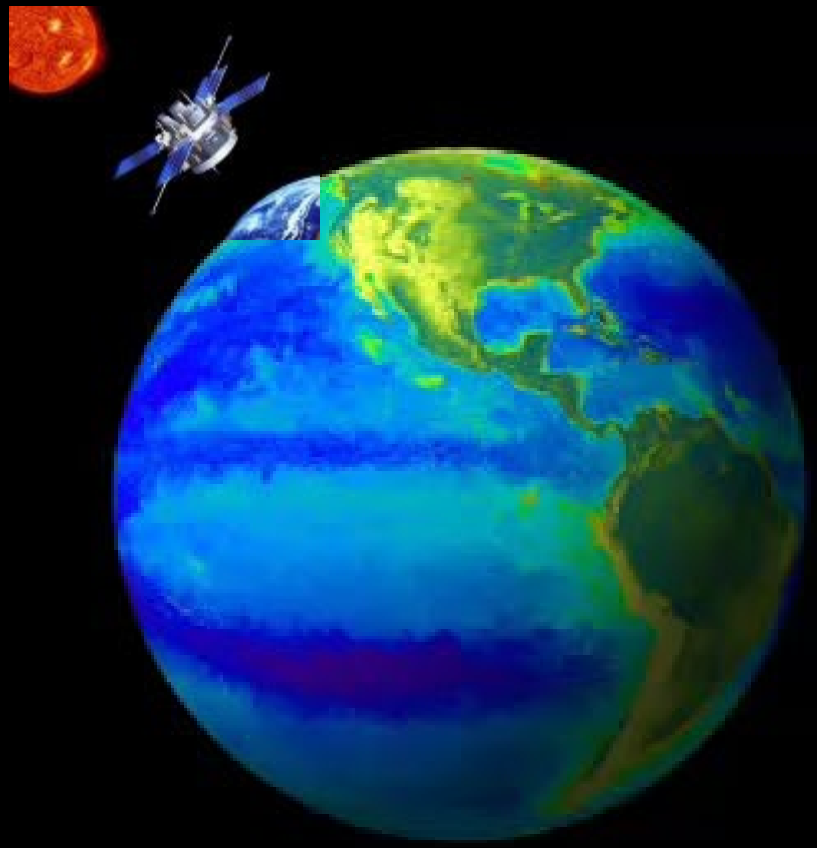
BioSpace25 - Biodiversity insight from Space
10 - 14 February 2025 | ESA-ESRIN | Frascati - Italy

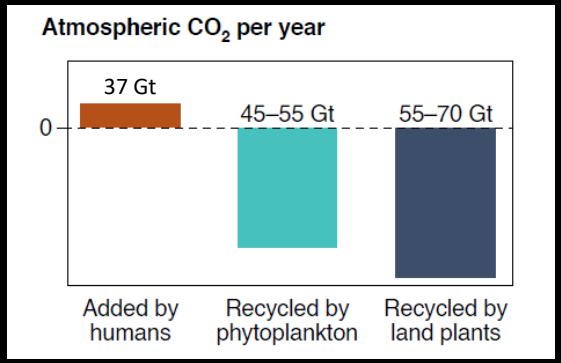
A satellite-genomics approach to explore phytoplankton iron ecophysiology in the global ocean

Pedro Ciarlini Junger, Roy El Hourany, Vitushanie Yogaranjan, Juan Pierella Karlusich, Chris Bowler

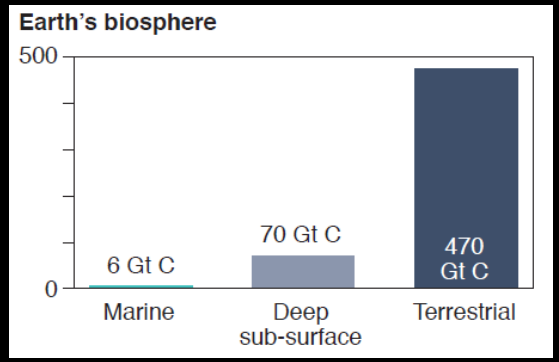
Plant & Algal Genomics, Institut de Biologie de l'École Normale Superieure (IBENS), Paris, France

Oceanic phytoplankton contribute to 50% of primary productivity on Earth

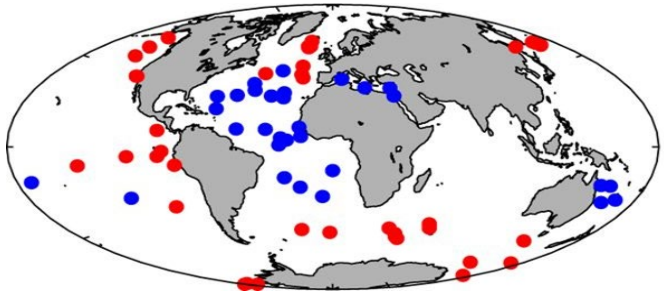




1% of Earth's photosynthetic biomass



Fe limits marine production in 30-40% of the ocean surface



Moore (2016) Phil. Trans. R. Soc. A

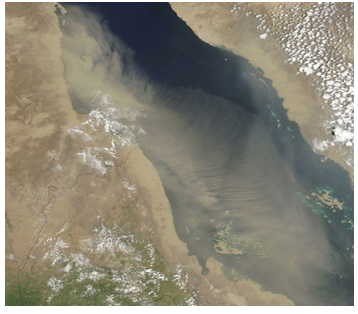
Experimental evidence of upper ocean primary nutrient limitation

N

Fe Very low **Fe** in the ocean (**<1 nM**)

