

© 2006 Encyclopædia Britannica, Inc.

Cd
Mn
Fe
Co
Mn
Fe
Mo
Ni
Cu
Fe
Co
Zn
Cd

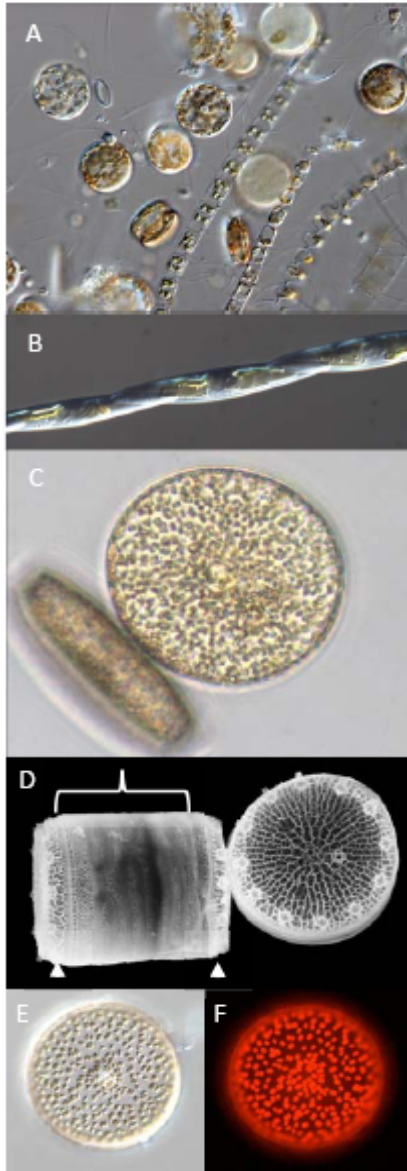
Biogeochemical cycling of trace metals in the sea

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 Univ. of British Columbia
 Vancouver, Canada



Fe
Ni
Co
Zn
Cd

Talk Outline



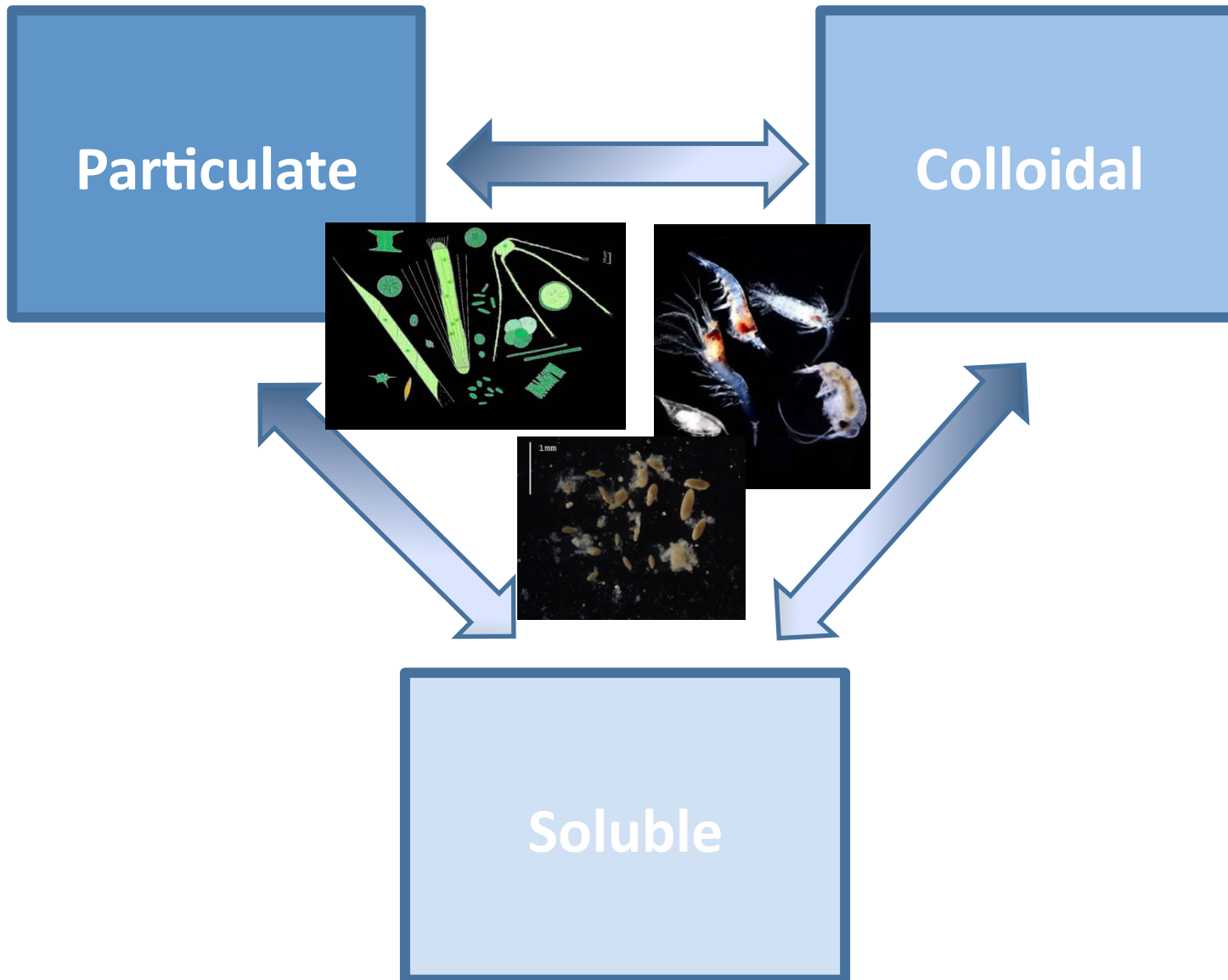
1. Modeling biota-trace metals interactions

2. An ecosystem model of biological Fe cycling

3. Highlighting recent findings, changing paradigms in the biogeochemical cycling of trace metals

Armbrust (2009)

Interactions between M and biota



Biological mechanisms mediating M transfer among pools

Soluble



Colloidal
Particulate

Colloidal
Particulate



Soluble

Transport M

- Accumulate M
- Package M into fecal material

- Efflux M
- Release ligands & other substances that bind M
- Remineralize M
- Digestive M dissolution

Biological mechanisms mediating M transfer among pools

Soluble



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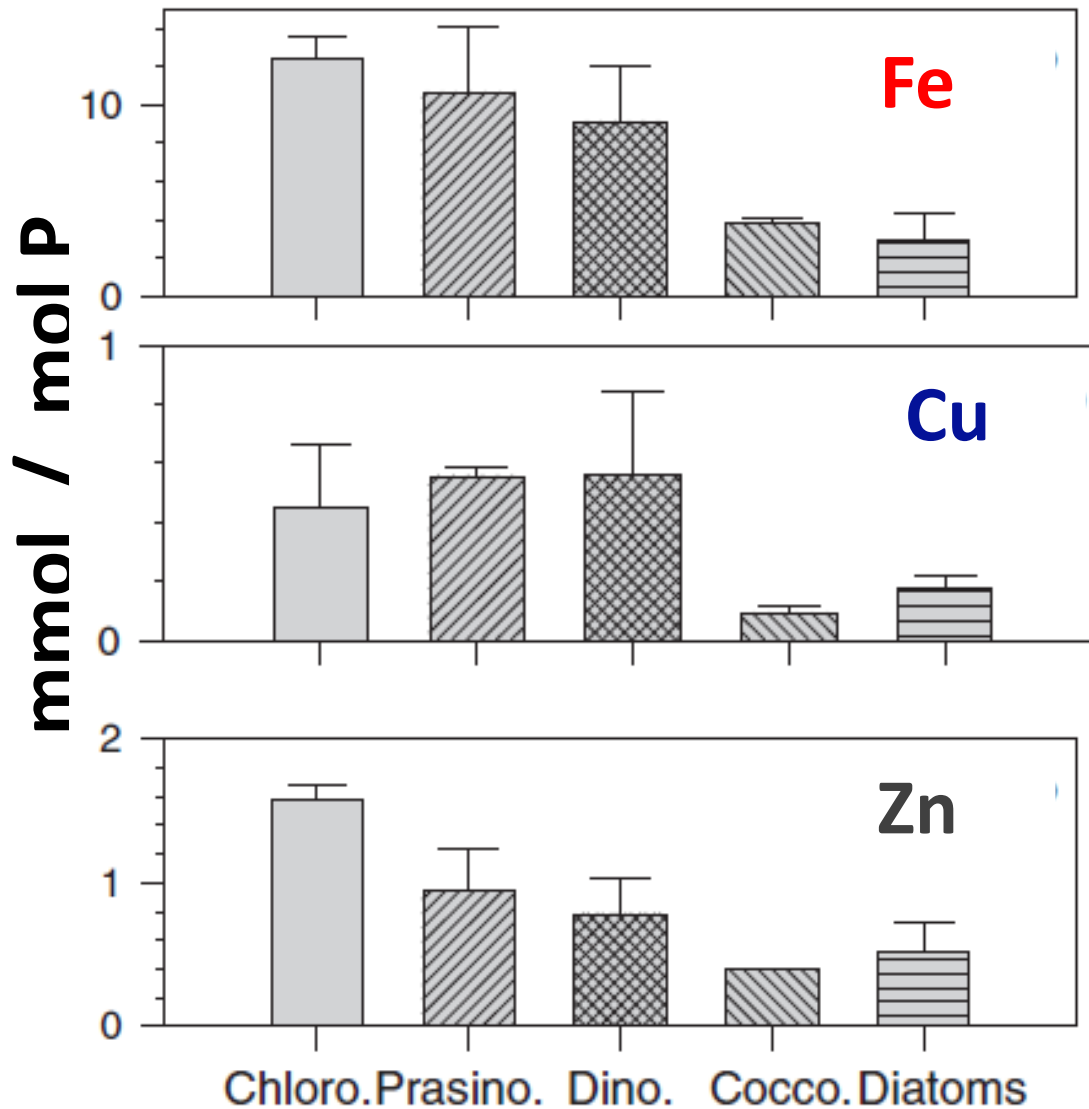
Soluble

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Taxonomic patterns of phytoplankton metal stoichiometry



Taxonomic variations: ~20 fold

Geographic provenance
(coastal vs. oceanic): ~4 fold

Environmental conditions
(light, nuts, [M]): up to 20 fold

Ferritin (Marchetti et al. 2009); Day/
night Fe homeostasis (Botebol et
al. 2015)

Models: functional groups ✓
good (specially if quotas can be
tweaked for in situ conditions)

What to use to normalize trace metal quotas, using P or C?

