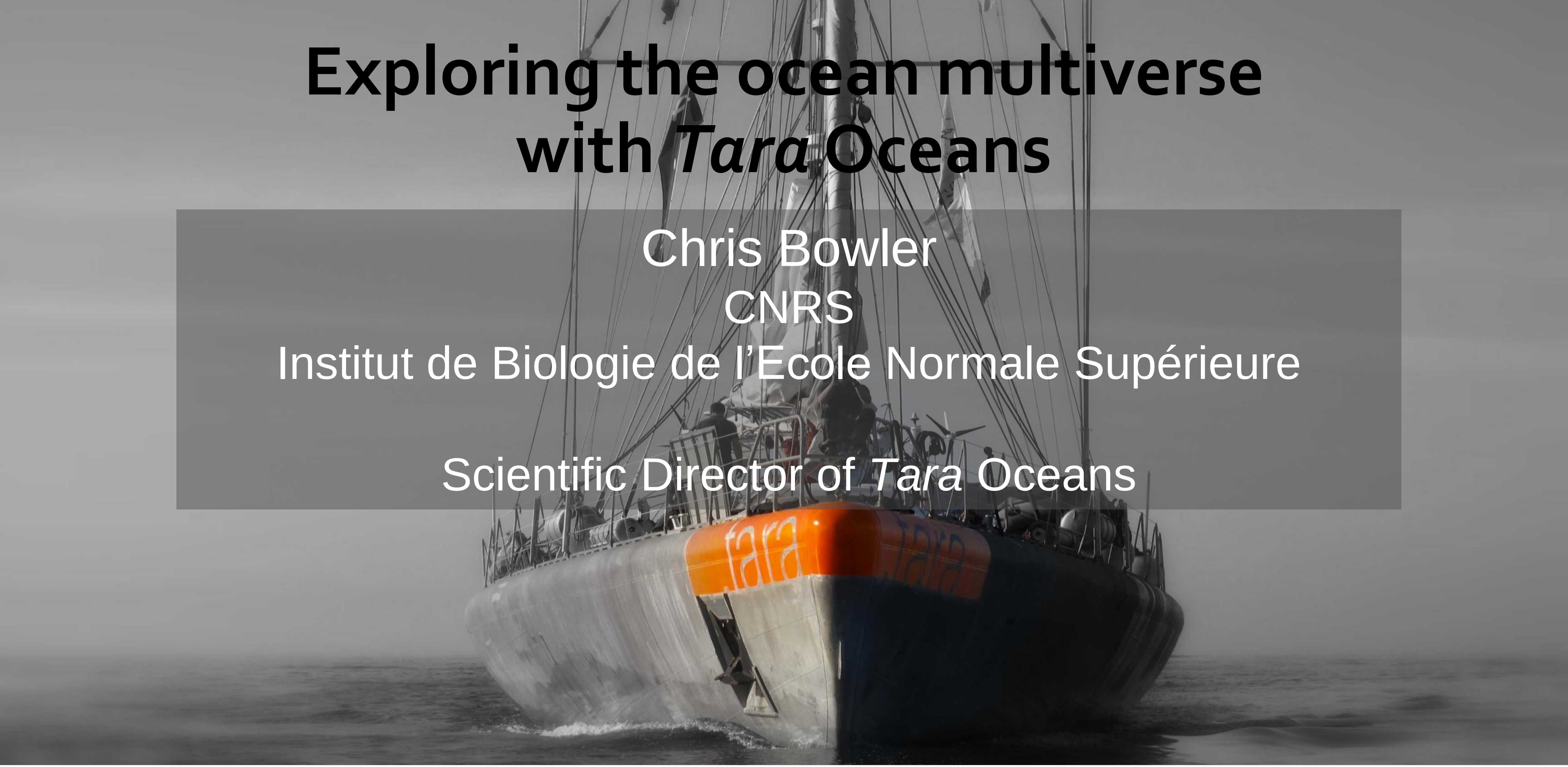


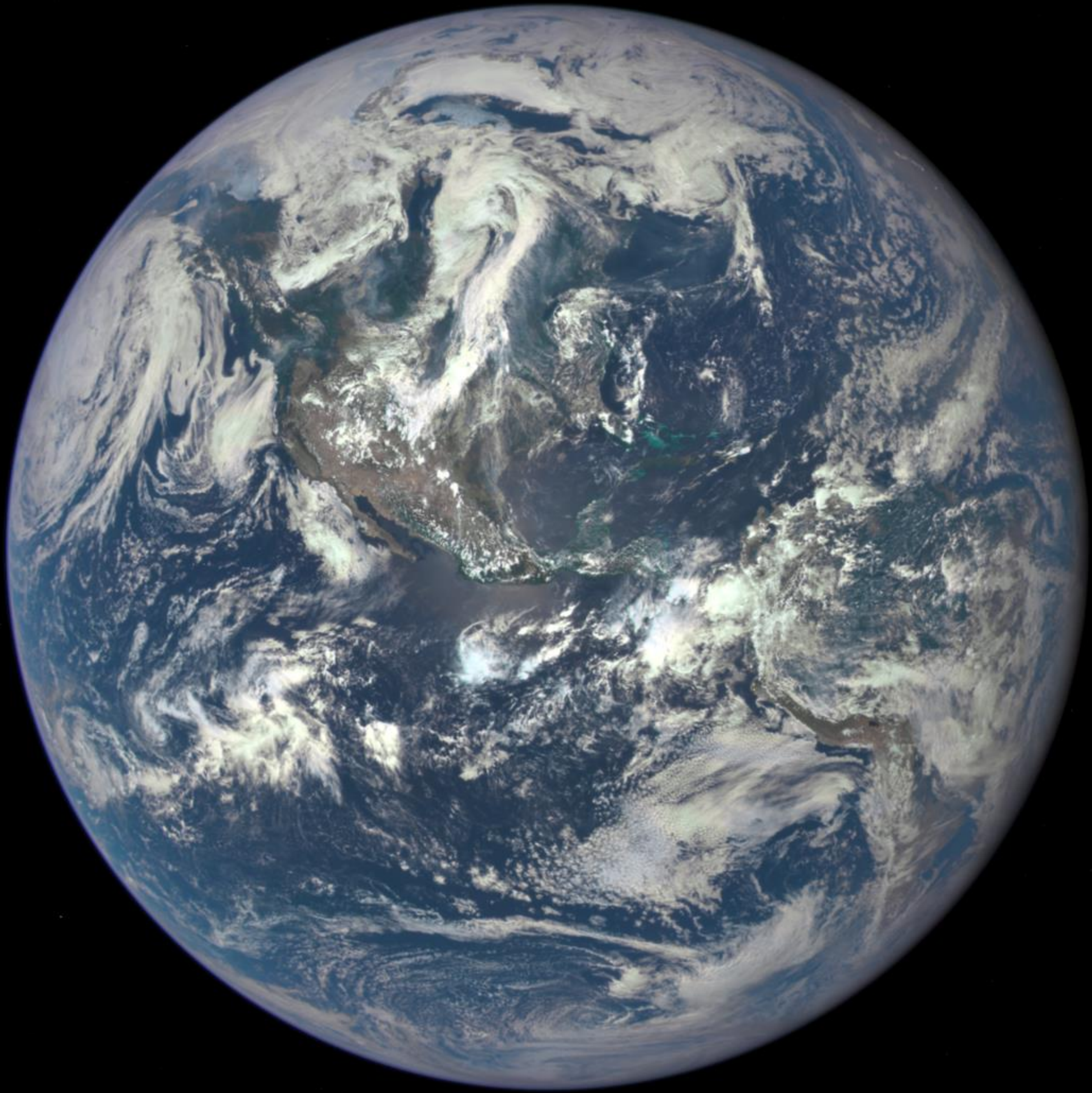
Exploring the ocean multiverse with *Tara* Oceans

Chris Bowler
CNRS
Institut de Biologie de l'Ecole Normale Supérieure

Scientific Director of *Tara* Oceans

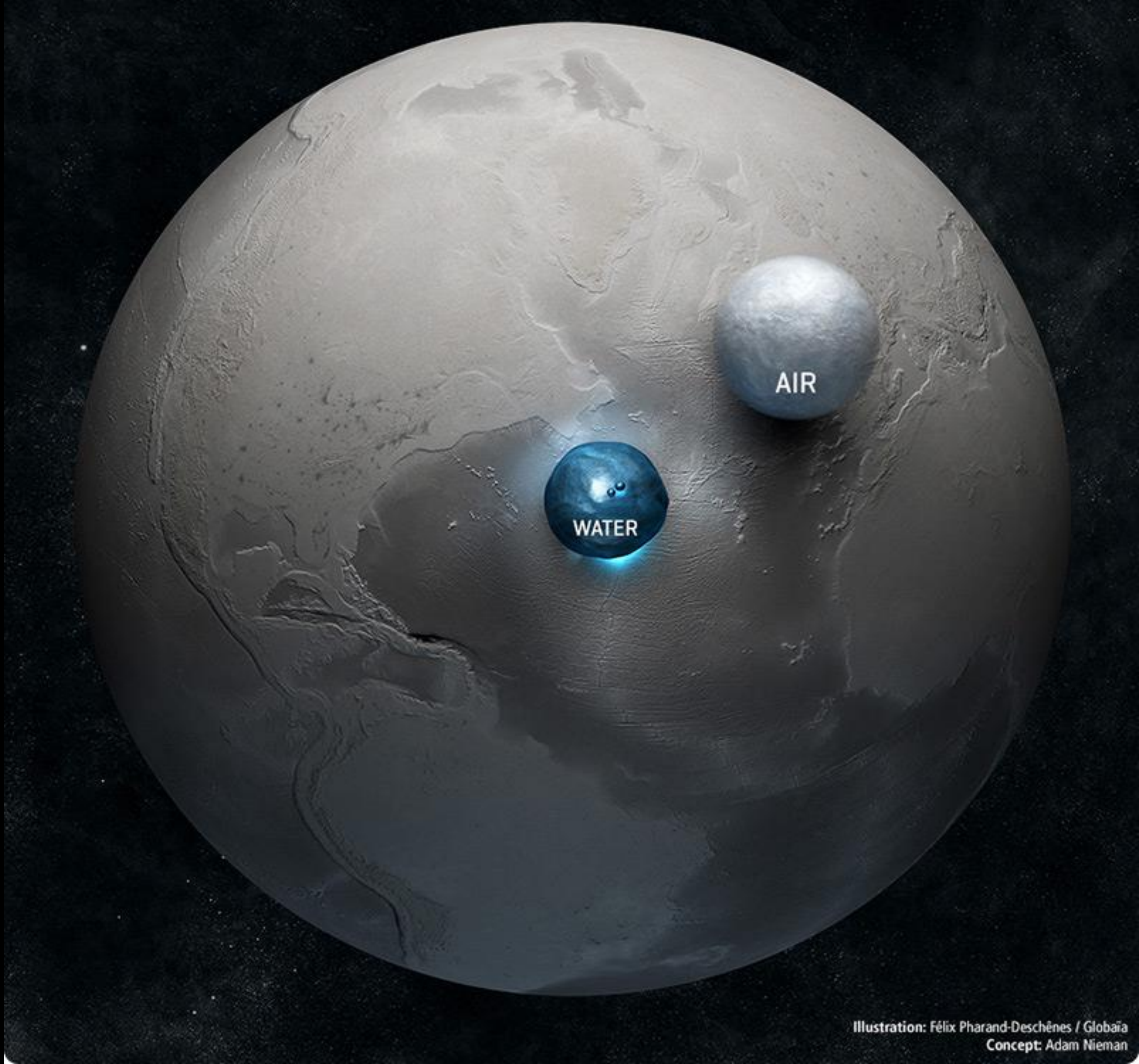
IBENS Institut de Biologie de l'Ecole Normale Supérieure
Inserm
EMBL
cnrs
cea
ENS ÉCOLE NORMALE SUPÉRIEURE
PSL RESEARCH UNIVERSITY PARIS

Although planet Earth looks mostly blue from space…



... water is relatively scarce.

Life appeared in, and is sustained by, the Ocean.



The Ocean
Our life support system

The Ocean covers 71% of our planet and is a Key player !

Ocean microbes perform 50% of photosynthesis on Earth.

The Ocean captures 25% of human CO2 emissions and 90% of the heat.

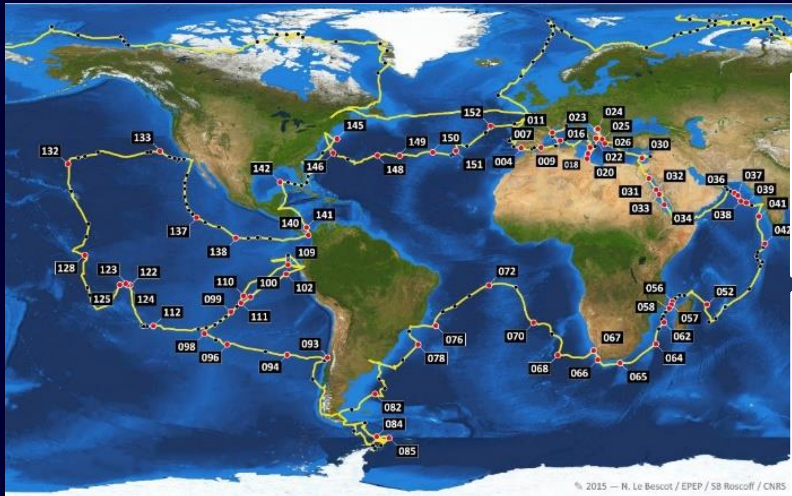
The Ocean regulates the temperature on Earth.

… and yet it is still poorly known !

TARA OCEANS

A four year expedition

- To explore marine planktonic ecosystems and their sensitivity to climate change-induced modifications to the ocean
- To popularize science
- To educate
- To improve ocean governance



Eric Karsenti

EMBL

cnrs

cea

Fondation tara océan explore and share

agnès b.

