TARA OCEANS 2009-2012

Forces that shape plankton communities

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 18*S* 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.

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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.

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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.

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Read the full article at http://dx.doi.org/10.1126/science.1261498

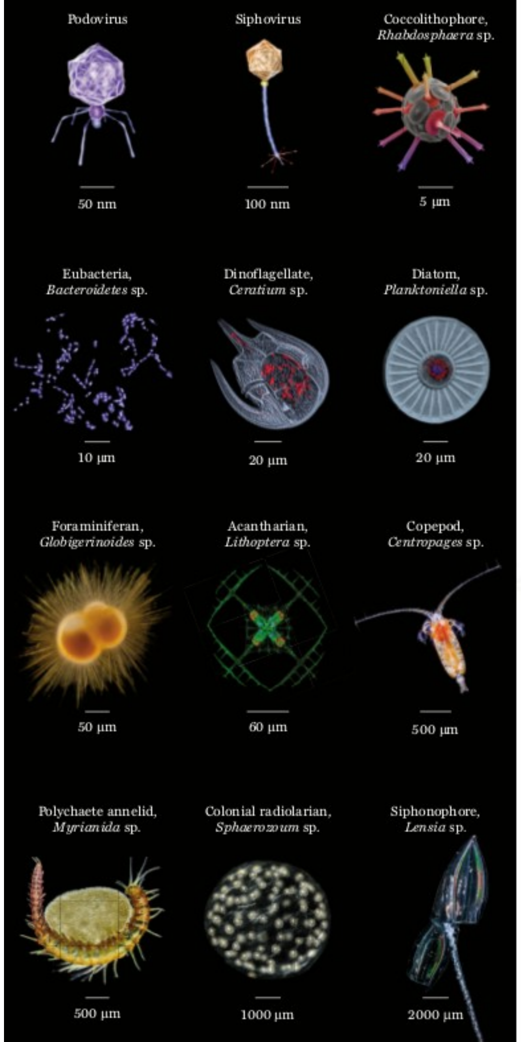
Determinants of community structure in the global plankton interactome

G. Lima-Mendez, K. Faust, N. Henry, J. Decelle, S. Colin, F.

Co-occurence network

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.



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.

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Read the full article at http://dx.doi.org/10.1126/science.1262073

Environmental characteristics of Agulhas rings affect interocean plankton transport

E. Villar,* G. K. Farrant, M. Follows, L. Garczarek, S. Speich, S.

Ocean choke-point impacts plankton

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.

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Read the full article at http://dx.doi.org/10.1126/science.1261447

Plankton diversity

TARA OCEANS 2009-2012

Protist diversity

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*

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generate an ocean ... million nonredund... prokaryotes, and p... enriched samples, ... stratification with ... driven by tempera... or geography. We i... and reveal that >7... man gut microbio... between these two

The list of author affiliations ... sunagawa@embl.de (S.S.); sacinas@icm.csic.es (S.G.A ... 1261359 (2015). Read the full article at h...

Patterns an... ocean vira...

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Viruses influence ec... size, diversity, metal... titative double-stran... (viromes) and whole... 43 Tara Oceans expe... terns and structure ... defined pelagic upp... and suggested that t... of viral protein clust... biogeographic patte... transported on ocea... mental conditions t... these investigations ... with analyses suppo... oceanic viral comm...

The list of author affiliation... E-mail: mbsulli@gmail.com ... 348, 1261498 (2015).

Plankton diversity

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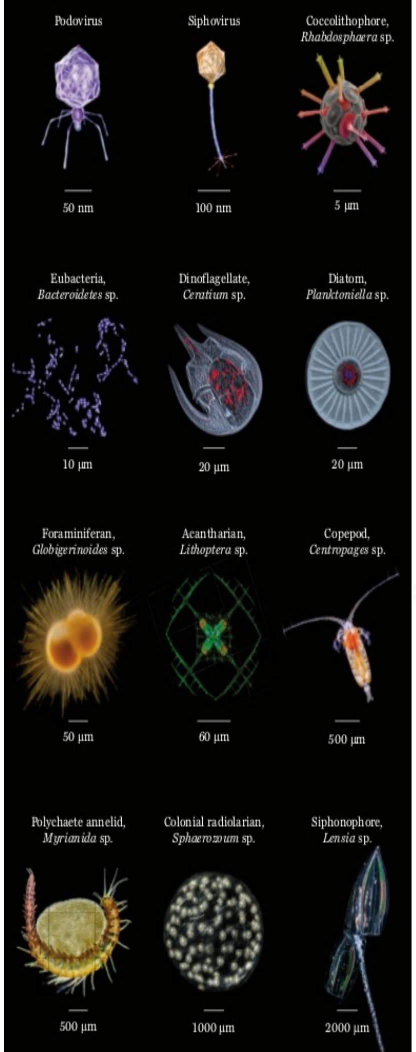

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Species interacti... factors. Here, as ... the photic zone i... organismal abun... factors are incon... found association... genetic groups to... and driven by bo... interactions amo... (mainly parasitic... hypotheses using... ships. We have th... research on ocea... nents into ocean...

Environm... of Agulha... plankton

E. Villar,* G. K. F... Audic, L. Bittner... A. Chase, J. R. De... Guidi, C. N. Hill, ... S. Malviya, E. Pel... E. Scalco, S. M. S... F. Vincent, A. Zin... Kandels-Lewis, ... Bork, E. Boss, C. ... B. Sullivan, S. Su... F. Not,* P. Hinga...

Agulhas rings pro... to circulate from ... influence on glob... role in plankton t... although the coa... ties is continuous... plankton diversit... populations. Mod... ring indicate that... cycling, shaping ... signatures as the ... The peculiar loca... vide a selective m... of Indian Ocean p...