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## Plankton network linked to ocean's biological carbon pump revealed

The ocean is the largest carbon sink on the planet. The community of planktonic organisms involved in the removal of carbon from the upper layers of the ocean has now been described by an interdisciplinary team bringing together oceanographers, biologists and computer scientists, principally from the CNRS, UPMC, Nantes University, VIB, EMBL and CEA. This first overview of the network of species linked to the oceanic biological pump has revealed some new players as well as the main bacterial functions participating in the process. It was obtained by analyzing samples collected by the *Tara Oceans* expedition in the nutrient-poor regions that cover most of the oceans. The scientists have also shown that the presence of a small number of bacterial and viral genes predicts variation in carbon export from the upper layers of the ocean. These findings should enable researchers to better understand the sensitivity of this network to a changing ocean and to better predict the effects that climate change will have on the functioning of the biological carbon pump, which is a key process for sequestering carbon at global scale. Published on 10 February 2016 on the website of the journal *Nature*, this work highlights the important role played by plankton in the climate system.

The ocean is the Earth's main carbon sink due to two principal mechanisms: the physical pump, which pulls surface waters rich in dissolved carbon dioxide down to deeper layers, where it becomes cut off from the atmosphere; and the biological pump, which fixes carbon, either in the tissue of organisms via photosynthesis, or in the calcareous shells of certain microorganisms. Part of this fixed carbon in the form of marine particles then sinks to the deep ocean (a process called carbon export), finally reaching the ocean floor where it is stored (it is said to be sequestered). The biological pump is thus one of the major biological processes that can sequester carbon on geological timescales.

The biological carbon pump in the ocean has been widely studied since the 1980s and involves the ocean's plankton. These tiny organisms are extraordinarily varied (plankton comprise viruses, bacteria and unicellular and multicellular eukaryotes<sup>1</sup>), produce half the world's oxygen from photosynthesis, and form the base of the oceanic food chain that feeds fish and marine mammals. A large number of studies have shown that the strength of the biological pump is directly correlated to the abundance of certain plankton species. However, the structure of the communities involved in carbon export has remained poorly understood.

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<sup>1</sup> These are uni- or multicellular organisms whose genetic material is contained within a nucleus (unlike bacteria and Archaea).



By analyzing samples collected by the *Tara Oceans* expedition (2009-2013), an interdisciplinary team bringing together biologists, computer scientists and oceanographers has shed new light on these planktonic species, their interactions, and the main functions associated with the biological pump, in particularly nutrient-poor ocean regions. Such regions represent more than 70% of the oceans' surface area. The researchers, principally from the CNRS, UPMC, Nantes University, VIB, EMBL and CEA (see list of laboratories below), made use of articles previously published in *Science* on 22 May 2015, and especially the first-ever survey of interactions between planktonic organisms<sup>2</sup>. They used computer analyses to describe the first 'planktonic social network' associated with carbon export in nutrient-poor regions. Many of the players involved, such as certain photosynthesizing algae (especially diatoms) and copepods (tiny shrimp-like organisms) were already known. However the role played by certain microorganisms (unicellular parasites, cyanobacteria and viruses) in carbon export was previously grossly underestimated.

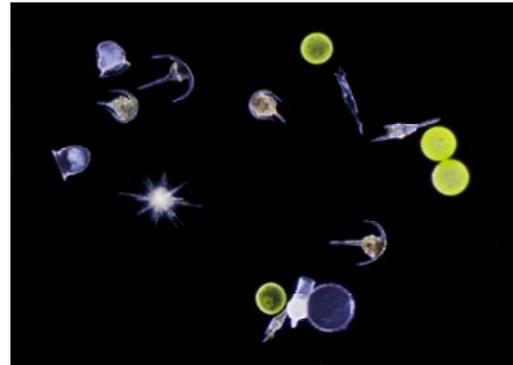
Going further, the researchers then characterized a network of functions, based this time on the analysis of the genes of bacteria and viruses. The Tara Oceans database thus enabled them to establish that the relative abundance of a small number of bacterial and viral genes can predict a significant proportion of variations in carbon export from the upper layers of the ocean to the deep ocean. Some of these genes are involved in photosynthesis and membrane transport, promoting among other things the formation of sediments and breakdown of organic aggregated material. However, the function of most of these genes is still unknown.

Understanding the structure of these networks and the function of the genes linked to carbon export opens up a wide range of possibilities, especially for modelling the biological processes associated with the oceanic carbon cycle. It should therefore be possible to test the robustness of these networks in various climate simulations, to better understand how different planktonic species affect the carbon cycle and climate regulation. One forthcoming objective is to repeat this work for nutrient-rich oceanic regions, to determine whether the planktonic networks are any different. A more complete picture of the biological carbon pump will also require the integration of both temporal and spatial dimensions.

<sup>2</sup> Lima-Mendez G, Faust K, Henry N, Decelle J, Colin S, Carcillo F, et al. Top-down determinants of community structure in the global plankton interactome. *Science*. 2015; 348: 1262073-1262073. doi: 10.1126/science.1262073



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Laboratoire "Evolution Paris Seine" (CNRS/UPMC), part of the Institut de Biologie Paris-Seine,  
Laboratoire d'Informatique de Nantes Atlantique (CNRS/Université de Nantes/École des Mines de Nantes),  
Institut de Biologie, Ecole Normale Supérieure (CNRS/ENS Paris/INSERM),  
Laboratoire "Adaptation et Diversité en Milieu Marin" (CNRS/UPMC), Roscoff Biological Station,  
CEA – Genoscope, Institut de Génétique,  
Laboratoire "Génomique Métabolique" (CNRS/CEA/Université Evry-Val-d'Essonne),  
Laboratoire "Information Génomique et Structurale" (CNRS/AMU),  
Laboratoire de Météorologie Dynamique (CNRS/UPMC/École Polytechnique/ENS Paris), part of IPSL.



- **In other countries**

EMBL (European Molecular Biology Laboratory) (Germany),  
Center for the Biology of Disease, VIB (Belgium),  
Department of Oceanography, University of Hawaii (USA),  
Department of Microbiology, The Ohio State University (USA),  
Dept of Earth, Atmospheric and Planetary Sciences, Massachusetts Institute of Technology (USA),  
University of Maine (USA),  
Institute for Chemical Research, Kyoto University (Japan),  
University of Bremen (Germany),  
Institute of Marine Sciences (Spain),  
Stazione Zoologica Anton Dohrn (Italy).

**Reference**

**Plankton networks driving carbon export in the oligotrophic ocean.** Lionel Guidi, Samuel Chaffron, Lucie Bittner, Damien Eveillard, Abdelhalim Larhlmi, Simon Roux, Youssef Darzi, Stephane Audic, Léo Berline, Jennifer Brum, Luis Pedro Coelho, Julio Cesar Ignacio Espinoza, Shruti Malviya, Shinichi Sunagawa, Céline Dimier, Stefanie Kandels-Lewis, Marc Picheral, Julie Poulain, Sarah Searson, Tara Oceans coordinators, Lars Stemann, Fabrice Not, Pascal Hingamp, Sabrina Speich, Mick Follows, Lee Karp-Boss, Emmanuel Boss, Hiroyuki Ogata, Stephane Pesant, Jean Weissenbach, Patrick Wincker, Silvia G. Acinas, Peer Bork, Colombar de Vargas, Daniele Iudicone, Matthew B. Sullivan, Jeroen Raes, Eric Karsenti, Chris Bowler, Gabriel Gorsky. Published on 10 February 2016 on the *Nature* website.  
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