Foundation VEOLIA ENVIRONNEMENT

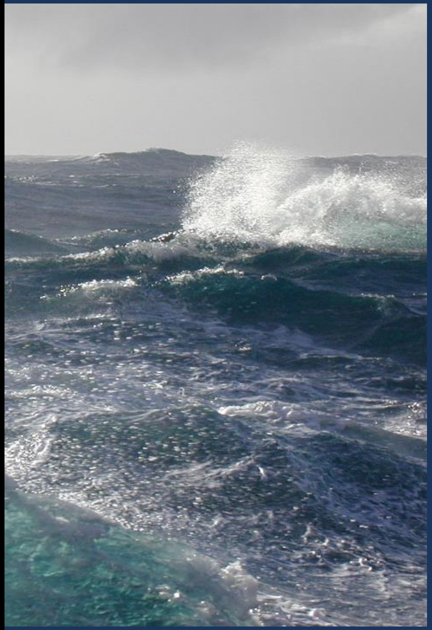
Région BRETAGNE

FONDATION PRINCE ALBERT II DE MONACO

WORLD COURIER A SERVICE NO ONE ELSE CAN DELIVER

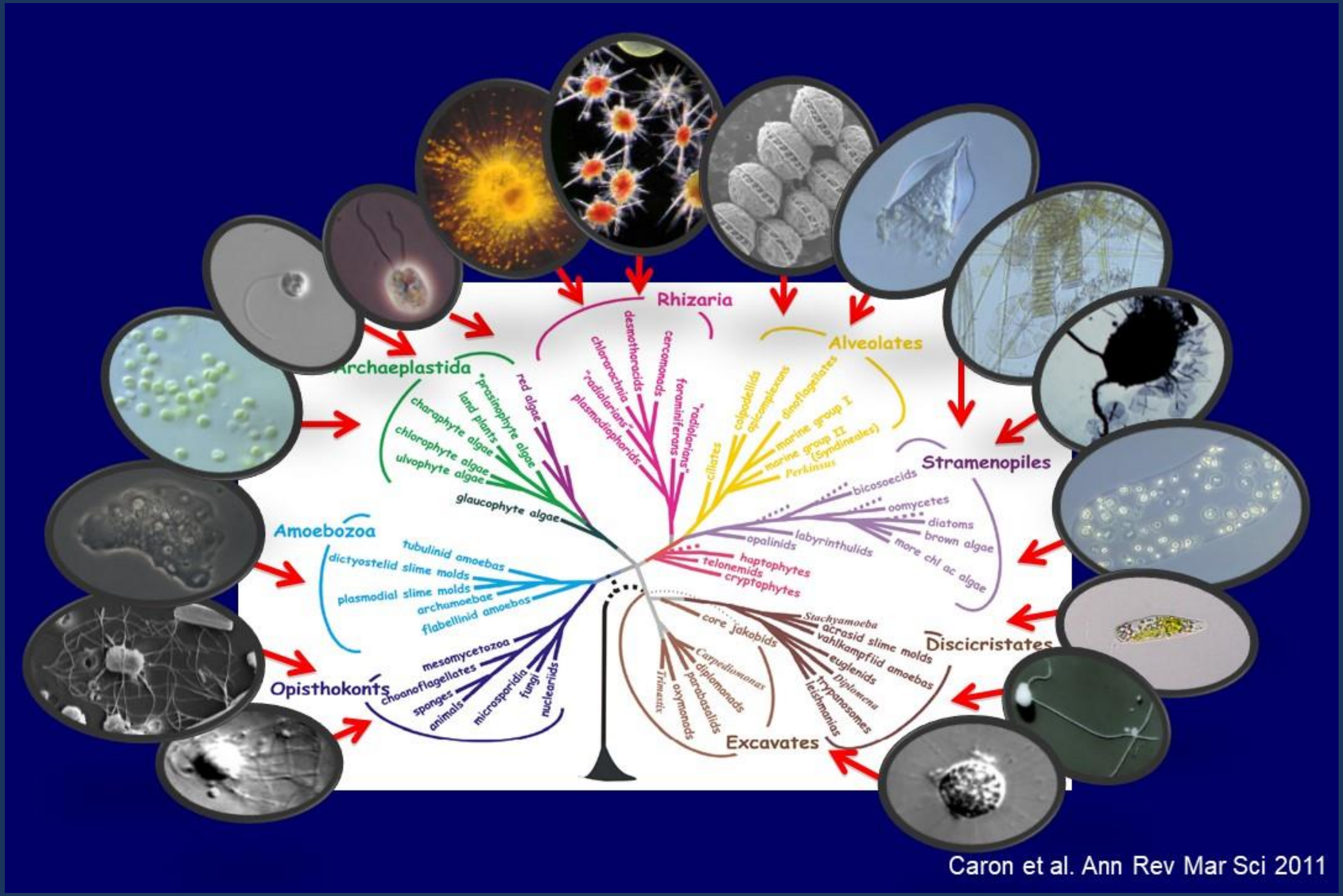
FONDATION EDF DiversiTerre

Who lives in the ocean ?



Plankton are very small

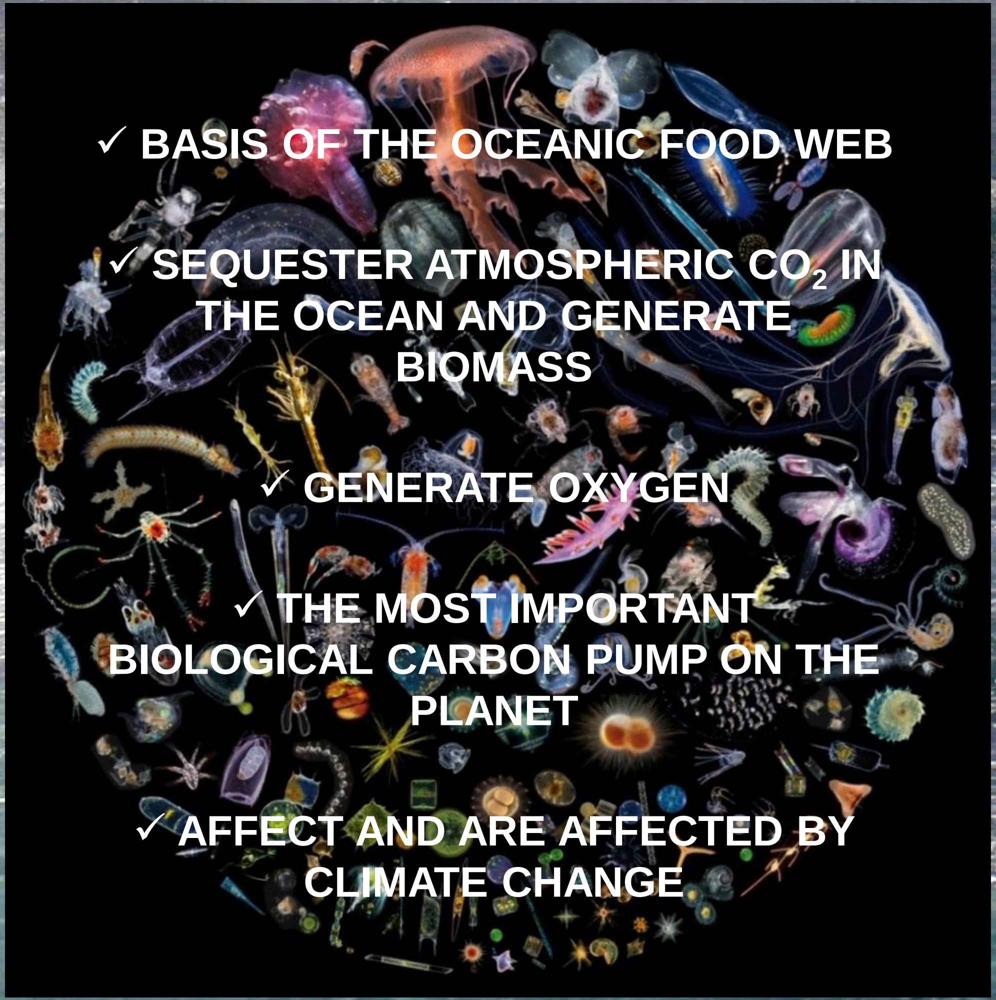
Marine micro-eukaryotes are found throughout the tree of life



TARA OCEANS

The Plankton

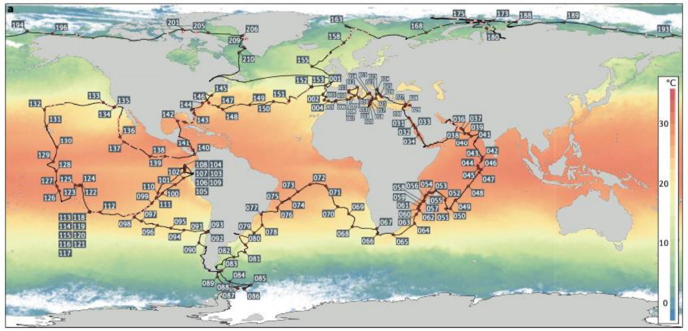
THE INVISIBLE MULTITUDE

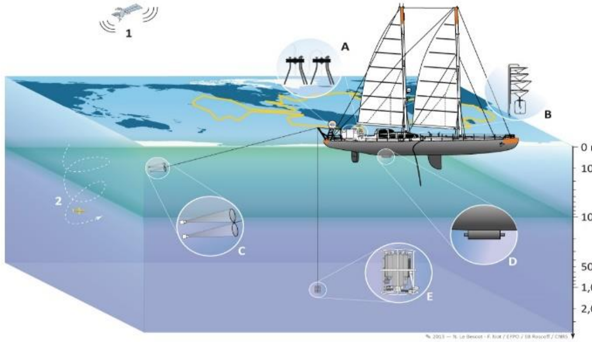


- ✓ BASIS OF THE OCEANIC FOOD WEB
- ✓ SEQUESTER ATMOSPHERIC CO_2 IN THE OCEAN AND GENERATE BIOMASS
- ✓ GENERATE OXYGEN
- ✓ THE MOST IMPORTANT BIOLOGICAL CARBON PUMP ON THE PLANET
- ✓ AFFECT AND ARE AFFECTED BY CLIMATE CHANGE

>65% of the biomass in the ocean

Tara Oceans: An eco-systems biology framework to understand a complex system at planetary scale

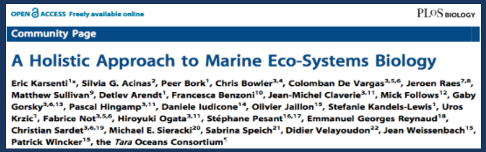




Global coverage

Standardized sampling and analysis pipelines

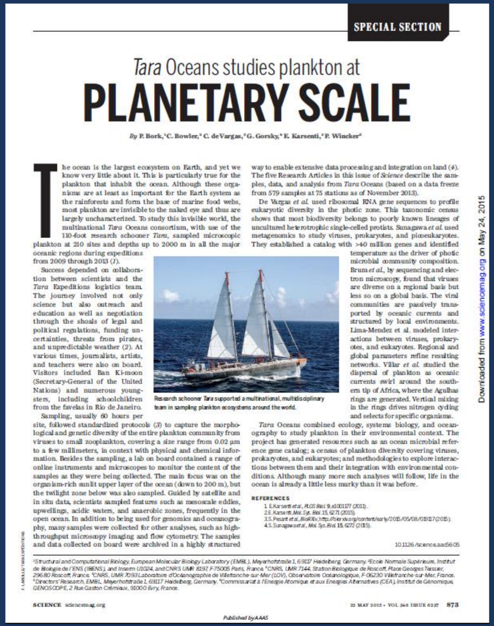
The entire community, from viruses to small animals



Who is there, what do they do, with whom, and why ?

TARA OCEANS

Science, May 22nd 2015



SPECIAL SECTION

Tara Oceans studies plankton at

PLANETARY SCALE

By P. Bork,* C. Bowler,* C. de Vargas,* G. Gorsky,* E. Karsenti,* P. Wincker*

Research schooner *Tara* supported a multinational, multidisciplinary team in sampling plankton ecosystems around the world.

Eukaryotic plankton diversity in the sunlit ocean

C. de Vargas,* S. Audic, N. Henry, J. Decelle, F. Mahé, R. Logares, E. Lara, C. Berney, N. Le Bescot, I. Probert, M. Carmichael, J. Poulain, S. Romac, S. Colin, J.-M. Aury, L. Bittner, S. Chaffron, M. Dunthorn, S. Engelen, O. Flegontova, L. Guidi, A. Horák, O. Jaillon, G. Lima-Mendez, J. Lukeš, S. Malviya, R. Morard, M. Mulot, E. Scalco, R. Siano, F. Vincent, A. Zingone, C. Dimier, M. Picheral, S. Searson, S. Kandels-Lewis, *Tara* Oceans Coordinators, S. G. Acinas, P. Bork, C. Bowler, G. Gorsky, N. Grimsley, P. Hingamp, D. Iudicone, F. Not, H. Ogata, S. Pesant, J. Raes, M. E. Sieracki, S. Speich, L. Stemmann, S. Sunagawa, J. Weissenbach, P. Wincker,* E. Karsenti*

Marine plankton support global biological and geochemical processes. Surveys of their biodiversity have hitherto been geographically restricted and have not accounted for the full range of plankton size. We assessed eukaryotic diversity from 334 size-fractionated photic-zone plankton communities collected across tropical and temperate oceans during the circumglobal *Tara* Oceans expedition. We analyzed 18S ribosomal DNA sequences across the intermediate plankton-size spectrum from the smallest unicellular eukaryotes (protists, >0.8 micrometers) to small animals of a few millimeters. Eukaryotic ribosomal diversity saturated at ~150,000 operational taxonomic units, about one-third of which could not be assigned to known eukaryotic groups. Diversity emerged at all taxonomic levels, both within the groups comprising the ~11,200 cataloged morphospecies of eukaryotic plankton and among twice as many other deep-branching lineages of unappreciated importance in plankton ecology studies. Most eukaryotic plankton biodiversity belonged to heterotrophic protistan groups, particularly those known to be parasites or symbiotic hosts.