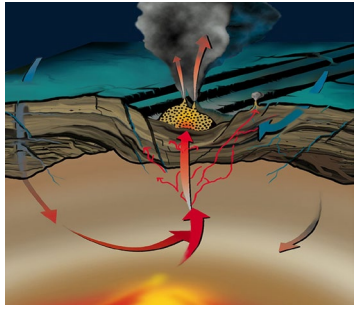
Natural iron fertilization of the ocean

Freshwater sediments

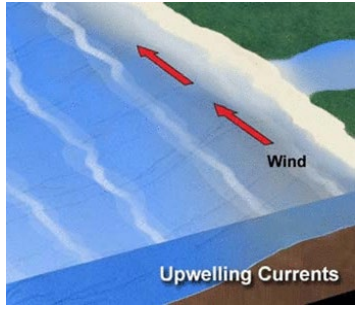


Dust

Melting Glaciers



Hydrothermal Vents
Volcanoes

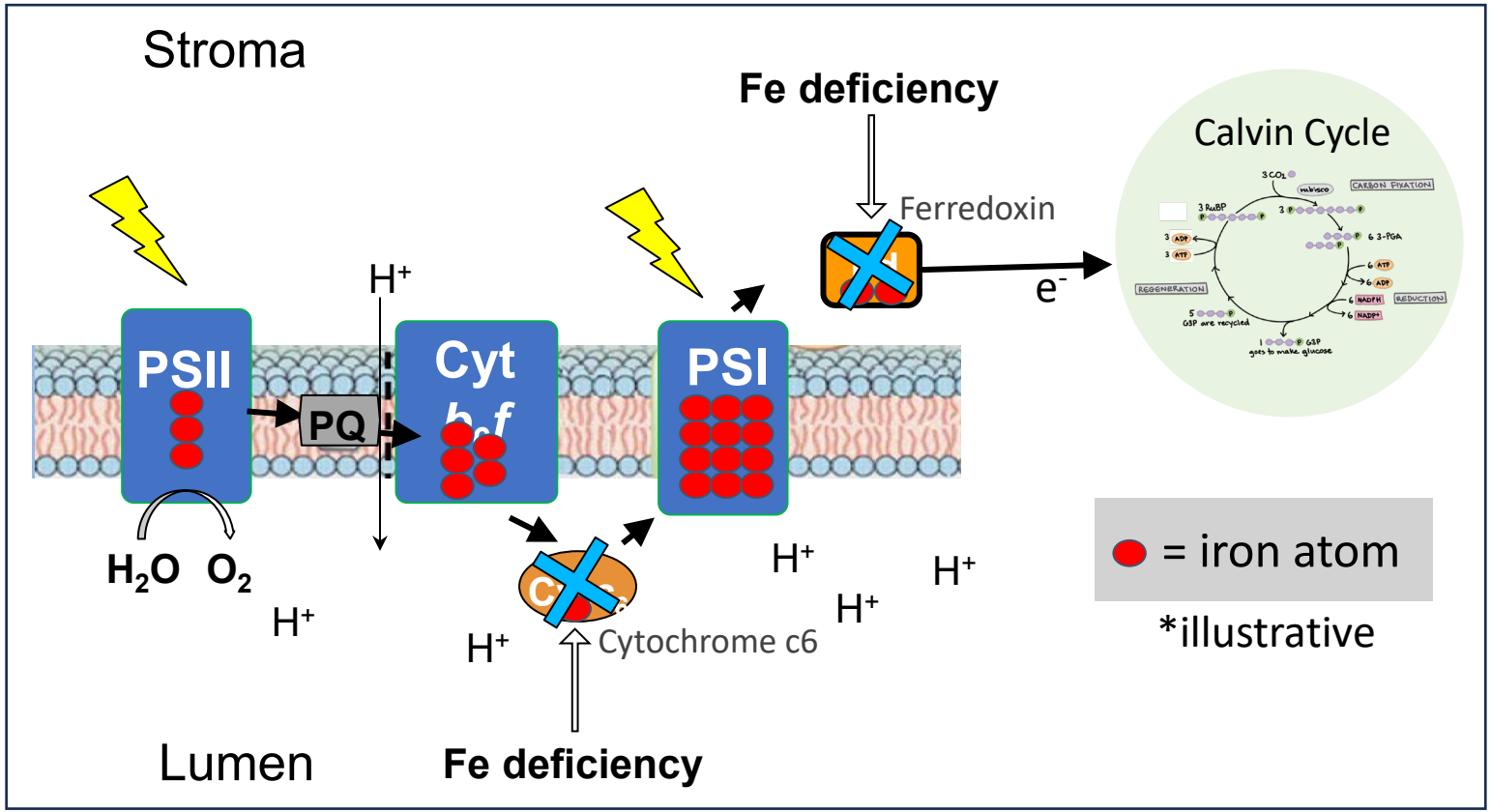


Upwelling

NASA Earth Observatory

Substitution of Fe-containing proteins by iron-free counterparts

Known molecular compensatory mechanisms to deal with iron deficiency



Substitution of Fe-containing proteins by iron-free counterparts

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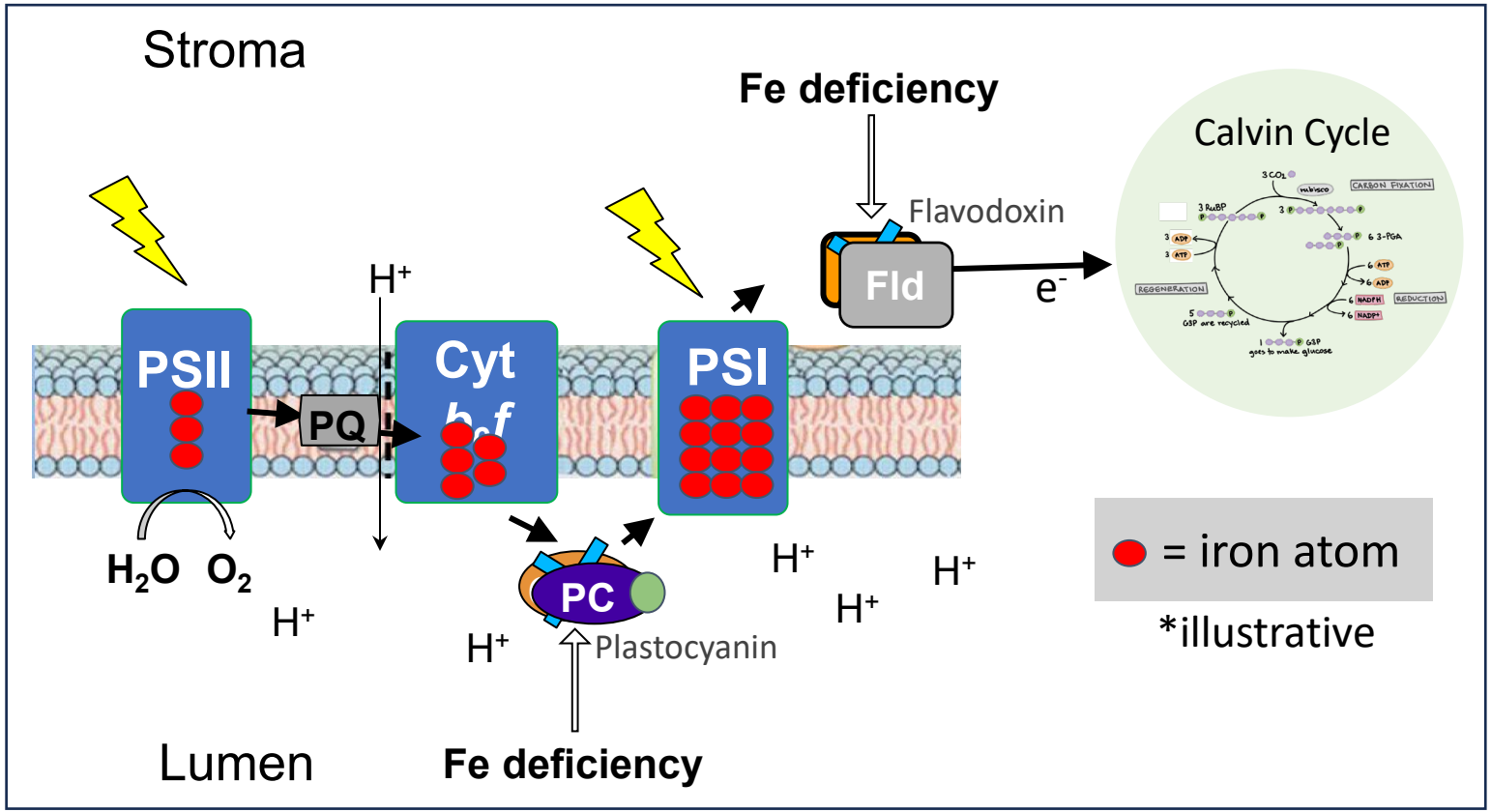
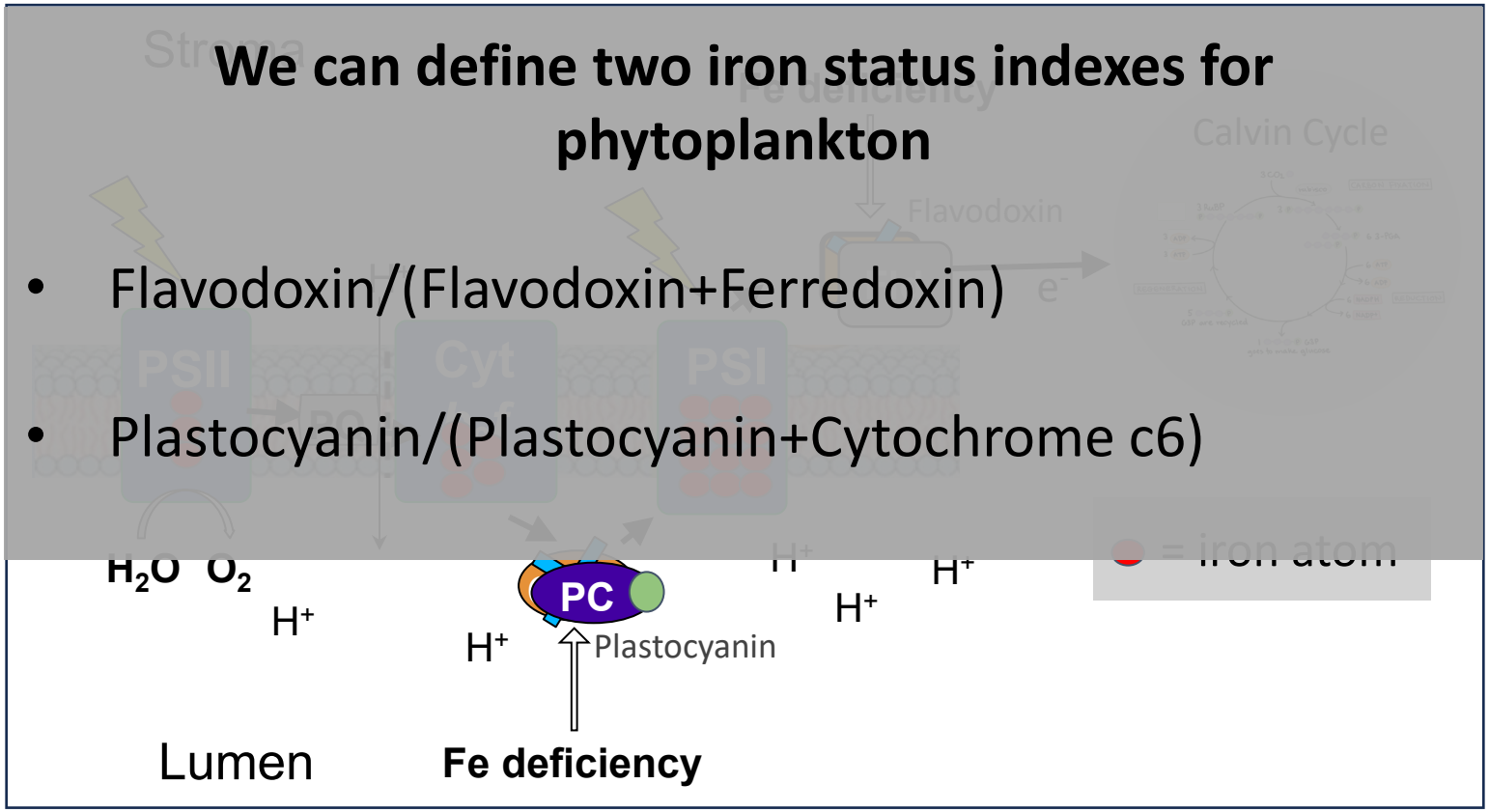


