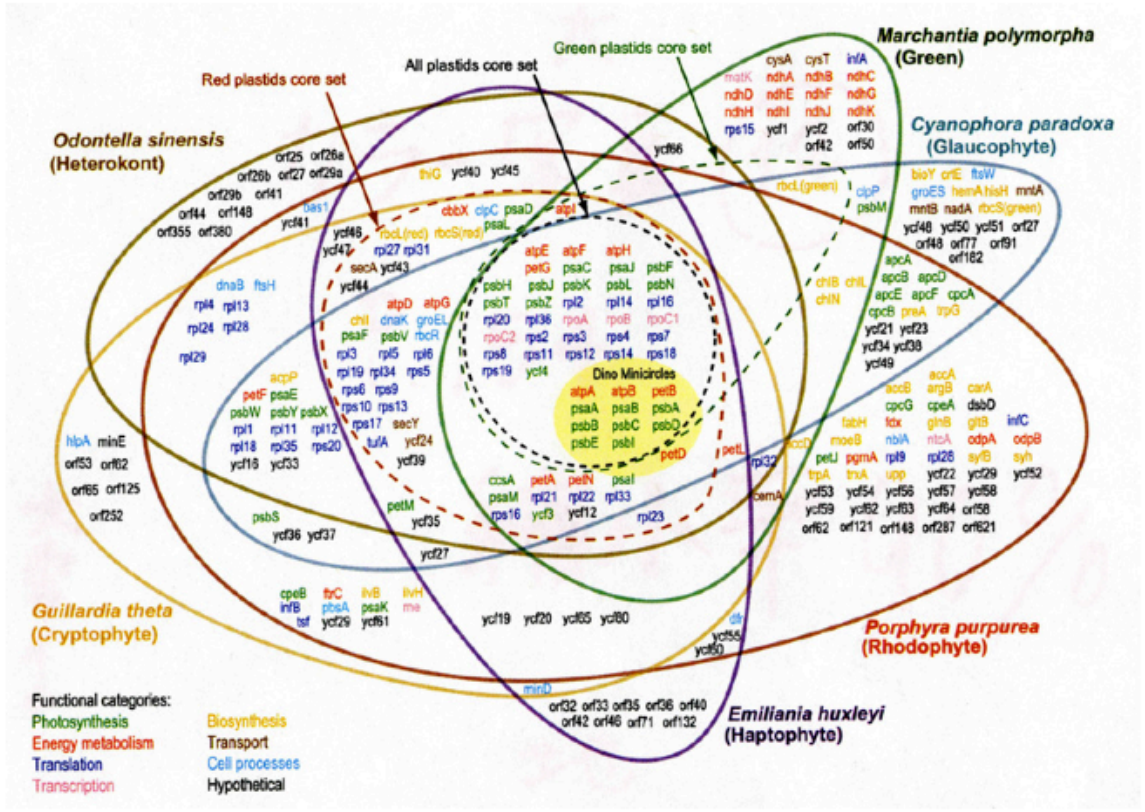
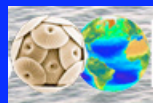


Figure 2. Venn diagram comparing the protein-coding gene content of six plastid genomes. Core sets of genes from all plastids, from red plastids, and from green plastids were inferred from all 36 photosynthetic plastid genomes published to date (Supplemental Information Table 1, http://www.dna-res.kazusa.or.jp/12/2/07/supplement/supplement_t1.html). Genes are colored depending on their functional category.

Supports red algal lineage of the haptophyte plastid Sanchez Puerta et al 2005

Biomes to genomes

- Despite a growing and broad understanding of coccolithophore evolution, biogeochemistry and ecology, many basic questions remain.
- *What are metabolic pathways and preferred sources of N, P and C?*
- *Biosynthesis and stability of alkenones?*
- *Influence of virus infection on loss terms and the cycling of S, C, N, P ?*
- *How and why to they calcify?*
- *How will all of these processes influence their distribution and activity in a future ocean?*
- These questions and more were used to rationalize the sequencing of a coccolithophore genome sequence.



The “oceanic genotype” represents only the potential biological capacity and sets an upper constraint on possible pathways and ecosystem rates. The realized structure and function of marine ecosystems, “oceanic phenotype”, reflects the complex interactions of individuals and populations with their physical and chemical environment and with each other.

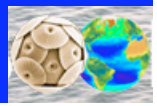
Doney et al. 2004 *Front. Ecol. Environ.*

Capacity?

Transcription?

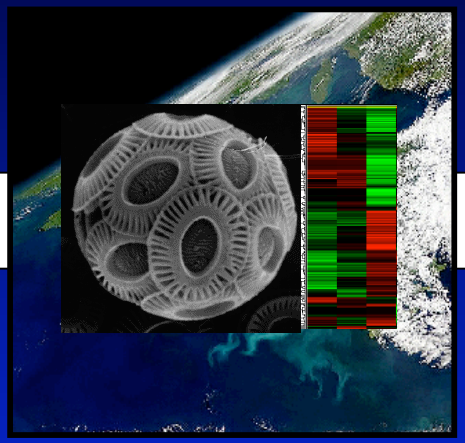
Activity?

Can studies at the genome level give predictive insight into structure and function of ocean ecosystems?



A changing ocean - predicting coccolithophore nutritional physiology and ecology

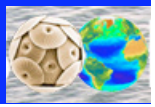
Temperature
CO_2
pH
N, P, Fe etc.



Ecology
Biogeochemistry
Climate

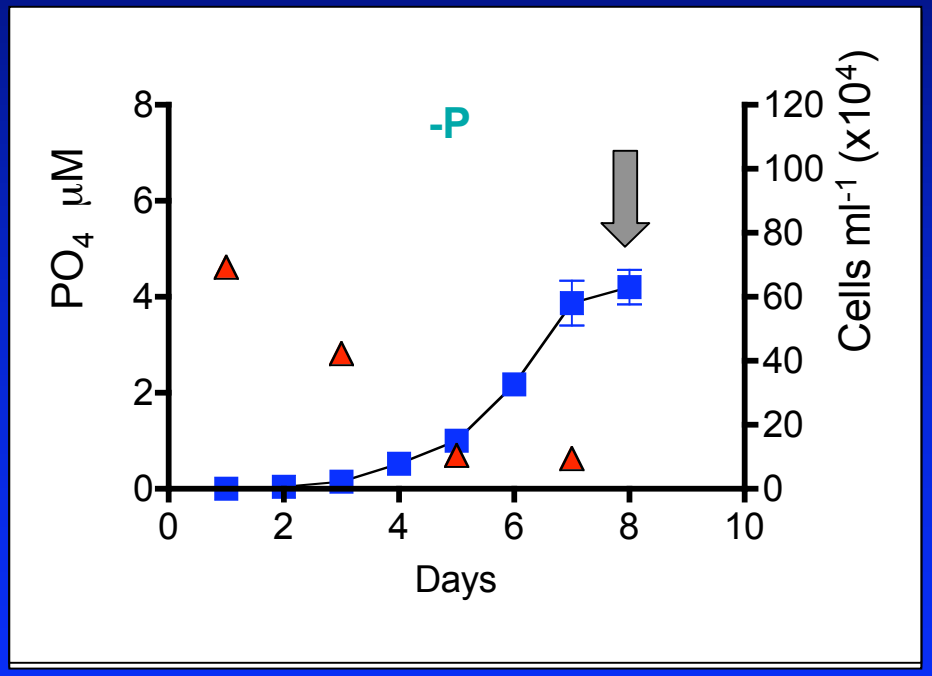
- *Emiliania huxleyi* (1516) responses to P and N deficiency
  - Validity of SAGE for gene expression profiling in the absence of a complete genome sequence.
- Molecular understanding of N, P and C metabolism
- Physiological ecology of field populations