The list of author affiliations is available in the full article online. *Corresponding author. E-mail: vargas@sb-roscoff.fr (C.d.V.); pwincker@genoscope.cns.fr (P.W.); karsenti@embl.de (E.K.) Cite as C. de Vargas et al., Science 348, 1261605 (2015).
Read the full article at http://dx.doi.org/10.1126/science.1261605

Structure and function of the global ocean microbiome

S. Sunagawa,* L. P. Coelho, S. Chaffron, J. R. Kultima, K. Labadie, G. Salazar, B. Djahanschiri, G. Zeller, D. R. Mende, A. Alberti, F. M. Cornejo-Castillo, P. I. Costea, C. Cruaud, F. d'Ovidio, S. Engelen, I. Ferrera, J. M. Gasol, L. Guidi, F. Hildebrand, F. Kokoszka, C. Lepoivre, G. Lima-Mendez, J. Poulain, B. T. Poulos, M. Royo-Llonch, H. Sarmento, S. Vieira-Silva, C. Dimier, M. Picheral, S. Searson, S. Kandels-Lewis, *Tara* Oceans Coordinators, C. Bowler, C. de Vargas, G. Gorsky, N. Grimsley, P. Hingamp, D. Iudicone, O. Jaillon, F. Not, H. Ogata, S. Pesant, S. Speich, L. Stemmann, M. B. Sullivan, J. Weissenbach, P. Wincker, E. Karsenti,* J. Raes,* S. G. Acinas,* P. Bork*

Microbes are dominant drivers of biogeochemical processes, yet drawing a global picture of functional diversity, microbial community structure, and their ecological determinants remains a grand challenge. We analyzed 7.2 terabases of metagenomic data from 243 *Tara* Oceans samples from 68 locations in epipelagic and mesopelagic waters across the globe to generate an ocean microbial reference gene catalog with >40 million nonredundant, mostly novel sequences from viruses, prokaryotes, and picoeukaryotes. Using 139 prokaryote-enriched samples, containing >35,000 species, we show vertical stratification with epipelagic community composition mostly driven by temperature rather than other environmental factors or geography. We identify ocean microbial core functionality and reveal that >73% of its abundance is shared with the human gut microbiome despite the physicochemical differences between these two ecosystems.

The list of author affiliations is available in the full article online. *Corresponding author. E-mail: sunagawa@embl.de (S.S.); karsenti@embl.de (E.K.); jeroen.raes@vib-kuleuven.be (J.R.); sacinas@icm.csic.es (S.G.A.); bork@embl.de (P.B.) Cite as S. Sunagawa et al., Science 348, 1261359 (2015).
Read the full article at http://dx.doi.org/10.1126/science.1261359

Patterns and ecological drivers of ocean viral communities

J. R. Brum, J. C. Ignacio-Espinoza, S. Roux, G. Doulcier, S. G. Acinas, A. Alberti, S. Chaffron, C. Cruaud, C. de Vargas, J. M. Gasol, G. Gorsky, A. C. Gregory, L. Guidi, P. Hingamp, D. Iudicone, F. Not, H. Ogata, S. Pesant, B. T. Poulos, S. M. Schwenck, S. Speich, C. Dimier, S. Kandels-Lewis, M. Picheral, S. Searson, *Tara* Oceans Coordinators, P. Bork, C. Bowler, S. Sunagawa, P. Wincker, E. Karsenti,* M. B. Sullivan*

Viruses influence ecosystems by modulating microbial population size, diversity, metabolic outputs, and gene flow. Here, we use quantitative double-stranded DNA (dsDNA) viral-fraction metagenomes (viromes) and whole viral community morphological data sets from 43 *Tara* Oceans expedition samples to assess viral community patterns and structure in the upper ocean. Protein cluster cataloging defined pelagic upper-ocean viral community pan and core gene sets and suggested that this sequence space is well-sampled. Analyses of viral protein clusters, populations, and morphology revealed biogeographic patterns whereby viral communities were passively transported on oceanic currents and locally structured by environmental conditions that affect host community structure. Together, these investigations establish a global ocean dsDNA viromic data set with analyses supporting the seed-bank hypothesis to explain how oceanic viral communities maintain high local diversity.

The list of author affiliations is available in the full article online. *Corresponding author. E-mail: mbsulli@gmail.com (M.B.S.); karsenti@embl.de (E.K.) Cite as Brum et al., Science 348, 1261498 (2015).
Read the full article at http://dx.doi.org/10.1126/science.1261498

Determinants of community structure in the global plankton interactome

G. Lima-Mendez, K. Faust, N. Henry, J. Decelle, S. Colin, F. Carcillo, S. Chaffron, J. C. Ignacio-Espinosa, S. Roux, F. Vincent, L. Bittner, Y. Darzi, J. Wang, S. Audic, L. Berline, G. Bontempi, A. M. Cabello, L. Coppola, F. M. Cornejo-Castillo, F. d'Ovidio, L. De Meester, I. Ferrera, M.-J. Garet-Delmas, L. Guidi, E. Lara, S. Pesant, M. Royo-Llonch, G. Salazar, P. Sánchez, M. Sebastian, C. Souffreau, C. Dimier, M. Picheral, S. Searson, S. Kandels-Lewis, *Tara* Oceans Coordinators, G. Gorsky, F. Not, H. Ogata, S. Speich, L. Stemmann, J. Weissenbach, P. Wincker, S. G. Acinas, S. Sunagawa, P. Bork, M. B. Sullivan, E. Karsenti, C. Bowler,* C. de Vargas,* J. Raes*

Species interaction networks are shaped by abiotic and biotic factors. Here, as part of the *Tara* Oceans project, we studied the photic zone interactome using environmental factors and organismal abundance profiles and found that environmental factors are incomplete predictors of community structure. We found associations across plankton functional types and phylogenetic groups to be nonrandomly distributed on the network and driven by both local and global patterns. We identified interactions among grazers, primary producers, viruses, and (mainly parasitic) symbionts and validated network-generated hypotheses using microscopy to confirm symbiotic relationships. We have thus provided a resource to support further research on ocean food webs and integrating biological components into ocean models.

The list of author affiliations is available in the full article online. *Corresponding author. E-mail: jeroen.raes@vib-kuleuven.be (J.R.); vargas@sb-roscoff.fr (C.d.V.); cbowler@biologie.ens.fr (C.B.); karsenti@embl.de (E.K.) Cite as G. Lima-Mendez et al., Science 348, 1262073 (2015).
Read the full article at http://dx.doi.org/10.1126/science.1262073

Plankton diversity

Tara Oceans sampled the smallest in the planktonic world, including viruses, bacteria, protists, and zooplankton. These spectacular and plentiful organisms form the microscopic basis of marine food webs. Analysis of their genes and genomes provides the basis for research insights into identities and interactions.

Environmental characteristics of Agulhas rings affect interocean plankton transport

E. Villar,* G. K. Farrant, M. Follows, L. Garczarek, S. Speich, S. Audic, L. Bittner, B. Blanke, J. R. Brum, C. Brunet, R. Casotti, A. Chase, J. R. Dolan, F. d'Ortenzio, J.-P. Gattuso, N. Grima, L. Guidi, C. N. Hill, O. Jahn, J.-L. Jamet, H. Le Goff, C. Lepoivre, S. Malviya, E. Pelletier, J.-B. Romagnan, S. Roux, S. Santini, E. Scalco, S. M. Schwenck, A. Tanaka, P. Testor, T. Vannier, F. Vincent, A. Zingone, C. Dimier, M. Picheral, S. Searson, S. Kandels-Lewis, *Tara* Oceans Coordinators, S. G. Acinas, P. Bork, E. Boss, C. de Vargas, G. Gorsky, H. Ogata, S. Pesant, M. B. Sullivan, S. Sunagawa, P. Wincker, E. Karsenti,* C. Bowler,* F. Not,* P. Hingamp,* D. Iudicone*

Agulhas rings provide the principal route for ocean waters to circulate from the Indo-Pacific to the Atlantic basin. Their influence on global ocean circulation is well known, but their role in plankton transport is largely unexplored. We show that, although the coarse taxonomic structure of plankton communities is continuous across the Agulhas choke point, South Atlantic plankton diversity is altered compared with Indian Ocean source populations. Modeling and in situ sampling of a young Agulhas ring indicate that strong vertical mixing drives complex nitrogen cycling, shaping community metabolism and biogeochemical signatures as the ring and associated plankton transit westward. The peculiar local environment inside Agulhas rings may provide a selective mechanism contributing to the limited dispersal of Indian Ocean plankton populations into the Atlantic.

The list of author affiliations is available in the full article online. *Corresponding author. E-mail: villar@igs.cnrs-mrs.fr (E.V.); not@sb-roscoff.fr (F.N.); hingamp@igs.cnrs-mrs.fr (P.H.); iudicone@szn.it (D.I.); karsenti@embl.de (E.K.); cbowler@biologie.ens.fr (C.B.) Cite as E. Villar et al., Science 348, 1261447 (2015).
Read the full article at http://dx.doi.org/10.1126/science.1261447

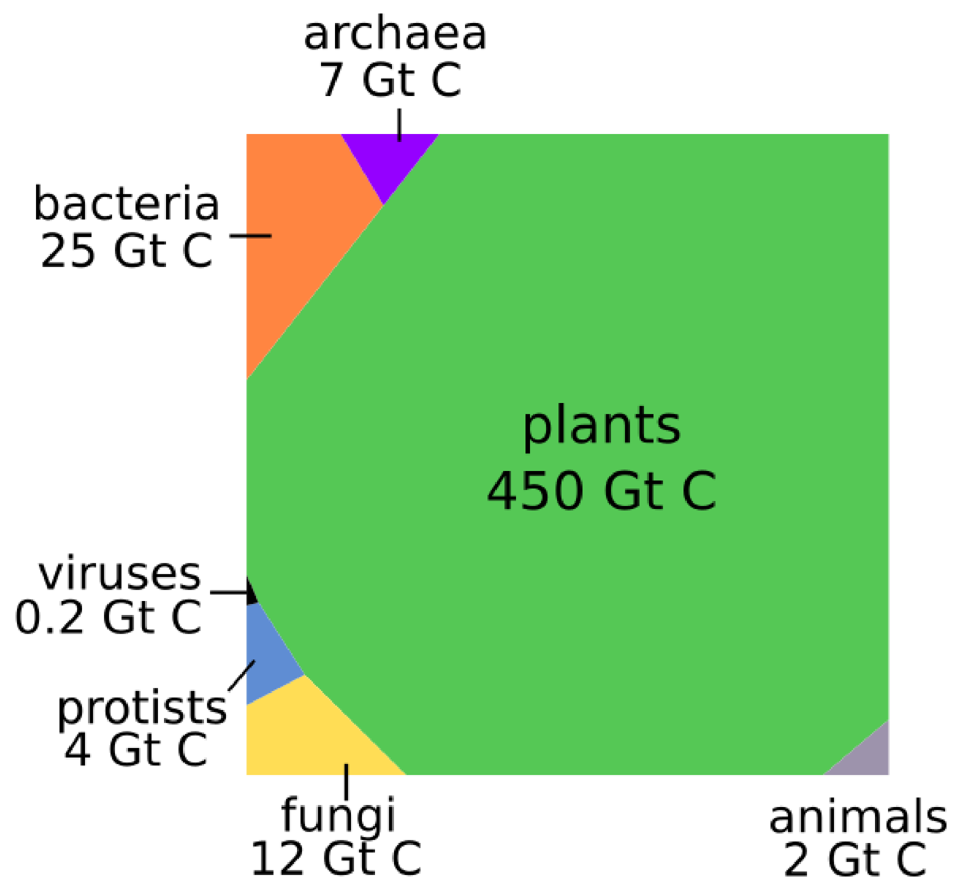
TARA OCEANS

Some very basic questions

- ☑ Which plankton group is the most abundant ?
- ☑ Which plankton group is the most diverse ?

TARA OCEANS

Biomass and number of species in terrestrial ecosystems



PNAS **The biomass distribution on Earth**

Yinon M. Bar-On[a], Rob Phillips[b,c], and Ron Milo[a,1]

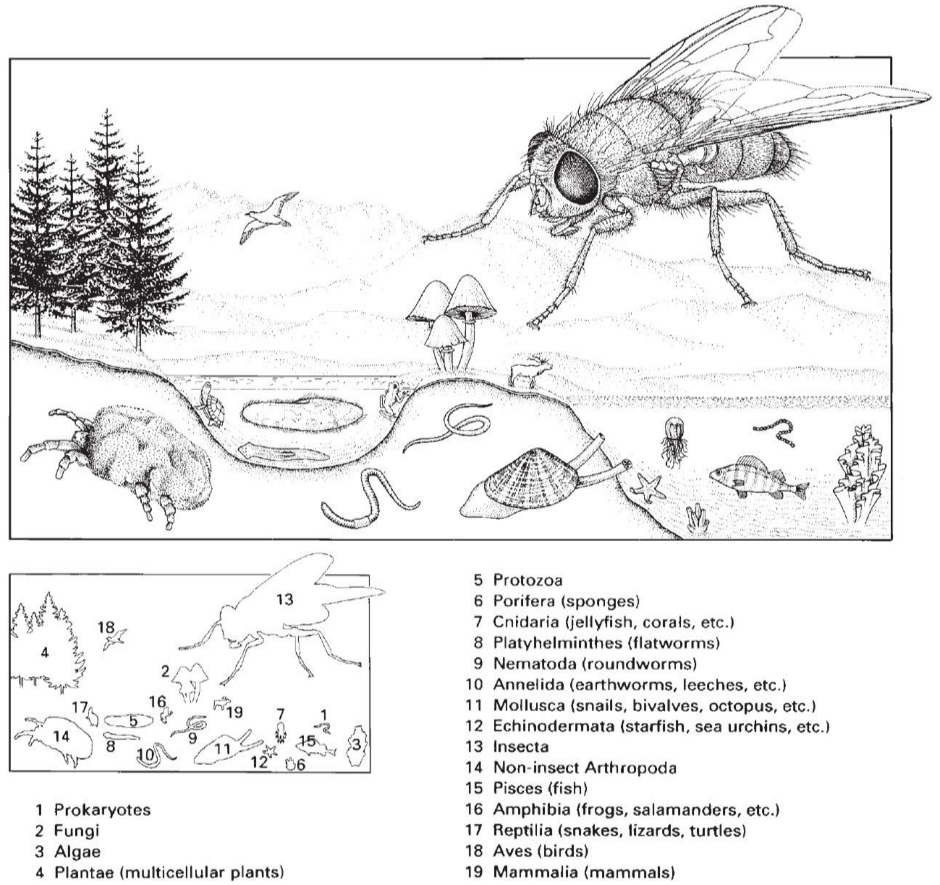
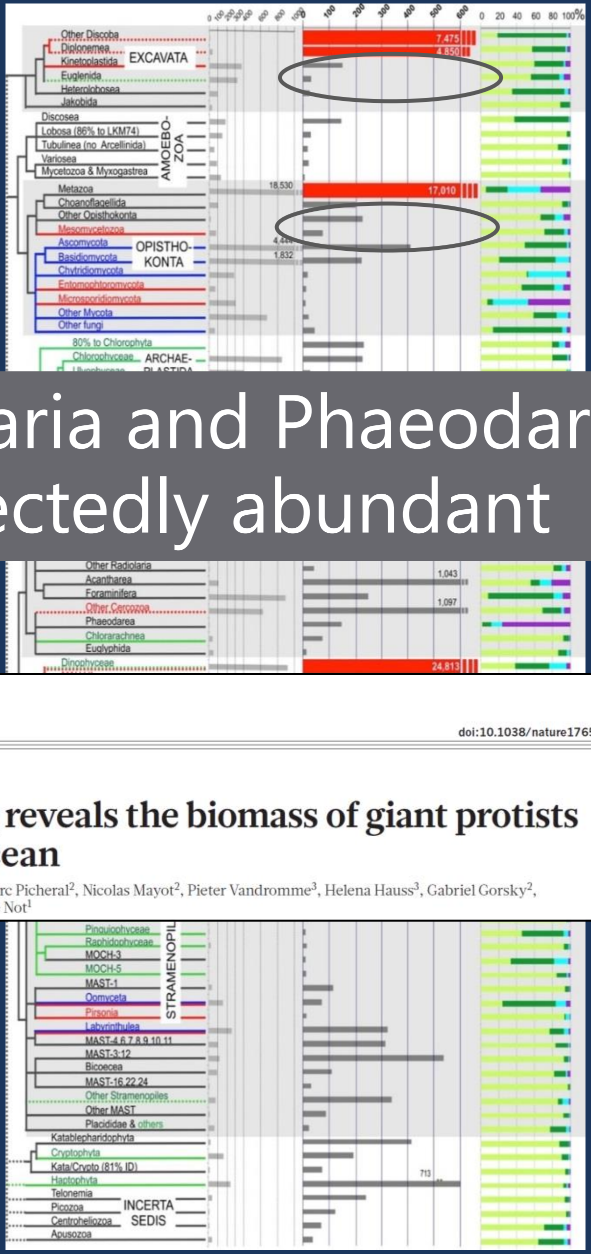


Fig. 1.1 Speciescape, in which the size of individual organisms is approximately proportional to the number of described species in the higher taxon that it represents. (After Wheeler 1990.)