Substitution of Fe-containing proteins by iron-free counterparts

Known molecular compensatory mechanisms to deal with iron deficiency

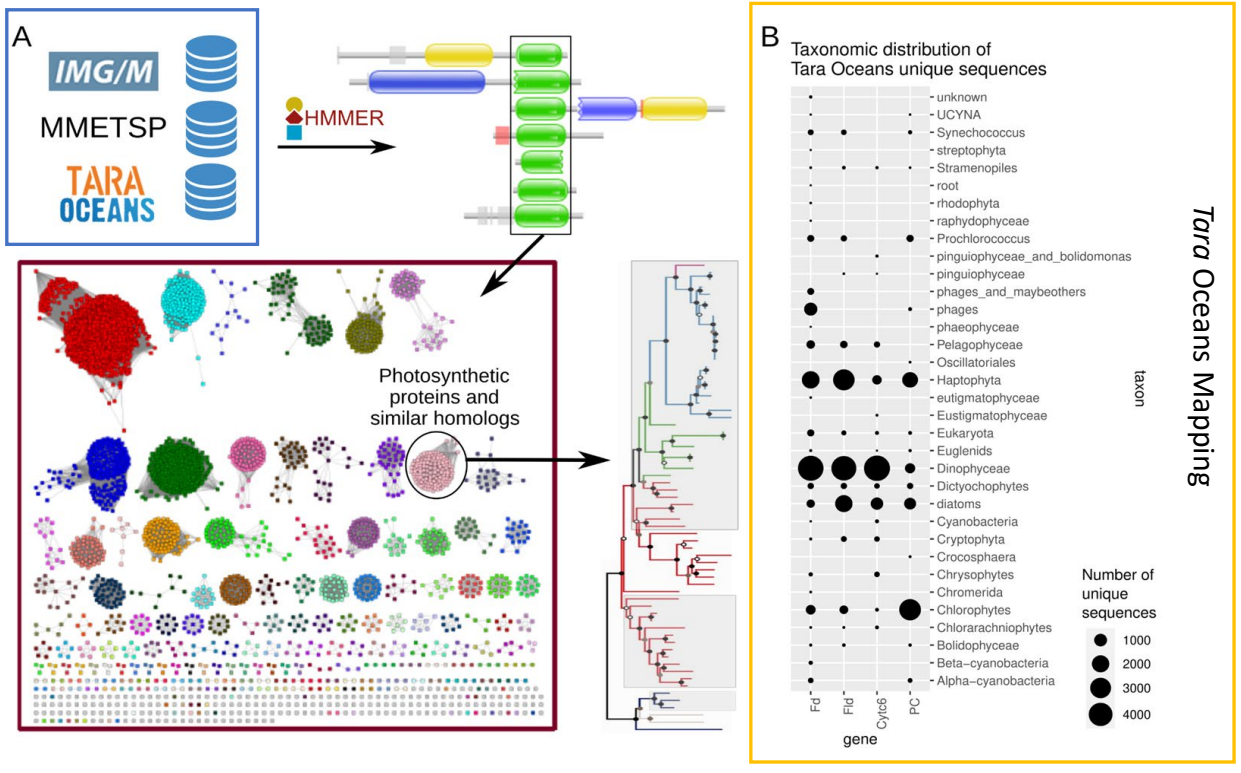
We can define two iron status indexes for phytoplankton

- Flavodoxin/(Flavodoxin+Ferredoxin)
- Plastocyanin/(Plastocyanin+Cytochrome c6)



MetaG and *MetaT* mapping against ref database

Functional and taxonomic annotation of *Tara* Oceans sequences coding for photosynthetic electron shuttles