photos: www.soes.soton.ac.uk, www.nasa.gov

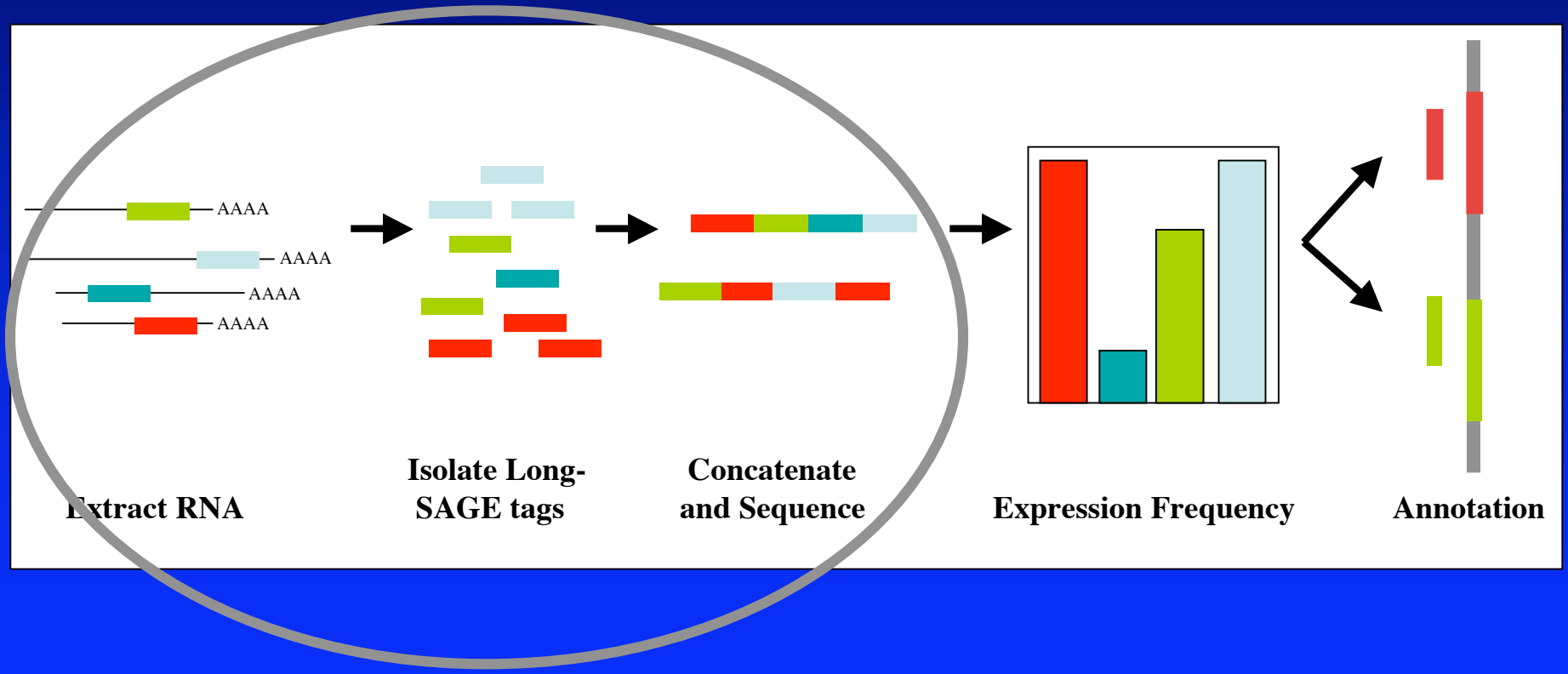


Global gene expression analyses

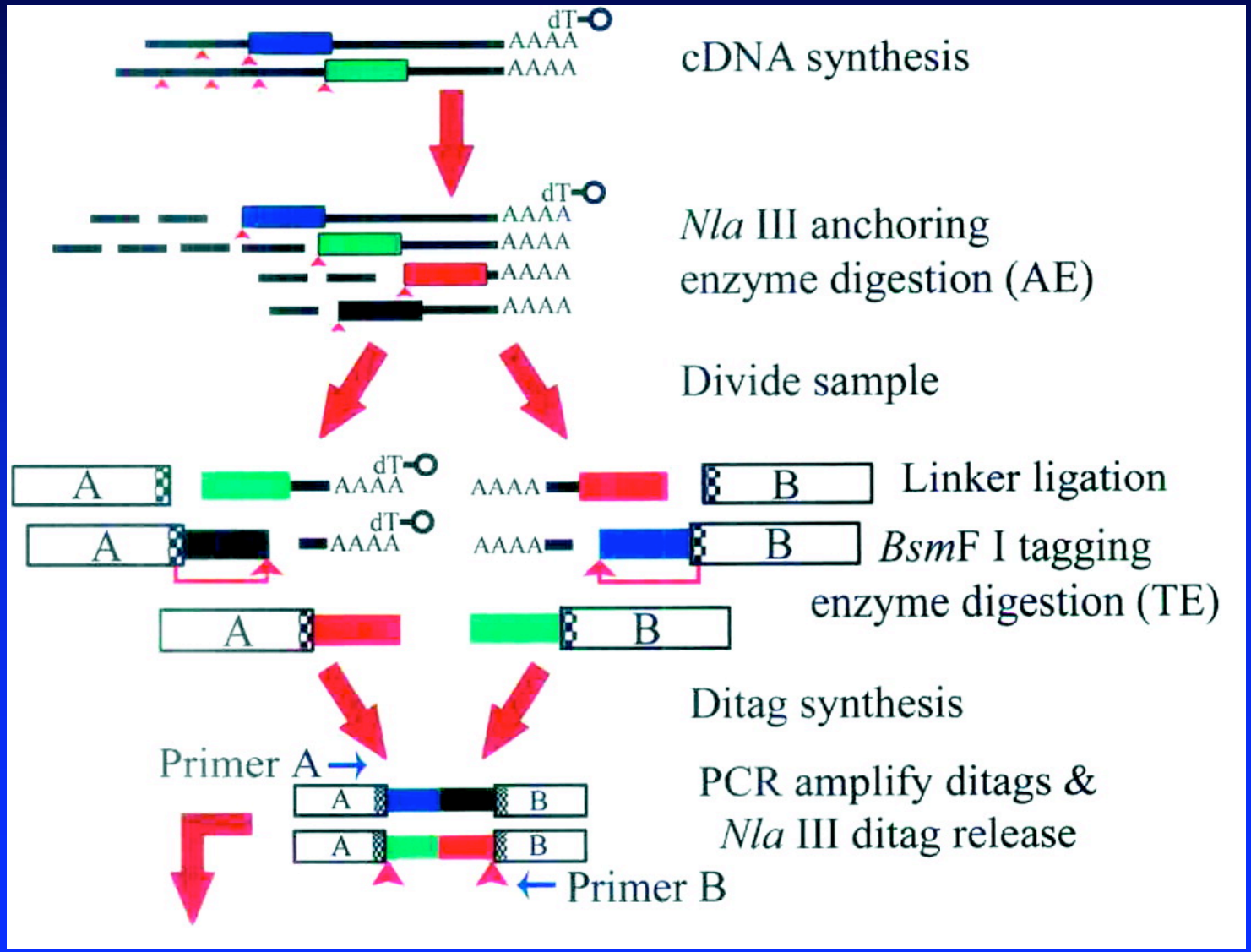
- Serial analysis of gene expression - SAGE
  - Velculescu et al. 1995 (14bp)
  - Saha et al. 2002 (21bp)
  - *Pfiesteria* Coyne et al. 2004
  - *Emiliania* Dyhrman et al. 2006
- Solexa/Illumina approach to SAGE has dramatically influenced through-put and cost.
- Analyses on *Aureoccocus* - and diatoms pending
- *E. huxleyi* : N and P stress responses
- Support the genome annotation



Long-SAGE


AAAA
AAAA
AAAA
AAAA
Extract RNA
Isolate Long-SAGE tags
Concatenate and Sequence
Expression Frequency
Annotation

Long-SAGE: tag isolation



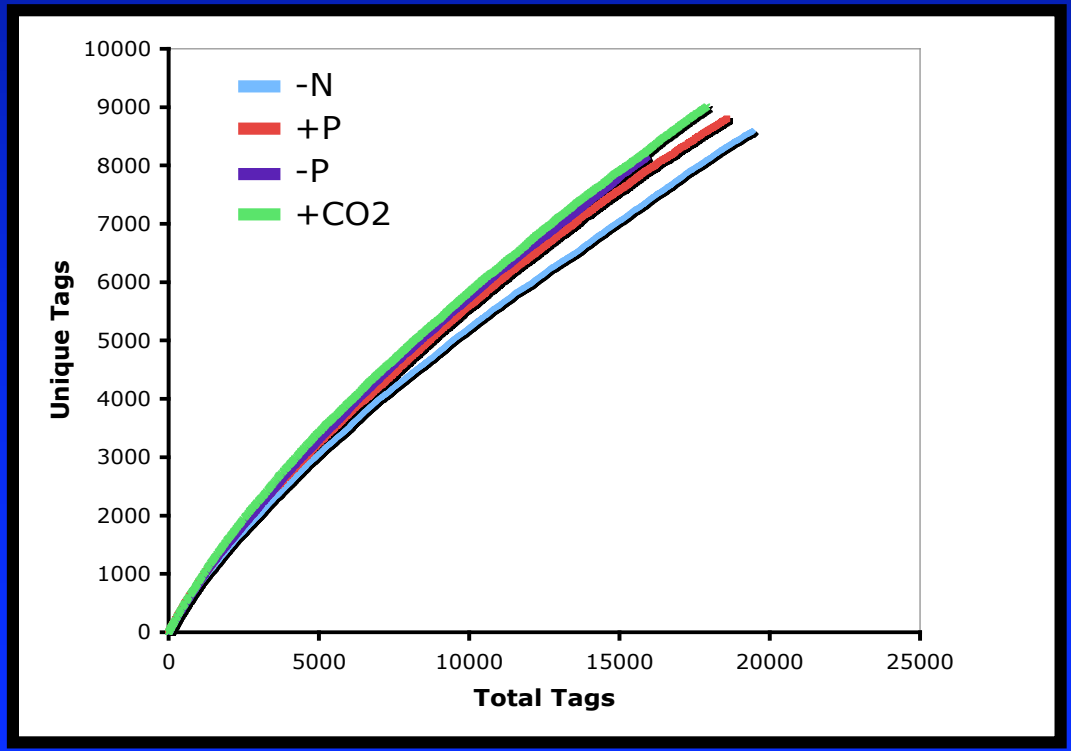
Long-Sage: library statistics

- Total tags sequenced ~ 55,000 across all libraries.
- Roughly 8,000 unique tags.
- Data suggests a unique tag count of ~ 30,000. Relationship of tag count to transcriptome size difficult to predict.

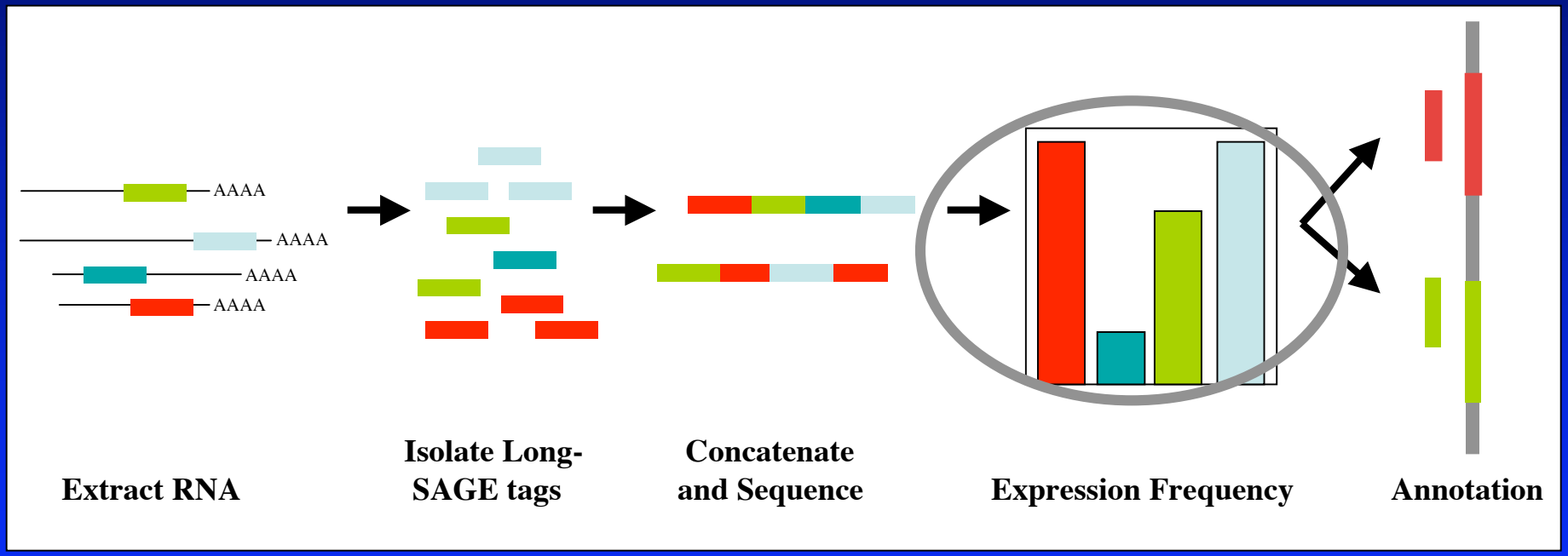
- Multiple tags map to a single gene.

- Single tag maps to multiple genes.

- Gene lacks *NlaIII* site.