- Interactions between M & C cycle: **normalize to cellular C**
- Geochemists prefer normalizing to P, issues:
 - P content is plastic (Sterner & Elser 2002) & affected by Fe nutrition (Price 2005)
 - P adsorbs to cell surface Fe-oxides (Sãnu-do-Wilhelmy et al. 2004; Fu et al. 2005)

Trend: different Cu:P quotas for green vs. red algae disappears if normalized to C

Data from Ho et al. 2003

Species	C:P (mol:mol)	Cu:P (mmol:mol)	Cu:C (μ mol:mol)	Mean Cu:P (mmol:mol)	Mean Cu:C (μ mol:mol)
Chlorophyceae	198 \pm 35	0.45 \pm 0.31	2.17 \pm 1.19		
Prasinophyceae	200 \pm 9	0.55 \pm 0.06	2.77 \pm 0.2	0.5	2.47
Dinophyceae	117 \pm 31	0.29 \pm 0.24	2.26 \pm 1.62		
Prymnesiophyceae	70 \pm 8	0.09 \pm 0.03	1.32 \pm 0.56		
Bacillariophyceae	62 \pm 22	0.17 \pm 0.09	2.8 \pm 1.4	0.18	2.13

Biological mechanisms mediating M transfer among pools

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Colloidal
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Soluble

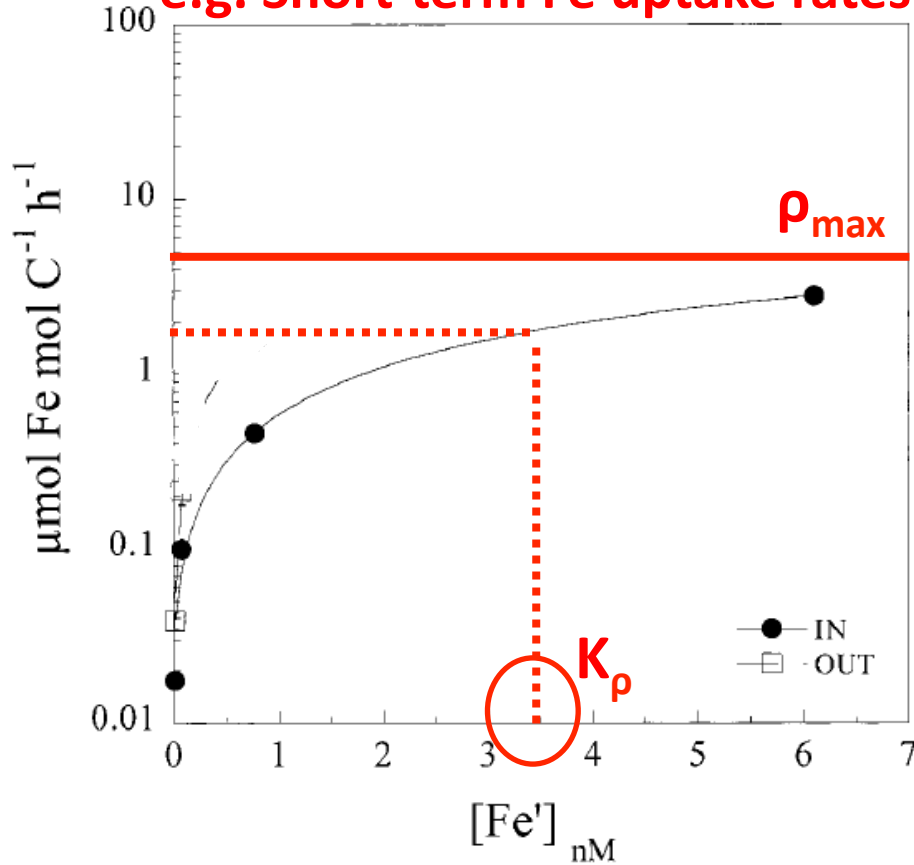
Transport M

- Accumulate M
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Half-saturation constant for **growth** (K_μ) vs. **short-term Fe uptake** (K_ρ) differ by orders of magnitude

e.g. Short-term Fe uptake rates



[Fe'] nM	K_μ (growth)	K_ρ (short-term uptake)
CULTURE	0.041	3.7
FIELD	~0.002	2.96

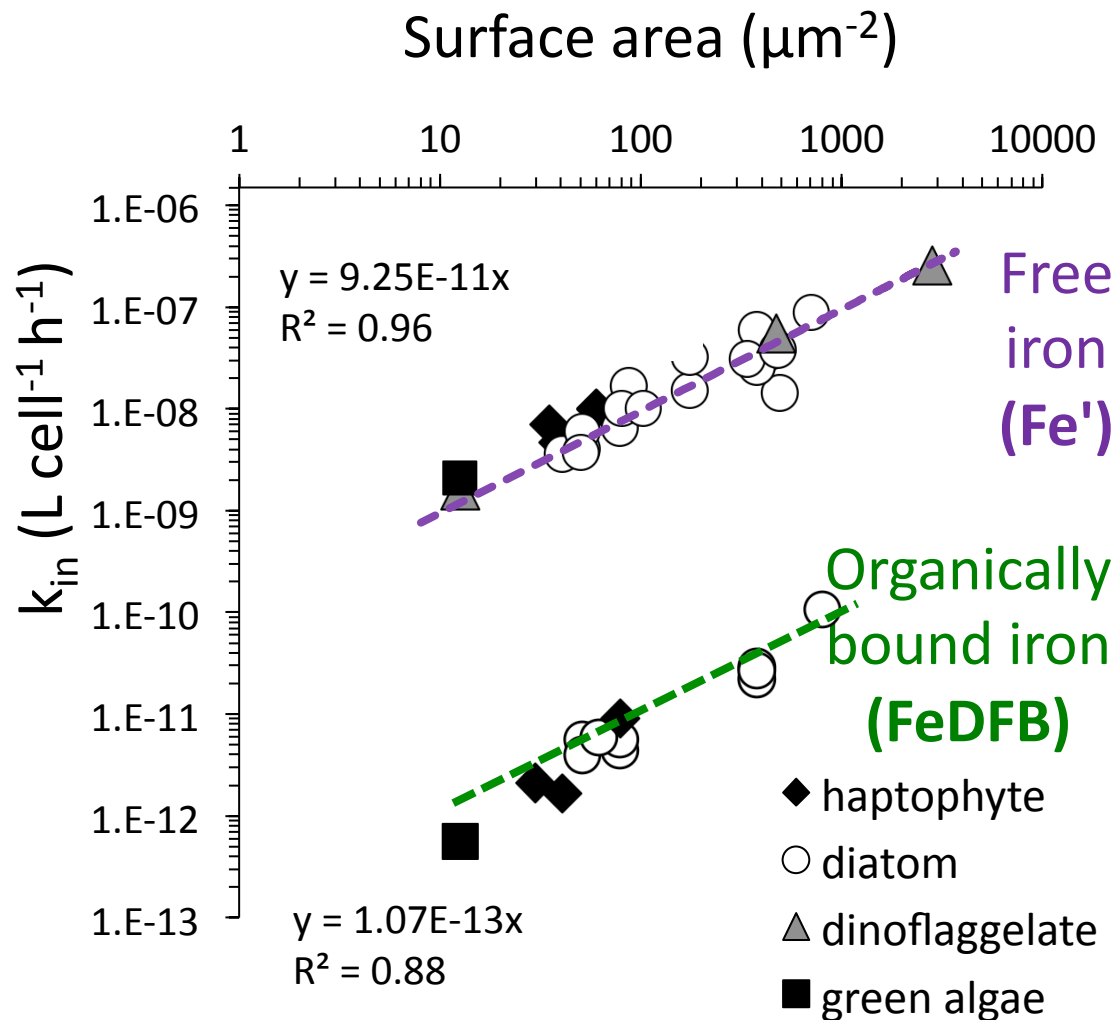
reviewed by Marchetti & Maldonado 2016

$\rho = \rho_{max} * [Fe] / (K_\rho + [Fe])$ (Michaelis-Menten 1913)
 $\mu = \mu_{max} * [Fe] / ([Fe] + K_\mu)$; (Monod 1942)

More K_ρ needed, but challenging Alternatives?

Alternative approaches to estimate short-term uptake rates (eg. when Fe concentrations are sub-saturating)

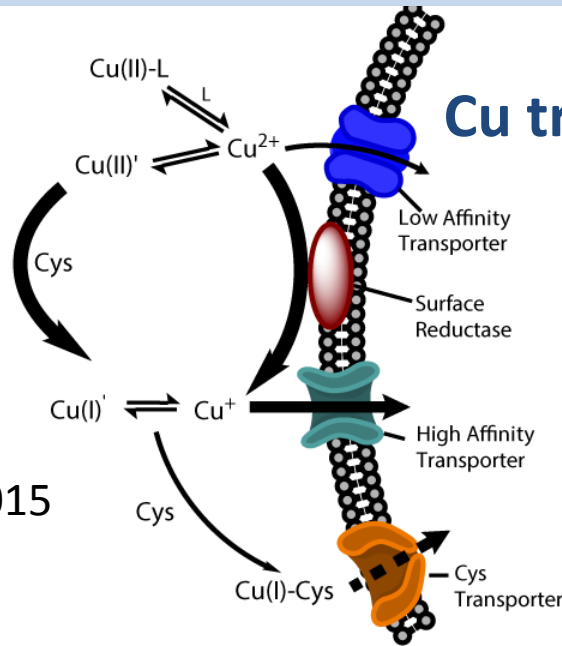
k_{in} = Fe uptake rate constant



- If you know phytoplankton functional group
- You can calculate SA & determine k_{in} from graph
- If you know [Fe], calculate $\rho = k_{in} * [\text{Fe}]$
- Excellent for modellers ✓

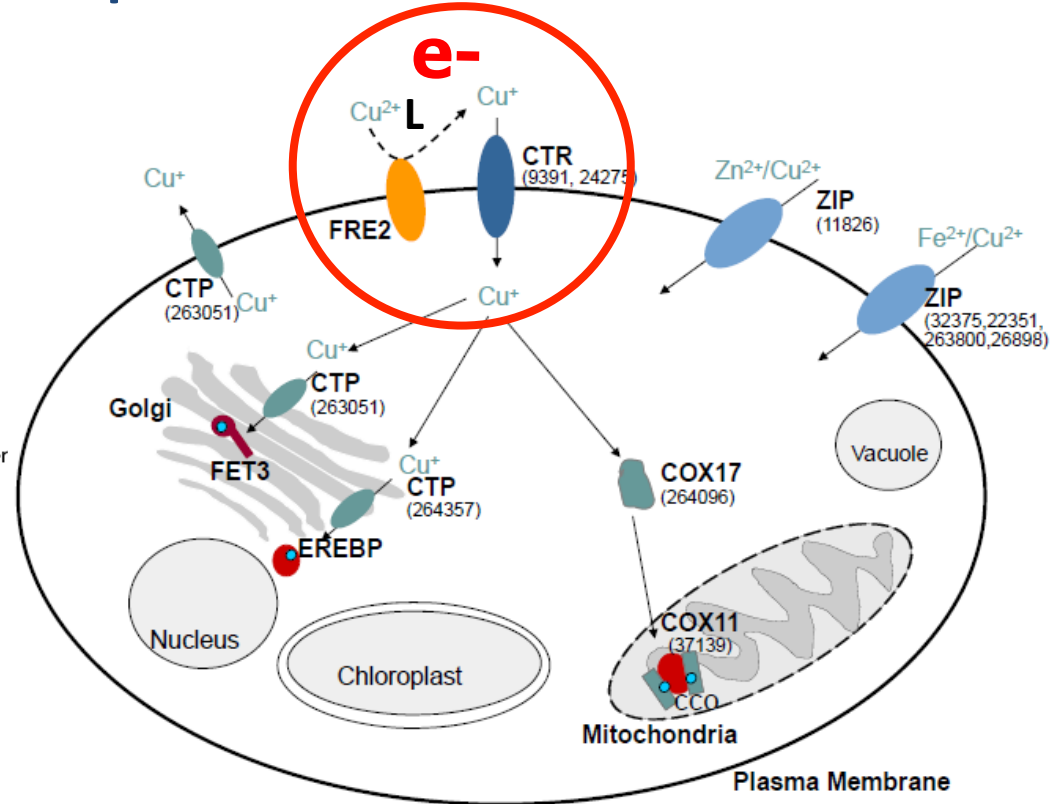
Organically bound trace metals are bioavailable (Fe, Cu, Zn...)

via weak L shuttle mechanism



Walsh et al. 2015

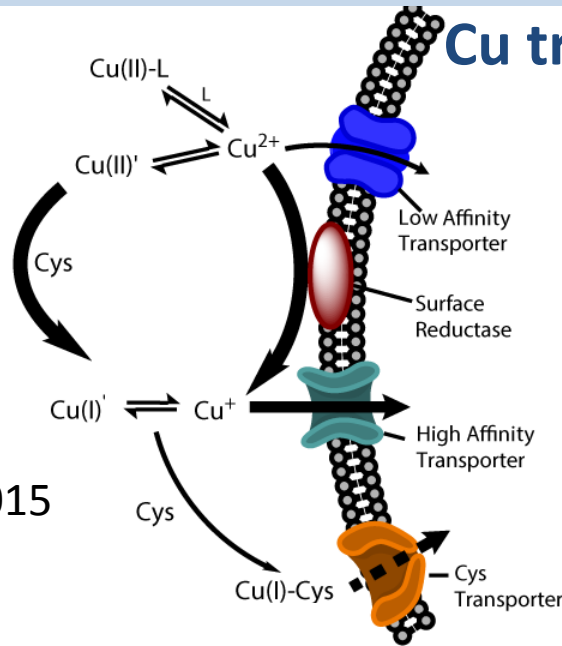
Cu transport from CuL *via membrane reductases*



Semeniuk et al. 2009, Guo et al. 2015,
 Semeniuk et al. 2015, Walsh et al. 2015

Organically bound trace metals are bioavailable (Fe, Cu, Zn...)