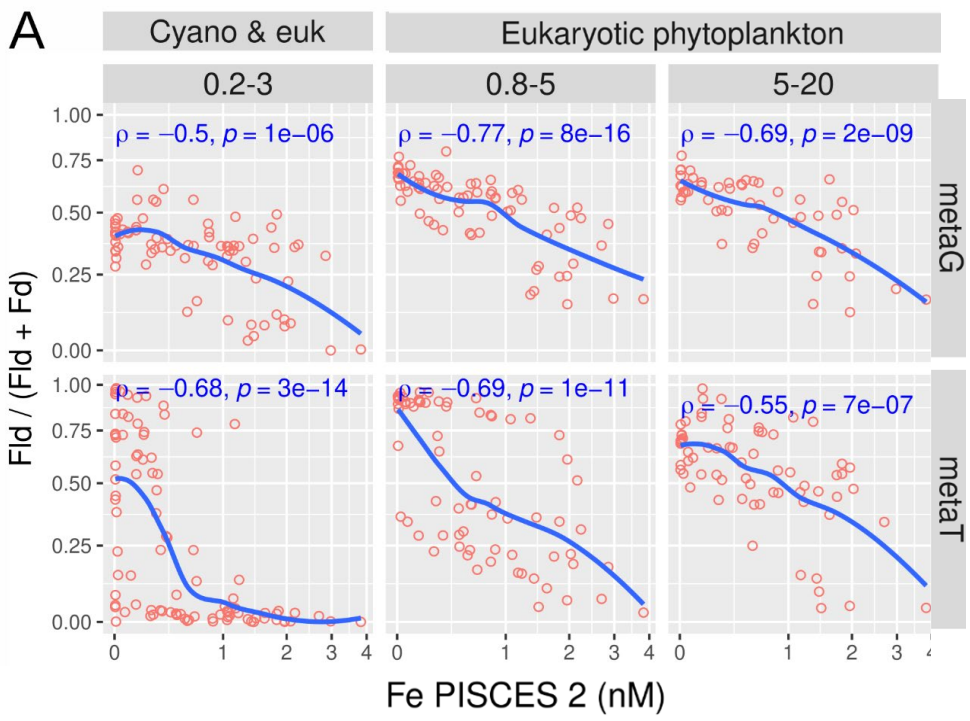
***Fld, Fd, PC, CytoC6* Reference Database**

Fld: 44,387 uni. seqs.
Fd: 105,119 uni. seqs.
CytoC6: 65,454 uni. seqs.
PC: 28,312 uni. Seqs

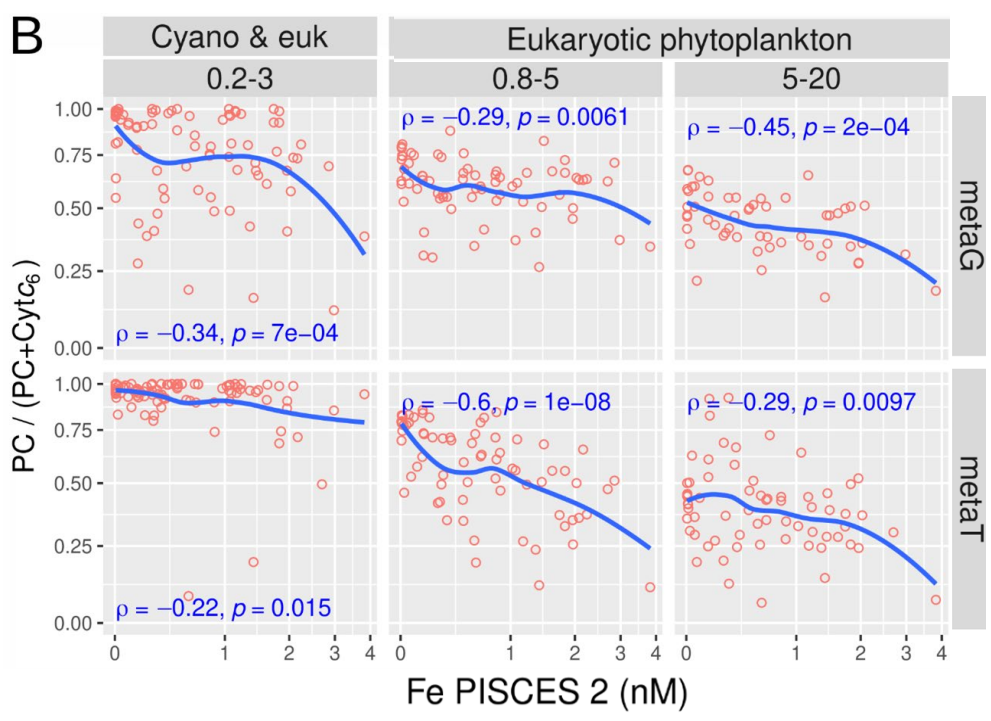
Pierella Karlusich et al. in prep.

Genomic indexes anti-correlated with iron concentration from biogeochemical models

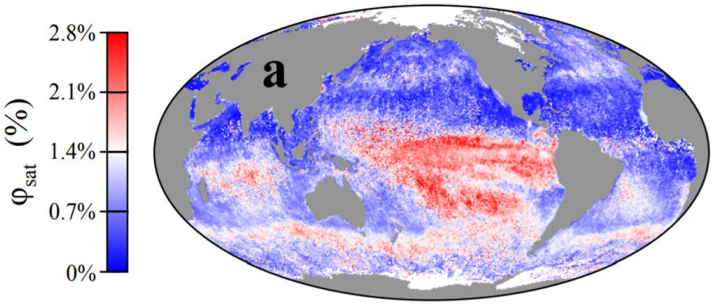
Flavodoxin index



Plastocyanin index



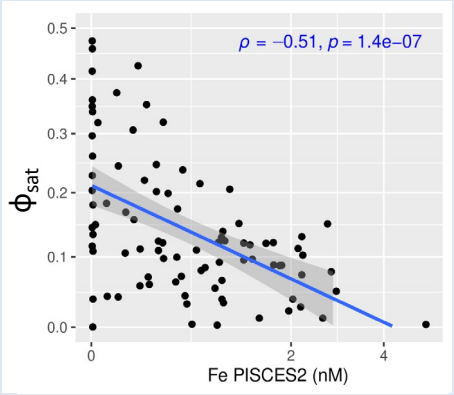
Genomic *Fe* status indexes correlates with fluorescence quantum yield