Long-SAGE: expression frequency



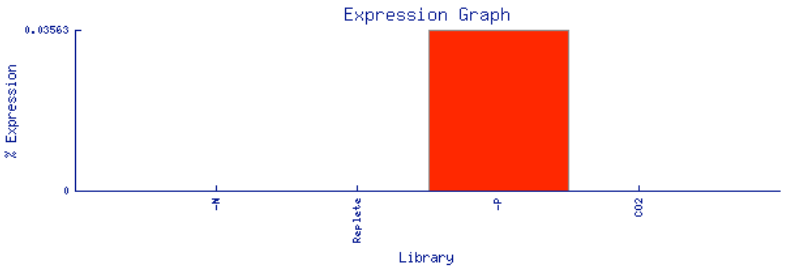
Long-SAGE: *E. huxleyi* tags up-regulated in low phosphorus conditions

SAGE Tag 12112

CATGAGGAGAGCGACACTTTG, This tag has not been assigned to an ORF

Library	Raw Count	Percentage
-N	0 of 14647	0.00000%
Replete	0 of 13682	0.00000%
-P	4 of 11225	0.03563%
+CO2	0 of 12787	0.00000%

[Details about SAGE libraries and statistics]

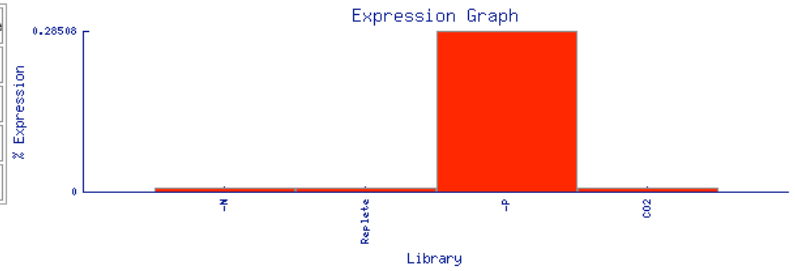


SAGE Tag 1855

CATGATTGTTAAGAAAGCGCA, This tag has not been assigned to an ORF

Library	Raw Count	Percentage
-N	1 of 14647	0.00683%
Replete	1 of 13682	0.00731%
-P	32 of 11225	0.28508%
+CO2	1 of 12787	0.00782%

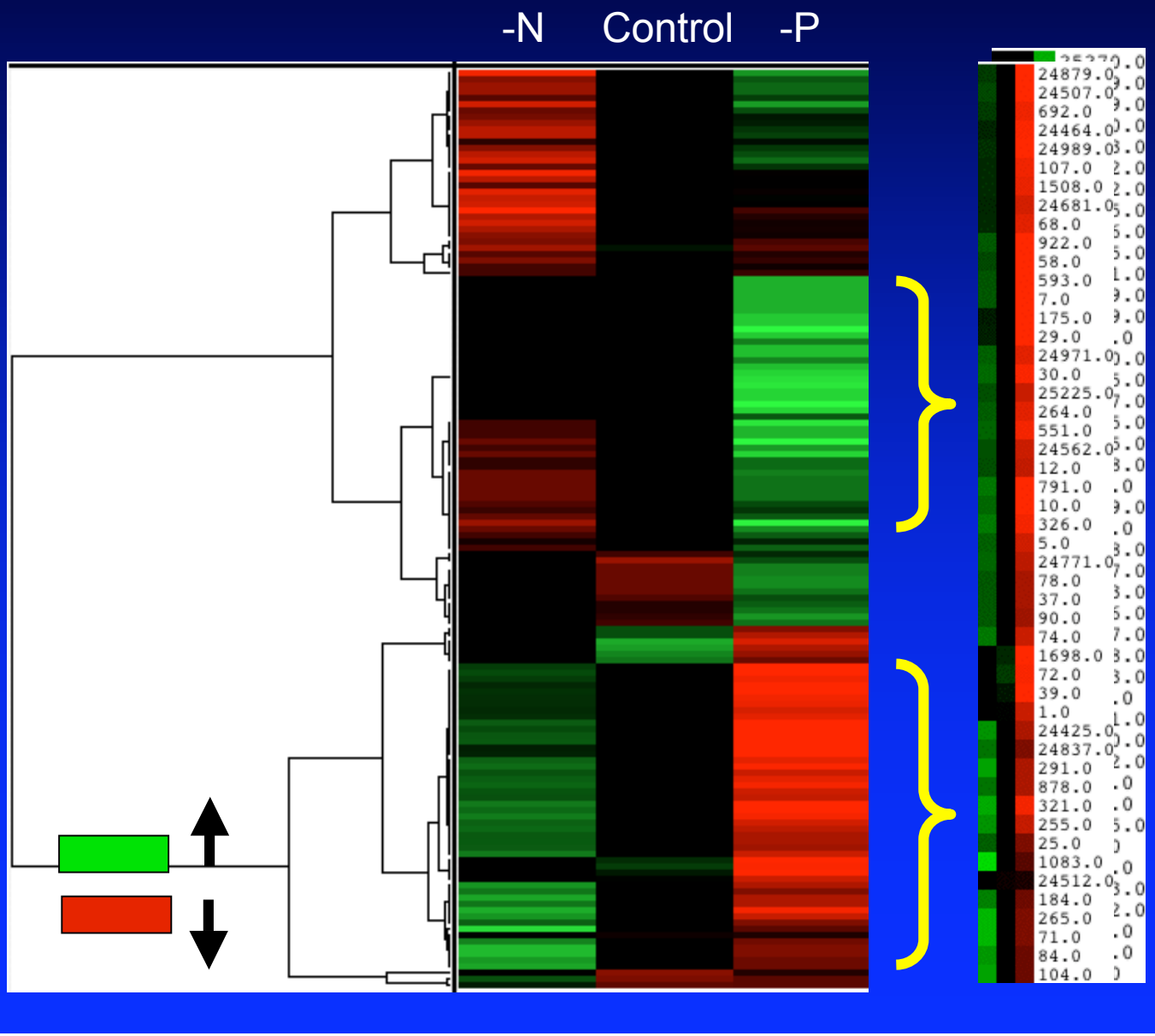
[Details about SAGE libraries and statistics]



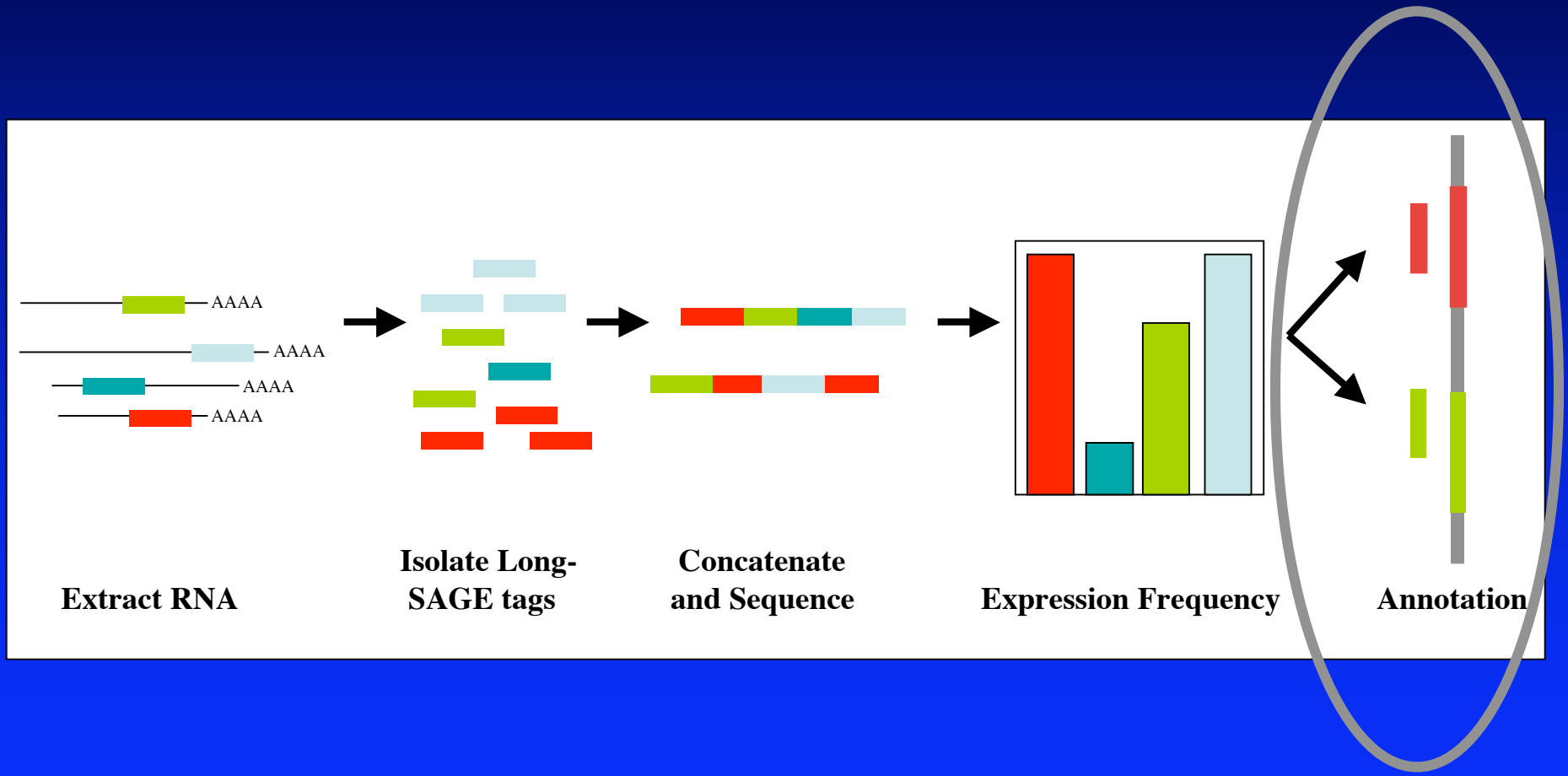
http://gmod.mbl.edu/perl/site/emiliania04?page=intro

Dyhrman et al. 2006

Long-SAGE: *E. huxleyi* clustering



Long-SAGE: annotation



Long-SAGE: *E. huxleyi* tag annotation

- Map tags to available *E. huxleyi* sequences for annotation
  - Direct match to the most 3' *NlaIII* restriction site

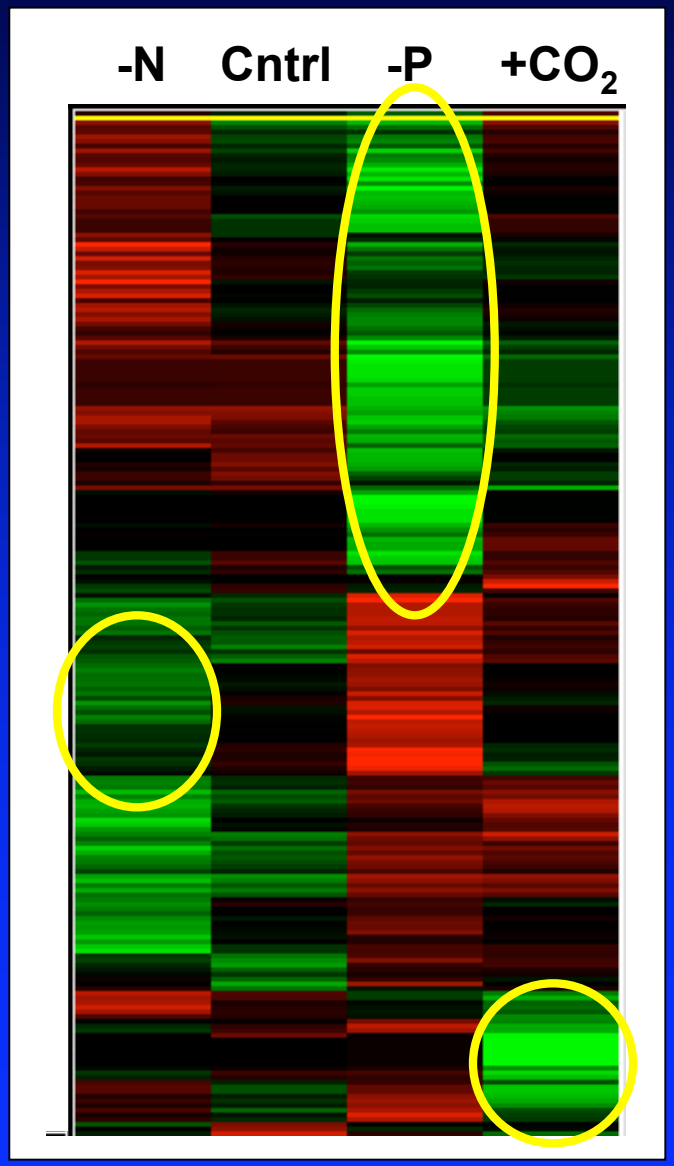
Tag mapped to EST or genome sequence with annotation

Tag ID	Sequence	Tag Type	OrfID	Description	-N	-P	Replete
12112	CATGAGGAGAGCGACACTTTG	PS	1884	putative inorganic pyrophosphatase [Arabidopsis thaliana] gi|15028285|gb|AAK76619.1| putative inorganic pyrophosphatase [Arabidopsis thaliana] gi|7671424|emb|CAB89365.1| inorganic pyrophosphatase-like protein [Arabidopsis thaliana] gi|12057177|emb|CAC1985	0.000	0.034	0.000

Scientific enquiries should be directed to sdyhrman@whoi.edu

This database is hosted by the JBPC GMOD Server. Bug reports and technical problems should be reported to biocomp@lists.mbl.edu.