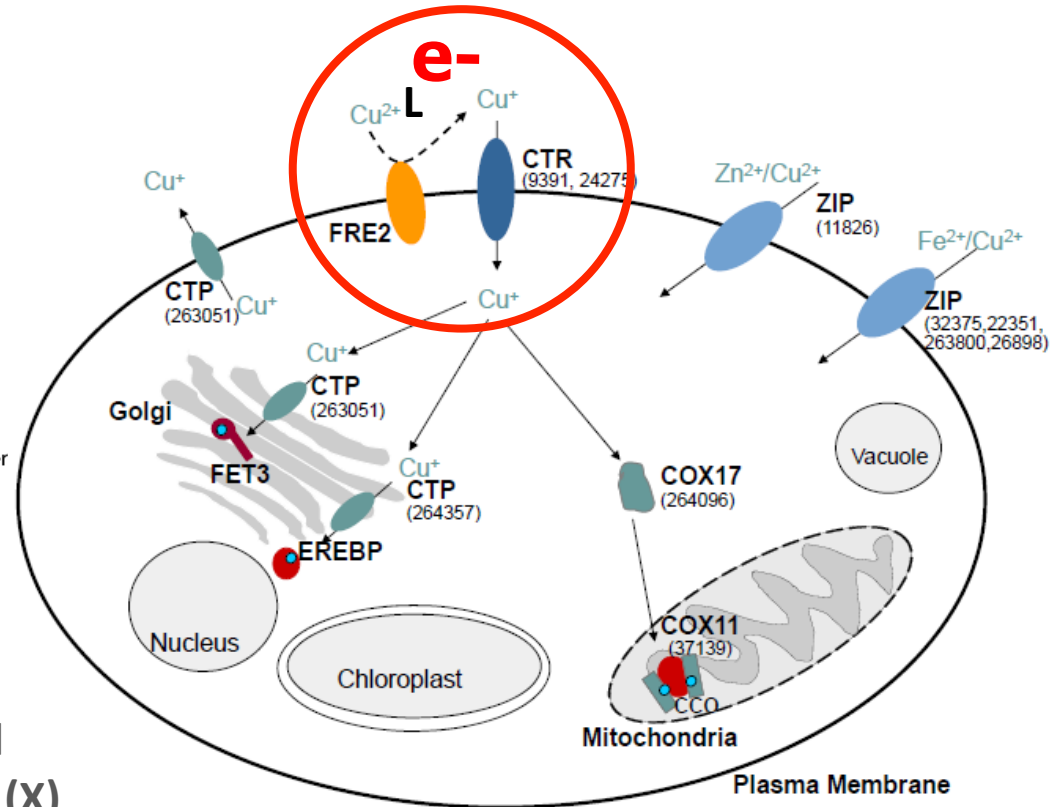
via weak L shuttle mechanism



Walsh et al. 2015

Cu transport from CuL

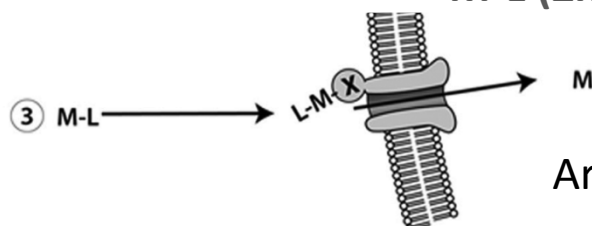
via membrane reductases



Semeniuk et al. 2009, Guo et al. 2015,
Semeniuk et al. 2015, Walsh et al. 2015

Zn transport

via ternary complex formation at the cell surface: transporter (X) M-L (ZnL)



Aristilde et al. 2012

Biological mechanisms mediating M transfer among pools

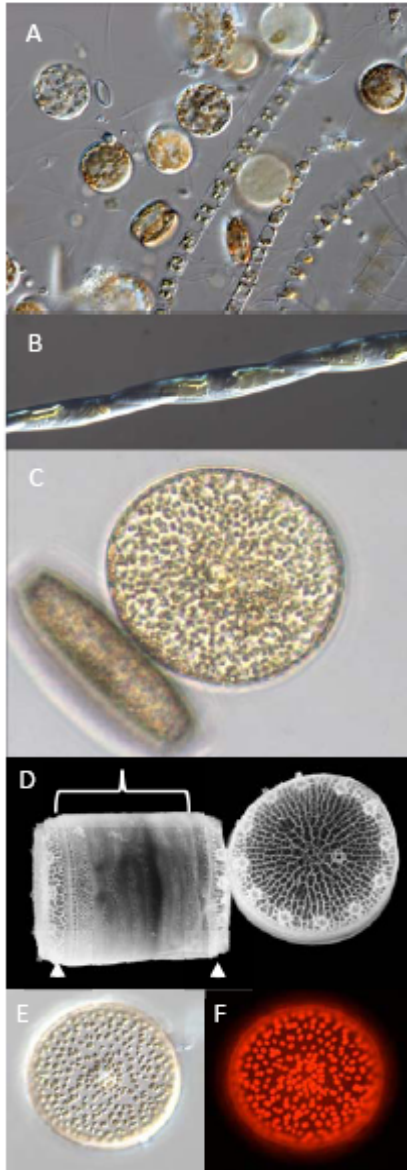


Transport M

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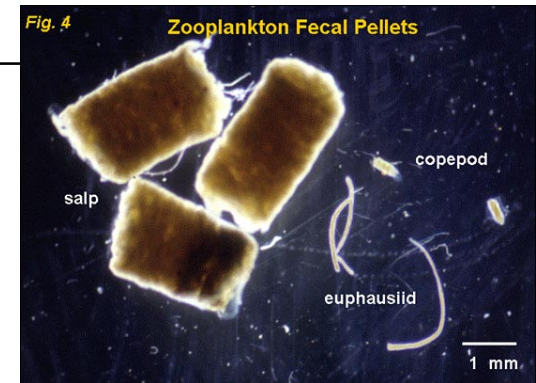
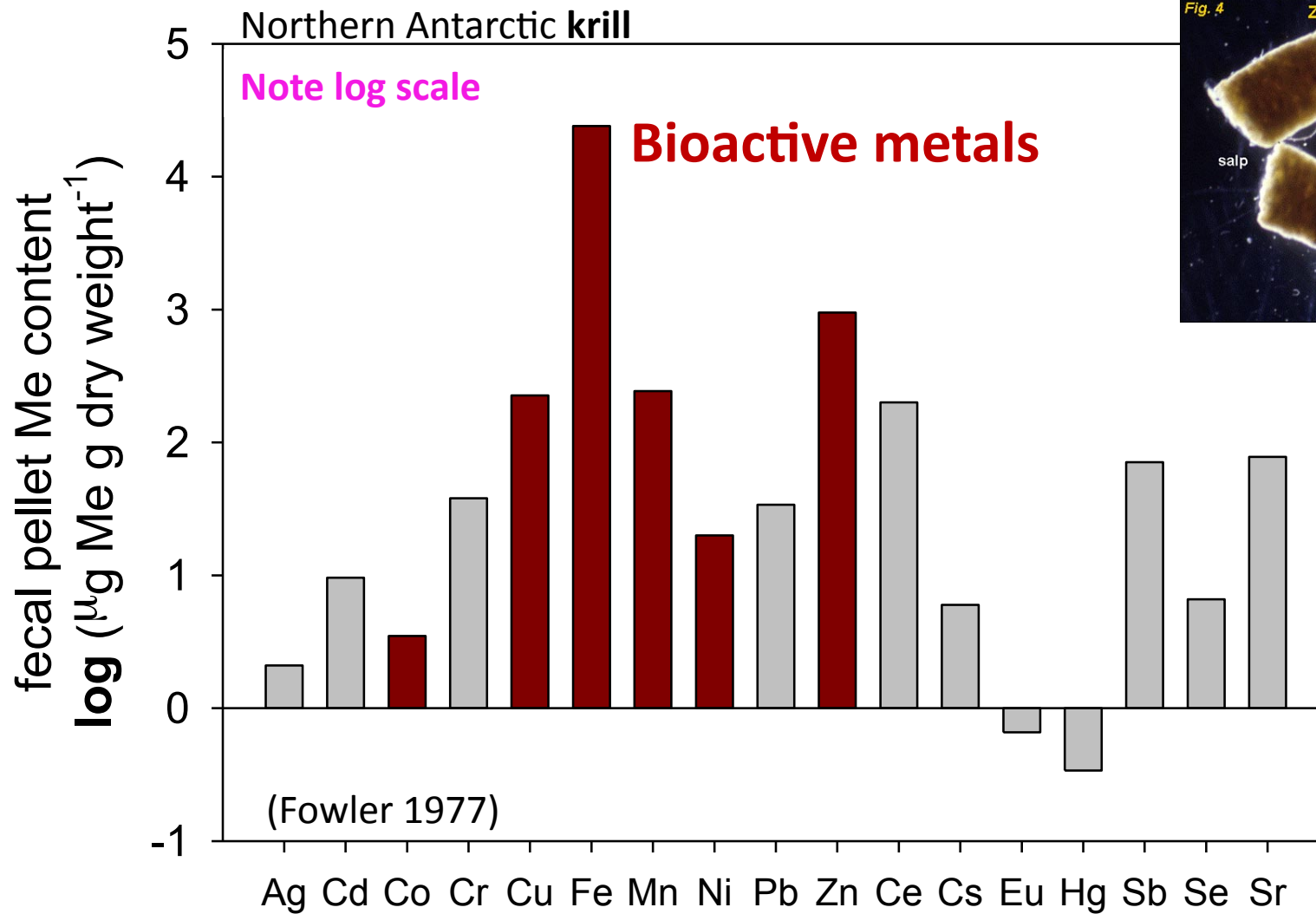
Talk Outline



- 1. Modeling biota-trace metal interactions**
- 2. An ecosystem model of biological Fe cycling**
- 3. Important recent findings, changing paradigms in biogeochemical cycling of trace elements**

Armbrust (2009)

Fecal material enriched in many M, including Fe



In Whale faeces:
 - Fe content
 ~ 10,000,000 X
 higher
 than Southern
 Ocean seawater