The Insects: An Outline of Entomology, P. J. Gullan, 5th edition, 2014

TARA OCEANS

A new world of marine protists



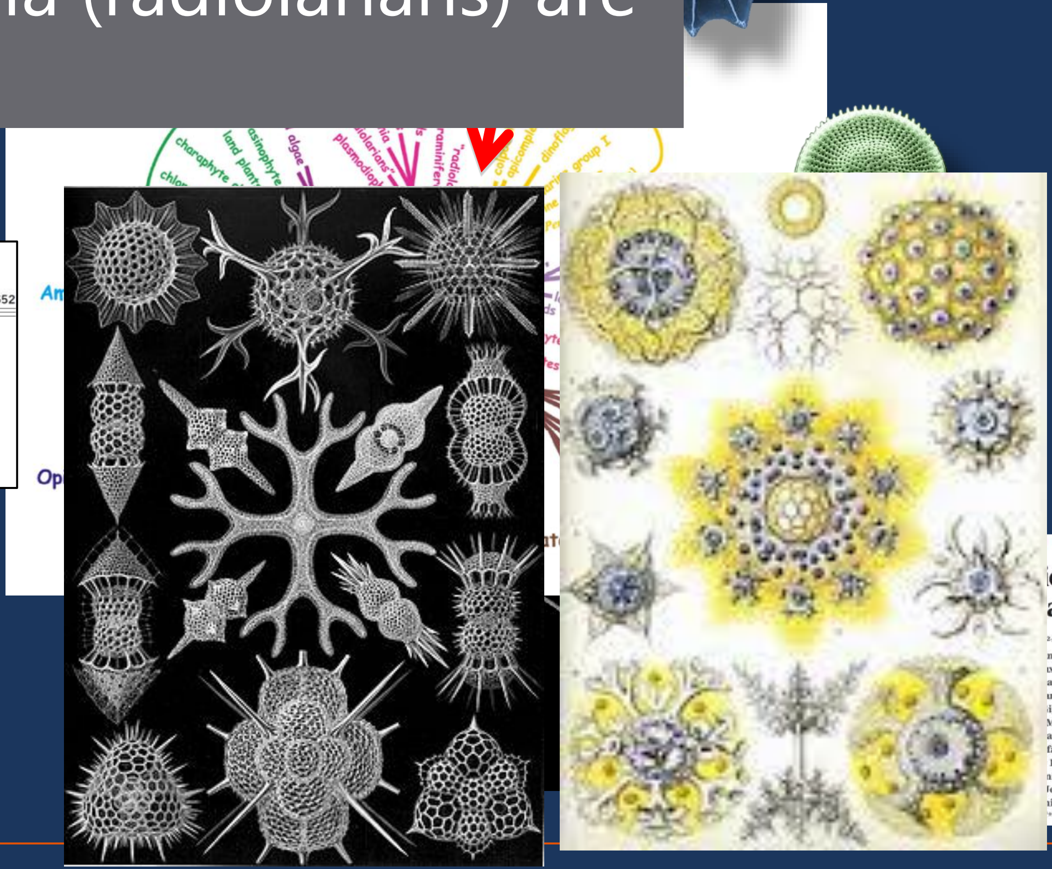
Collodaria and Phaeodaria (radiolarians) are unexpectedly abundant

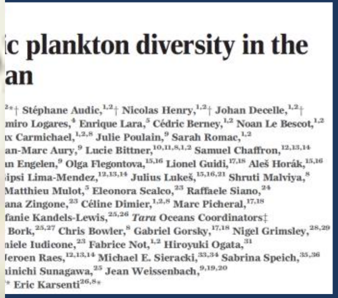
LETTER

doi:10.1038/nature17652

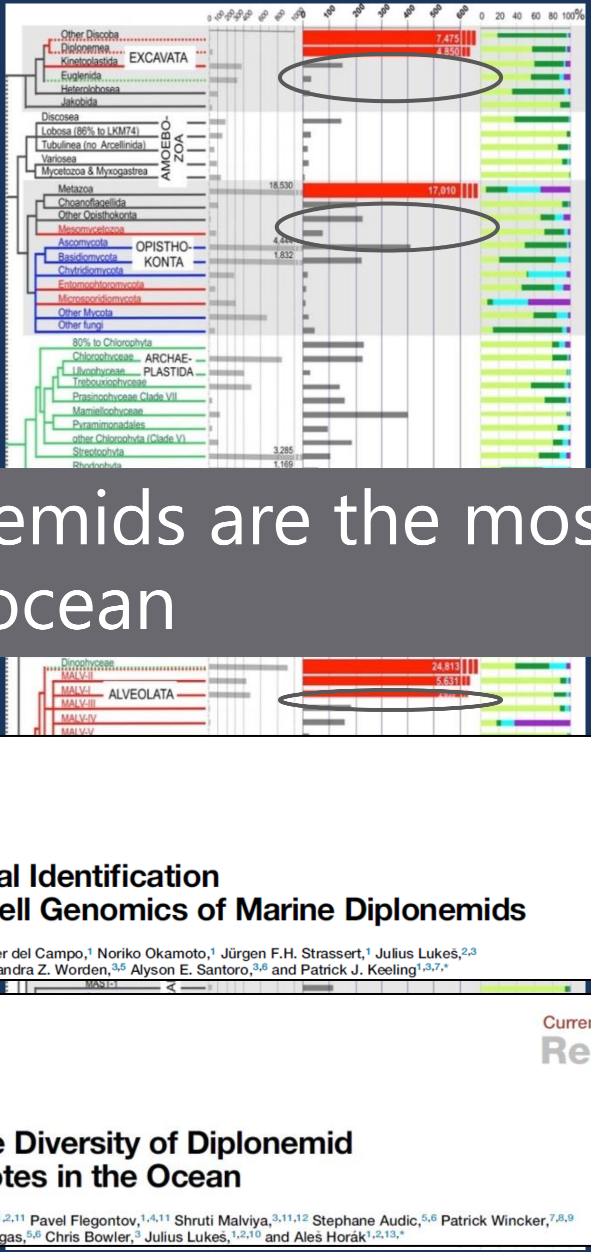
In situ imaging reveals the biomass of giant protists in the global ocean

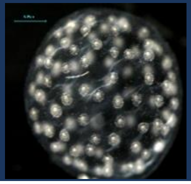
Tristan Biard[1,2], Lars Stemmann[2], Marc Picheral[2], Nicolas Mayot[2], Pieter Vandromme[3], Helena Hauss[3], Gabriel Gorsky[2], Lionel Guidi[2], Rainer Kiko[3] & Fabrice Not[1]

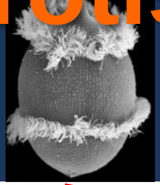


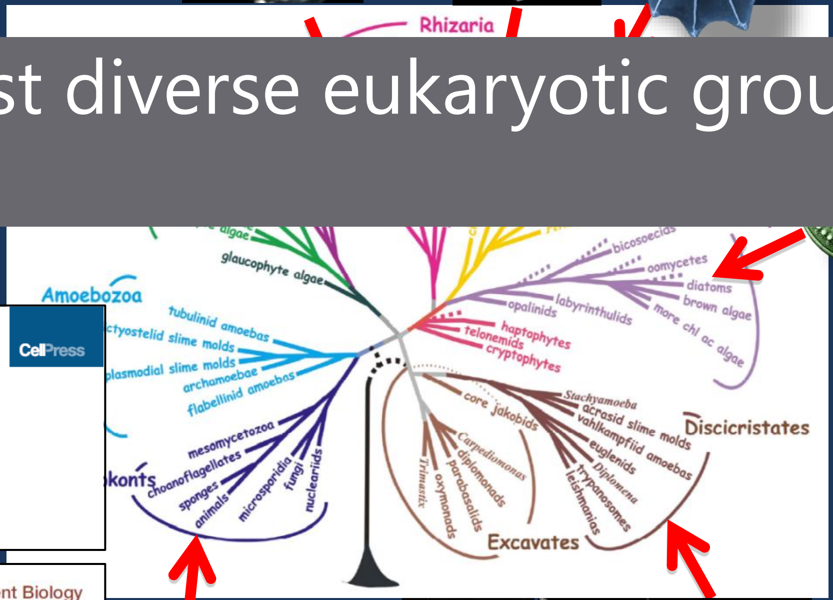


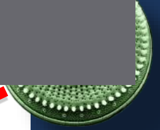
A new world of marine protists











Diplonemids are the most diverse eukaryotic group in the ocean

Current Biology
Report
CellPress

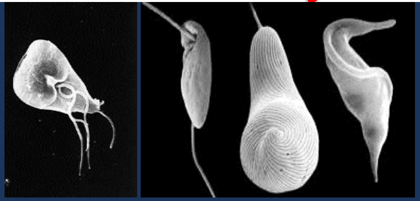
Morphological Identification and Single-Cell Genomics of Marine Diplonemids

Ryan M.R. Gawryluk,[1,*] Javier del Campo,[1] Noriko Okamoto,[1] Jürgen F.H. Strassert,[1] Julius Lukeš,[2,3] Thomas A. Richards,[3,4] Alexandra Z. Worden,[3,5] Alyson E. Santoro,[3,6] and Patrick J. Keeling[1,3,7,*]

CellPress
Current Biology
Report

Extreme Diversity of Diplonemid Eukaryotes in the Ocean

Olga Flegontova,[1,2,11] Pavel Flegontov,[1,4,11] Shruti Malviya,[3,11,12] Stephane Audic,[5,6] Patrick Wincker,[7,8,9] Colomban de Vargas,[5,6] Chris Bowler,[3] Julius Lukeš,[1,2,10] and Aleš Horák[1,2,13,*]



OCEAN PLANKTON

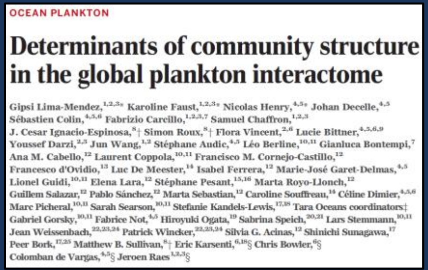
Eukaryotic plankton diversity in the sunlit ocean

Colomban de Vargas, Stéphane Audic, Nicolas Henry, Johan Decelle, Frédéric Mahé, Ramiro Logares, Enrique Lara, Cédric Berney, Noan Le Bescot, Ian Probert, Margaux Carmichael, Julie Poulain, Sarah Romac, Sébastien Colin, Jean-Marc Aury, Lucie Bittner, Samuel Chaffron, Micah Dunthorn, Stefan Engelen, Olga Flegontova, Lionel Guidi, Aleš Horák, Olivier Jaillon, Gipsi Lima-Mendez, Julius Lukeš, Shruti Malviya, Raphael Morard, Matthieu Mulot, Eleonora Scalco, Raffaele Siano, Flora Vincent, Adriana Zingone, Céline Dimier, Marc Picheral, Sarah Searson, Stefanie Kandels-Lewis, *Tara* Oceans Coordinators, Silvia G. Acinas, Peer Bork, Chris Bowler, Gabriel Gorsky, Nigel Grimsley, Pascal Hingamp, Daniele Iudicone, Fabrice Not, Hiroyuki Ogata, Stephane Pesant, Jeroen Raes, Michael E. Sieracki, Sabrina Speich, Lars Stemmann, Shinichi Sunagawa, Jean Weissenbach, Patrick Wincker, Eric Karsenti