Long-SAGE: *E. huxleyi* tag annotation



- Up-regulated by P stress

Alkaline phosphatase*

Phosphate permease

- Up-regulated by N stress

High affinity nitrate transporter

Amino acid transporter

Urease

- Up-regulated by increased CO_2

Many tags that map to genes with unknown function

Up-regulated

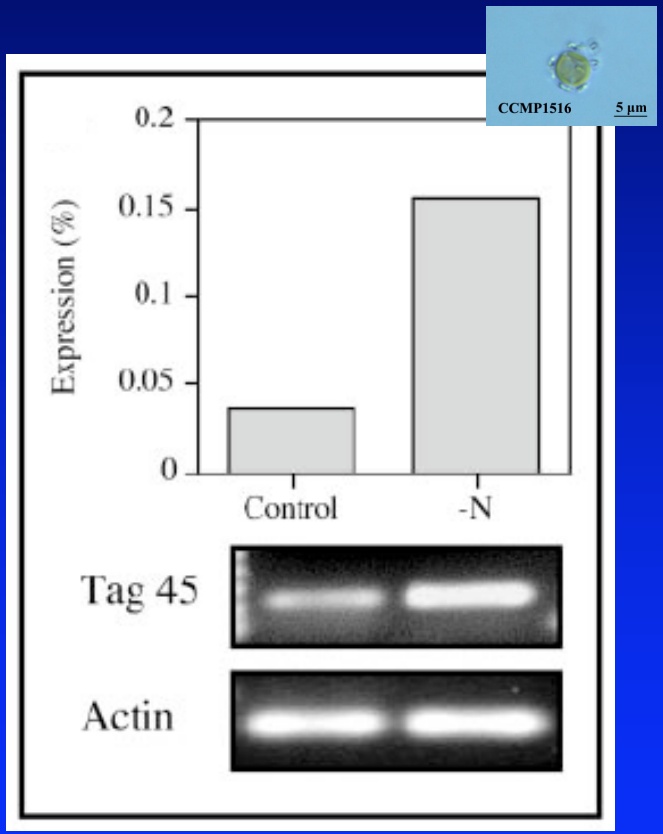
Down-regulated

Long-SAGE: *E. huxleyi* tag validation

P related
Inorganic pyrophosphatase
Phosphate-repressible permease
Polyphosphate synthetase
Alkaline phosphatase

N related
High affinity nitrate transporter*
Urease

C related
Carbonic anhydrase

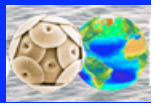


Dyhrman et al. 2006

Beyond the transcriptome

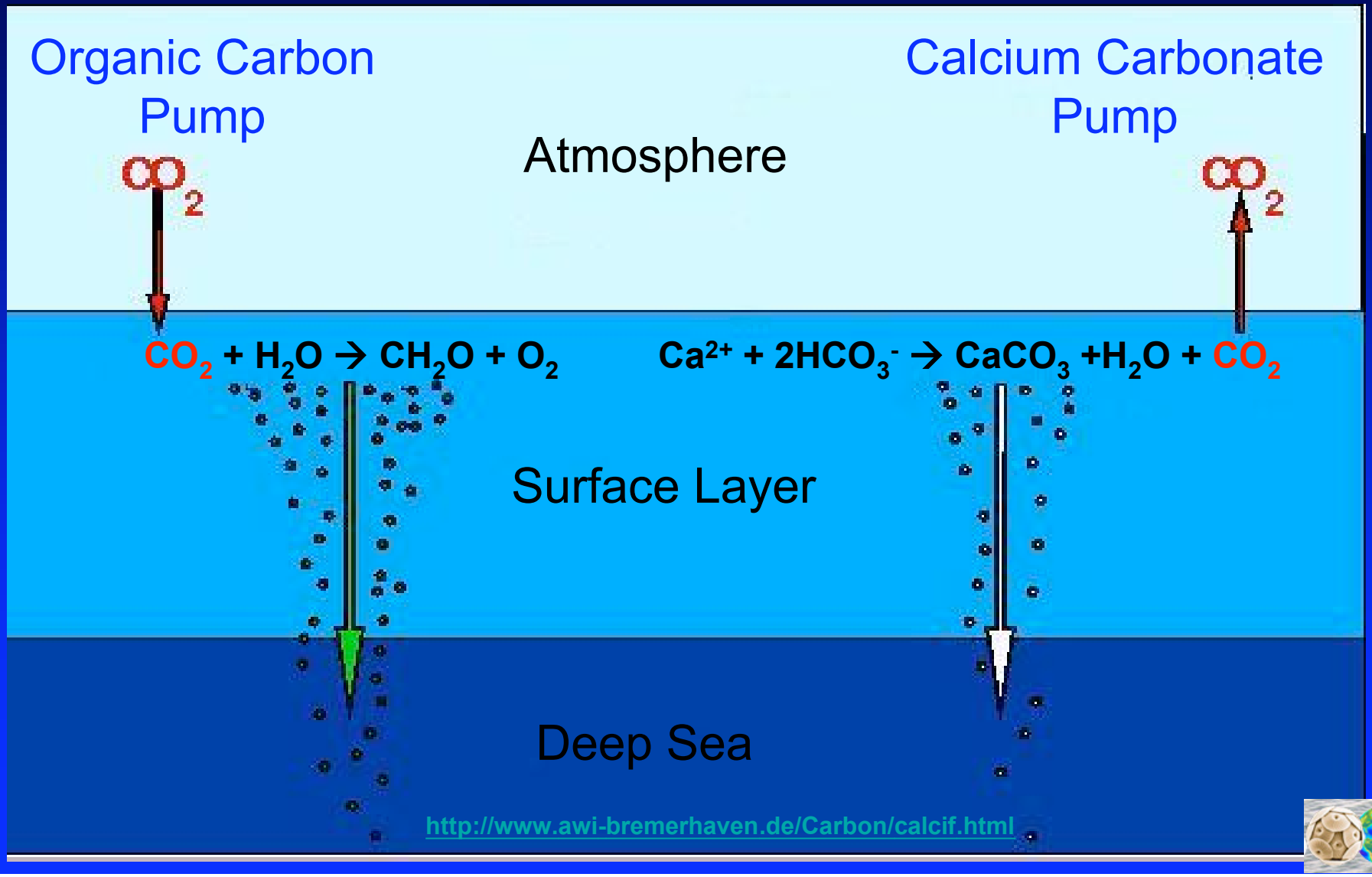
- *What are metabolic pathways and preferred sources of N, P and C?*
- *Biosynthesis and stability of alkenones?*
- *Influence of virus infection on loss terms and the cycling of S, C, N, P ?*
- *How and why to they calcify?*

- How do we get at genes with no known function?
  - *One of the E. huxleyi alkaline phosphatases has a very high Vmax but no database homology.*
  - *Only identified with molecular/biochemical characterization (Xu et al 2006, Landry et al. 2006)*
- Development of a genetic system may be needed to identify genes involved with calcification etc.
- So - what does the future hold?



Back to the Future

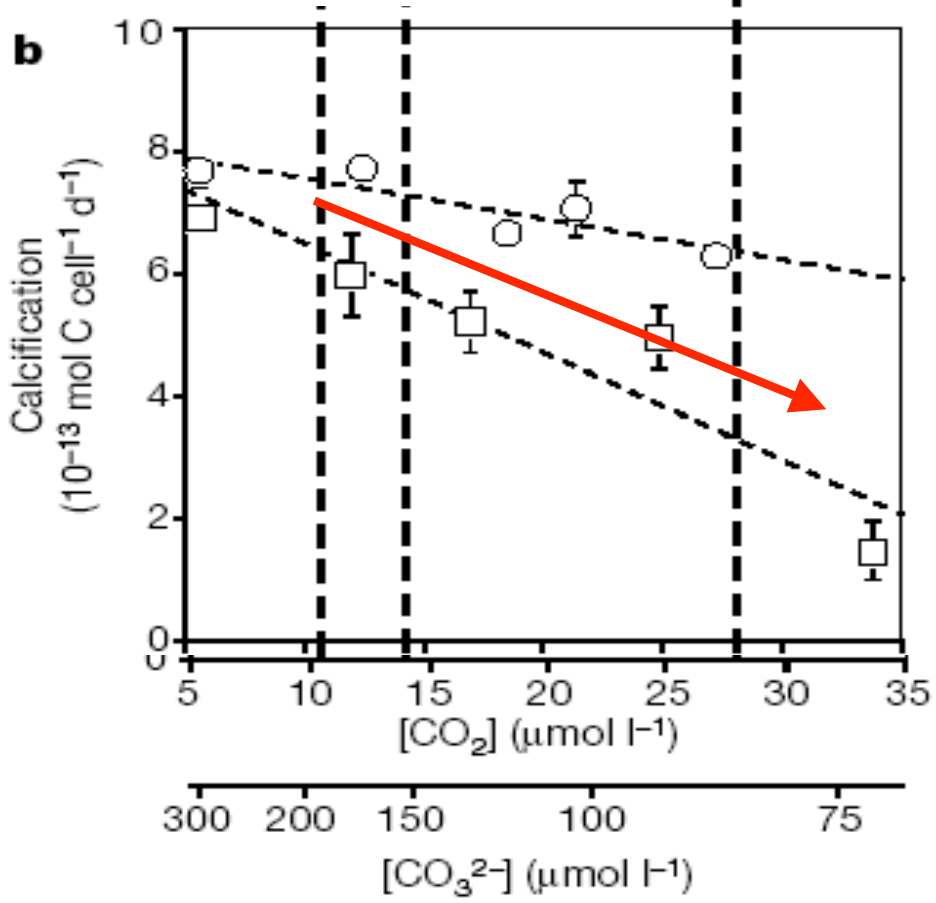
- Coccolithophore responses to high CO_2