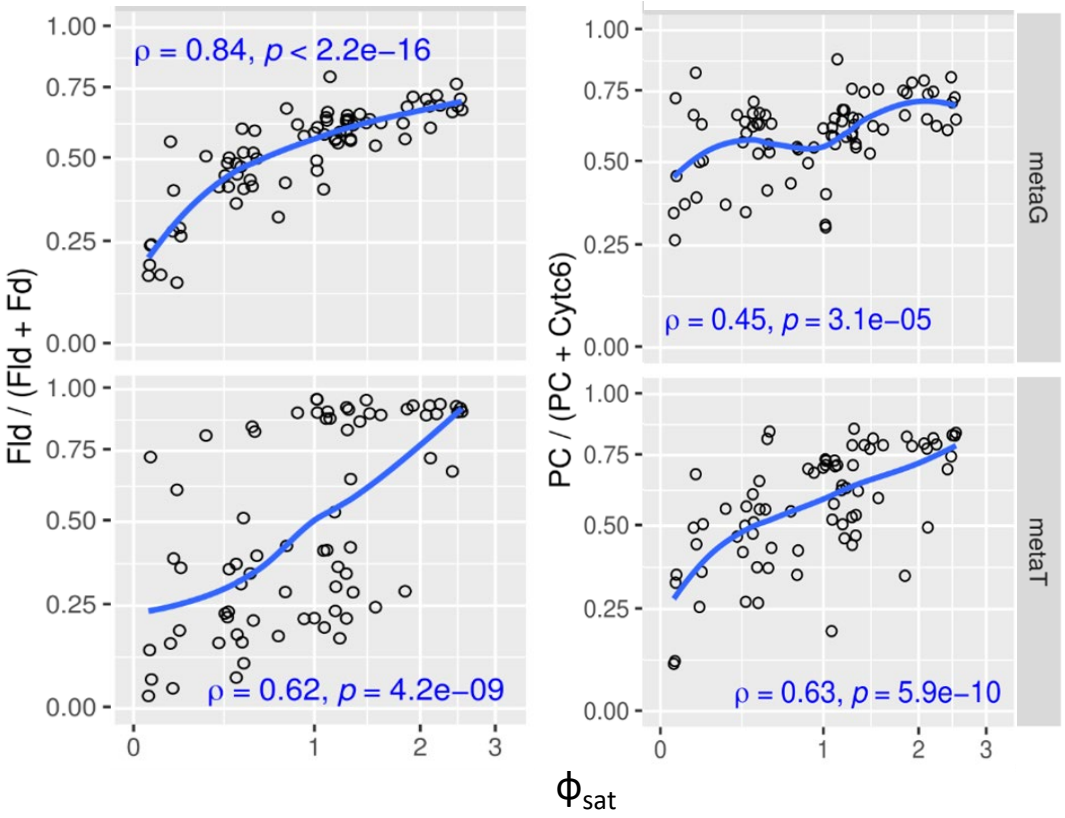


Satellite-detected fluorescence reveals global physiology of ocean phytoplankton

M. J. Behrenfeld[1], T. K. Westberry[1], E. S. Boss[2], R. T. O'Malley[1], D. A. Siegel[3], J. D. Wiggert[4], B. A. Franz[5], C. R. McClain[5], G. C. Feldman[5], S. C. Doney[6], J. K. Moore[7], G. Dall'Olmo[1], A. J. Milligan[1], I. Lima[6], and

Strong anti-correlation between fQY and modeled iron in TO stations



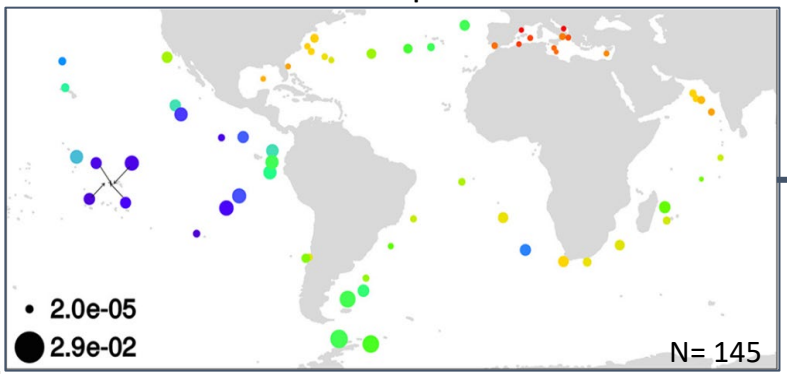


Generating a global biogeography of phytoplankton *Fe* nutritional status

Metagenomes

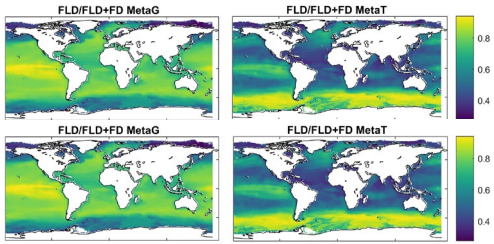
Metatranscriptomes

Tara Oceans patterns



Random Forest

Fe gene stress ratios biogeography



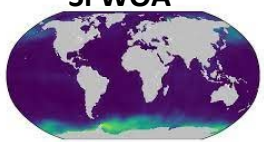
Validation

Predictors

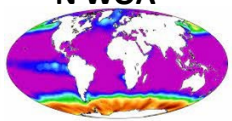
Monthly 4km

SST, Chla, iPAR, Fluorescence in the red

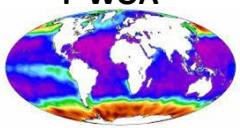
Si WOA



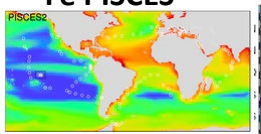
N WOA



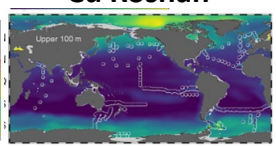
P WOA



Fe PISCES



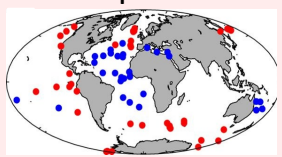
Cu Roshan



Bottle experiments

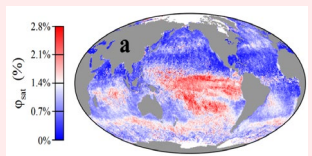
N

Fe



Moore (2016) *Phil Trans R Soc A*

Satellite



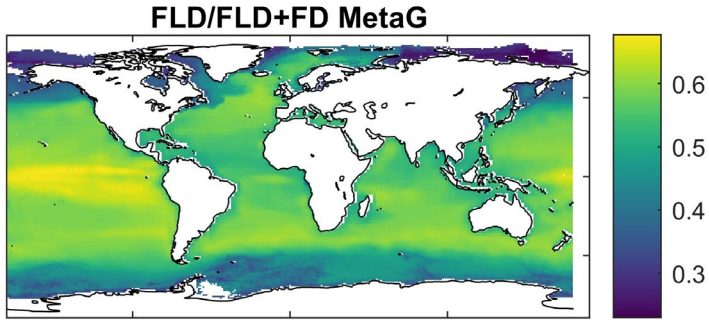
Behrenfeld et al 2009 *Biogeosciences*

Tpac in-situ *Fe* data

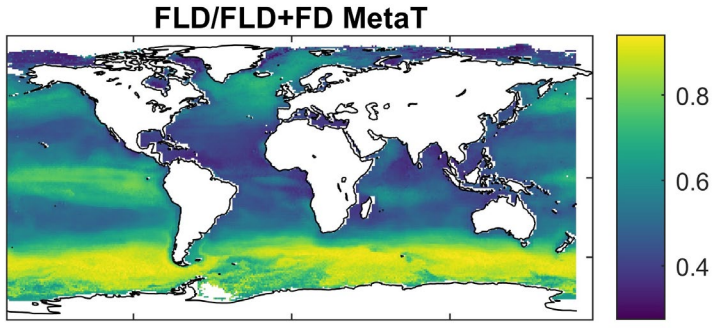
Lombard (2023) *Sci. Data*

Global maps of predicted iron genes ratios

Substitution of Ferredoxin (Fd) by Flavodoxin (Fld)