TARA OCEANS

Defining the plankton interactome in the global ocean

a.k.a The Ocean's facebook



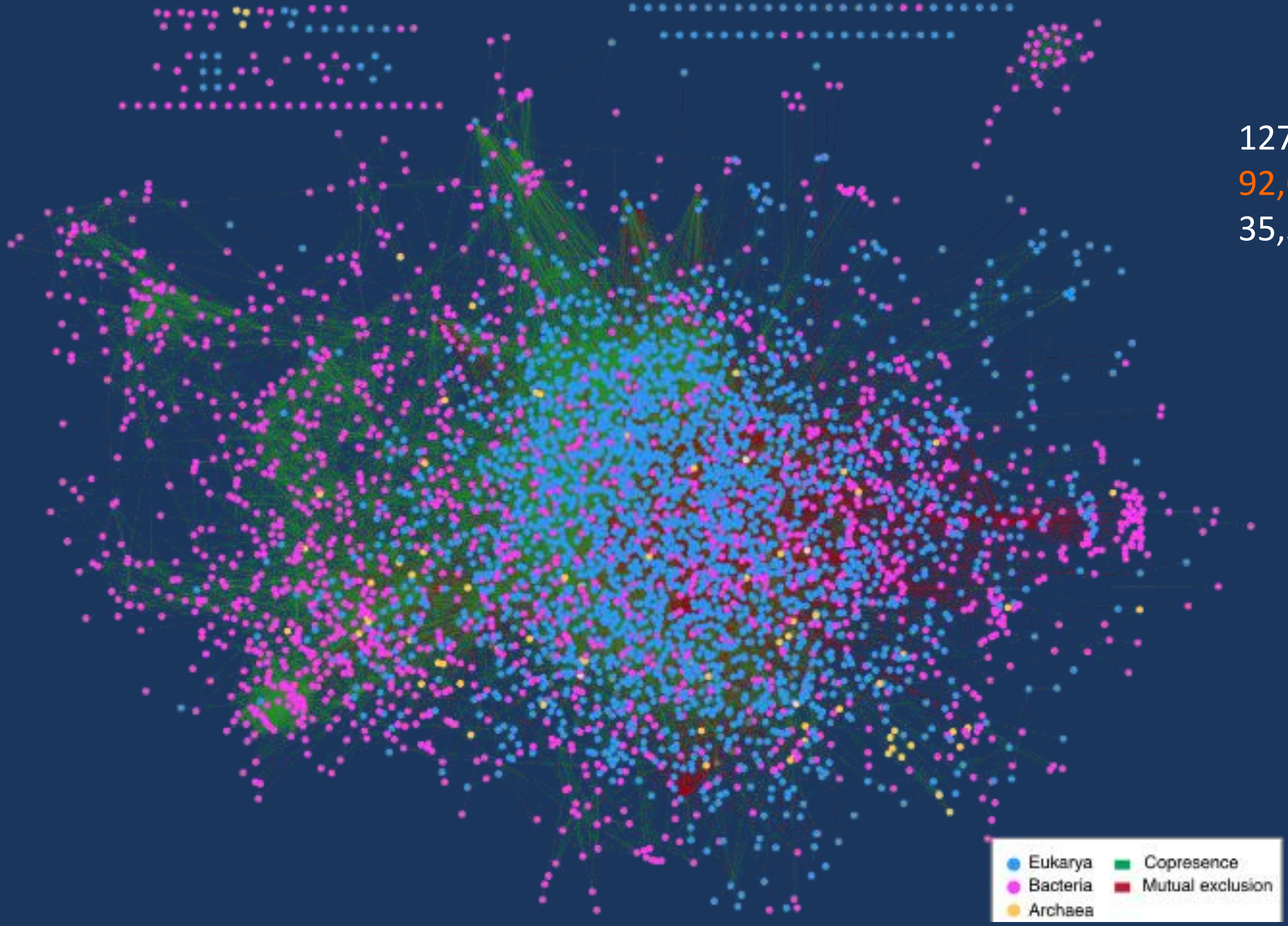
OCEAN PLANKTON

Determinants of community structure in the global plankton interactome

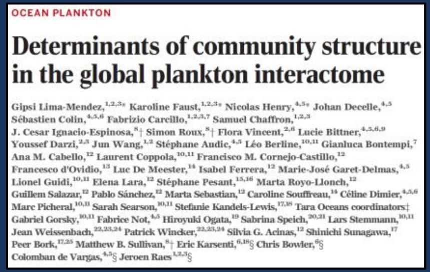
Gipsi Lima-Mendez,[1,2,3]* Karoline Faust,[1,2,3]* Nicolas Henry,[4,5]* Johan Decelle,[4,5] Sébastien Colin,[4,5,6] Fabrizio Carcillo,[1,2,3,7] Samuel Chaffron,[1,2,3] J. Cesar Ignacio-Espinosa,[8]† Simon Roux,[8]† Flora Vincent,[2,6] Lucie Bittner,[4,5,6,9] Youssef Darzi,[2,3] Jun Wang,[1,2] Stéphane Audic,[4,5] Léo Berline,[10,11] Gianluca Bontempi,[7] Ana M. Cabello,[12] Laurent Coppola,[10,11] Francisco M. Cornejo-Castillo,[12] Francesco d'Ovidio,[13] Luc De Meester,[14] Isabel Ferrera,[12] Marie-José Garet-Delmas,[4,5] Lionel Guidi,[10,11] Elena Lara,[12] Stéphane Pesant,[15,16] Marta Royo-Llonch,[12] Guillem Salazar,[12] Pablo Sánchez,[12] Marta Sebastian,[12] Caroline Souffreau,[14] Céline Dimier,[4,5,6] Marc Picheral,[10,11] Sarah Searson,[10,11] Stefanie Kandels-Lewis,[17,18] Tara Oceans coordinators‡ Gabriel Gorsky,[10,11] Fabrice Not,[4,5] Hiroyuki Ogata,[19] Sabrina Speich,[20,21] Lars Stemmann,[10,11] Jean Weissenbach,[22,23,24] Patrick Wincker,[22,23,24] Silvia G. Acinas,[12] Shinichi Sunagawa,[17] Peer Bork,[17,25] Matthew B. Sullivan,[8]† Eric Karsenti,[6,18]§ Chris Bowler,[6]§ Colomban de Vargas,[4,5]§ Jeroen Raes[1,2,3]§

TARA OCEANS

The global plankton interactome – an integrated "network of networks"



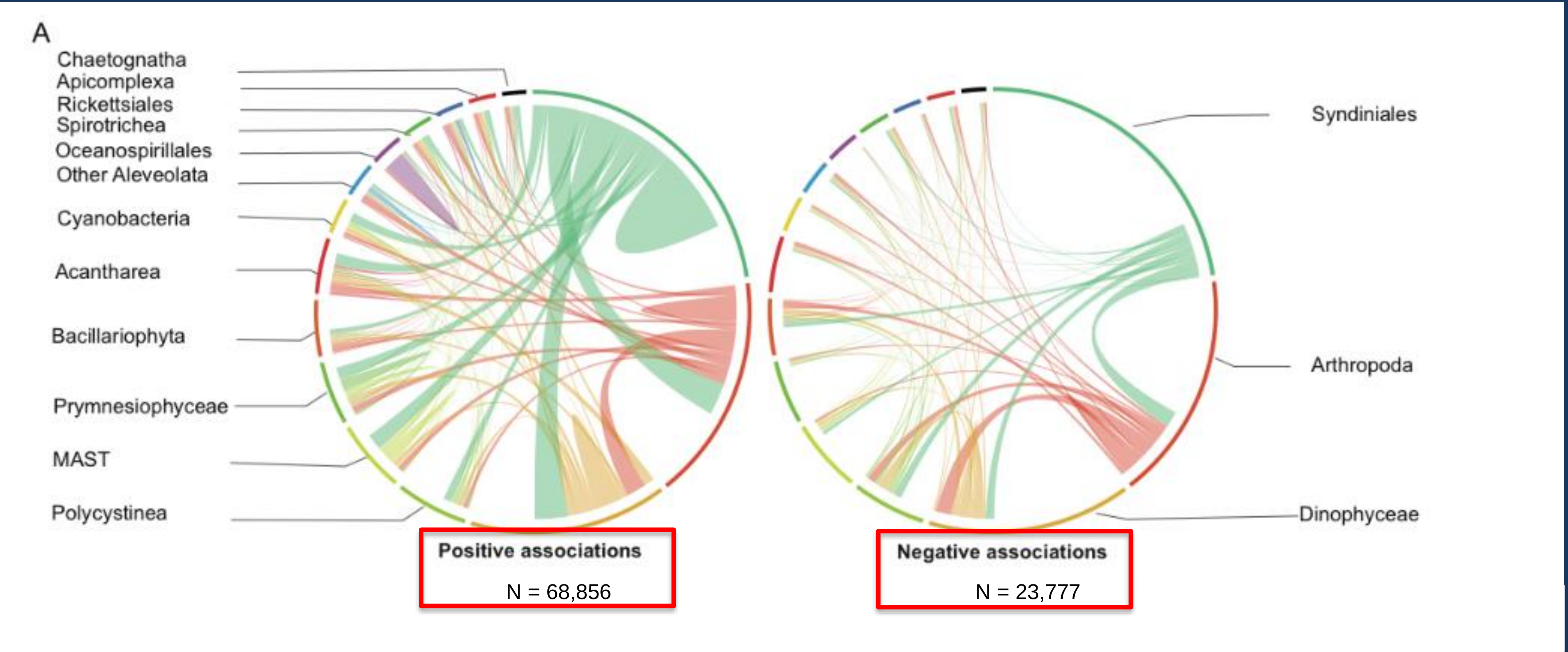
127,995 associations
92,633 taxon-taxon
35,362 taxon-env


OCEAN PLANKTON

Determinants of community structure in the global plankton interactome

Gipsi Lima-Mendez,[1,2,3*] Karoline Faust,[1,2,3*] Nicolas Henry,[4,5*] Johan Decelle,[4,5] Sébastien Colin,[4,5,6] Fabrizio Carcillo,[1,2,3,7] Samuel Chaffron,[1,2,3] J. Cesar Ignacio-Espinosa,[8]† Simon Roux,[8]† Flora Vincent,[2,6] Lucie Bittner,[4,5,6,9] Youssef Darzi,[2,3] Jun Wang,[1,2] Stéphane Audic,[4,5] Léo Berline,[10,11] Gianluca Bontempi,[7] Ana M. Cabello,[12] Laurent Coppola,[10,11] Francisco M. Cornejo-Castillo,[12] Francesco d'Ovidio,[13] Luc De Meester,[14] Isabel Ferrera,[12] Marie-José Garet-Delmas,[4,5] Lionel Guidi,[10,11] Elena Lara,[12] Stéphane Pesant,[15,16] Marta Royo-Llonch,[12] Guillem Salazar,[12] Pablo Sánchez,[12] Marta Sebastian,[12] Caroline Souffreau,[14] Céline Dimier,[4,5,6] Marc Picheral,[10,11] Sarah Searson,[10,11] Stefanie Kandels-Lewis,[17,18] Tara Oceans coordinators‡ Gabriel Gorsky,[10,11] Fabrice Not,[4,5] Hiroyuki Ogata,[19] Sabrina Speich,[20,21] Lars Stemmann,[10,11] Jean Weissenbach,[22,23,24] Patrick Wincker,[22,23,24] Silvia G. Acinas,[12] Shinichi Sunagawa,[17] Peer Bork,[17,25] Matthew B. Sullivan,[8]† Eric Karsenti,[6,18]§ Chris Bowler,[6]§ Colomban de Vargas,[4,5]§ Jeroen Raes[1,2,3]§

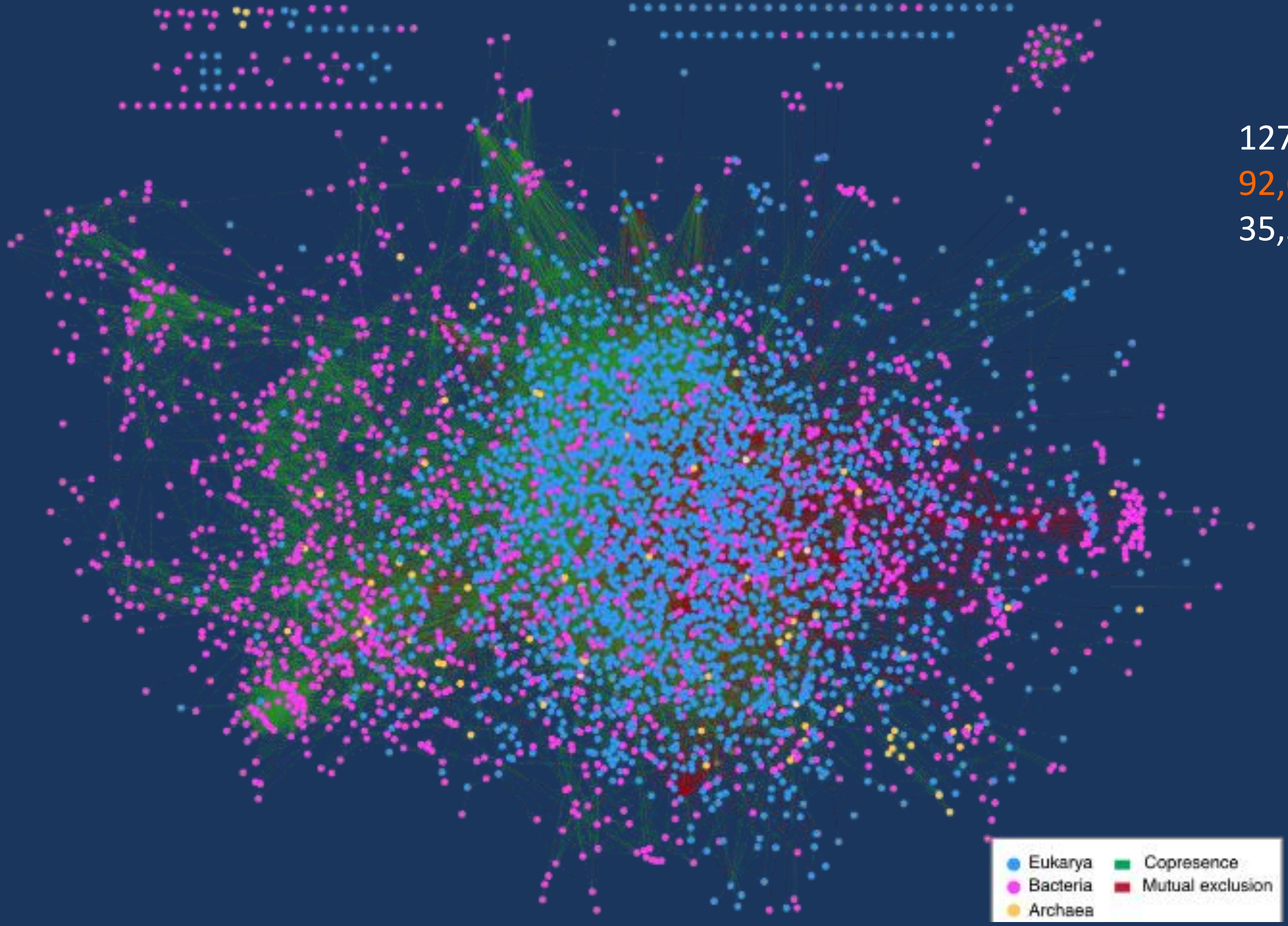
Most interactions are positive …



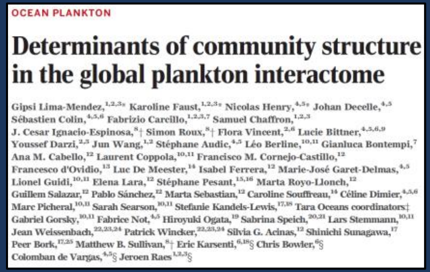
Cooperation is more important than competition