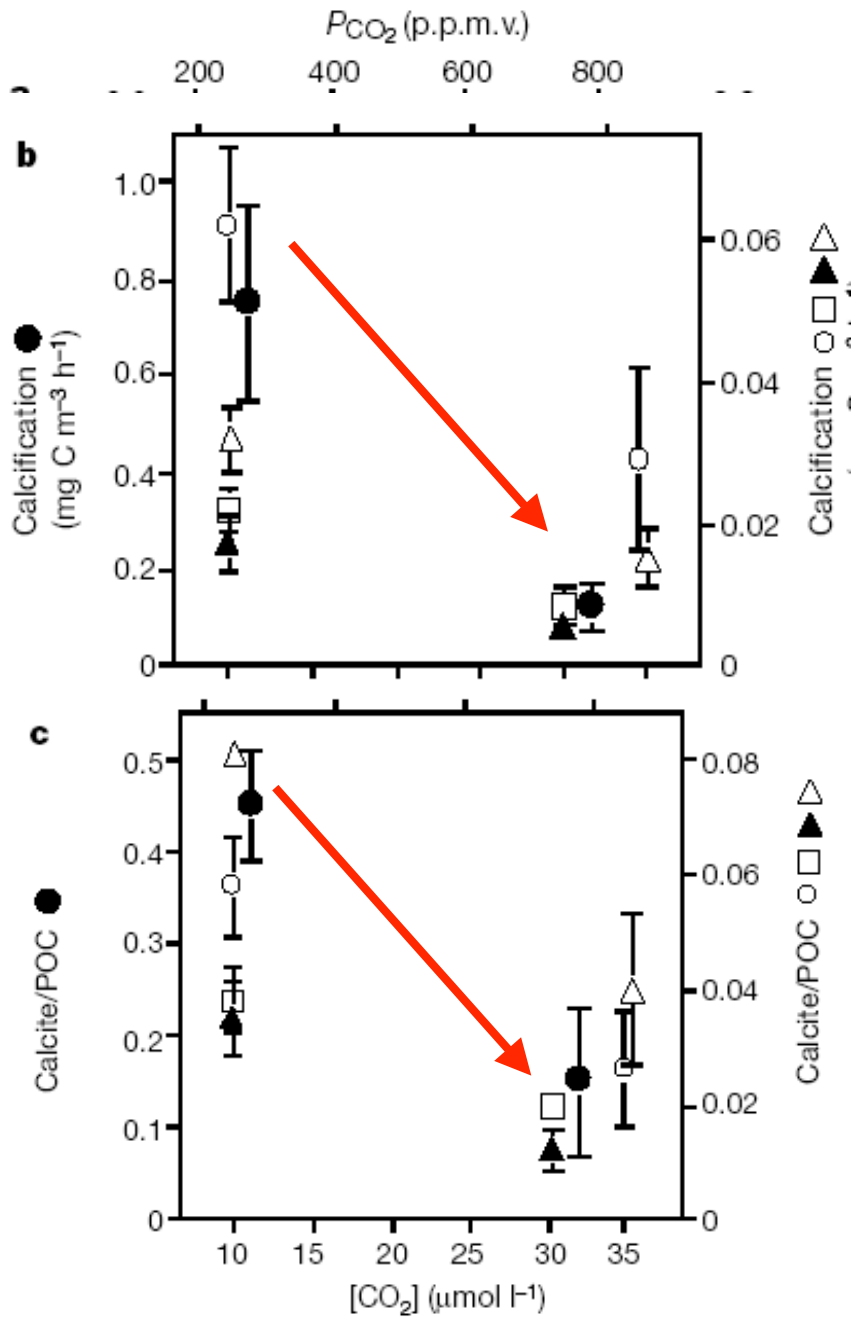


Reduced calcification of marine plankton in response to increased atmospheric CO_2

Ulf Riebesell *, Ingrid Zondervan*, Björn Rost*, Philippe D. Tortell†, Richard E. Zeebe*‡ & François M. M. Morel†

Culture studies with variable CO_2 concentrations generated by adding acid



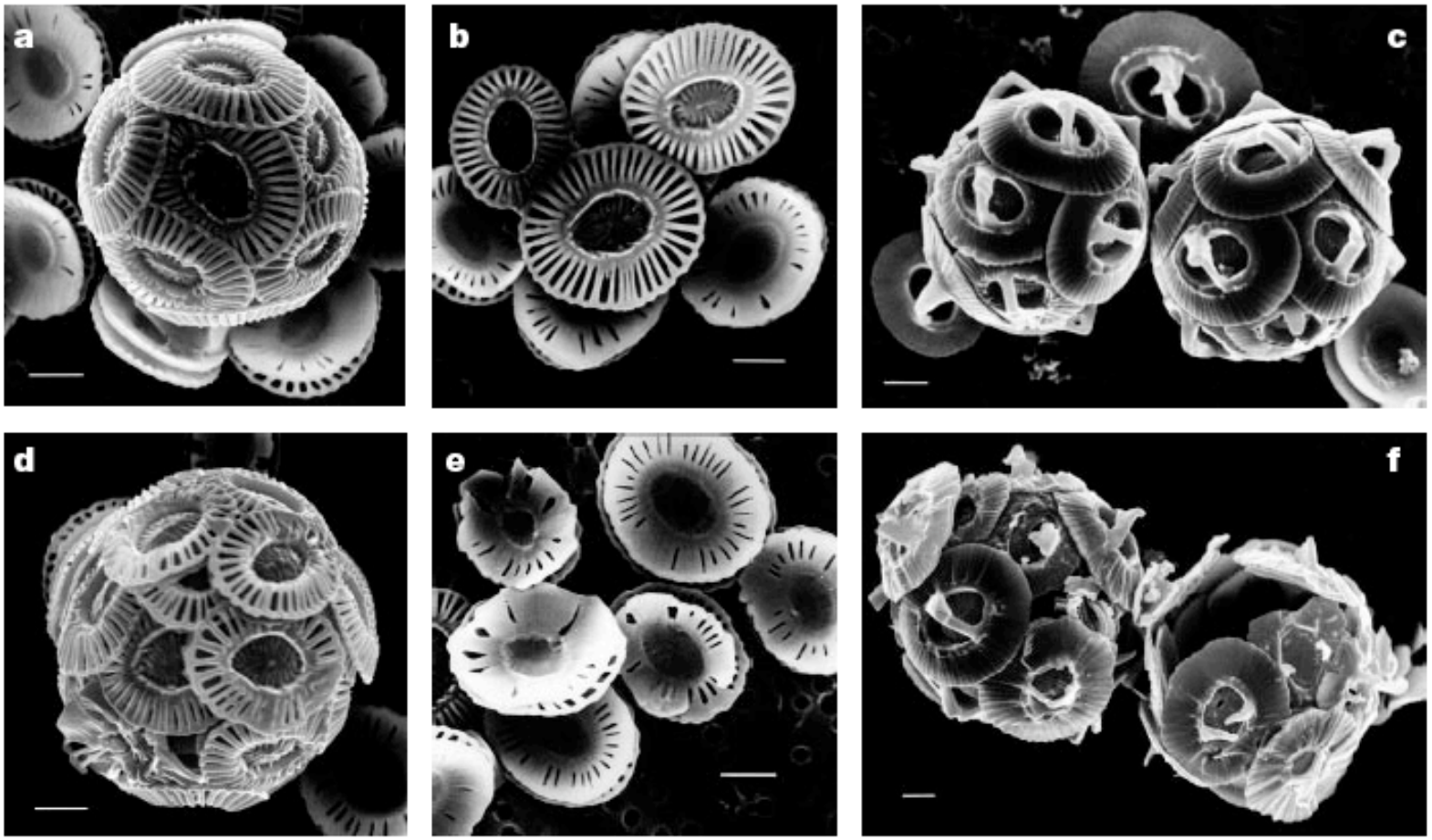


Similar results observed for field populations in the subarctic North Pacific.

Reduced calcification of marine plankton in response to increased atmospheric CO_2

Ulf Riebesell *, Ingrid Zondervan*, Björn Rost*, Philippe D. Tortell†, Richard E. Zeebe*‡ & François M. M. Morel†

Normal CO_2

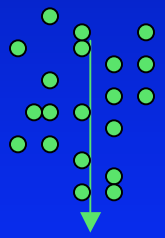


High CO_2

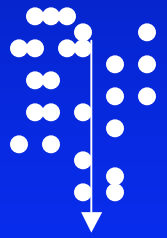
Back to the Future

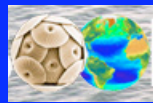
- Coccolithophore responses to high CO_2
- Decrease in calcification observed for *Emiliania huxleyi, Gephyrocapsa oceanica*, negligble change observed for *Coccolithus pelagicus*.

$$CO_2 + H_2O \rightarrow CH_2O + O_2$$

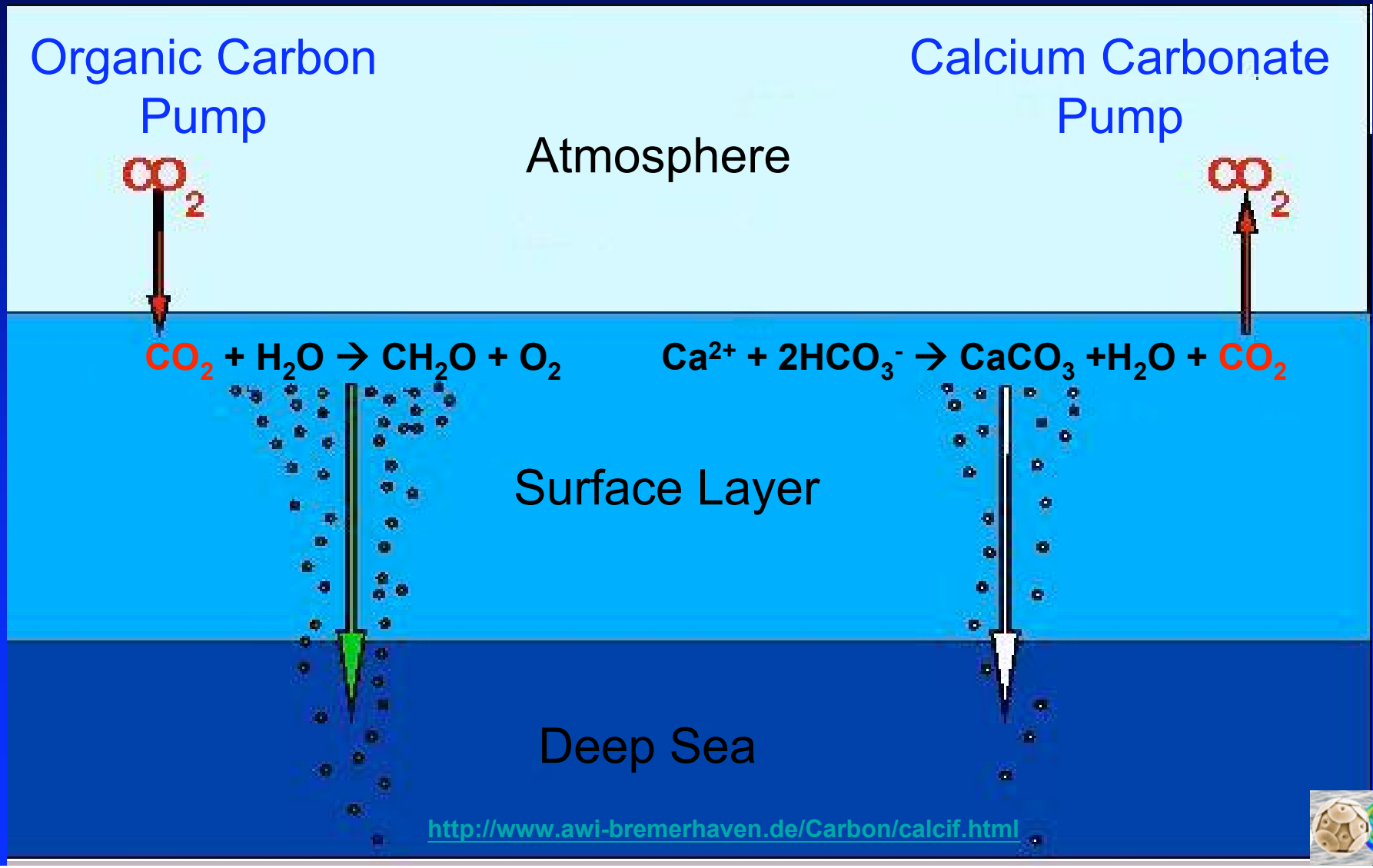


$$Ca^{2+} + 2HCO_3^- \rightarrow CaCO_3 + H_2O + CO_2$$





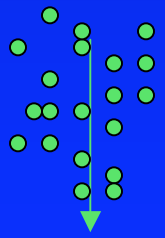
Negative feedback on CO_2?