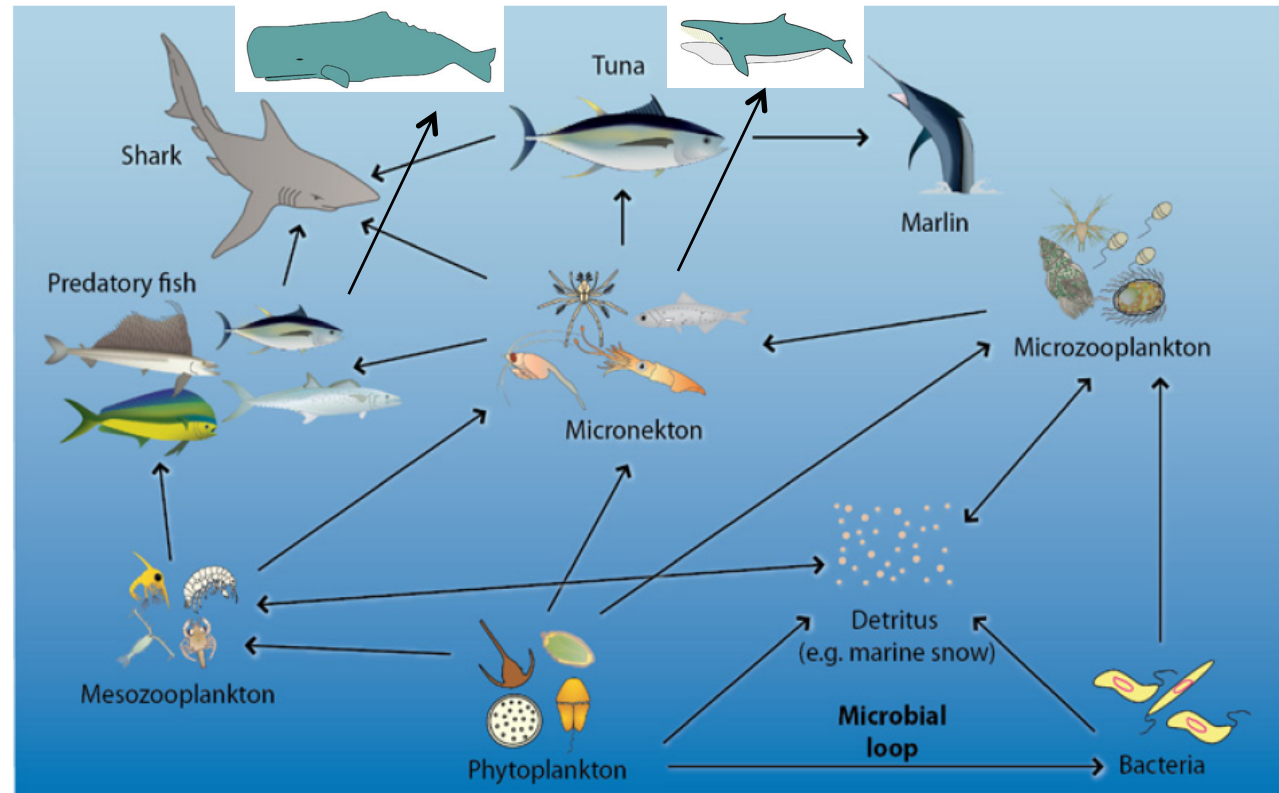
(Ratnarajah et al
 2014, 2016)

How important are these fecal Fe sources for phytoplankton growth?

Biological Fe cycling in a realistic food webs (eg. Southern Ocean)



- organisms feeding in multiple trophic levels

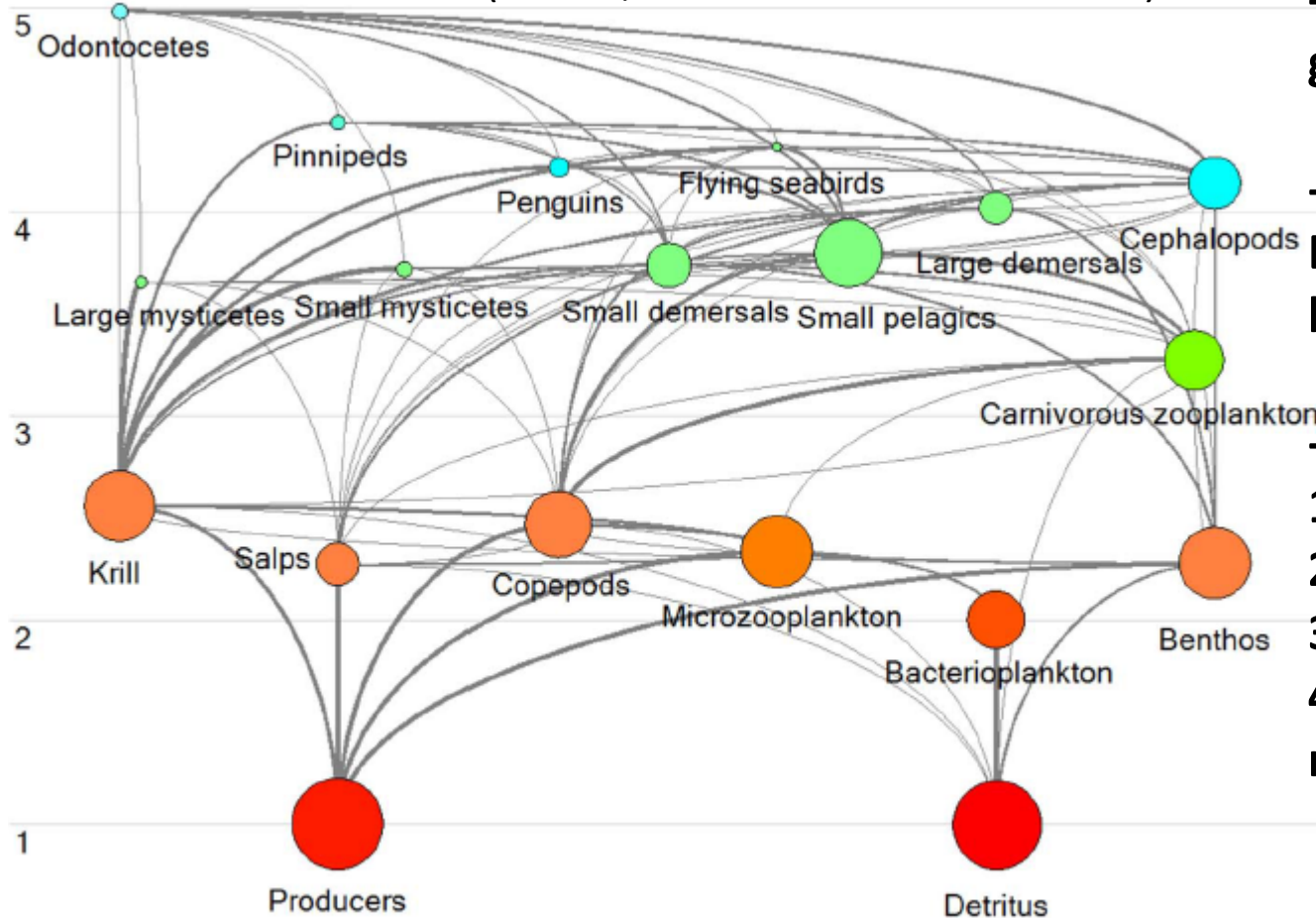


A Possible Approach Biological Fe cycling

(Christensen & Walters 2004)

Mass balance ecosystem models (Ecopath) e.g. Southern Ocean

(Surma, Pakhomov & Pitchet 2014)



- 19 Functional groups

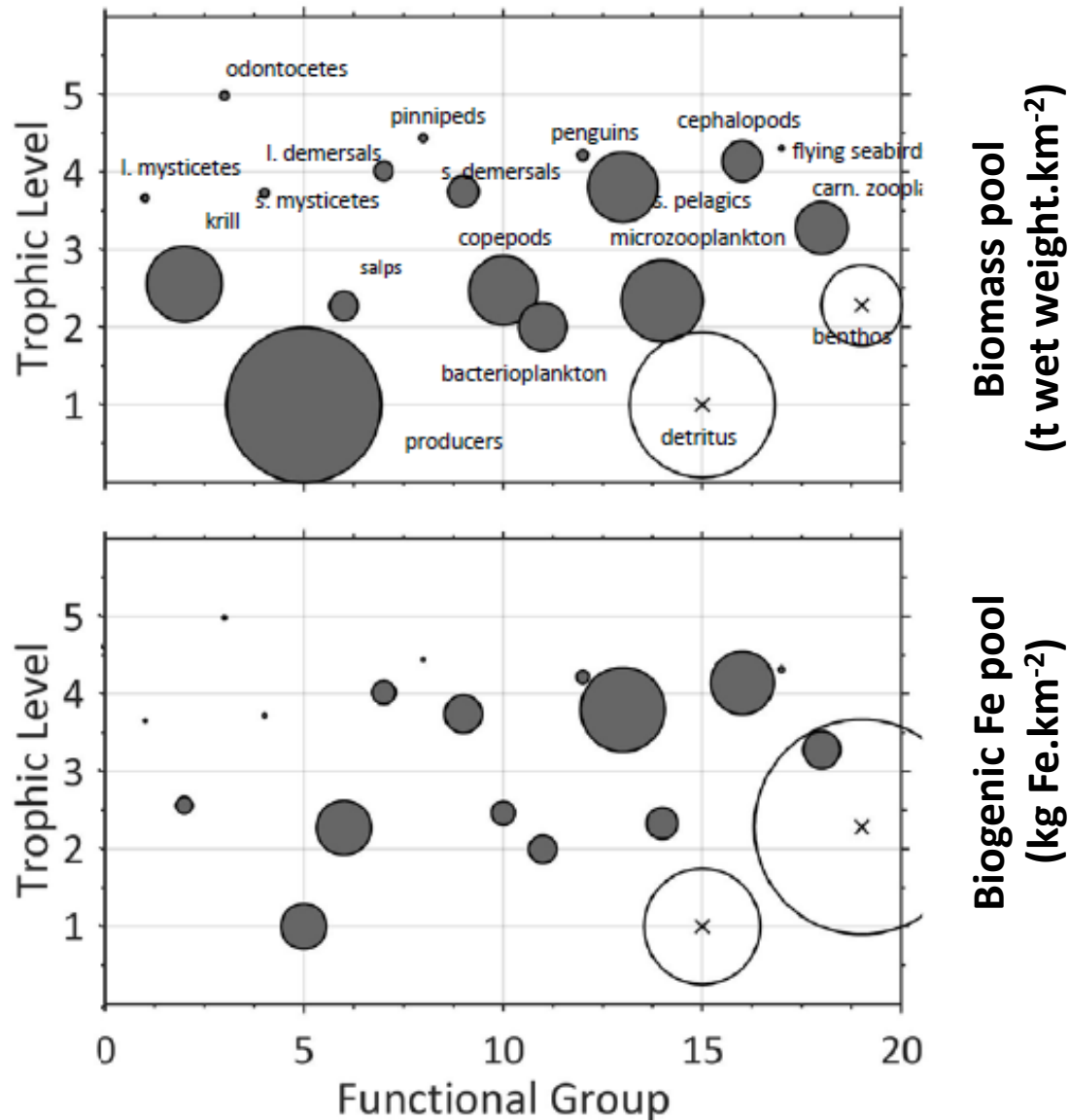
- for each group:
Biomass gains balanced by biomass losses

- Parameters:

1. Biomass (B ; t/km^2)
2. Production (P ; y^{-1}) / B
3. Consumption (Q ; y^{-1}) / B
4. Diet composition matrix

To each groups we assigned Fe content & calculate Biogenic Fe pools, Fe associated with production, Fe consumption & Fe recycled

