

Micromonas project meeting

January 2010



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Microbial oceanography

Urgency

Mechanistic knowledge of marine carbon-cycle is weak

Very diverse microbial communities – bacteria, archaea and protists

Many uncultured; interactions not known

Today –

Project rationale/goals

Introduction to *Micromonas*

ALEX MOVE

THIS: 10+ years behind *Chlamy*/Plant



Picoplankton Do Some Heavy Lifting

<2-3 μm diameter

Tiny unicellular plants called picoplankton play an unexpectedly large role in the transport of organic matter to the deep ocean.

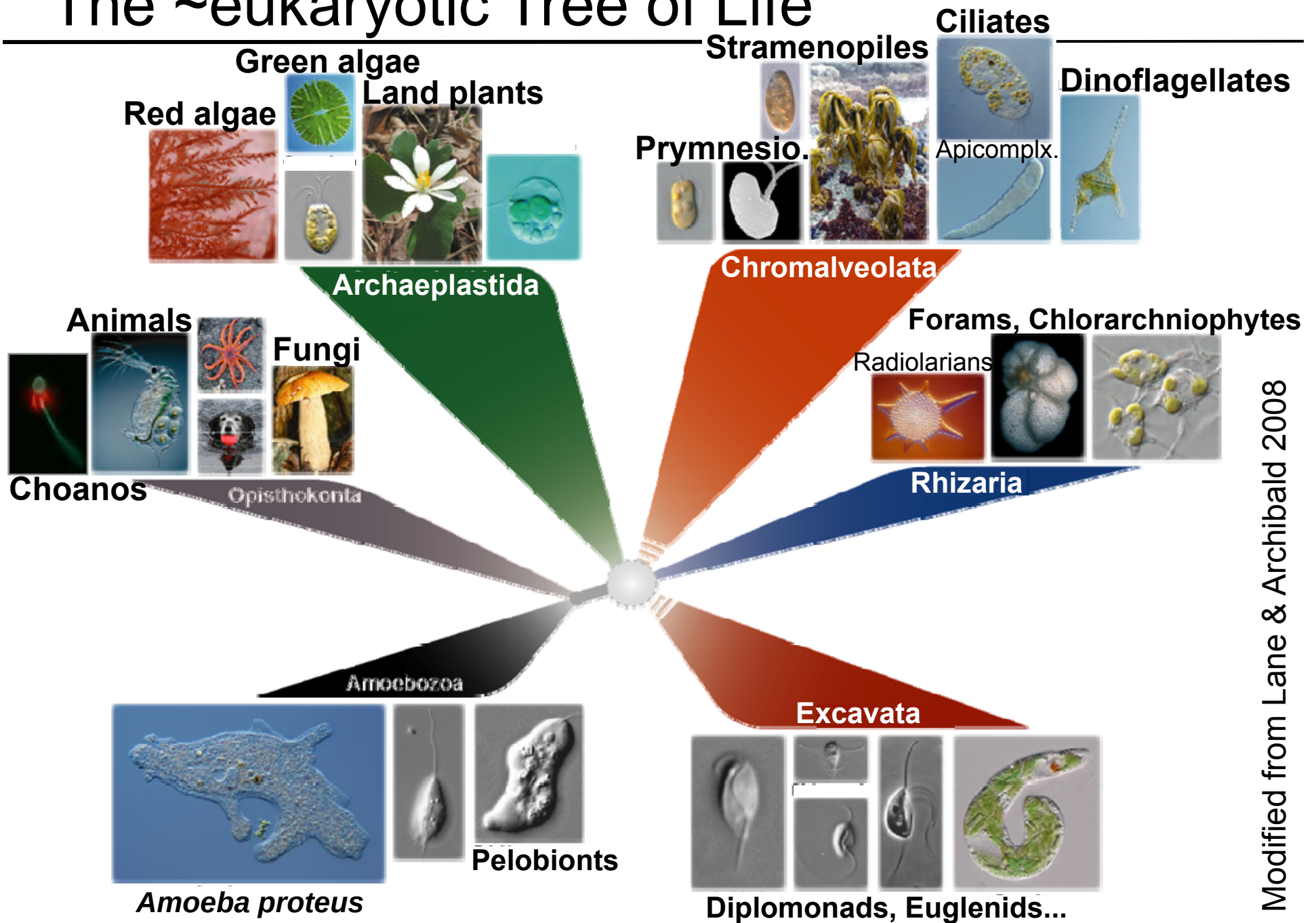
Richardson & Jackson *Science* 2007

Prochlorococcus
Synechococcus } **Cyanobacteria**

Picophytoeukaryotes,
e.g. *Micromonas*

Bill Li's arctic results

The ~eukaryotic Tree of Life

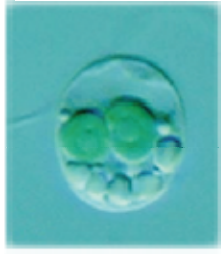


Modified from Lane & Archibald 2008

Green algae



Land plants



Archaeplastida



Ancestral green algae were of fundamental importance to the eukaryotic 'greening' that shaped Earth ecosystems