Lima-Mendez et al. Science (2015)

The global plankton interactome – a playground to discover new interactions



127,995 associations
92,633 taxon-taxon
35,362 taxon-env


OCEAN PLANKTON

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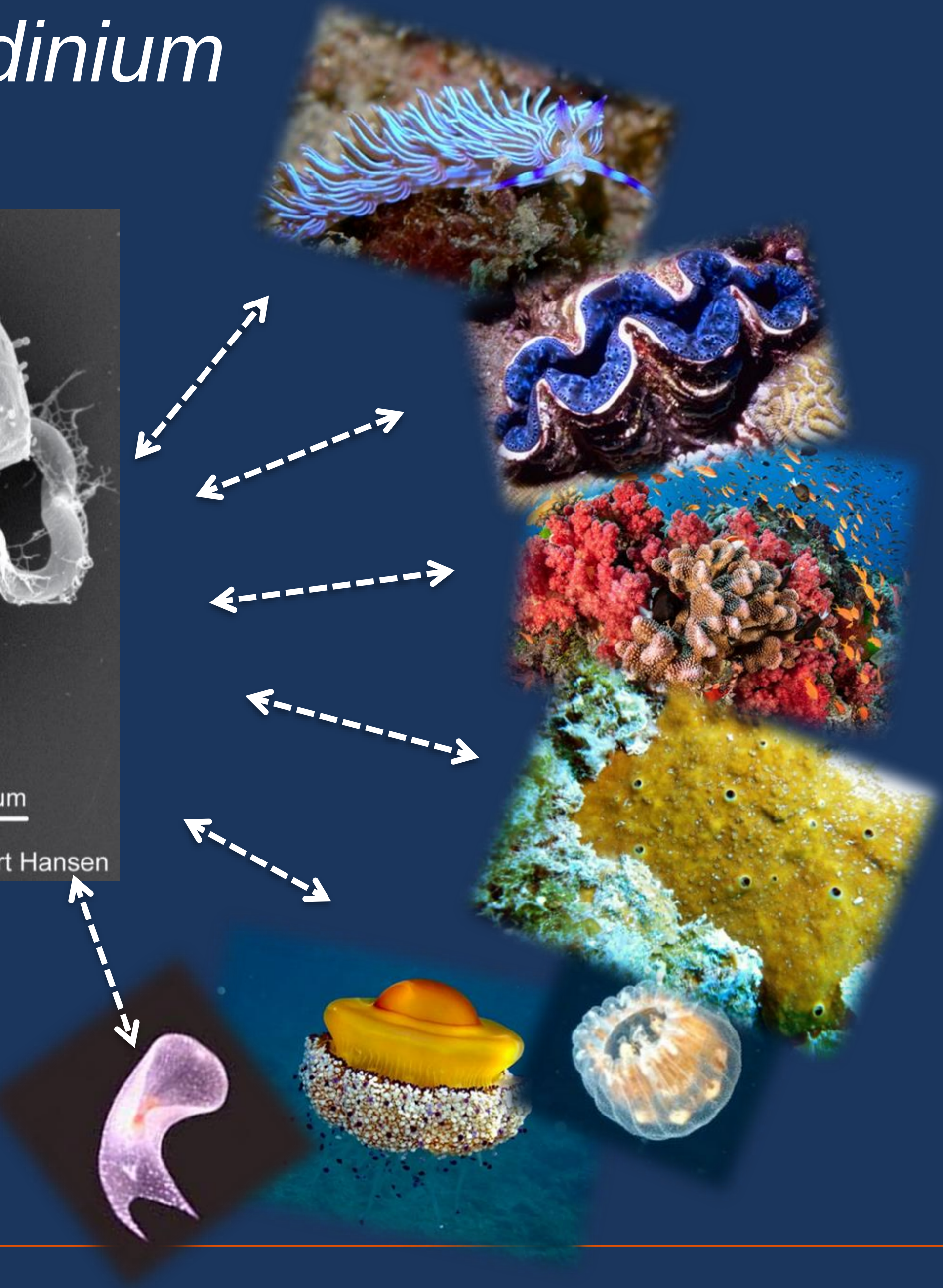
TARA OCEANS

The super symbiont *Symbiodinium*



➔ Do we find *Symbiodinium* in symbiosis with plankton ?

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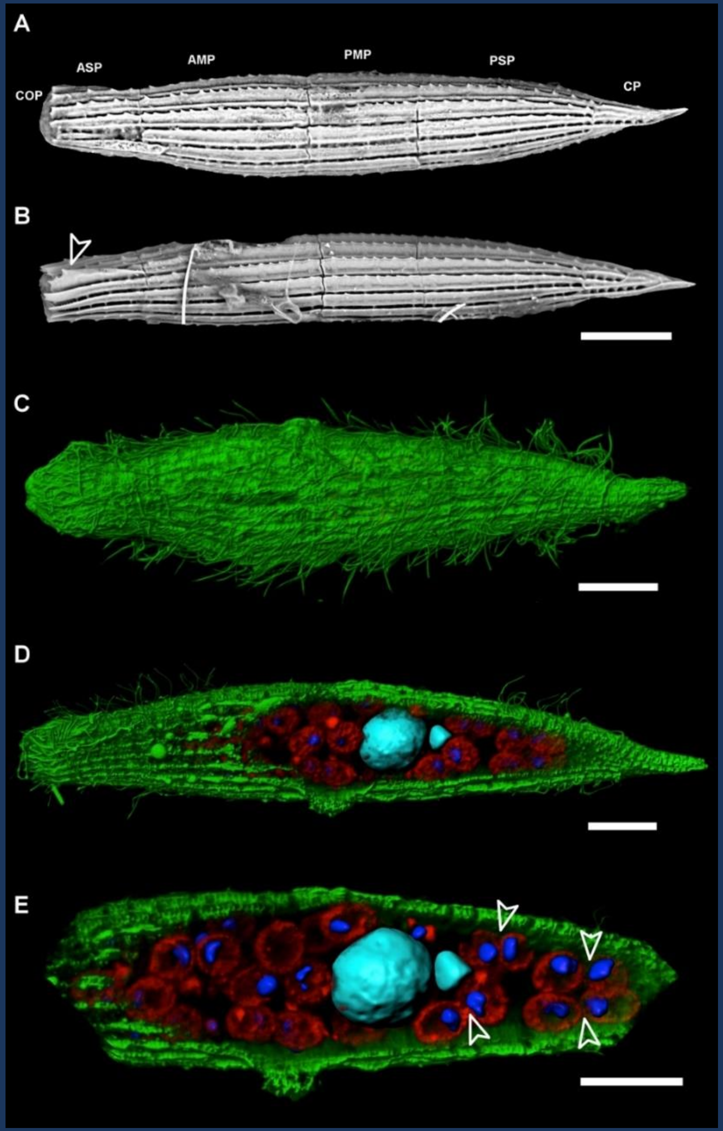
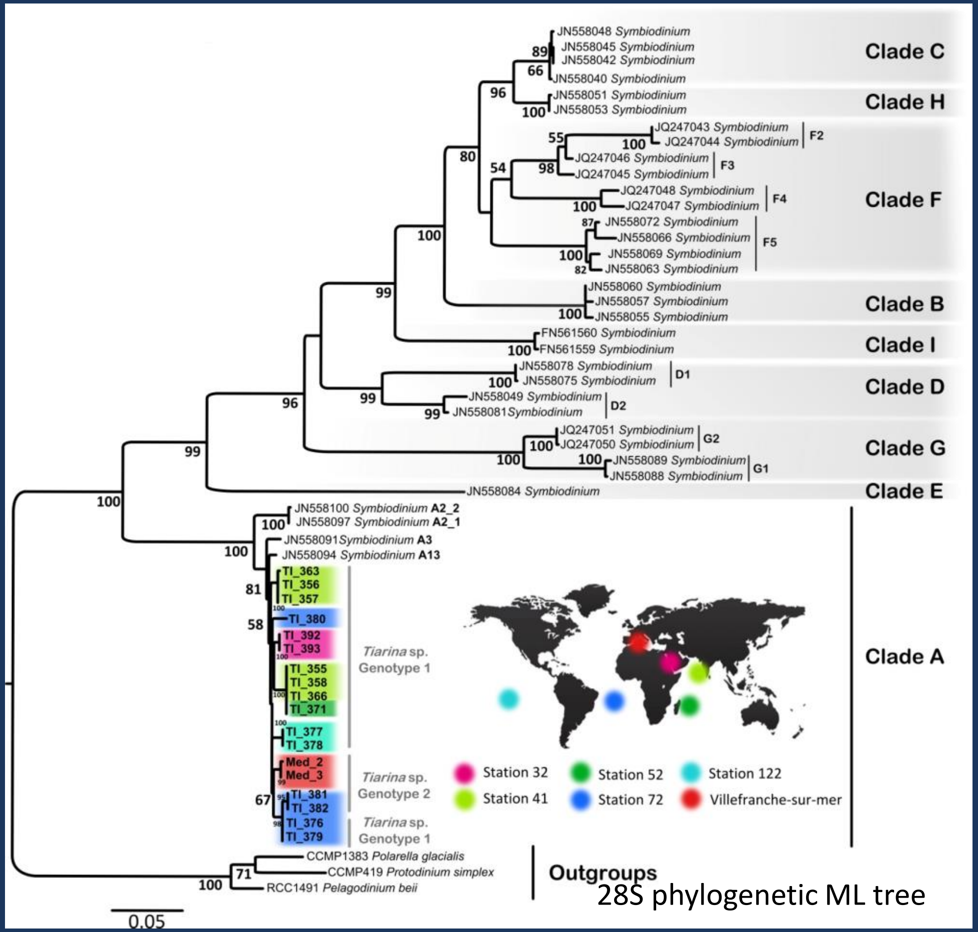
Symbiodinium in symbiosis with a planktonic ciliate

…widely distributed in the ocean





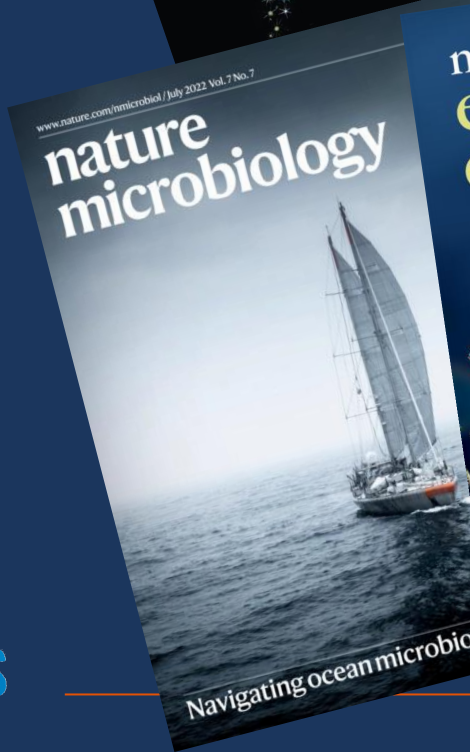
28S phylogenetic ML tree

The ISME Journal (2015), 1–13
www.nature.com/ismej

ORIGINAL ARTICLE

The symbiotic life of *Symbiodinium* in the open ocean within a new species of calcifying ciliate (*Tiarina* sp.)

Solenn Mordret[1,2,5], Sarah Romac[1,2], Nicolas Henry[1,2], Sébastien Colin[1,2], Margaux Carmichael[1,2], Cédric Berney[1,2], Stéphane Audic[1,2], Daniel J Richter[1,2], Xavier Pochon[3,4], Colomban de Vargas[1,2] and Johan Decelle[1,2,6]



The international journal of science / 8 June 2023

nature

The *Tara*'s inspiring 20 years at sea

A research ship's voyages to understand marine biodiversity show how visionary thinking can boost understanding of the natural world – and help to better preserve it.

FRANÇOIS AURAT/TARA OCEAN FOUNDATION

The *Tara* during its 100,000-kilometre voyage around the Pacific Ocean.

Scientists have known for decades that the biodiversity we know is a fraction of the biodiversity that exists. Even when it comes to perhaps the simplest measure, the number of species, researchers estimate that there could be anywhere between 3 million and 100 million species, of which some 1.7 million have been described. Every year, the names of some 10,000 new ones get added to the list.

Gathering good biodiversity data can be a mission in itself, especially on marine biodiversity. One dependable source is a schooner called *Tara*, which celebrates 20 years at sea as a research ship this year. *Tara* has been to the Arctic Ocean and the Mediterranean Sea. Last week, researchers reported the results of its latest voyage, Tara Pacific, a two-year expedition across the Pacific Ocean, published in a collection of articles in Springer Nature journals (go.nature.com/45puzhk).

Coral reefs are among Earth's most diverse ecosystems, supporting 25% of marine life and providing services such as food, jobs and coastal protection to nearly one billion people worldwide. One region of the Pacific, the Coral Triangle – which includes the waters of Indonesia, Malaysia and the Philippines – has around 75% of the world's coral species. But these nurseries for marine life are under threat: globally, around 50% of living corals have been lost since the 1950s (T. D. Eddy *et al. One Earth* **4**, 1278–1285; 2021). Moreover, climate change poses a large risk to their continued survival.

One of Tara Pacific's research groups has been focusing on genetic diversity – in particular, that of microbial communities (bacteria and archaea) living in Pacific Ocean corals. The scientists, led by marine microbiologist Pierre Galand at the Banyuls Oceanological Observatory in Banyuls-sur-Mer, France, collected more than 5,000 samples, and focused on analysing the 16S ribosomal DNA marker gene, which is used to identify and classify microorganisms. They found around half a million distinct DNA sequences known as amplicon sequence variants (ASVs), which can be used as a measure of the genetic diversity in a sample (*Nature* https://doi.org/kddz; 2023). From these data, the researchers estimated that the microbial diversity of coral reefs globally is probably around 2.8 million ASVs (P. E. Galand *et al. Nature Commun.* **14**, 3039; 2023). For comparison, this is close to the lower end of one genetic-diversity estimate of all of Earth's bacterial and archaeal communities – a proposed range of 2.72 million and 5.44 million ASVs (S. Louca *et al. PLoS Biol.* **17**, e3000106; 2019). Galand and his colleagues' work, which builds on smaller-scale studies of coral reefs (M. Chiarello *et al. Proc. R. Soc. B* **287**, 20200642; 2020), confirms that Earth's microbial genetic diversity is much higher and richer than previously thought.