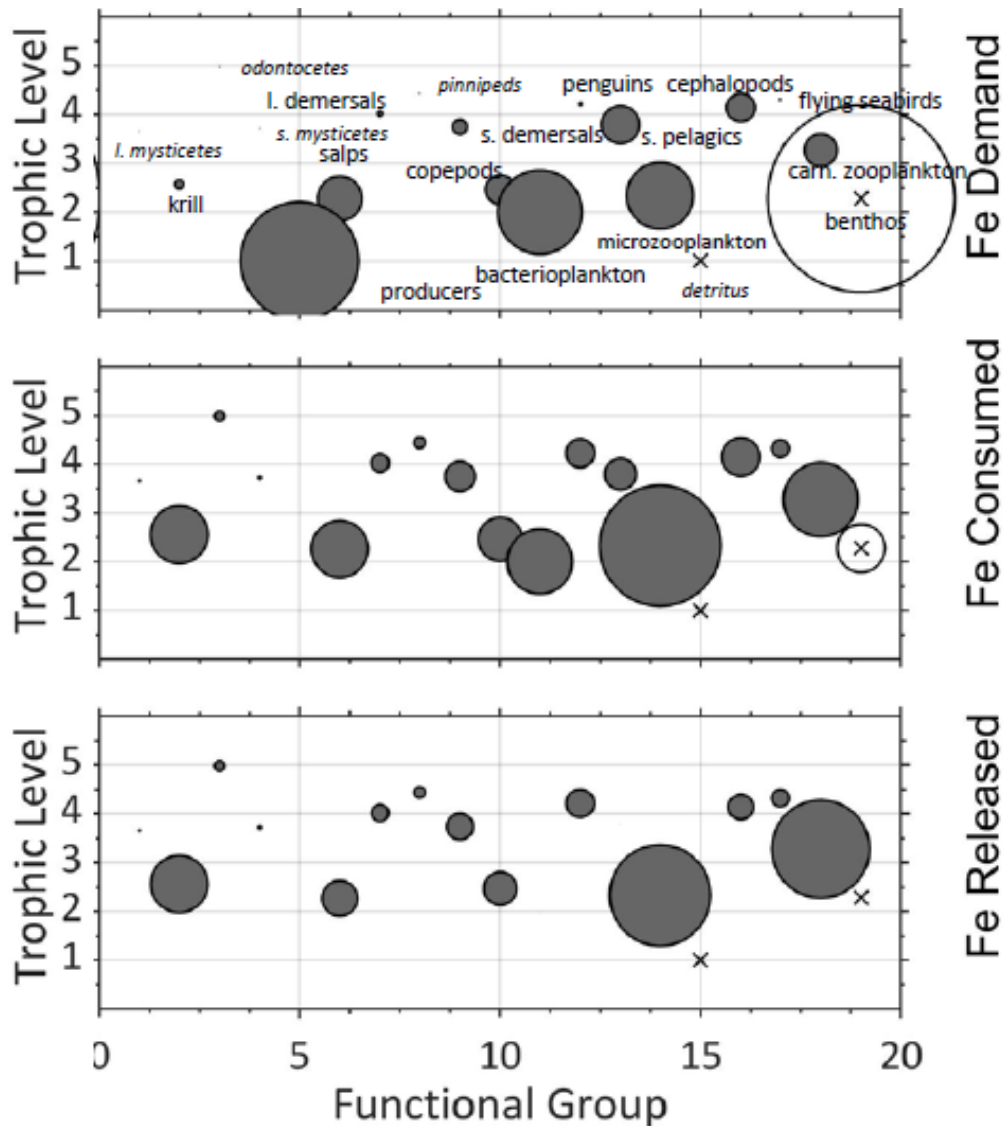
Biomass & Biogenic Fe pools in Southern Ocean ecosystem model



Biggest Fe pools

- Small pelagic fish
- Cephalopods
- Salps
- Small demersal fish

Annual Fe demand, consumption & released by functional groups in the Southern Ocean ($\text{kg Fe.km}^{-2}.\text{y}^{-1}$)



Greatest Fe demand by phytoplankton, bacteria, & microzooplankton

Greatest Fe consumers from prey microzooplankton, carnivorous zooplankton, bacteria, krill & salps

The key recyclers

microzooplankton & carnivorous zooplankton (70% total)

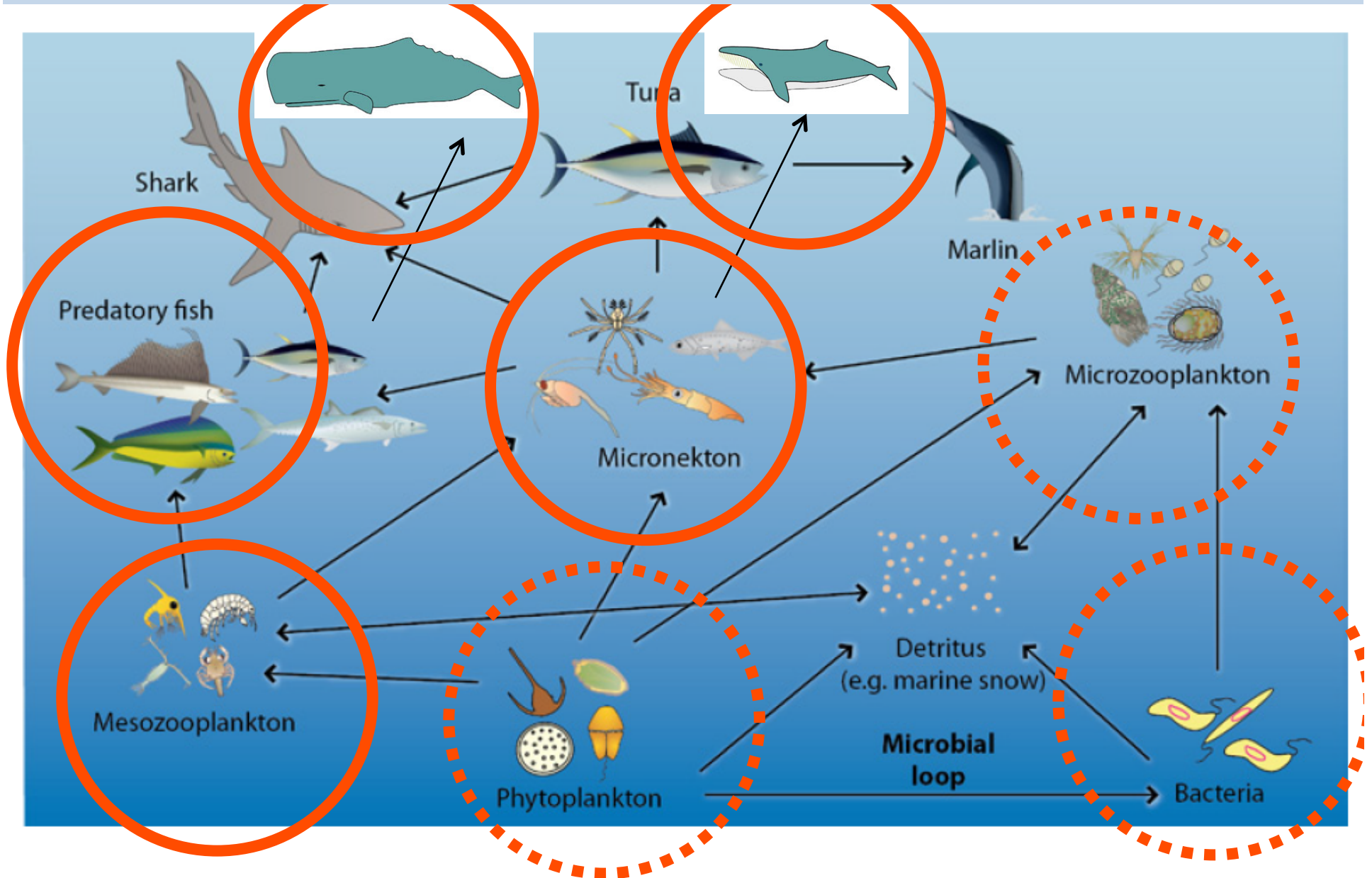
Total Fe recycling $29 \text{ kg Fe.km}^{-2} \text{ y}^{-2}$

$\approx =$

phytoplankton & bacteria

Fe demand = $22 \text{ kg Fe.km}^{-2} \text{ y}^{-2}$

A call for estimates of essential M content in more organisms



Talk Outline



Armbrust (2009)

1. Modeling biota-trace metal interactions
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Transcriptomics reveals M homeostasis & uptake mechanisms