Persistence in modern oceans

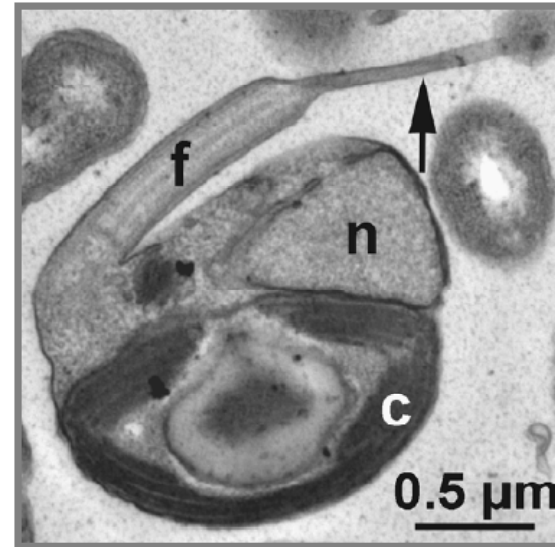
pico-prasinophytes

Ostreococcus



Worden et al. 2004

Micromonas



Worden et al. 2009

Ostreococcus ~ 13 Mb genome (Derelle et al '06, Palenik et al '07)

Micromonas (2 isolates) ~ 21 Mb each } CCMP1545
(*Chlamy* ~ 120 Mb) & RCC299

Pros: Reduced genomes, low redundancy, few repeats

Cons: No genetic system (overcome this w/RNAseq & RNAi?)

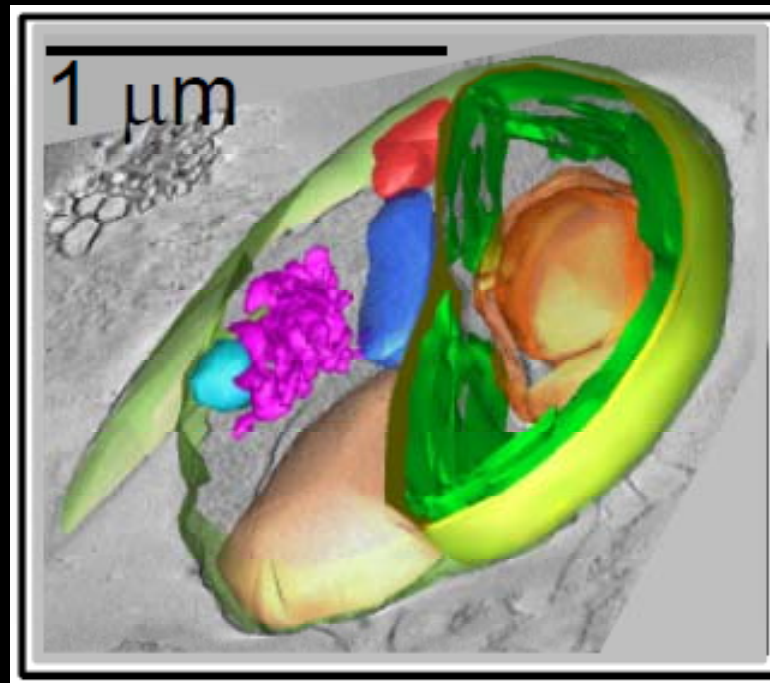
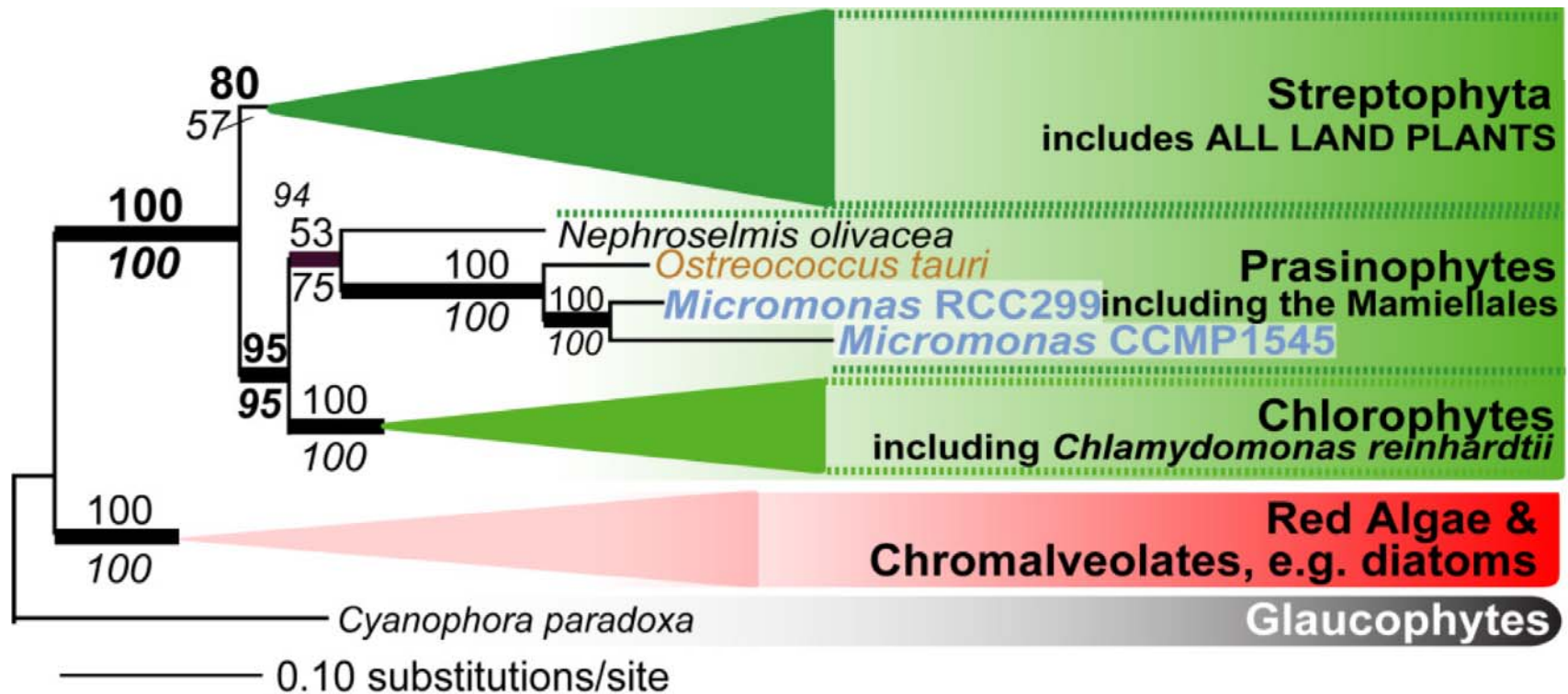