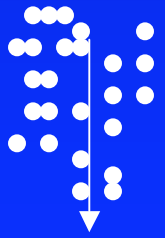
Back to the Future

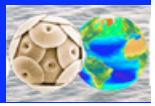
- Coccolithophore responses to high CO_2
- Decrease in calcification observed for *Emiliania huxleyi, Gephyrocapsa oceanica*, negligble change observed for *Coccolithus pelagicus*
- But.. The carbonate system was modified by directly adjusting pH
- pH controls the relative proportions of the carbonate species while DIC remains constant.
- Many researchers are suggesting that bubbling CO_2 enriched air through sea water (increasing both CO_2 and DIC) is more realistic.

$$CO_2 + H_2O \rightarrow CH_2O + O_2$$



$$Ca^{2+} + 2HCO_3^- \rightarrow CaCO_3 + H_2O + CO_2$$



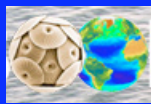


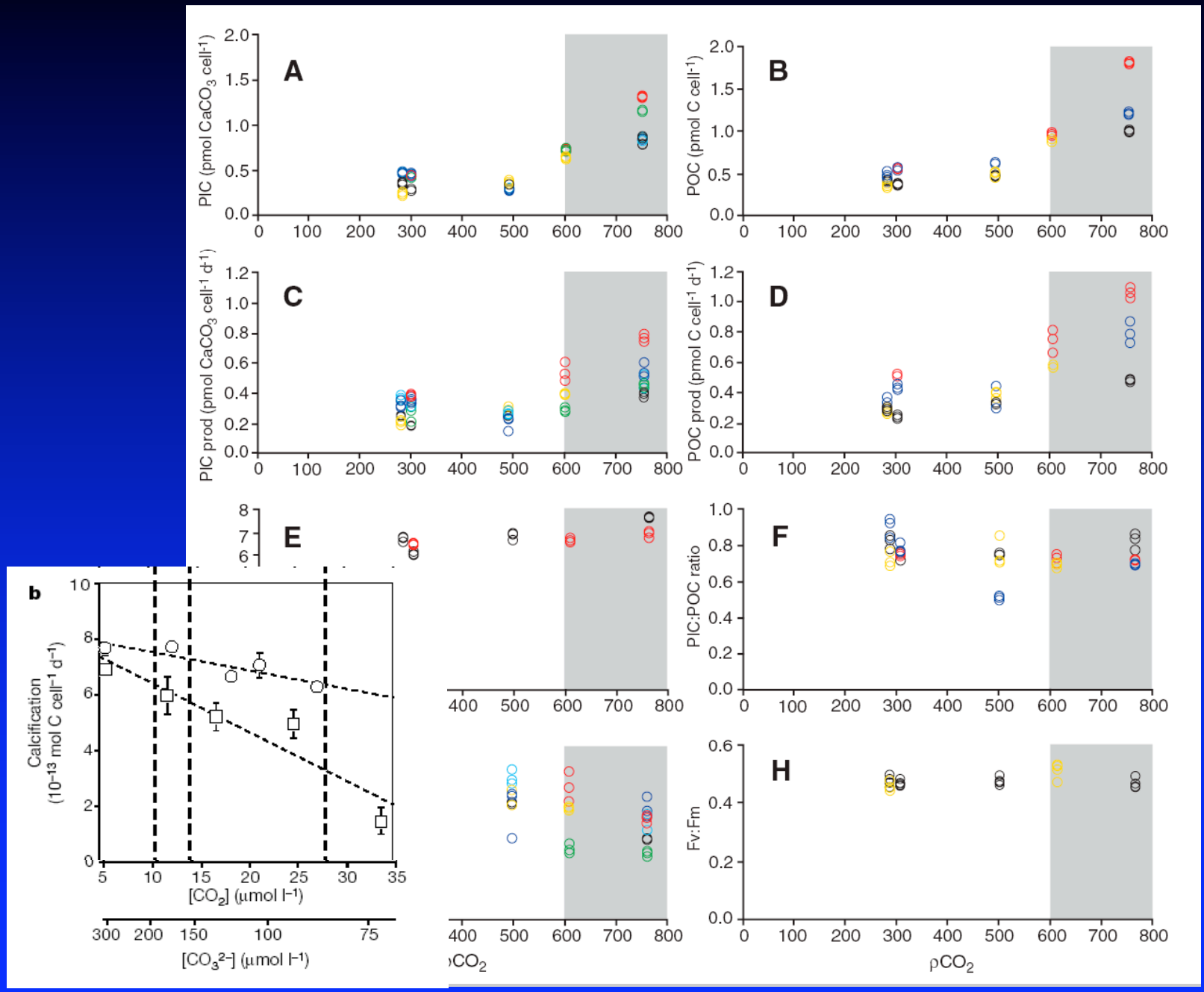
Back to the Future with CO_2 bubbling…

Phytoplankton Calcification in a High-CO_2 World

M. Debora Iglesias-Rodriguez,[1]* Paul R. Halloran,[2]* Rosalind E. M. Rickaby,[2]
Ian R. Hall,[3] Elena Colmenero-Hidalgo,[3]† John R. Gittins,[1] Darryl R. H. Green,[1]
Toby Tyrrell,[1] Samantha J. Gibbs,[1] Peter von Dassow,[4] Eric Rehm,[5]
E. Virginia Armbrust,[5] Karin P. Boessenkool[3]

Ocean acidification in response to rising atmospheric CO_2 partial pressures is widely expected to reduce calcification by marine organisms. From the mid-Mesozoic, coccolithophores have been major calcium carbonate producers in the world's oceans, today accounting for about a third of the total marine $CaCO_3$ production. Here, we present laboratory evidence that calcification and net primary production in the coccolithophore species *Emiliania huxleyi* are significantly increased by high CO_2 partial pressures. Field evidence from the deep ocean is consistent with these laboratory conclusions, indicating that over the past 220 years there has been a 40% increase in average coccolith mass. Our findings show that coccolithophores are already responding and will probably continue to respond to rising atmospheric CO_2 partial pressures, which has important implications for biogeochemical modeling of future oceans and climate.




A
PIC (pmol CaCO3 cell-1)
B
POC (pmol C cell-1)
C
PIC prod (pmol CaCO3 cell-1 d-1)
D
POC prod (pmol C cell-1 d-1)
E
F
PIC:POC ratio
H
Fv:Fm
pCO2
b
Calcification (10-13 mol C cell-1 d-1)
[CO2] (µmol l-1)
[CO32-] (µmol l-1)

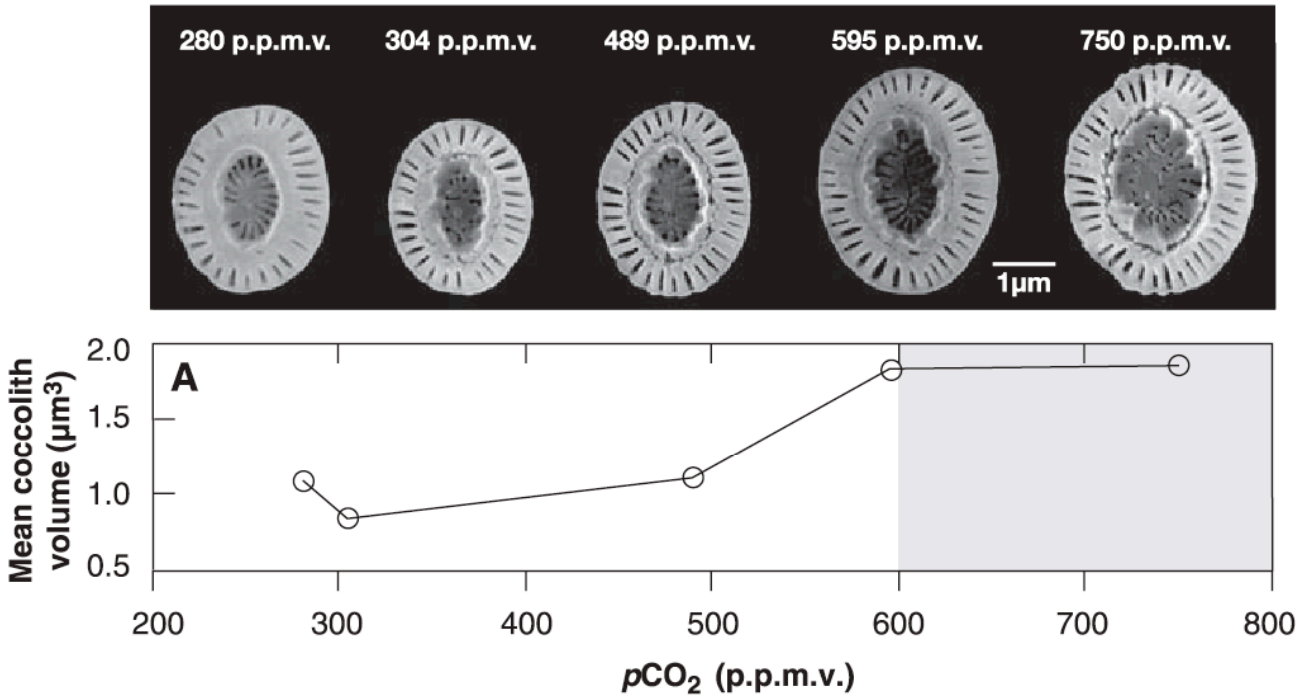


Fig. 2. Coccolith volume and $CaCO_3$ per cell. Increasing coccolith volume is closely coupled with increasing $CaCO_3$ per cell, indicating down-core measurement of coccolith mass to be representative of $CaCO_3$ production. Scanning electron microscope (SEM) images show typical coccoliths from each culture with Pco_2 values from 280 to 750 ppmv of CO_2, of where the measured volume was converted to length using the formula for a heavily calcified coccolith (*27*).