e.g. Uncovering strategies of 50 diatom species to meet their Fe demands

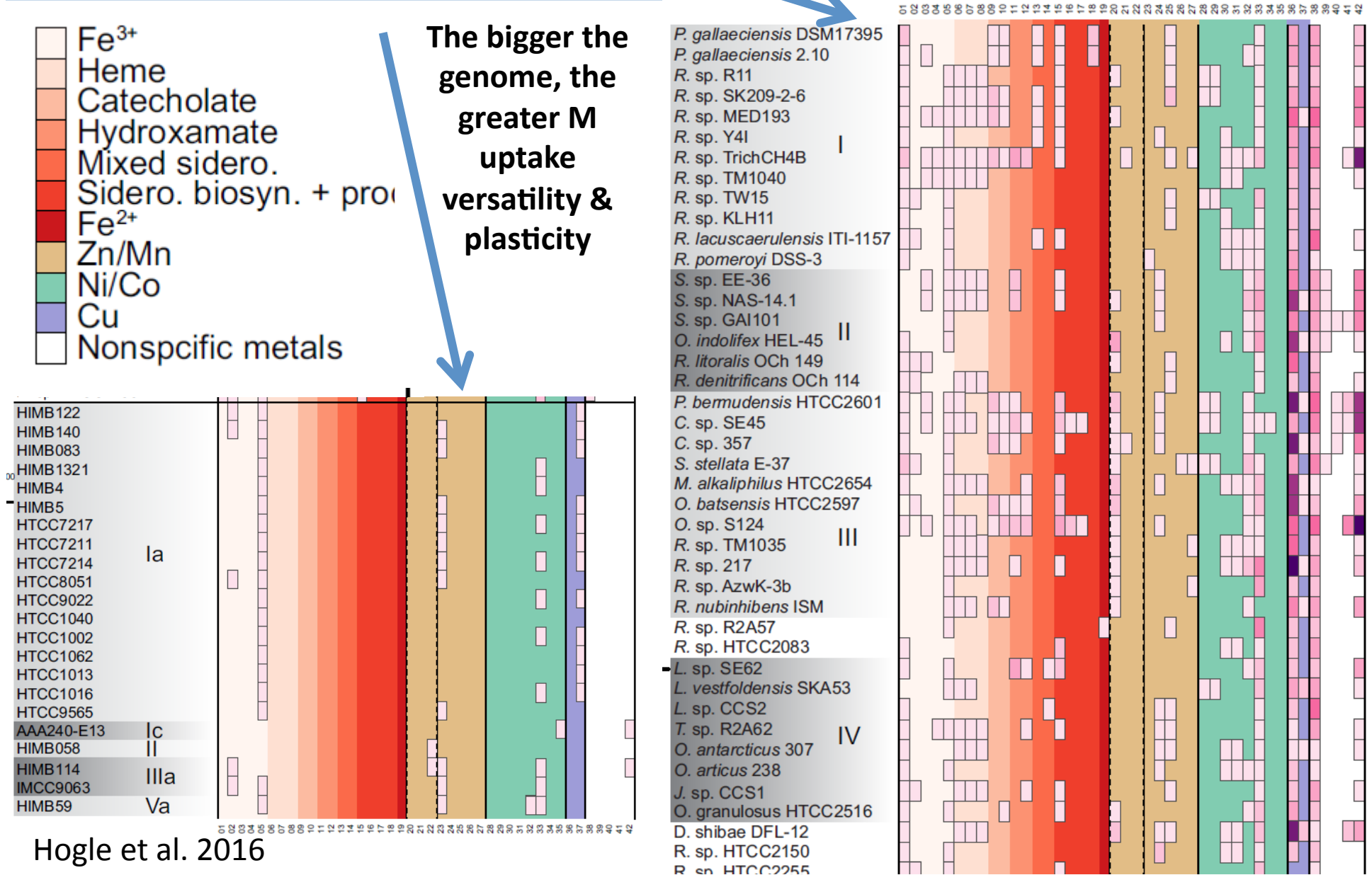
Goussman et al. 2015

Source	Genus species strain	Class	Uptake			Storage		Redox				SOD			
			FRE	FET	FTR	FTN	petF	FLDA-I	FLDA-II	CYTC6	PCYN	CuZn	Fe	Mn	Ni
MMETSP0316-18	<i>Amphora coffeaeformis</i> CCMP127	Bacillariophyceae	1	1	2	2	1	1	1	1	0	1	0	2	2
MMETSP1065	<i>Amphiprora paludosa</i> CCMP125		2	1	1	2	0	0	1	1	0	1	0	1	2
MMETSP0724-27	<i>Amphiprora</i> sp. CCMP467		2	1	1	1	1	1	0	1	0	1	0	2	2
JGI	^a <i>Phaeodactylum tricorutum</i>		2	0	0	1	0	1	1	1	0	1	0	2	1
MMETSP0017	<i>Cylindrotheca closterium</i> KMMCC:B-181		2	1	0	1	0	1	0	1	0	1	0	1	1
MMETSP0014	<i>Nitzschia</i> sp. RCC80		0	1	1	2	0	0	0	1	0	1	0	2	2
MMETSP0744-47	<i>Nitzschia punctata</i> CCMP561		1	0	2	1	0	1	1	1	0	2	0	2	2
JGI	^a <i>Fragilariopsis cylindrus</i>		1	3	1	1	0	1	1	1	1	1	0	2	1
MMETSP0733-36	^a <i>Fragilariopsis kerguelensis</i> L26-C5		4	2	0	1	0	1	2	1	3	1	0	2	1
MMETSP1352	<i>Stauroneis constricta</i> CCMP1120		1	0	0	0	1	1	1	2	0	1	0	2	0
MMETSP0139-42	<i>Pseudo-nitzschia australis</i> 10249 10 AB		1	0	0	1	0	1	1	1	0	0	0	1	1
MMETSP1060	<i>Pseudo-nitzschia pungens</i> cf. <i>cingulata</i>		0	0	1	1	0	0	0	0	0	0	0	2	1
MMETSP1061	<i>Pseudo-nitzschia pungens</i> cf. <i>pungens</i>		0	1	0	2	0	0	0	1	0	0	0	1	1
JGI	^a <i>Pseudo-nitzschia multiseriis</i>		1	0	1	2	0	1	1	1	0	1	0	2	1
internal	<i>Pseudo-nitzschia granii</i>		0	0	0	1	0	0	1	1	1	1	0	2	1
MMETSP0329	<i>Pseudo-nitzschia arenysensis</i> B593		1	1	1	1	0	0	0	1	1	1	0	2	1
MMETSP0327	<i>Pseudo-nitzschia delicatissima</i> B596	0	1	1	1	0	0	0	1	0	1	0	1	0	
MMETSP1423	<i>Pseudo-nitzschia heimii</i>	1	1	1	1	0	1	1	1	3	0	0	2	1	
MMETSP1394	<i>Asterionellopsis glacialis</i>	Fragilariophyceae	1	2	1	1	0	1	0	1	0	0	1	2	1
MMETSP1360	<i>Licmophora</i> sp.		1	0	0	1	0	0	1	1	0	1	0	2	1
MMETSP0786	<i>Thalassionema frauenfeldii</i> CCMP 1798		1	2	0	2	2	1	1	0	0	1	1	2	2
MMETSP1176	<i>Synedropsis recta</i> cf. CCMP1620		1	1	1	1	0	1	2	1	0	1	0	2	0
MMETSP0009	<i>Grammatophora oceanica</i>		1	1	1	0	1	0	0	1	0	1	0	1	1
MMETSP1361	<i>Nanofrustulum</i> sp.		3	2	2	4	0	0	0	1	0	2	0	2	2

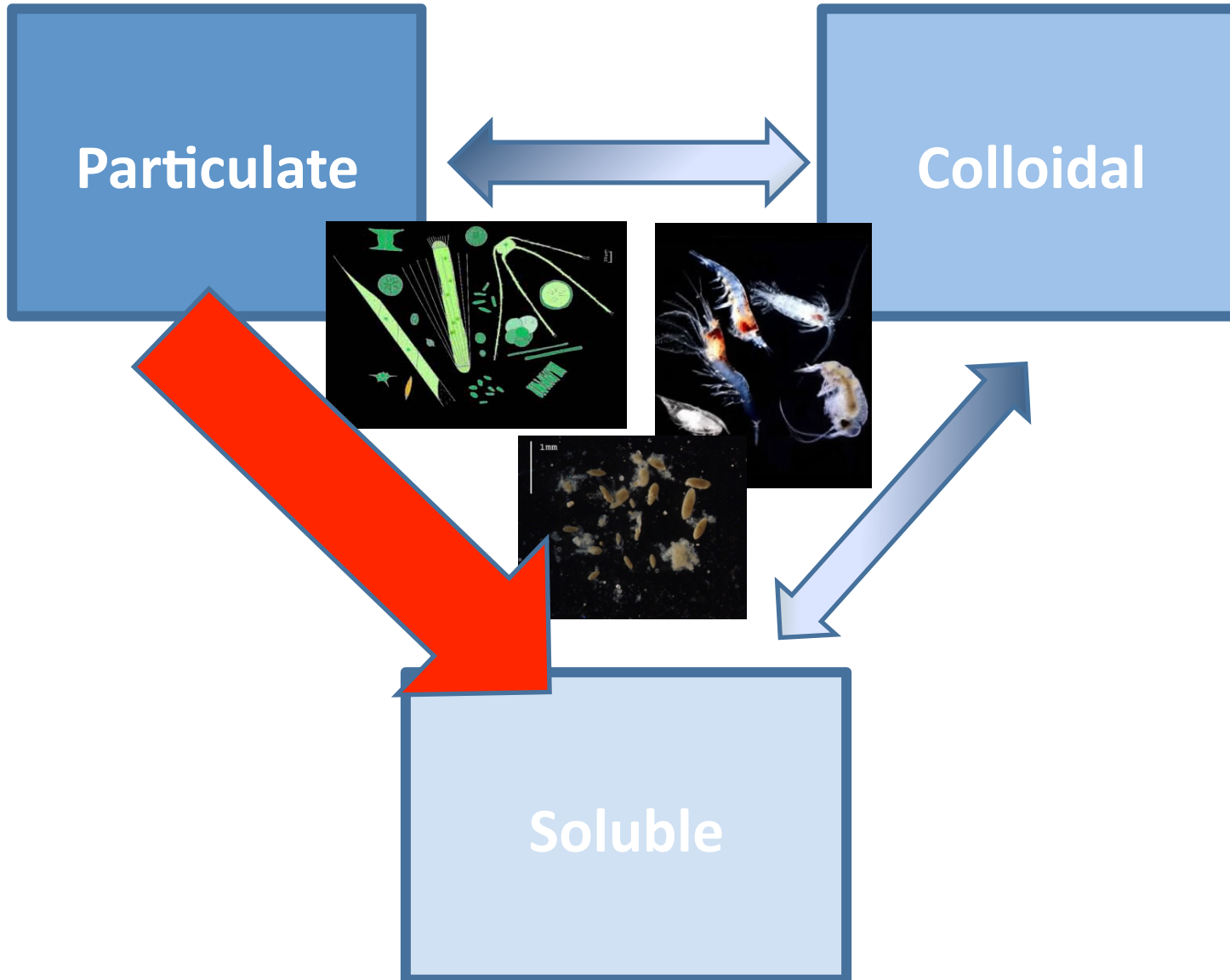
In theory, a brave modeler/biologist may calculate M demand based on principles of biochemistry (as John Raven)