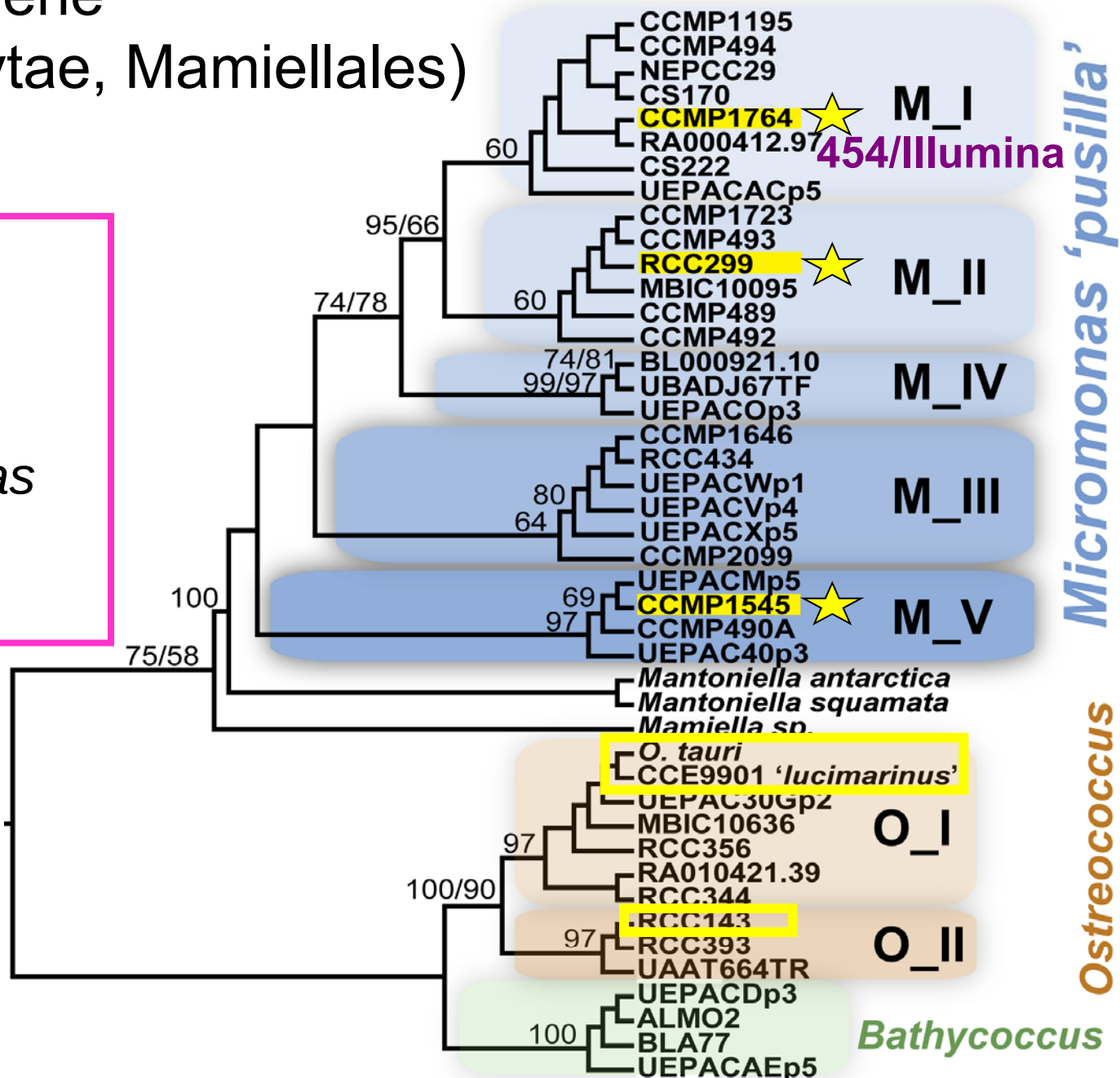
Image: Worden Deerinck, Terada, Oniyashi & Ellisman