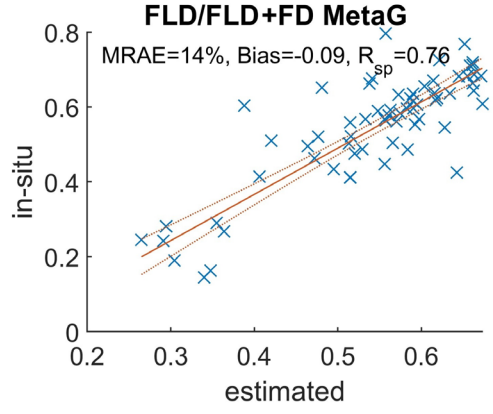
Variance explained = 76%

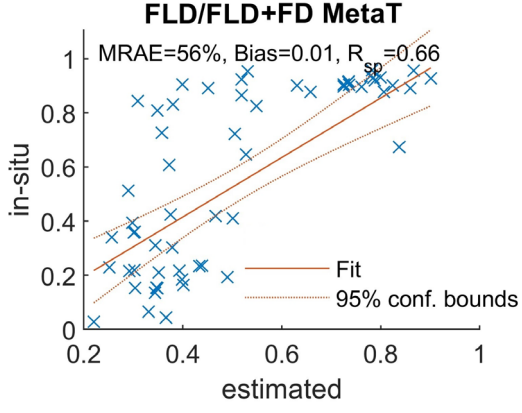


Variance explained = 66%

Fe Defficiency

Fe Replete



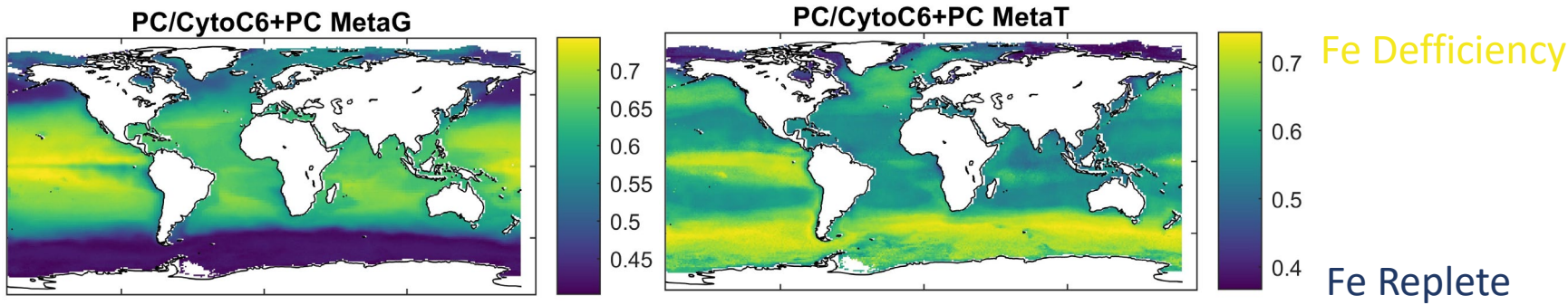


∗ Leave-one-out cross-validation

MRAE – Mean Relative Absolute Error

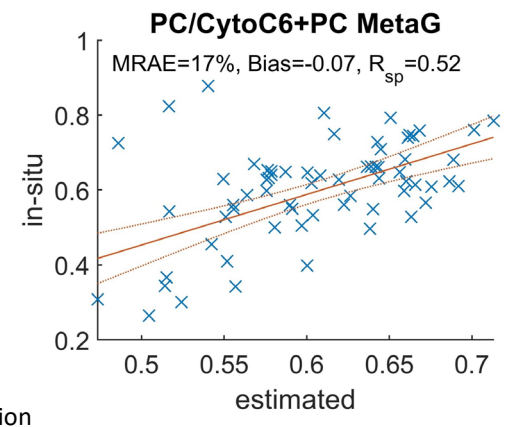
Global maps of predicted iron genes ratios

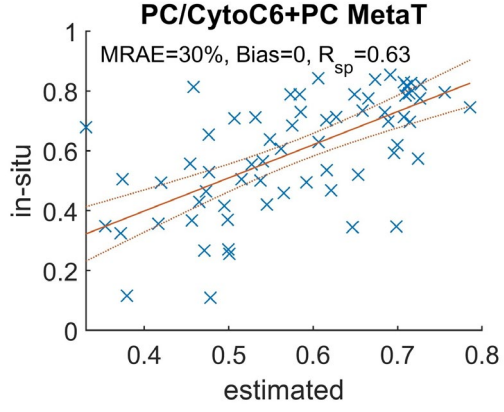
Substitution of cytochrome C6 (CytoC6) by plastocyanin (PC)



Variance explained = 52%

Variance explained = 63%

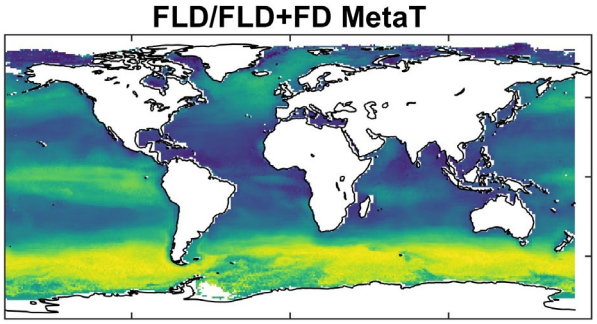


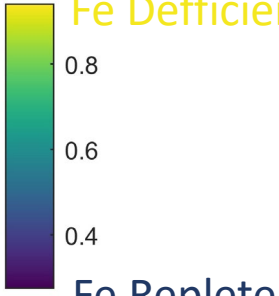


∗ Leave-one-out cross-validation

MRAE – Mean Relative Absolute Error

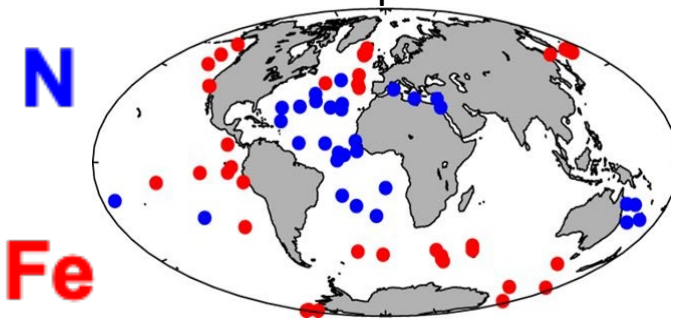
MetaT-based flavodoxin index is a proxy of Fe limitation defined by bottle experiments