Genomics reveals diversity in trace metal acquisition mechanisms

eg. *Alphaproteobacteria* (SAR11) vs. *Roseobacter* lineages

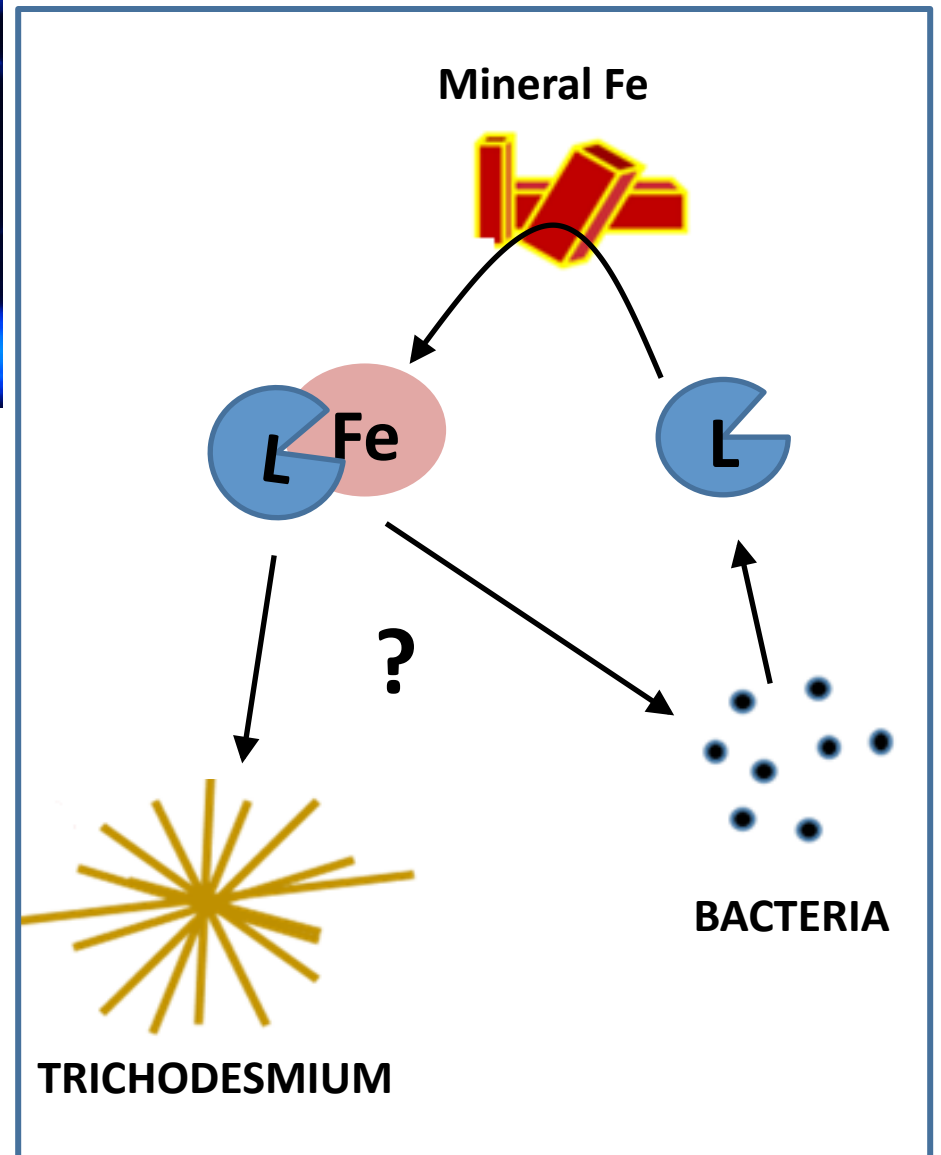


Interactions between M and biota



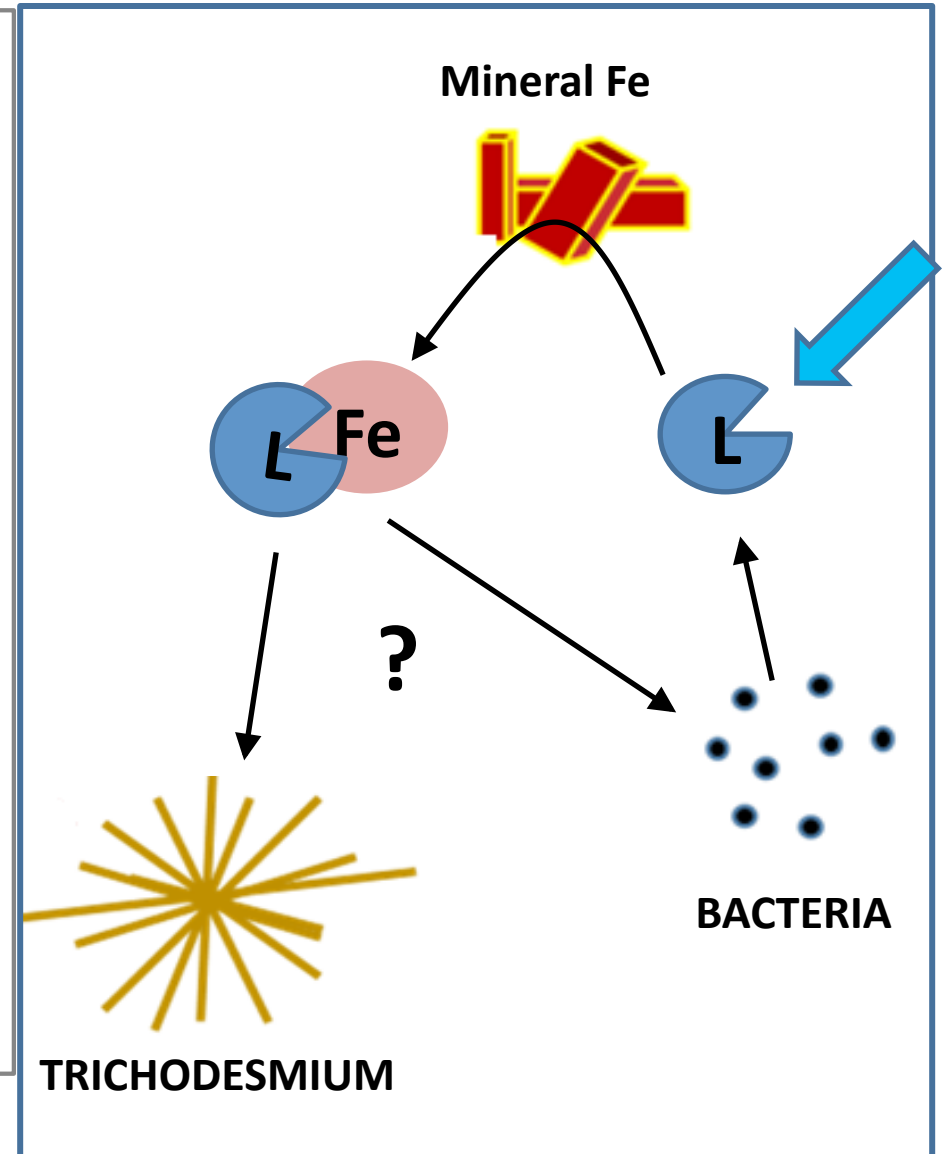
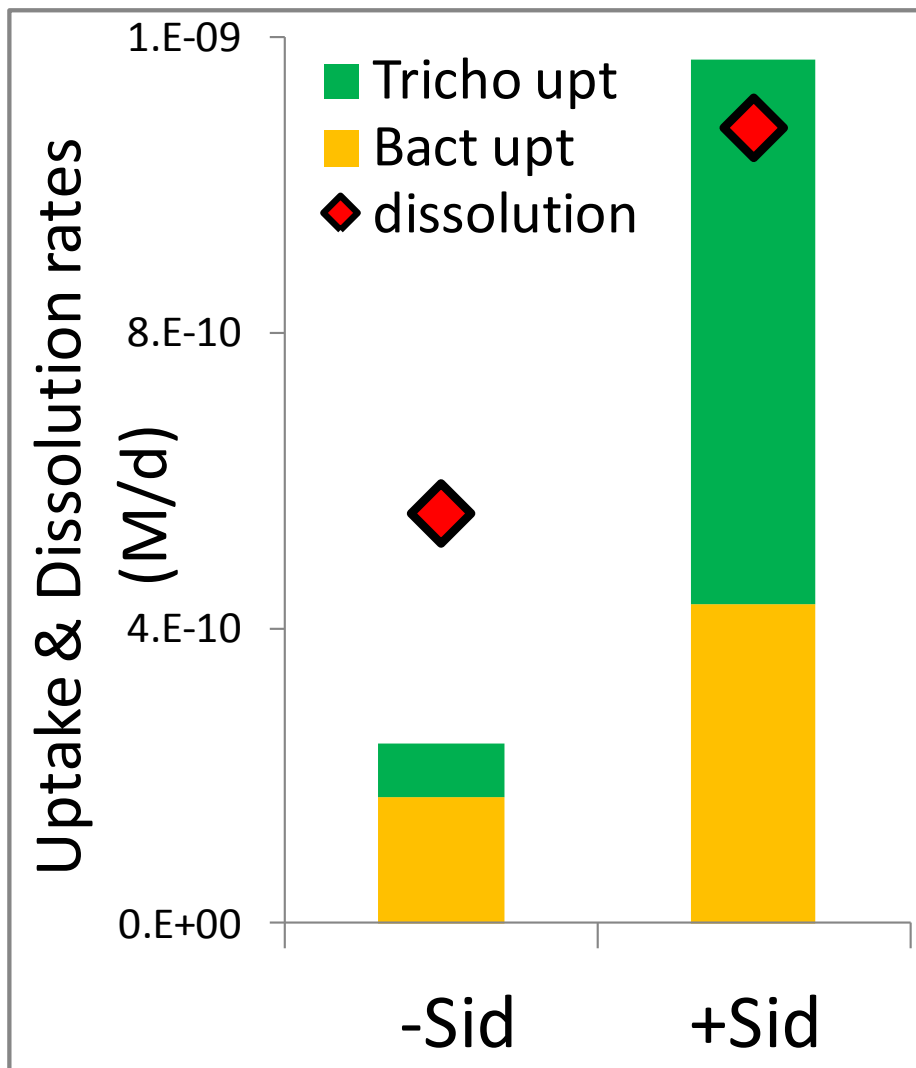
Dust Iron Utilization by Natural *Trichodesmium* Assisted by Bacteria

Shaked et al



Dust Iron Utilization by Natural *Trichodesmium* Assisted by Bacteria

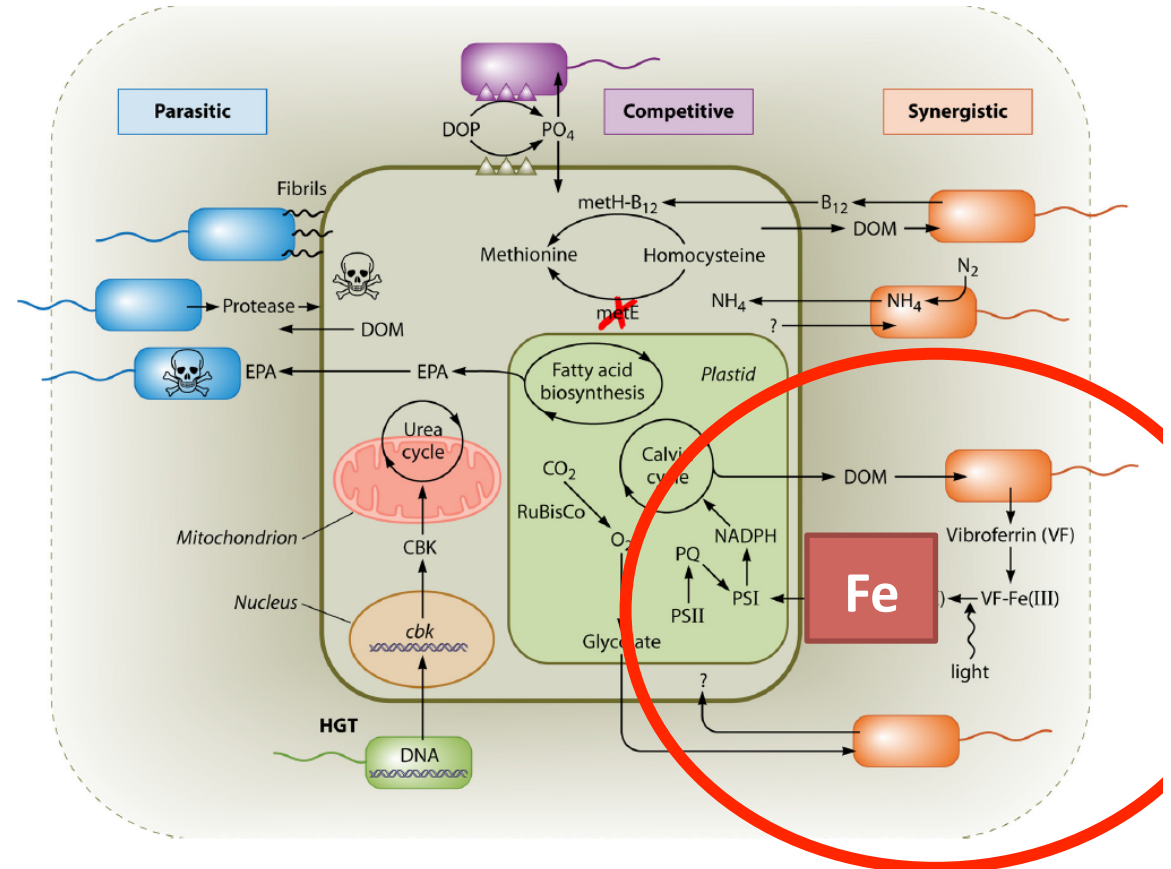
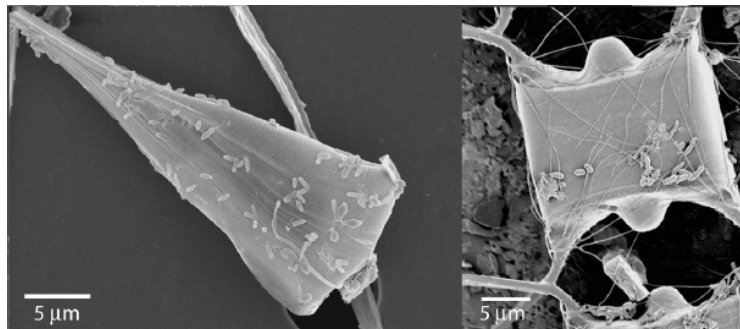
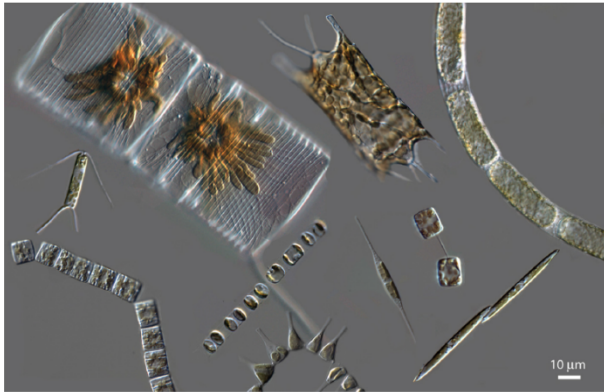
Shaked et al



⁵⁵Fe-Ox, Natural colonies, Red Sea, Mar 2016

Phytoplankton & associated bacteria are teaming-up to acquire M

signaling molecules & exchange of nutrients



Amin et al. 2009, 2012, 2016

mutualistic interaction

Mixotrophs (organisms that can switch nutritional modes) are widespread in the ocean: affect M cycling