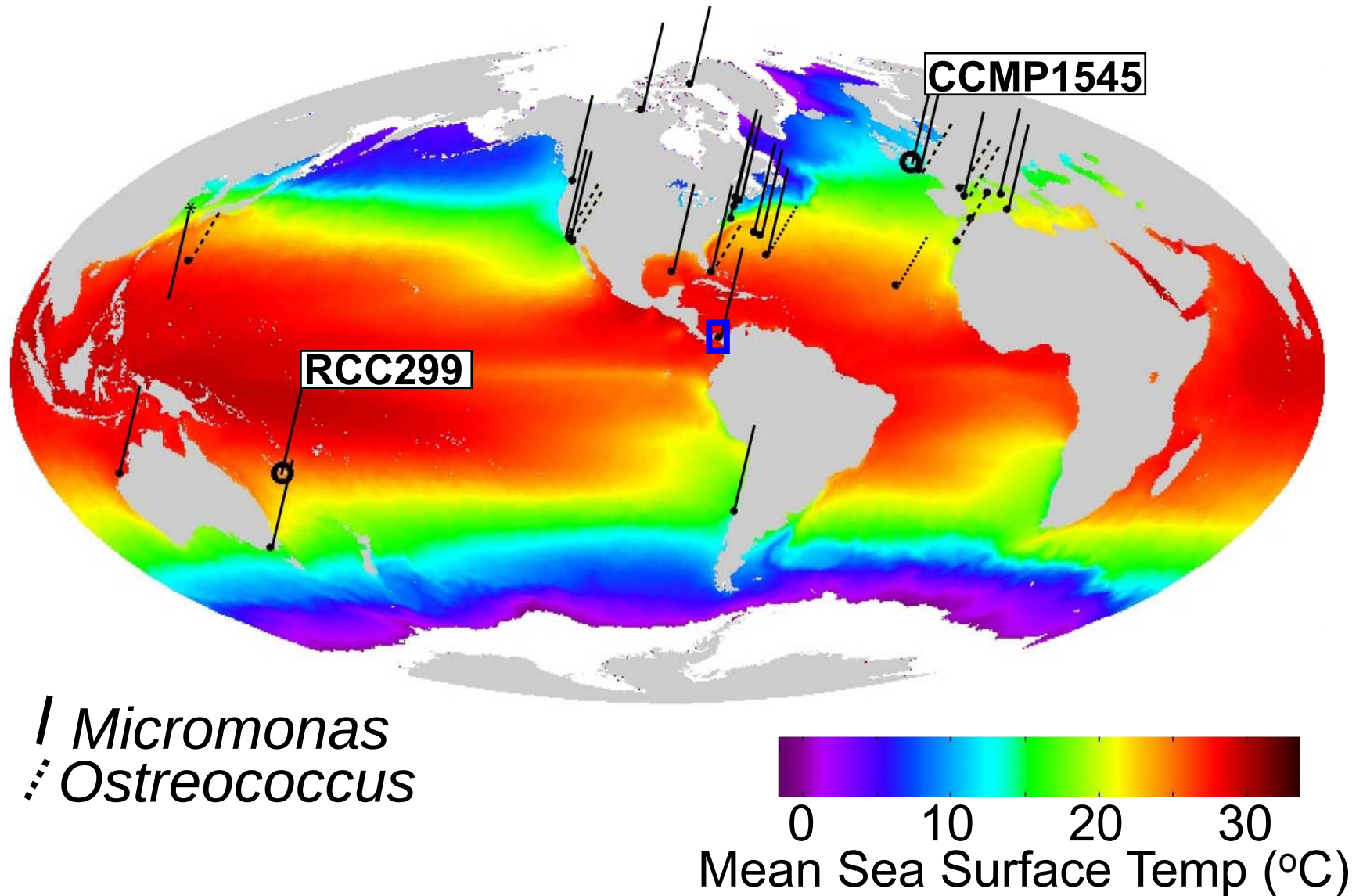
18S rRNA gene (Prasinophytae, Mamiellales)

Cryptic
species??