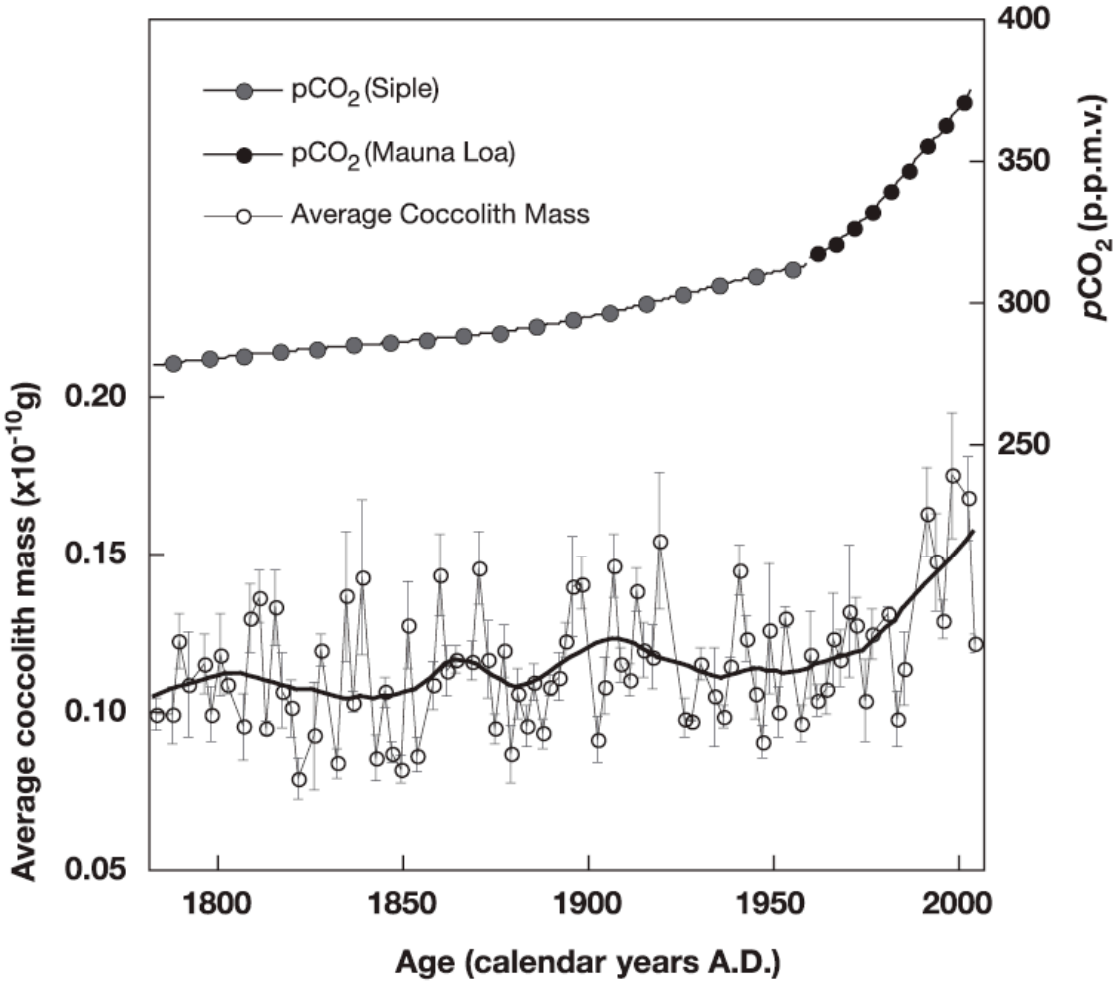
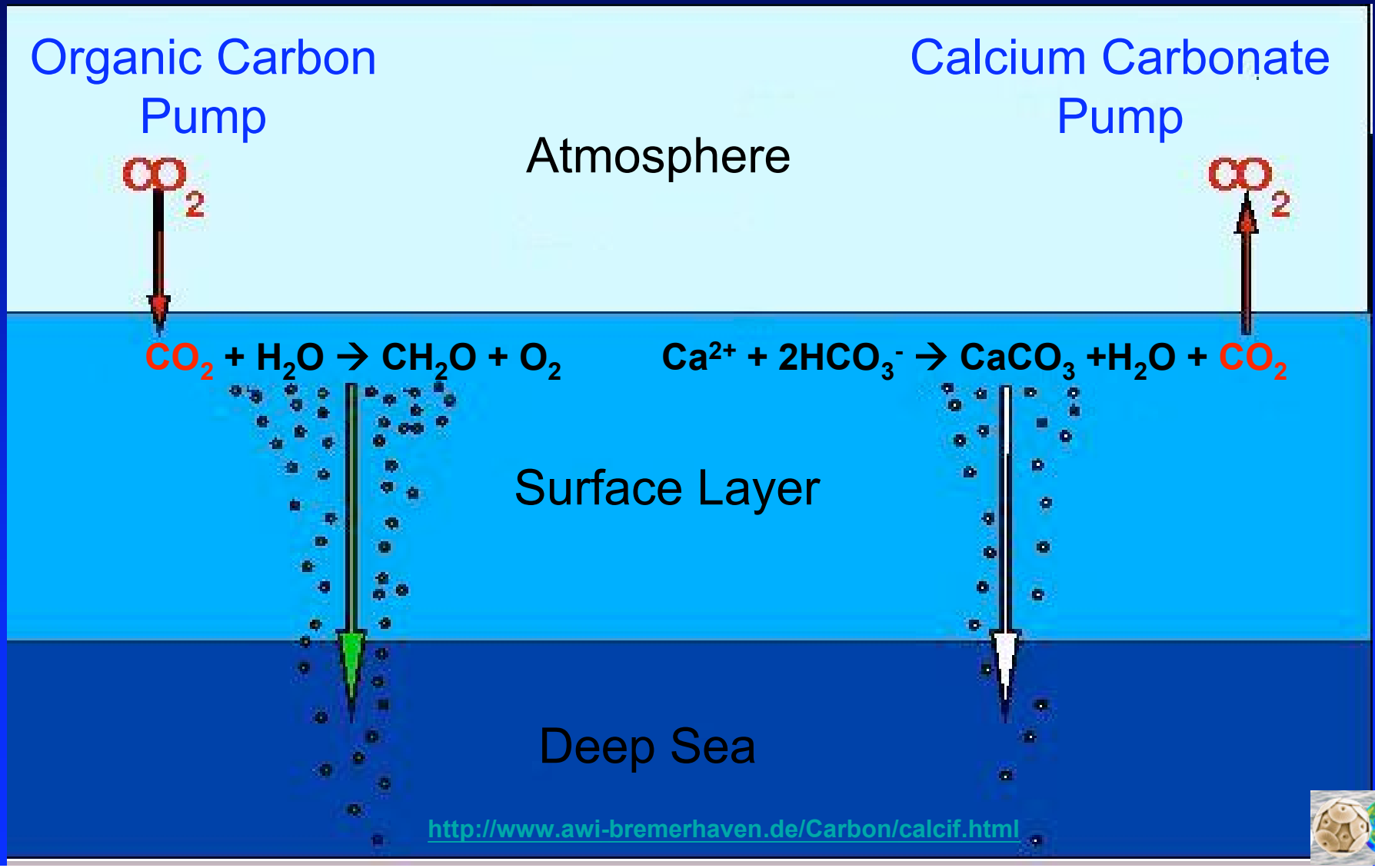
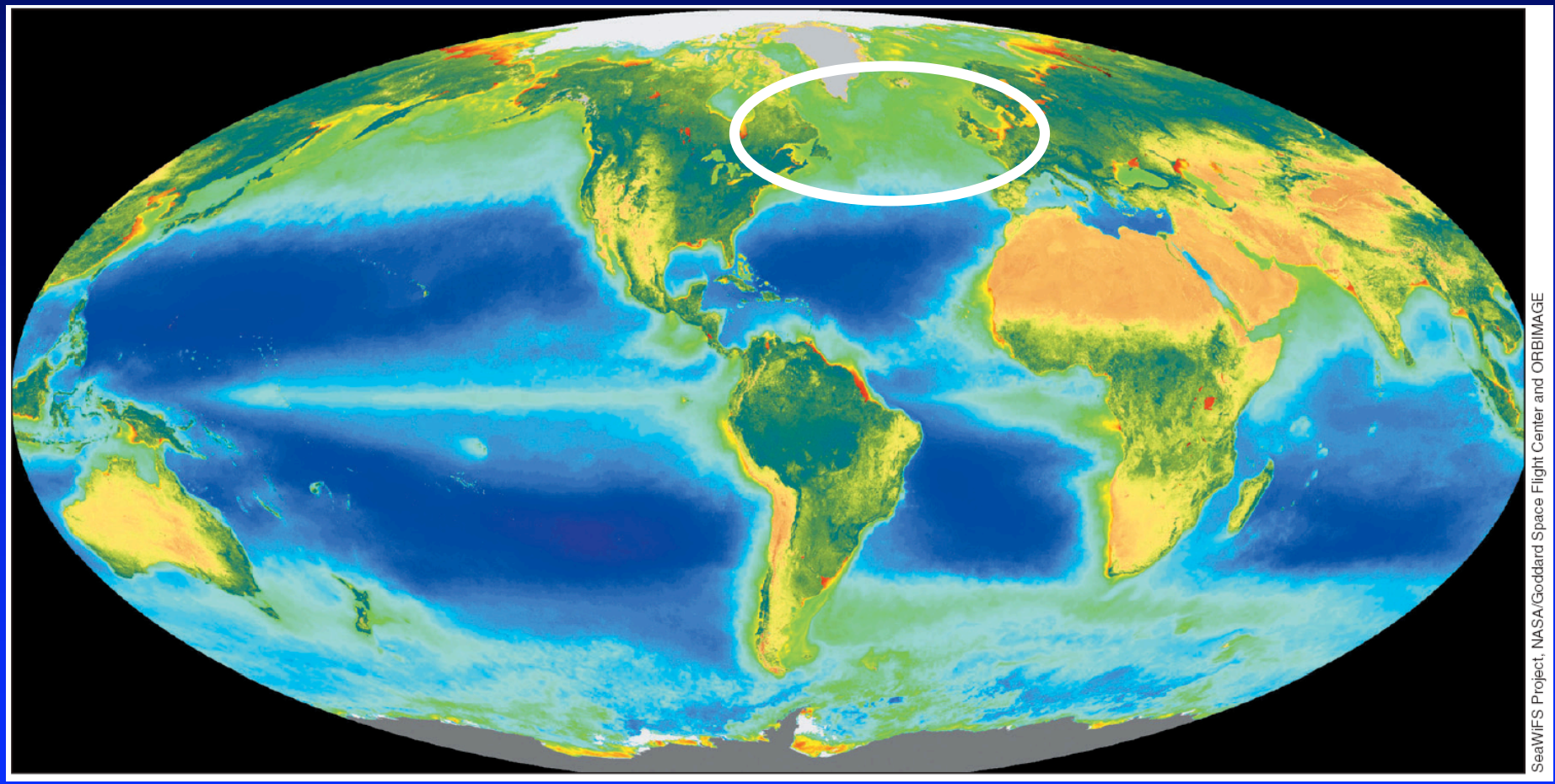


Fig. 4. Average mass of $CaCO_3$ per coccolith in core RAPID 21-12-B and atmospheric CO_2. The average mass of $CaCO_3$ per coccolith in core RAPID 21-12-B (open circles) increased from 1.08×10^{-11} to 1.55×10^{-11} g between 1780 and the modern day, with an accelerated increase over recent decades. The increase in average coccolith mass correlates with rising atmospheric Pco_2, as recorded in the Siple ice core (gray circles) (*26*) and instrumentally at Mauna Loa (black circles) (*38*), every 10th and 5th data point shown, respectively. Error bars represent 1 SD as calculated from replicate analyses. Samples with a standard deviation greater than 0.05 were discarded. The smoothed curve for the average coccolith mass was calculated using a 20% locally weighted least-squares error method.