**e.g. Phytoplankton
that can also ingest prey**



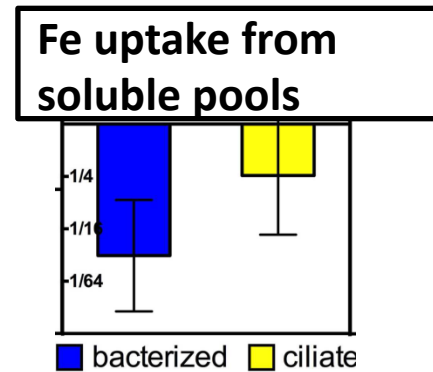
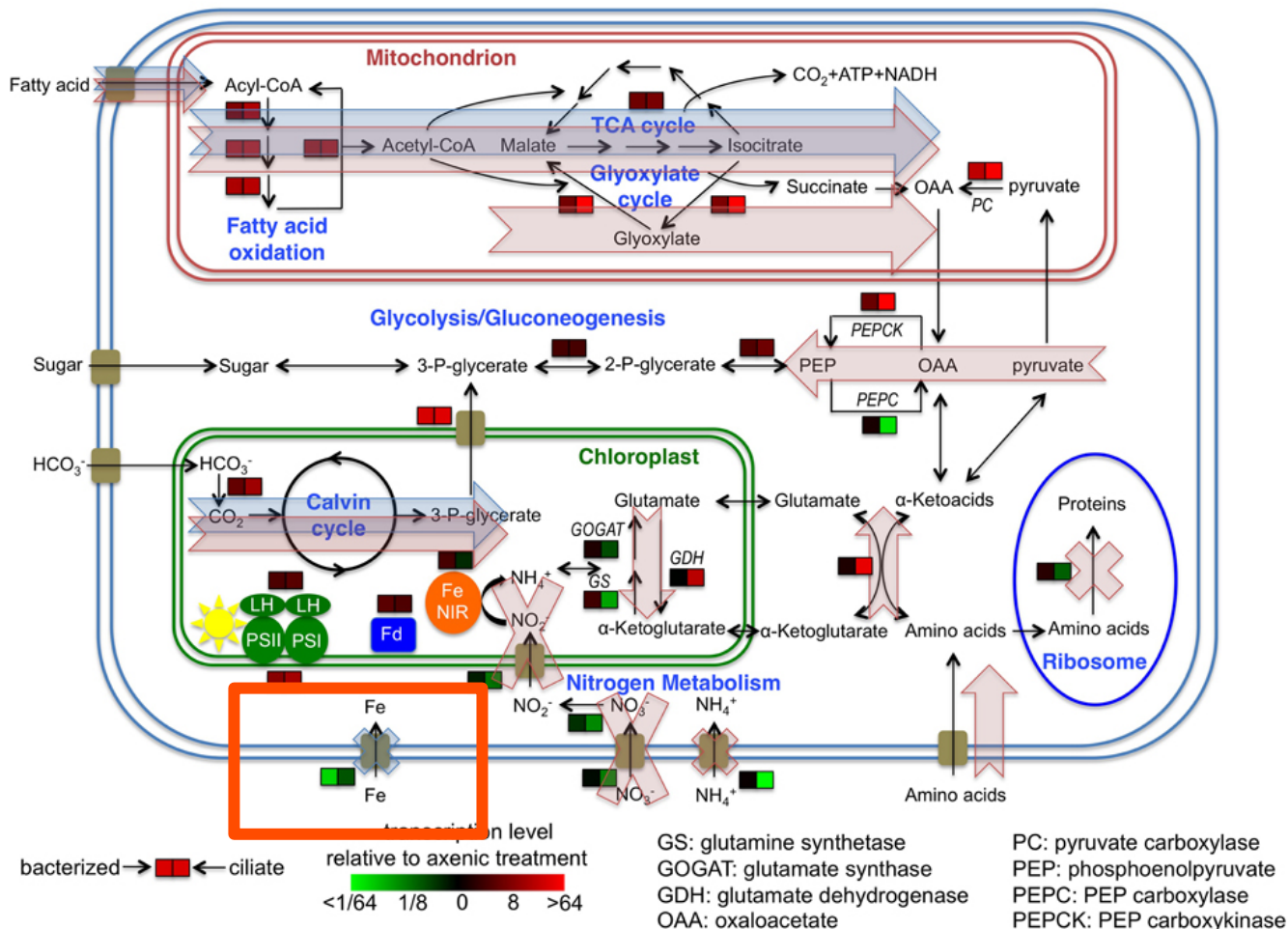
Prymnesium parvum

Review by Stoecker et al. 2016

Mixotrophs (organisms that can switch nutritional modes) are widespread in the ocean: affect M cycling

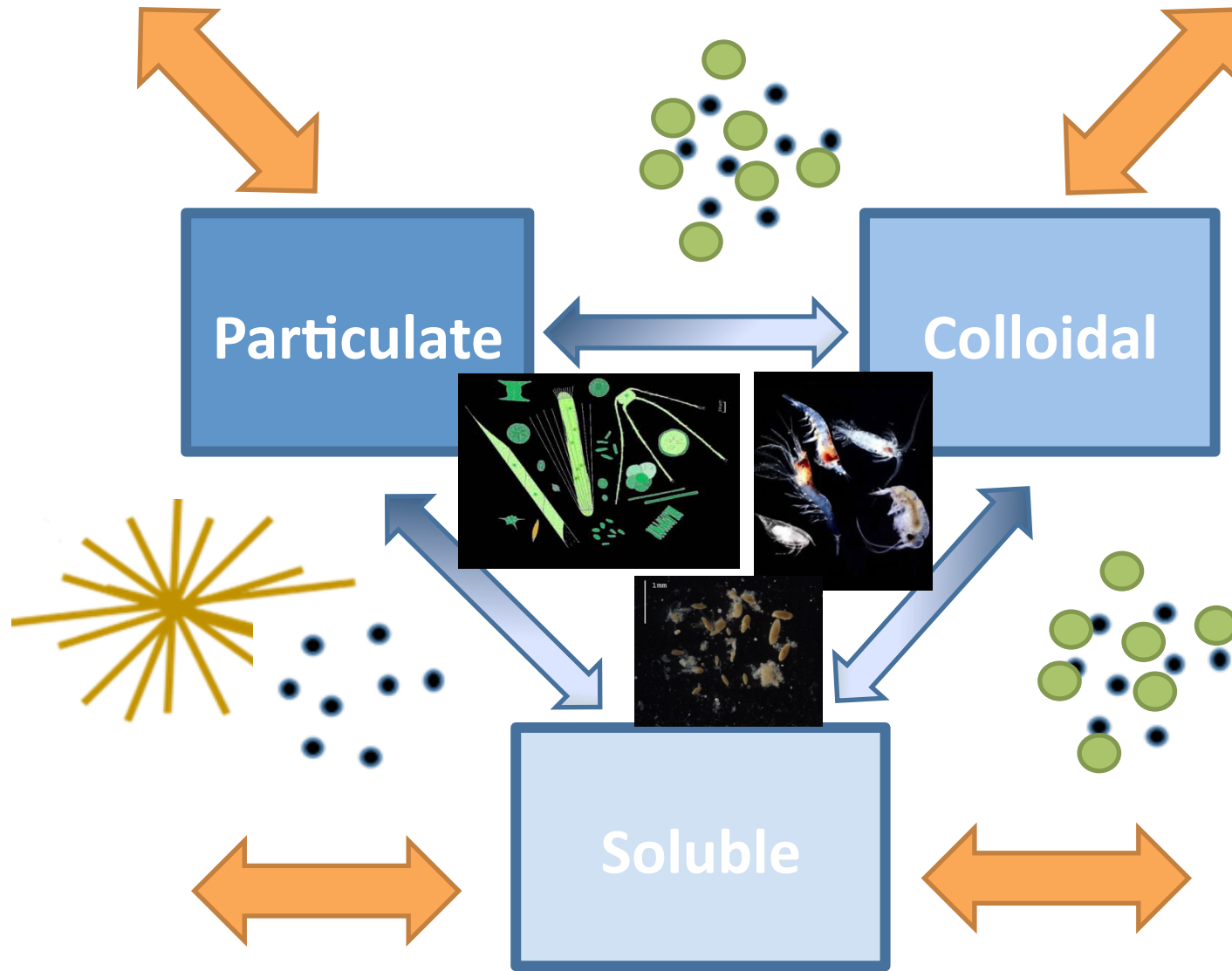
Prymnesium parvum responds to prey (bacteria vs. ciliates) & changes metal acquisition
Liu et al. 2015 (Maranger et al. 1998)

Phytoplankton acquiring their Fe ration from prey



Prymnesium parvum

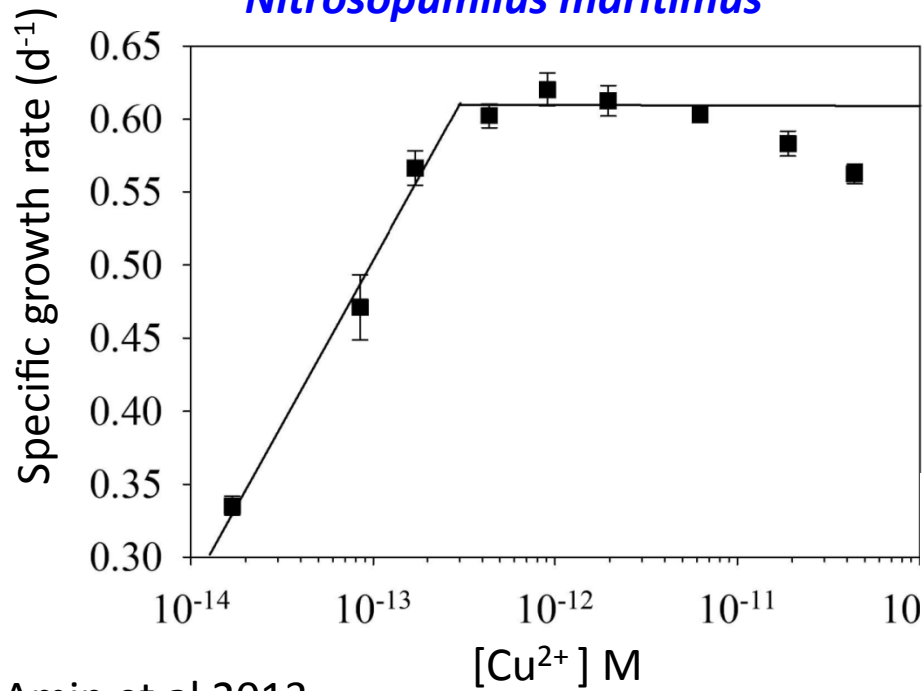
Interactions between M and biota



Interaction between M and nutrient cycles

Cu concentrations in the ocean may limit processes in the N cycle

Ammonium Oxidizing Archaea *Nitrosopumilus maritimus*



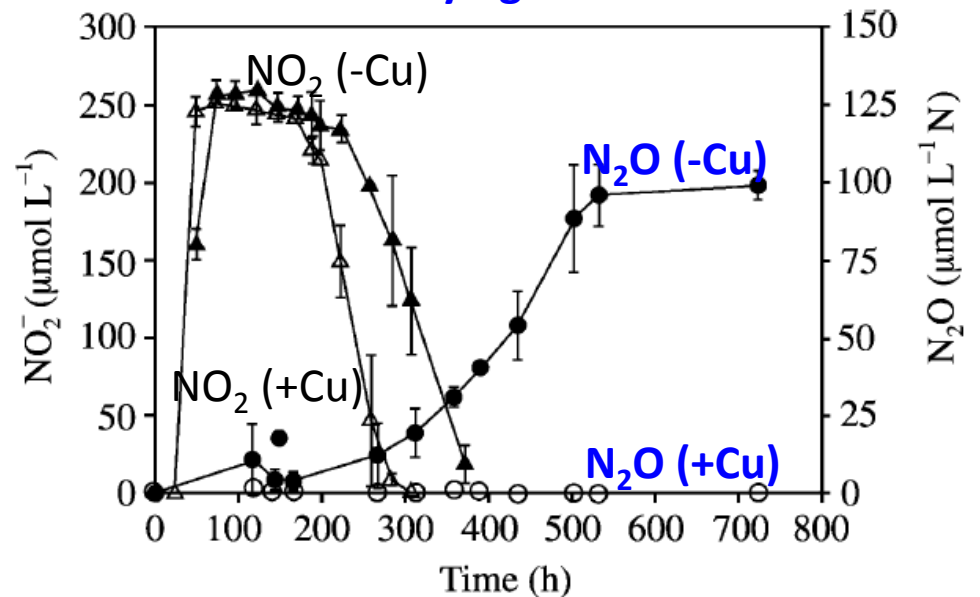
Amin et al 2013

Cu containing proteins involved in e- transport:
Nitrosopumilus maritimus (27)

Candidatus Nitrosopelagicus brevis (12)

Santoro et al. 2015

Denitrifying Bacteria



Granger & Ward 2003

SUMMARY and Future Directions

- Incredible diversity of mechanisms to acquire metals, and deal with changes in trace metal availability.
- Organisms are accessing multiple M pools & are mediating the transfer of metals between pools
- To better understand biogeochemical cycles of M we need to study the interactions between microorganisms, and M nutrition in higher trophic levels
- Concentrations of other M, besides Fe, may not affect PP, but they may control community composition & cycles of macronutrients