Multiple
Micromonas
clades
co-exist

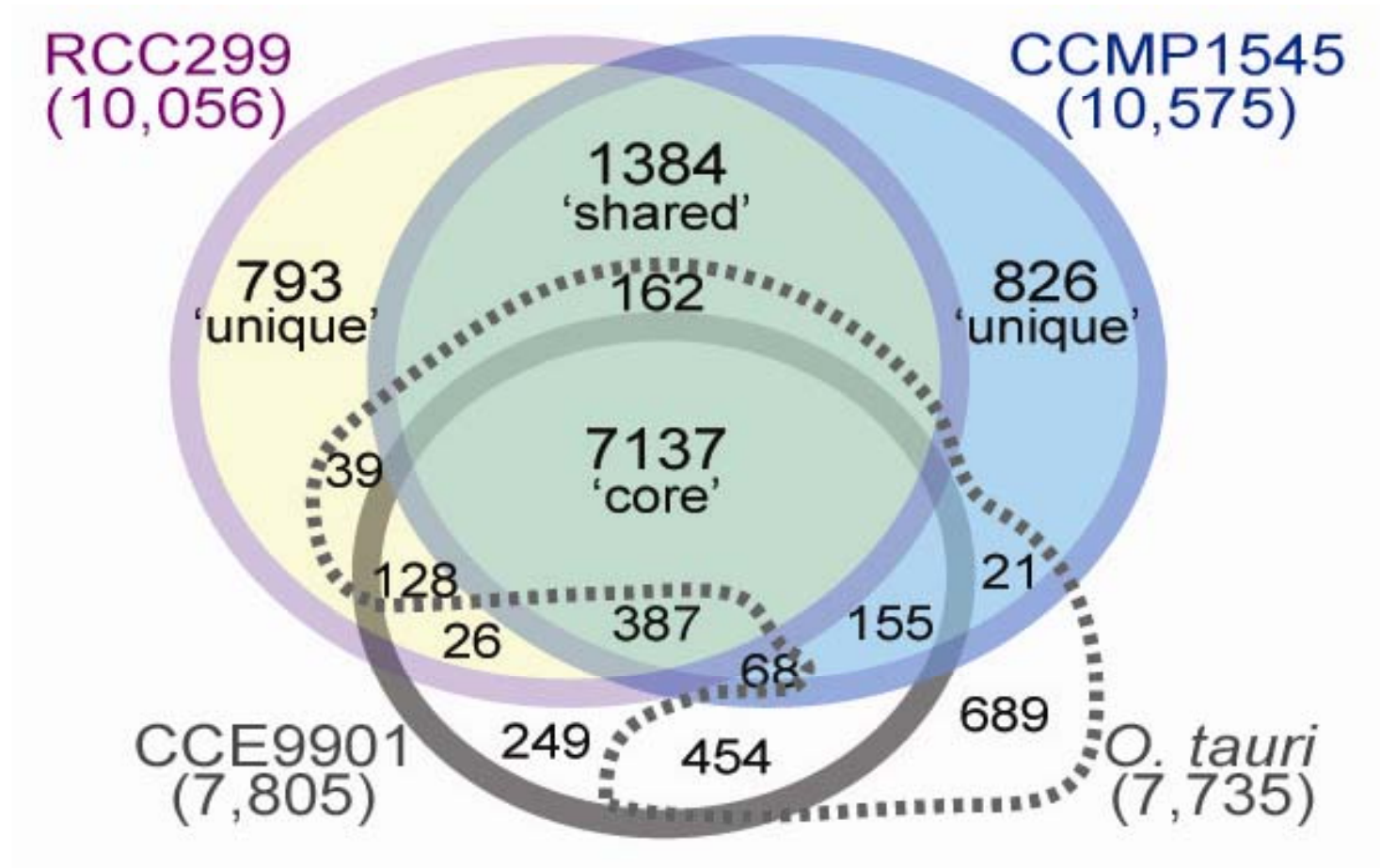


Micromonas is globally distributed



At most 90% of genes shared by *Micro* strains

‘Unexpected’ divergence for same eukaryotic ‘species’



97% 18S rDNA identity

Insights to co-existence?...differentiation?

‘unique’
RCC299 or CCMP1545



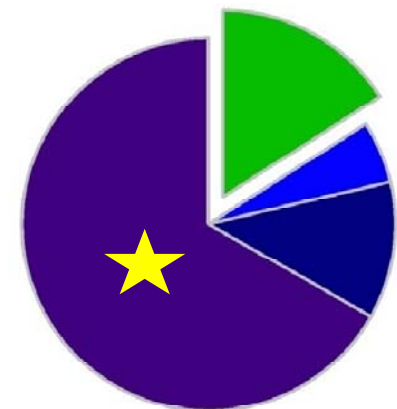
most ‘uniques’
affiliate with:
Transport
Chromalveolates,
Opisthokonts &
Bacteria

‘shared’ in Micro
but not Ostreo



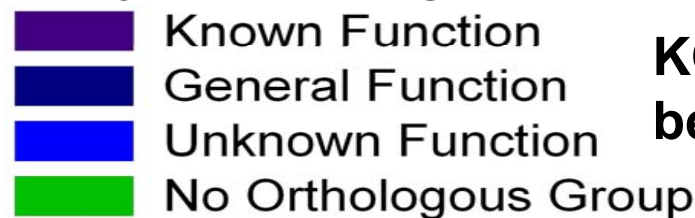
Cell motility

‘core’
all Mamiellales



most ‘core’
affiliate with:
Sex
other Green
Lineage Orgs.