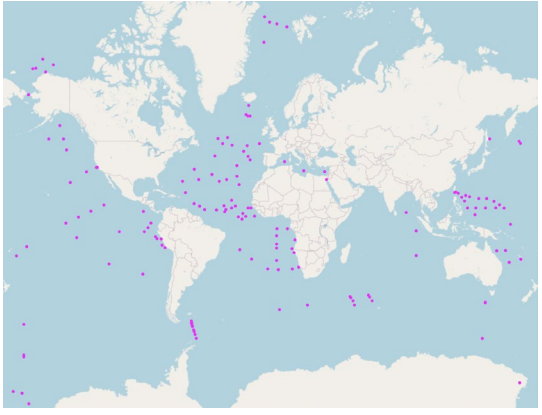
Variance explained = 66%

Bottle experiments

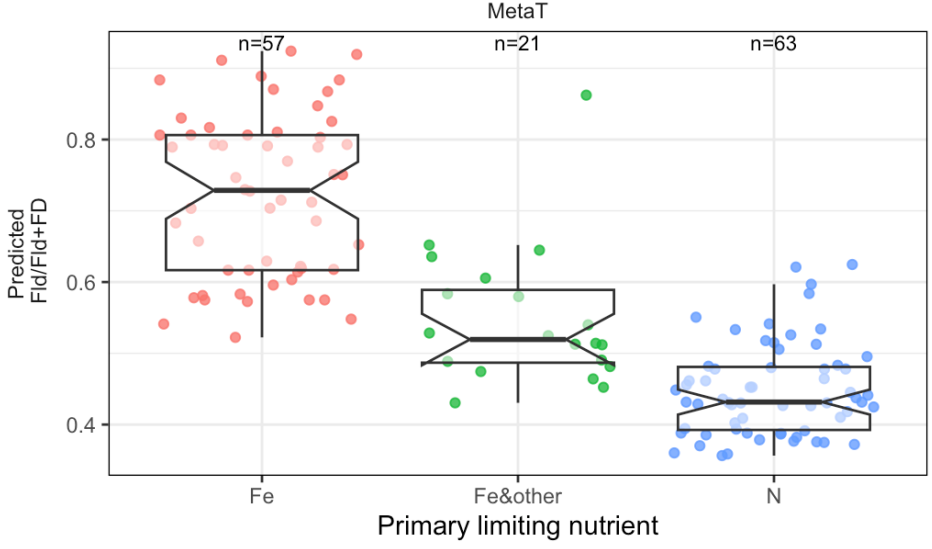


Moore (2016) Phil Trans R Soc A

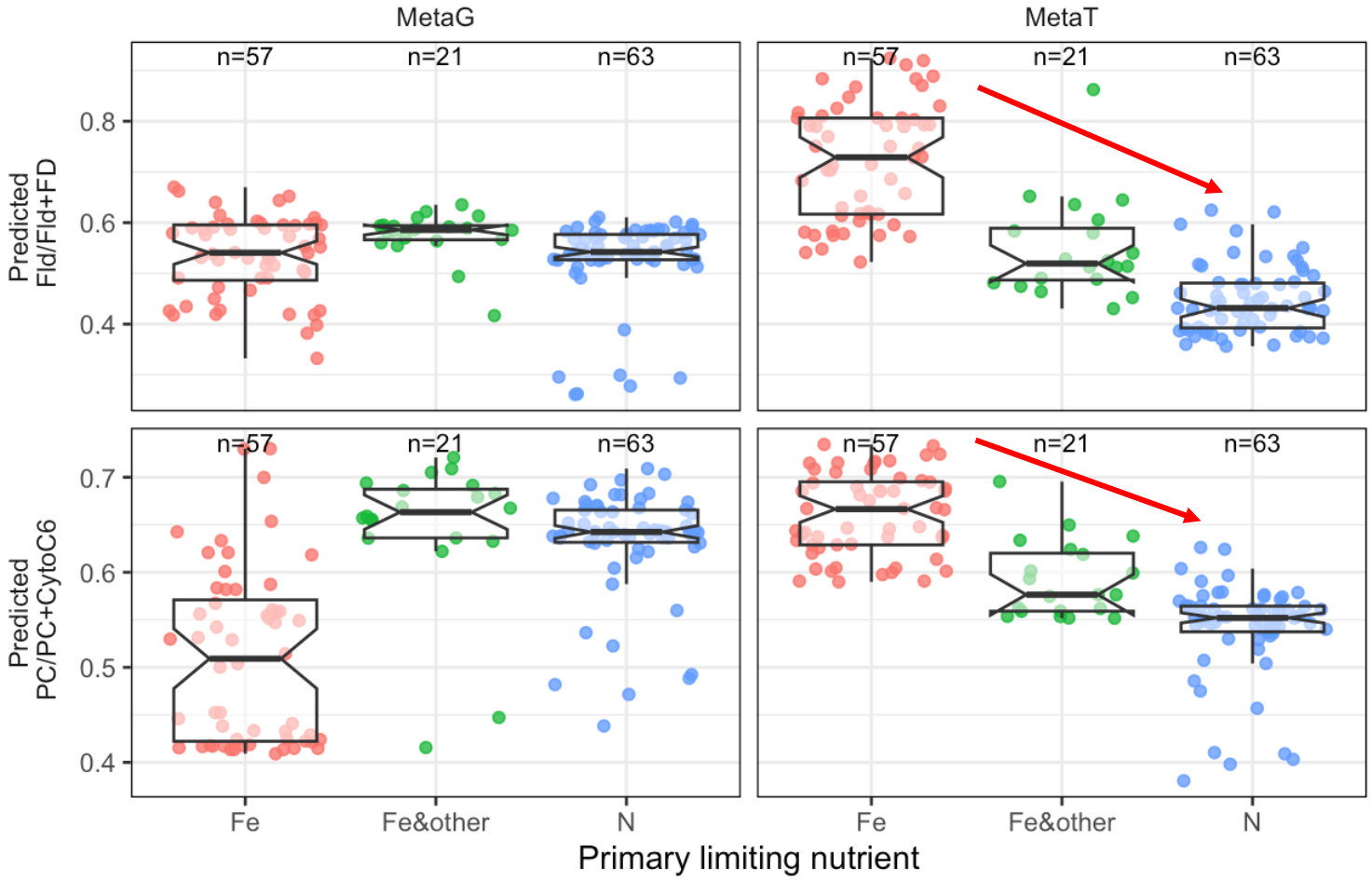
Bottle experiments



Georeferences



metaT-based ratios are better proxies of *Fe* limitation defined by bottle experiments



Iron stress genes/transcripts in the *Tara* Pacific

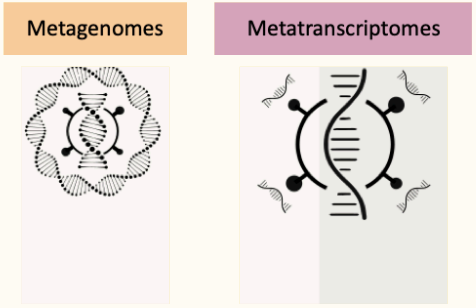
1. Further validating the approach by correlating gene ratios with in-situ iron measurements
2. Increasing observations for ML algorithms

Fld, Fd, PC, CytoC6
Reference Database

Fld: 44,387 uni. seqs.
Fd: 105,119 uni. seqs.
CytoC6: 65,454 uni. seqs.
PC: 28,312 uni. Seqs

Mapping

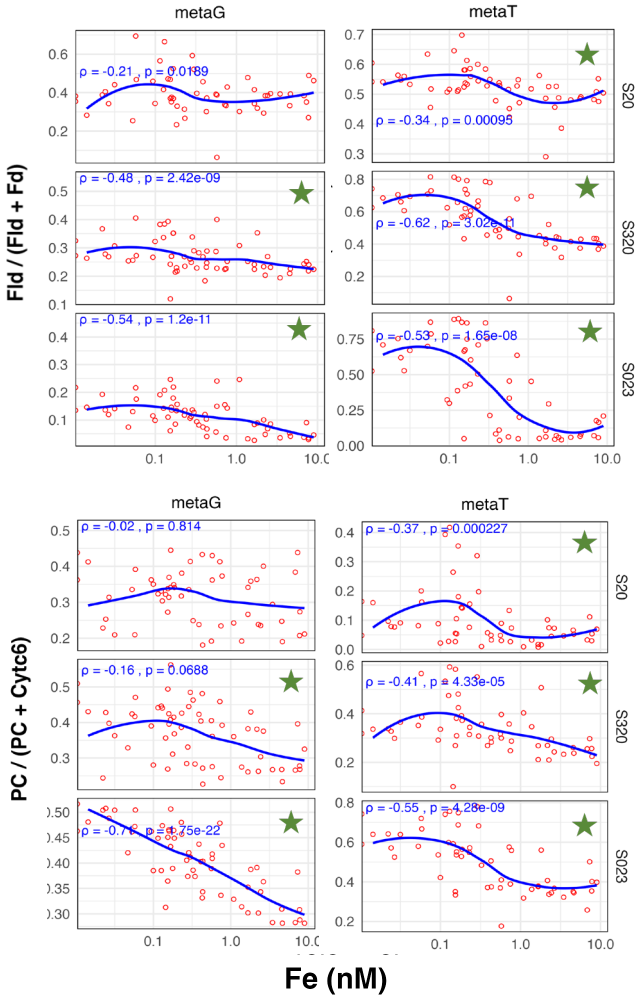
tara PACIFIC



Tara Pacific (2016-2018)