> **"The research has a stirring and unusual back story."**

The research ship has a stirring and unusual back story. Its original captain was Peter Blake, a much-decorated professional yachtsman from New Zealand. After retirement, Blake became an environmental envoy to the United Nations but was killed by pirates at the mouth of the Amazon River while on an expedition in 2001. Agnès Troublé, a French fashion designer known as Agnès B, and her son Etienne Bourgois acquired the boat, determined to continue Blake's original vision. They established the Tara Ocean Foundation and invited scientists and research funders to join them on various missions.

The logistics of converting a schooner into a floating laboratory and taking it on a 100,000-kilometre journey cannot be underestimated, especially considering the present complicated relations between Pacific nations. And then there's the logistics of the research itself: organizing 3,000 dives; sending samples for PCR analysis en route; keeping the voyage on track.

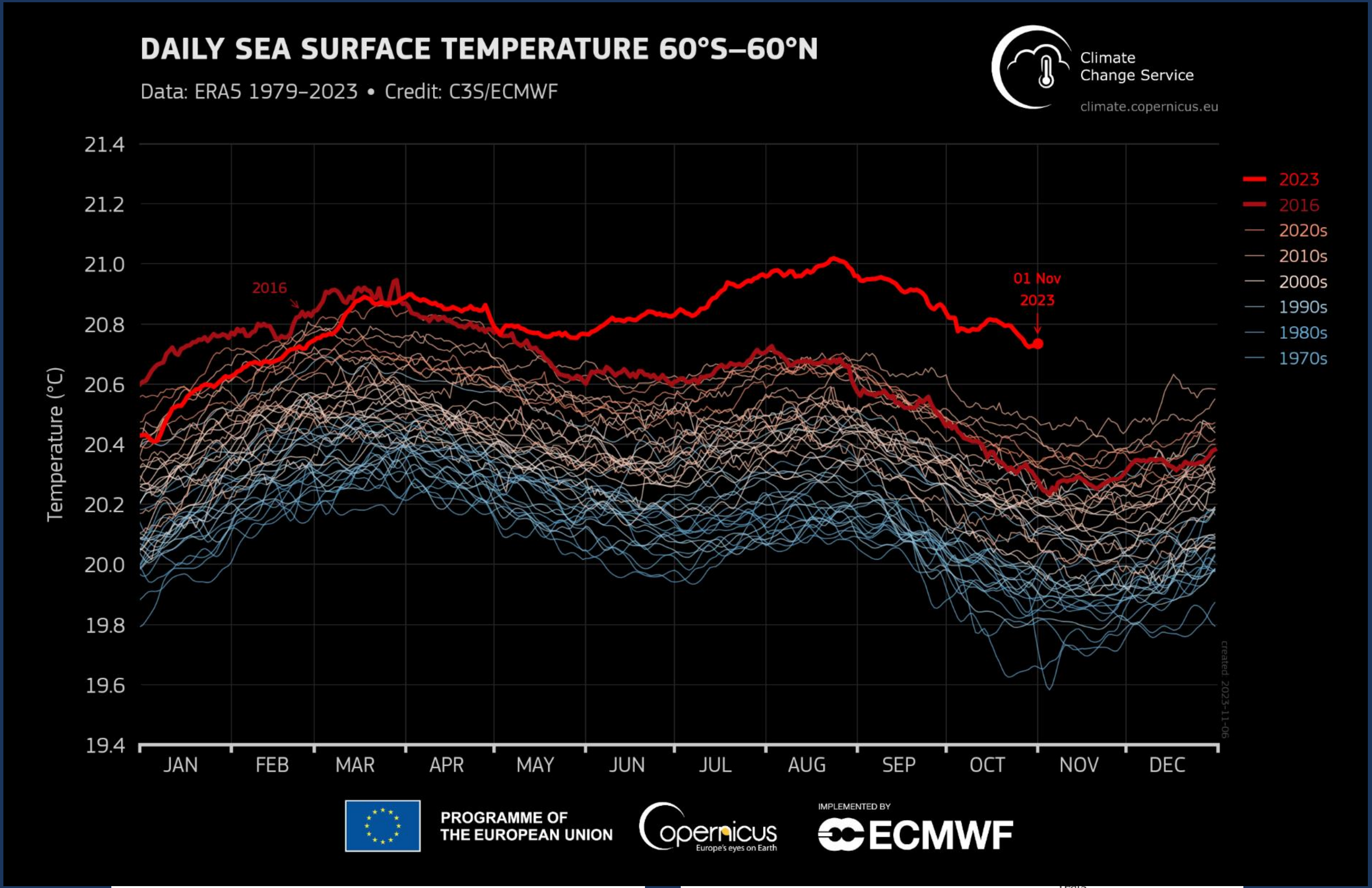
Researchers must continue to build on the work being reported and refine our understanding of the importance of diversity for safeguarding ecosystem stability and function. The project is a great example of visionary thinkers such as Troublé and Bourgois working closely with funders and scientists to help us to understand the breathtaking diversity of the world around us before it is too late. When it comes to preserving the natural systems we all depend on, more such collaborations are needed.

TARA OCEANS

Tara Oceans and climate change

Homo sapiens – the superpower

Consequences of human



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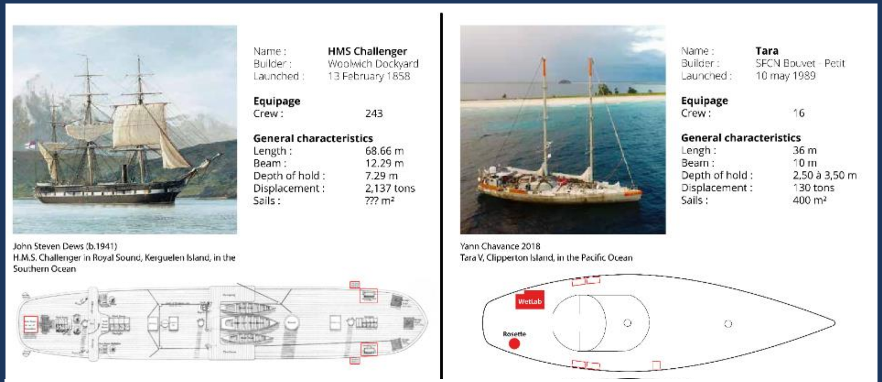
Tara Oceans and climate change

- ✔ Digging into the past - Evidence for effects of ocean acidification

Evidence of the effects of ocean acidification on marine ecosystems ?

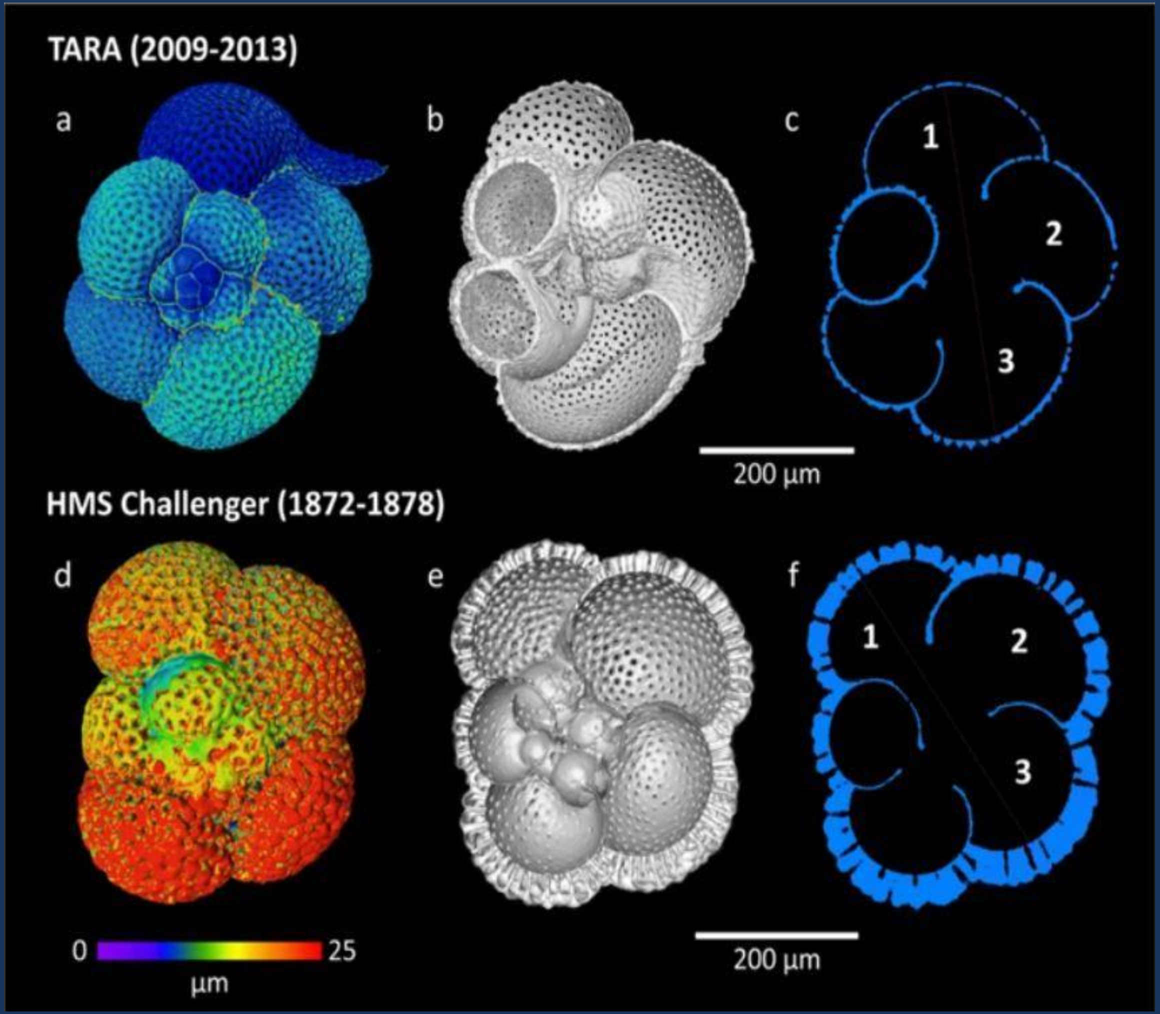


Foraminifera calcification has decreased in the last 150 years

SCIENTIFIC REPORTS
natureresearch

Quantifying the Effect of Anthropogenic Climate Change on Calcifying Plankton

Lyndsey Fox[1,2*], Stephen Stukins[1], Thomas Hill[1] & C. Giles Miller[1]