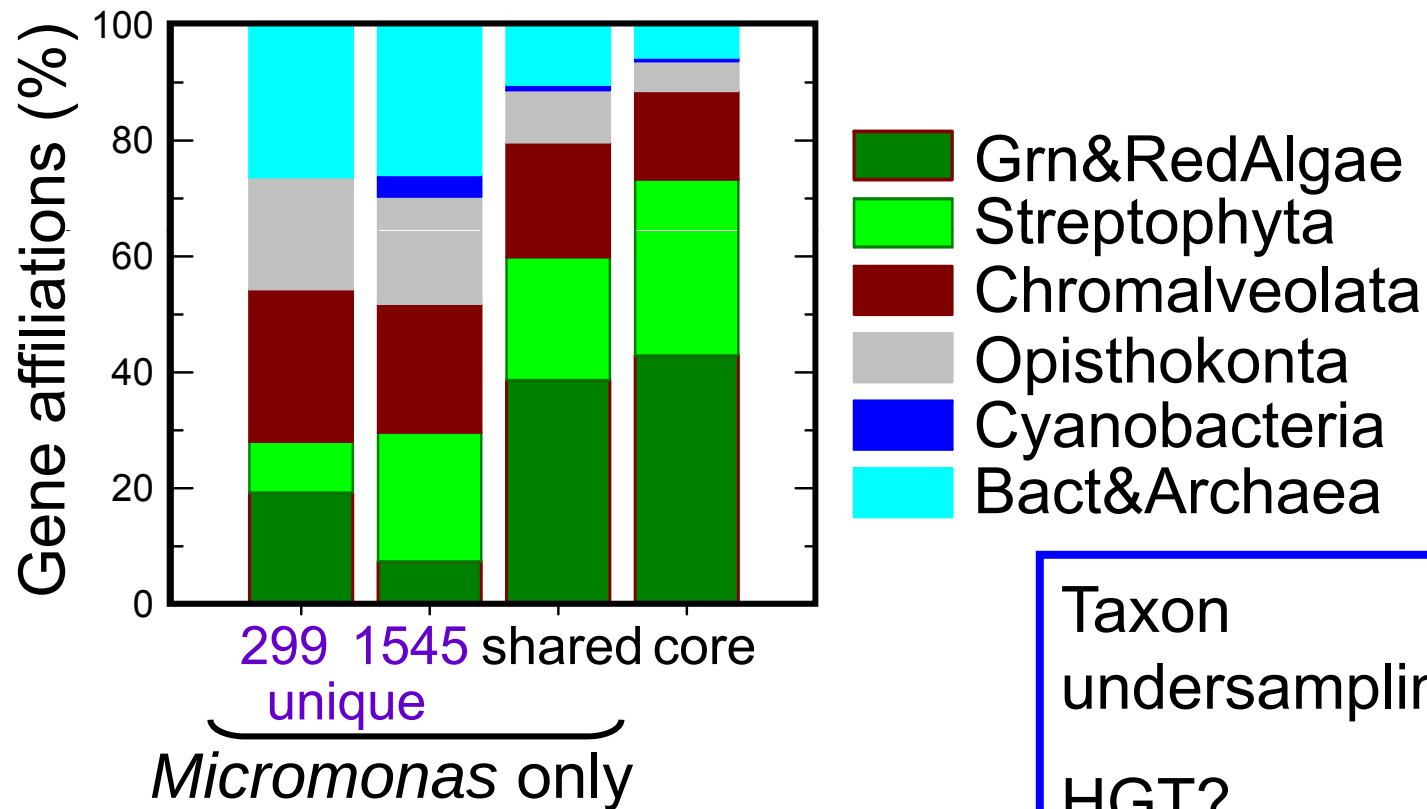
EuKaryotic Orthologous Groups (KOGs)



**KOG
bearing**

Mixed lineage affiliations – a trend

also seen in diatoms

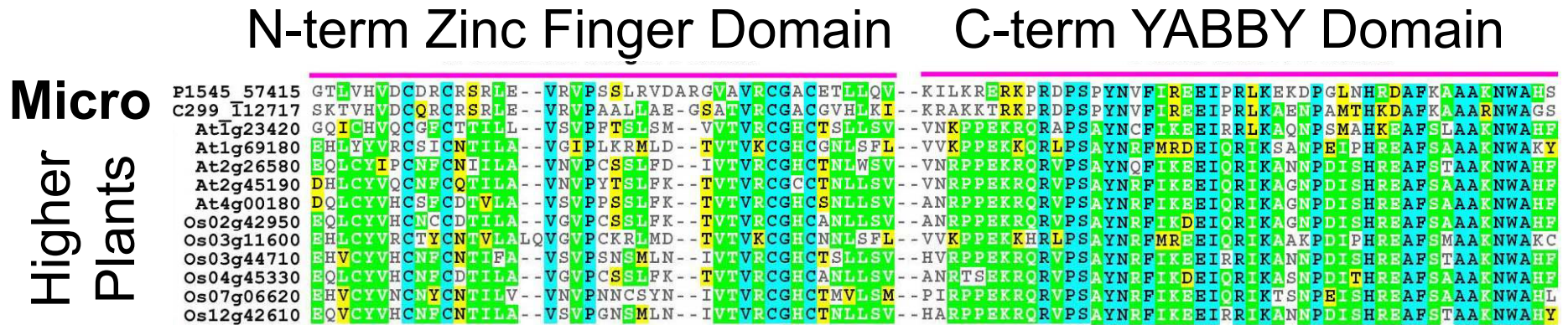


Taxon
undersampling?
HGT?
Loss/divergence?

collaboration w/Allen & Badger in Worden et al. *Science* 2009

Reconstructing the ancestor

YABBY



The potential importance of cooption...