Abundance of mapped genes and transcripts

Flavodoxin and plastocyanin indexes in the *Tara* Pacific



- **Flavodoxin** and **plastocyanin** indexes strongly anti-correlated with **in-situ iron** measurements
- Correlations were more pronounced in the smaller size-fractions
- Correlations were mostly **stronger** in the **metatranscriptomic** than in the metagenomic data

Conclusions

- We found **patterns** of gene and transcript abundances **consistent with biogeochemical models**, **iron concentration measurements**, and **satellite remote sensing**, suggesting these ratios can work as good **genomic proxies for iron limitation in the ocean**

- We used the prevalence of phytoplankton genes and transcripts involved in iron responses to develop **maps of inferred nutrient stress** across the global ocean. The ***metaT* predictions** were **more coherent with bottle experiments.**

- The ***metaT* indexes correlated better** with **iron in-situ measurements** in *Tara* Pacific

- Although we highlight the need for increasing in-situ observations, our workflow provides the foundation for **linking genomics and remote sensing** to monitor phytoplankton iron nutritional status in the global ocean

Perspective & Recommendations

- **Perspective:** to generate an enhanced dataset of genes and transcripts mapped in more metagenomes and metatranscriptomes to train machine learning algorithms linking genomic and remote sensing data

- **Recommendations:**

1. The **transcript ratios** are **good proxies of phytoplankton stress,** and can inform **EBVs (physiology),** which can be **linked to remote sensing metrics**

2. We highlight the need for increasing recurrent in-situ observations (DNA & RNA sequencing), **particularly in underrepresented ocean regions**, to improve predictions of phytoplankton diversity & physiology

3. Keep **working together in inter-disciplinary efforts**

Acknowledgements

Juan Pierella Karlusich
(MIT)

Roy El Hourany
(Université du Littoral Côte d'Opale)

Éric Pelletier
(CEA/Genoscope)

Alessandro Tagliabue
(University of Liverpool)

Vitushanie Yogaranjan
(IBENS)

Chris Bowler
(IBENS)

Plant & Algal Genomics Team

IBENS
Institut de Biologie de l'Ecole Normale Supérieure

ENS
ÉCOLE NORMALE SUPÉRIEURE

PSL
RESEARCH UNIVERSITY PARIS

Inserm
La science pour la santé
From science to health

cnrs

TARA OCEANS

MARCO-BOLO
STRENGTHENING BIODIVERSITY OBSERVATION IN SUPPORT OF DECISION MAKING

Thank you!

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ENS ÉCOLE NORMALE SUPÉRIEURE | PSL RESEARCH UNIVERSITY PARIS | IBENS Institut de Biologie de l'Ecole Normale Supérieure | Inserm La science pour la santé From science to health | cnrs | TARA OCEANS

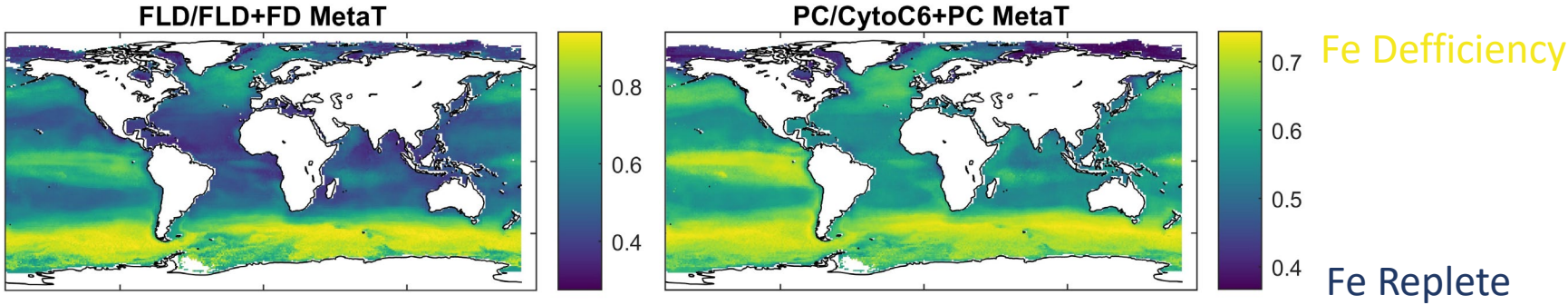
Plant & Algal Genomics (Bowler's Team)

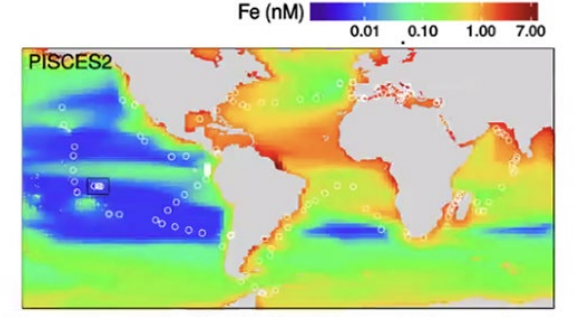
Ecology & Evolutionary Biology Section

Extra slides

pjunger@bio.ens.psl.eu

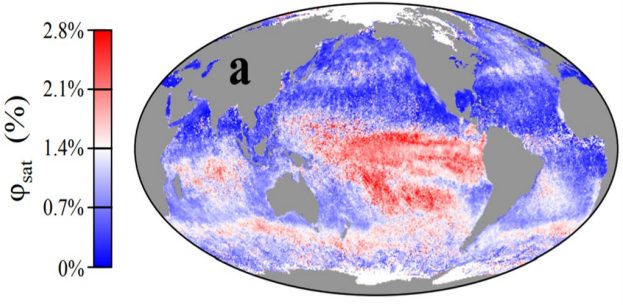
Predictions were coherent with biogeochemical models, remote sensing, and genomic data





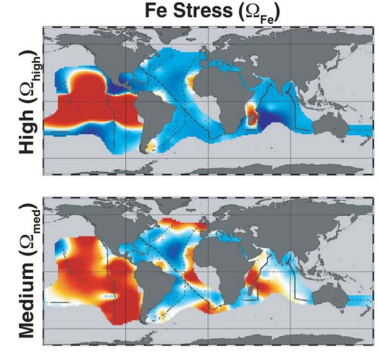
Caputi et al. (2019) *Global Biog. Cycles*

Satellite



Behrenfeld et al 2009
Biogeosciences

Prochlorococcus metagenomes



Ustick et al 2021 *Science*, *372*(6539), 287-291

Iron correlations with Fld and PC indexes in the main phytoplankton groups