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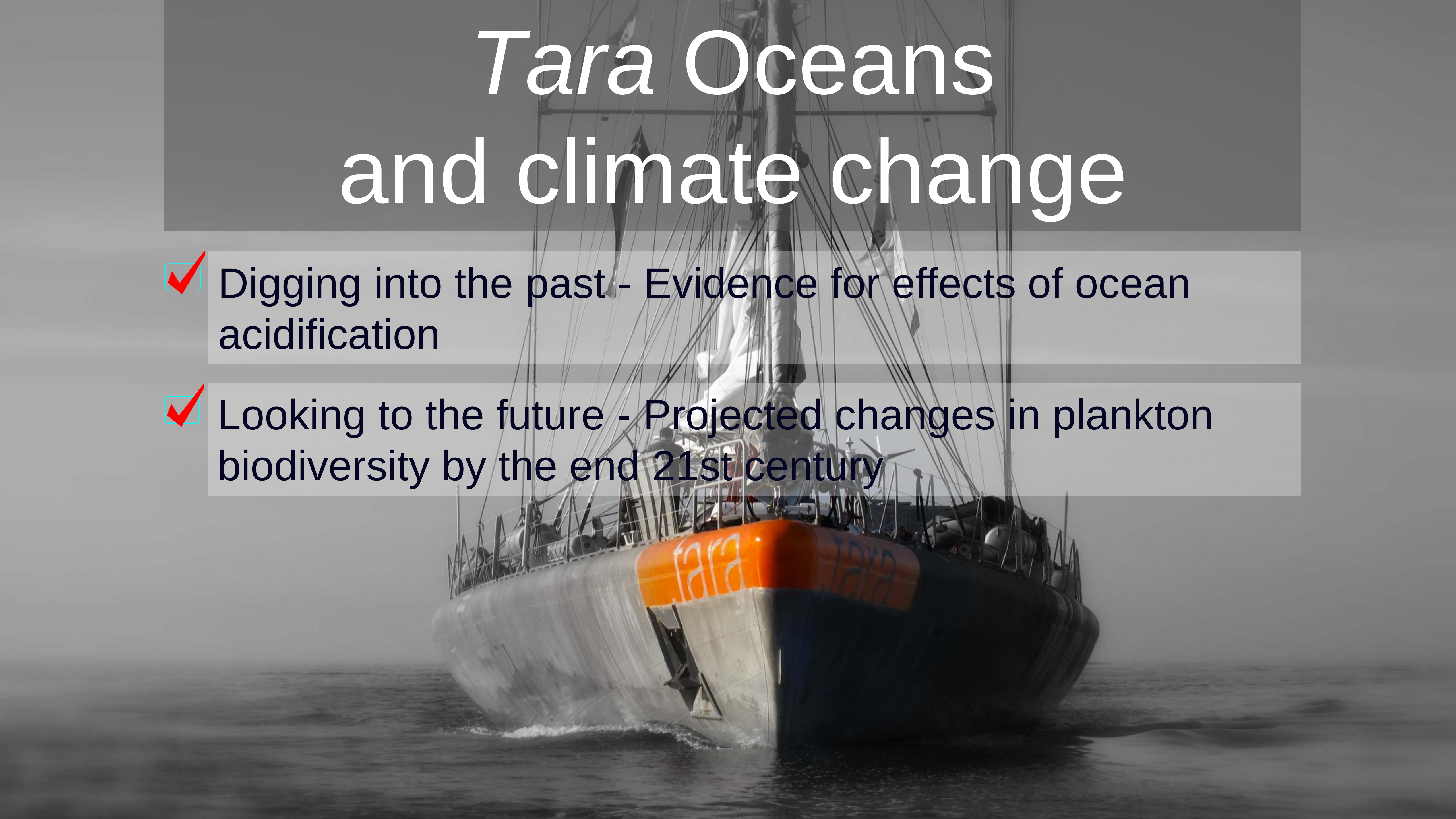
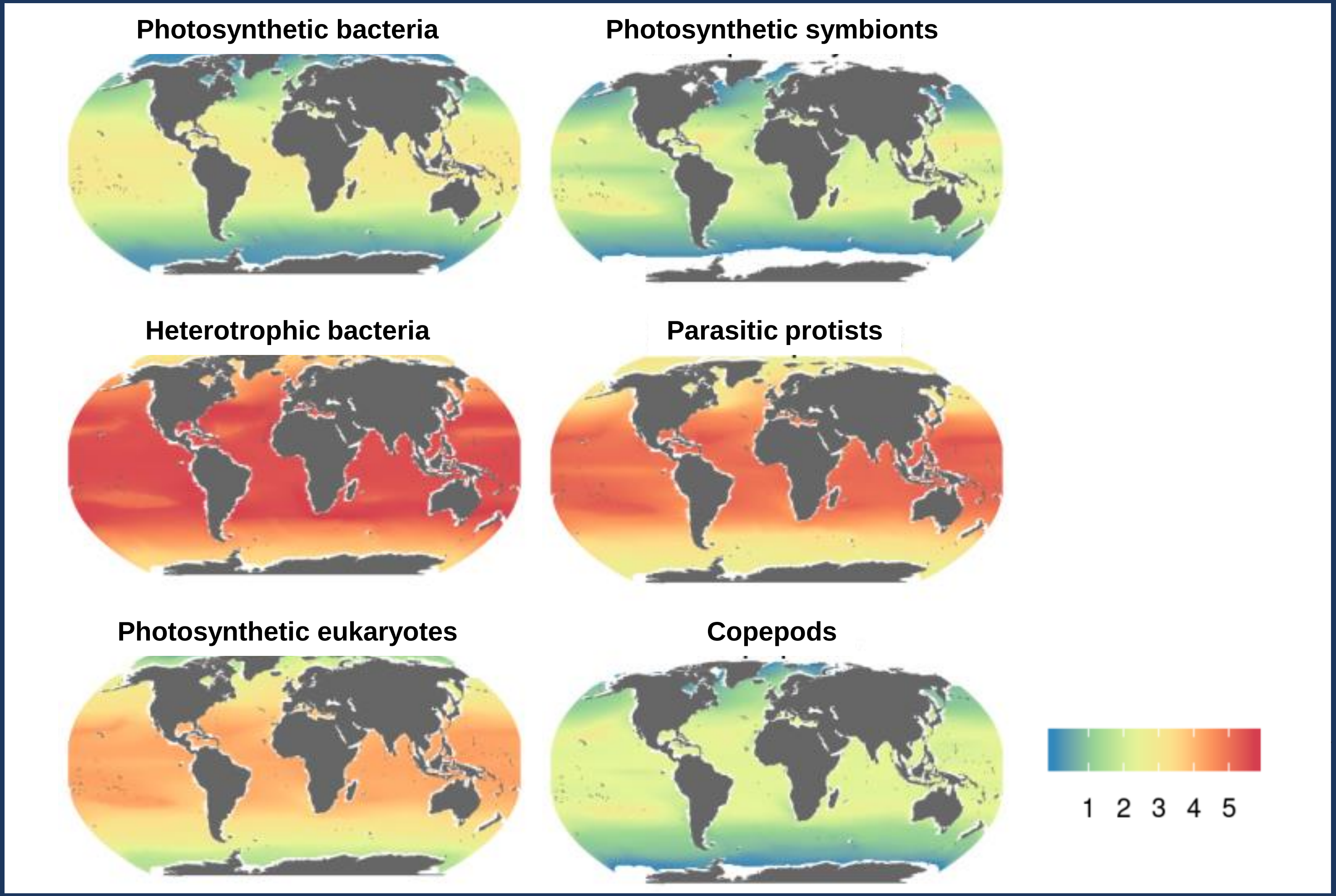
Tara Oceans and climate change

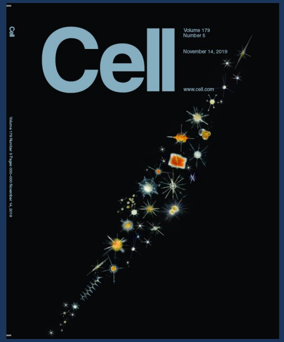
- ✓ Digging into the past - Evidence for effects of ocean acidification
- ✓ Looking to the future - Projected changes in plankton biodiversity by the end 21st century



Current patterns of diversity of major plankton functional groups



Six plankton functional groups have highly explanatory GAMs



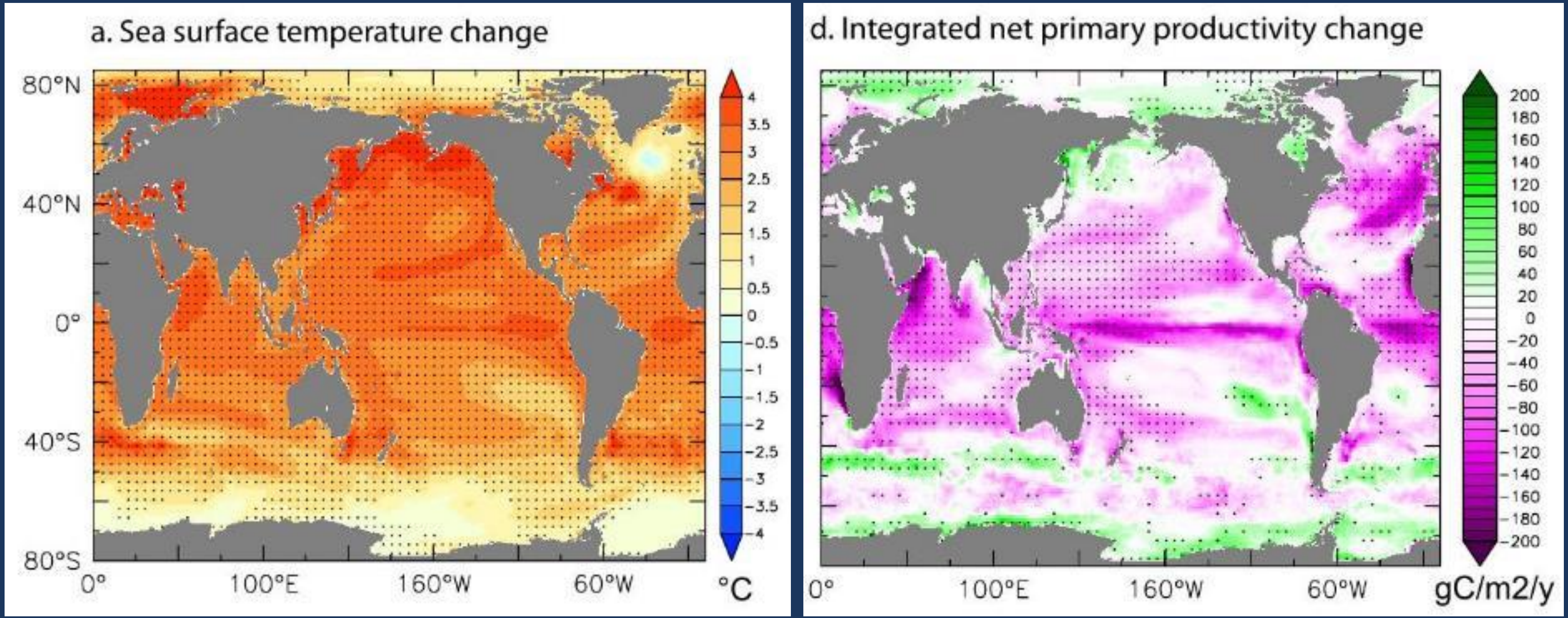

Cell
Article

Global Trends in Marine Plankton Diversity across Kingdoms of Life

Federico M. Ibarbalz,[1] Nicolas Henry,[2,3] Manoela C. Brandão,[4] Séverine Martini,[4] Greta Busseni,[5] Hannah Byrne,[6] Luis Pedro Coelho,[7] Hisashi Endo,[8] Josep M. Gasol,[9,10] Ann C. Gregory,[11] Frédéric Mahé,[12,13] Janaina Rigonato,[14] Marta Royo-Llonch,[9] Guillem Salazar,[15] Isabel Sanz-Sáez,[9] Eleonora Scalco,[5] Dodji Soviadan,[4] Ahmed A. Zayed,[11] Adriana Zingone,[5] Karine Labadie,[16] Joannie Ferland,[17] Claudie Marec,[17] Stefanie Kandels,[18,19] Marc Picheral,[4]

TARA OCEANS

Projected changes in ocean temperatures and primary productivity by 2100



IPCC CMIP5 model outputs
Bopp et al. 2013
Dots show areas of highest certainty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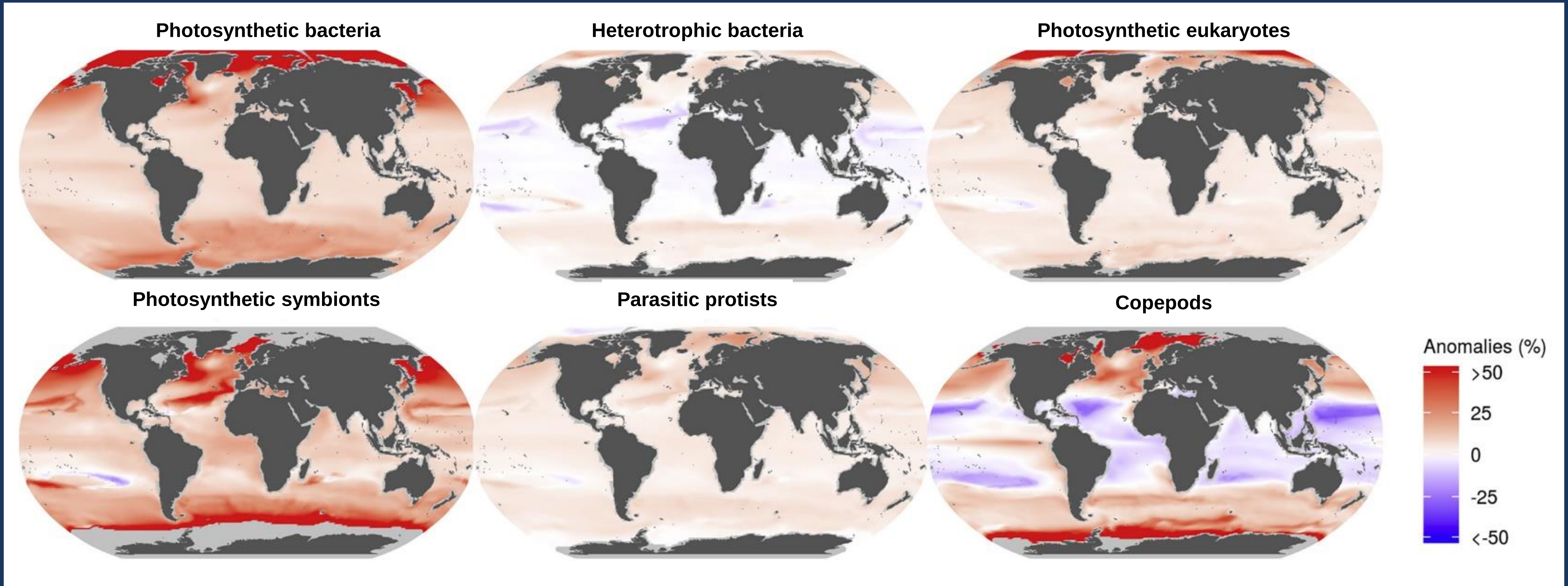
TARA OCEANS

Projected diversity anomalies by end of 21st century

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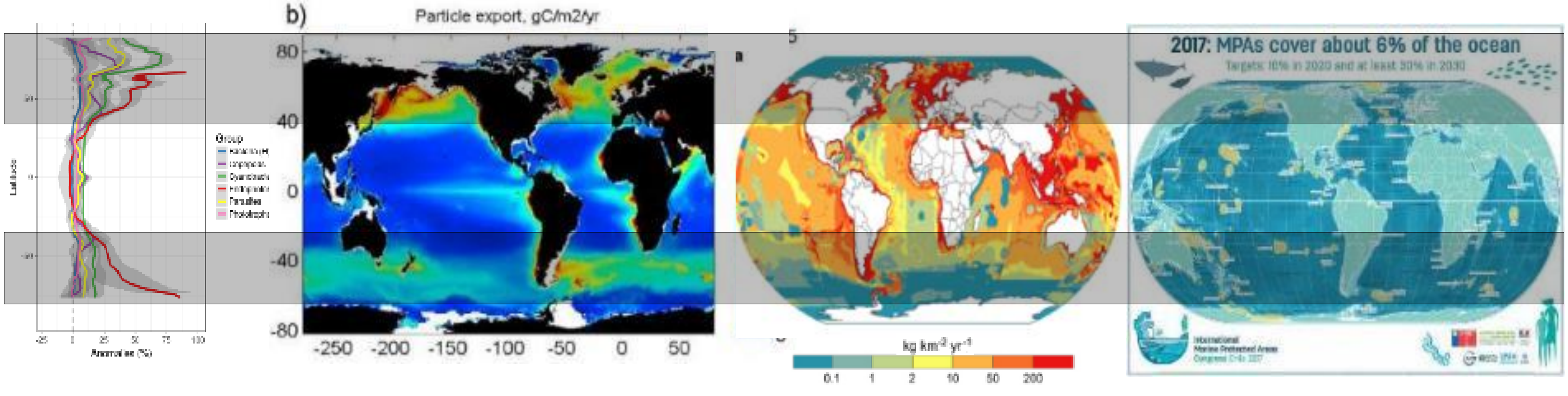
Projected effects of diversity changes on marine ecosystems, fisheries, and biogeochemical cycles

Diversity anomalies | C export | Fish catch | Density of Marine Protected Areas (MPAs)

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The *Tara* Oceans multiverse

- ☑ Our eco-systems biology approach has shed light on a complex invisible ecosystem at global scale
- ☑ Multiple new discoveries have been made about ocean life, together with a wealth of open-access resources
- ☑ Provides a baseline for understanding the effects of climate change on marine ecosystems

TARA OCEANS

CNRS EMBL cea FFEM Fonds Français pour l'Environnement Mondial OCEANOMICS

Fondation Louis D.
Institut de France

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20 YEARS
FOR THE OCEAN