Also see genes implicated in
obesity, breast cancer, etc.

An indication of degree of taxon undersampling?

Would less reduced algal genomes tell more about ancestor?

Ecological considerations

>Primed for life in low nutrient environments

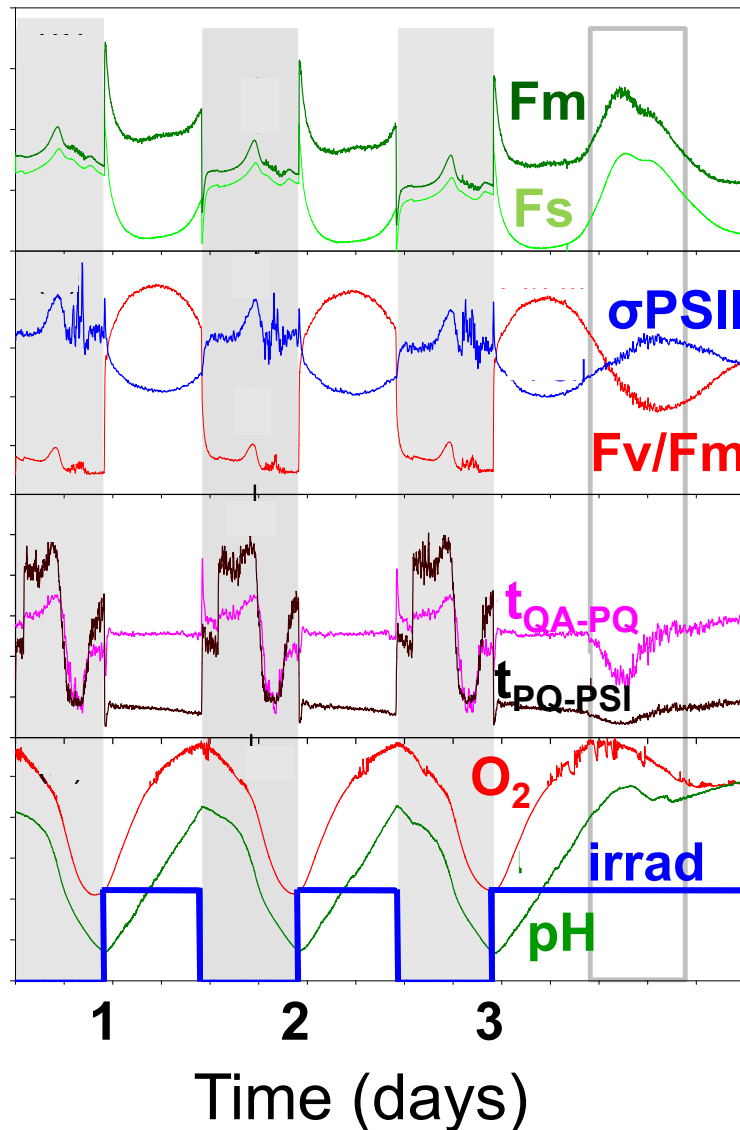
Things like nitrogen transport may not be 'niche defining' (you die if you aren't good at N)

Can genes reveal 'subtleties' not currently considered?

(need controlling factors for developing mechanistic carbon cycling models)

Need gene function(s)

*pH*stats for systems biology



Kolber et al.

> *pH*-chemostats
(Kolber, exps. at MBARI)

> Continuous flow
cytometry (?)