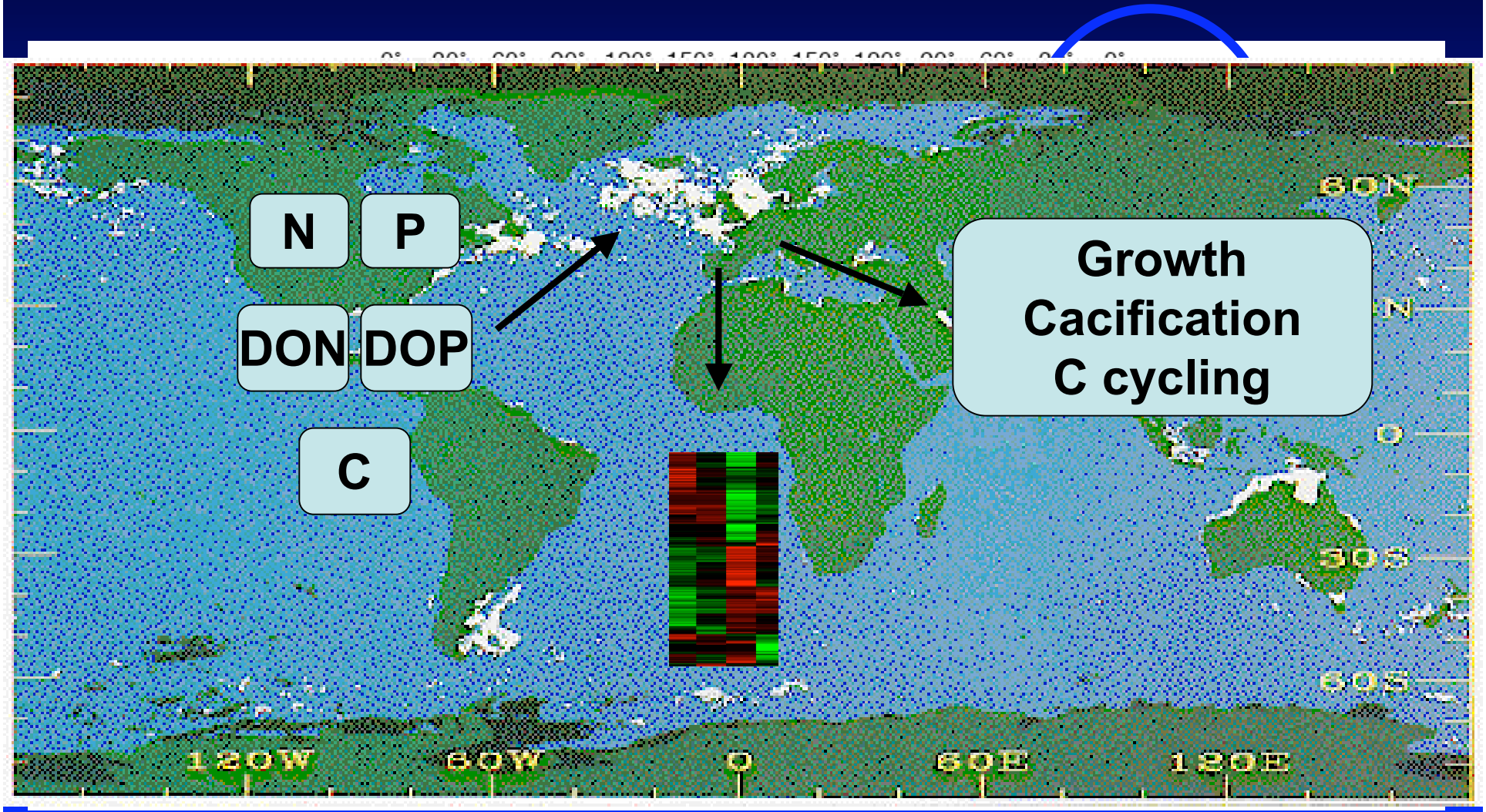
Negative feedback on CO_2??????
Or…Positive feedback on CO_2



Linking the genome to physiological ecology



North Atlantic is a CO_2 sink



Graphic: www.noc.soton.ac.uk, Brown and Yoder 1994

Preliminary “ocean phenotype” data

Sample 5m niskins
Sample incubations

↓

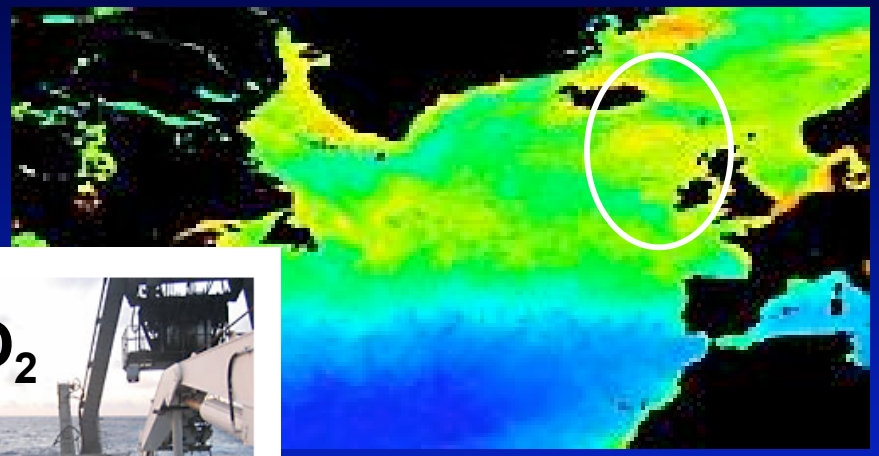
Collect 0.5-0.75L
onto GF/F

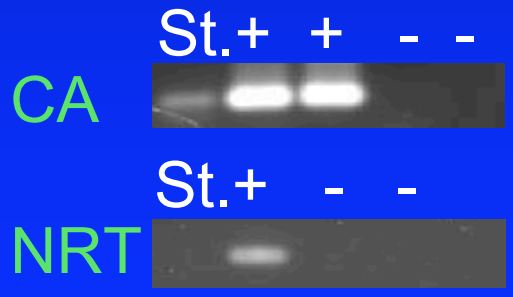
↓

Store in RNA
extraction buffer

↓

Examine gene
expression



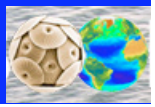


Gene targets and expression pattern

Transcript	Functional Category	# 33	# 85	# 57 Incubation
Actin	Cell Structure	■	■	■
Nitrate transporter	N Metabolism		■	■
Pyrophosphatase	P Metabolism		■	■
δ Carbonic anhydrase	C Metabolism		■	■
O_2 evolving enhancer	Photosynthesis			■

■ Band Detected ■ Band Not Detected

Special thanks to Dave Hutchins and Louie Wurch



The take home message…

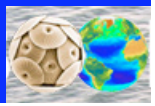
- Coccolithophores are really cool - in part because the dynamics of this one group can dramatically influence carbon cycling

- Of the coccolithophores, *Emiliania huxleyi* is emerging as increasingly important model for studies of …
  - *Paleo climate reconstruction*
  - *S cycling*
  - *Viral dynamics*
  - *Carbon cycling*

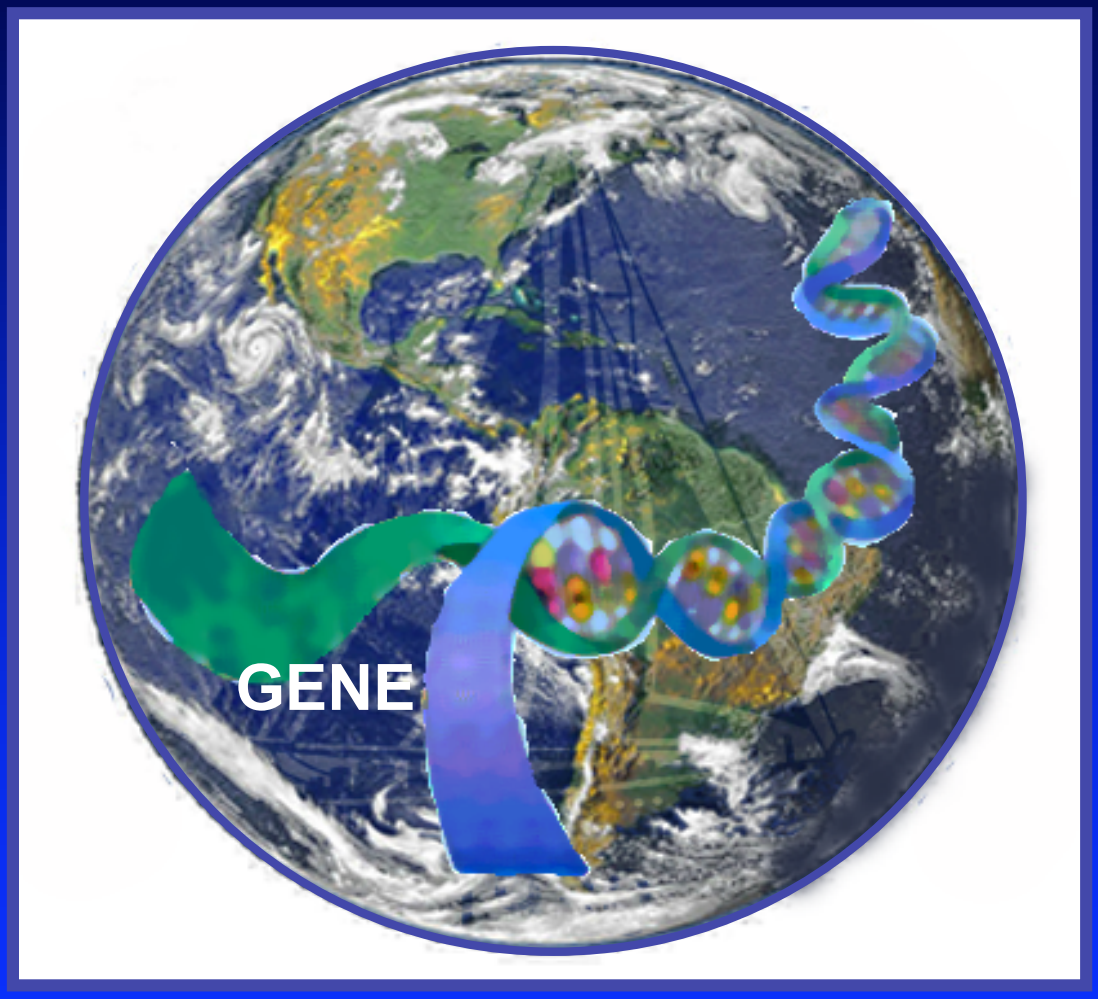
- Anatomy of a eukaryotic genome project "euks are challenging"

- Transcriptome profiling for aiding genome annotation and moving beyond "capacity"
  - *Introduction to SAGE*
  - *N and P scavenging in E. huxleyi*

- What does the future hold? … The challenges of prediction in microbial oceanography
  - *Two different CO_2 responses*




INGRAHAM


GENE