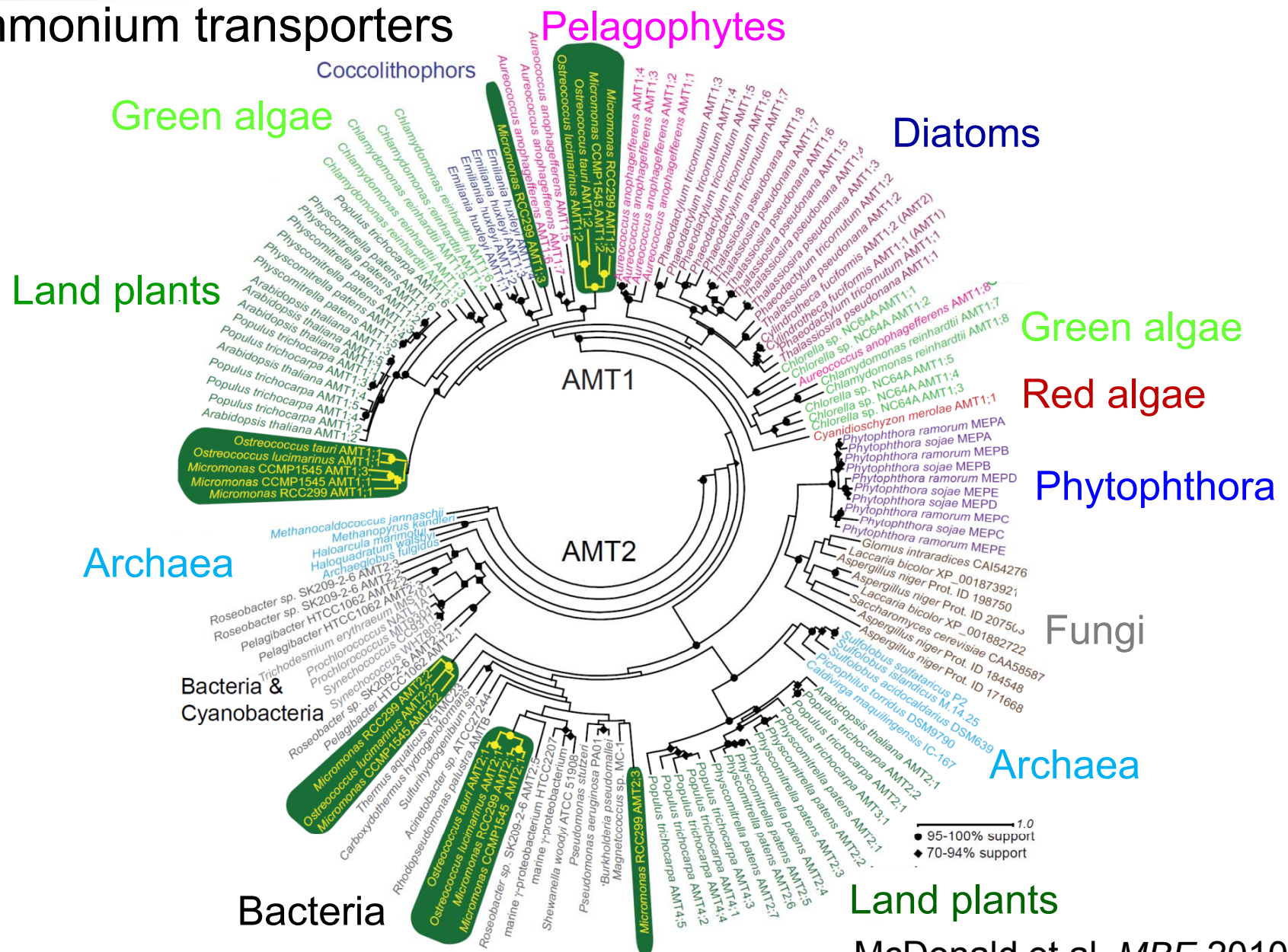
> 1st round Solid
rest Illumina (directional)

> Blended arrays
(tiling & gene probe)

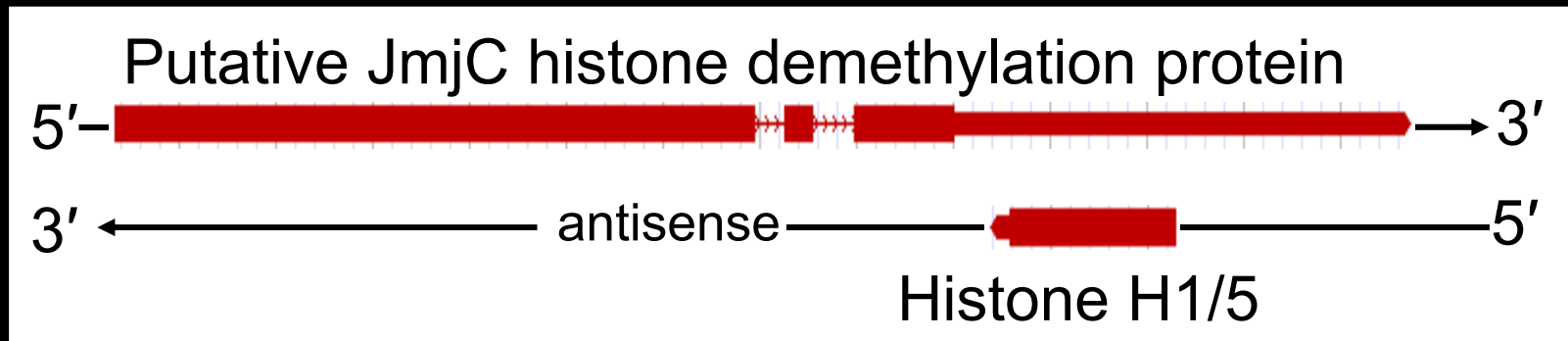
> Proteomics (PNNL)
(reannotate genome)

> Pathway modeling
(J. Stuart, UCSC)

Ammonium transporters

McDonald et al. *MBE* 2010

Can COPs help us investigate function?



Often one pair member is of unknown function...

% genes forming COPs >> other genomes analyzed to date

4-9% (Human)

1.7-14% (Mouse)

7% (Arabidopsis)

22% (Fruit fly)

Project goals

Cultured
model
organisms

Targeted
'reference'
genomes
(uncultureds)

Environ.
transcriptomics –
activity & function
assembly of
communities

Real time *in situ* measurements

Biogeochemical processes

Meeting goals



*'It is not the powers that you have,
but the way you choose to use them...'*

- Albus Dumbledore

Thank you!

