

**FINAL CRUISE REPORT OF THE TARA OCEANS MISSION IN
THE UNITED STATES WATERS
2009 - 2013**

Report recipient

Office for science et technology
ATTN : Yves Frenot / conseiller@ambascience-usa.org

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Office of Ocean and Polar Affairs
U.S. Department of State
Eisenhower Executive Office Building
1650 Pennsylvania Avenue
Washington, DC 20504
U.S.A.

TARA OCEANS FINAL CRUISE REPORT

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CRUISE NAME: Tara Oceans

RESEARCH VESSEL: Tara

CHIEF SCIENTIST: Eric Karsenti

Research unit: European Molecular Biology Laboratory

Adresse:

Phone: 0033623068397

E-mail: Karsenti@embl.de

RESEARCH UNIT: a consortium of scientists mainly from France's National Centre for Scientific Research (CNRS), the European Molecular Biology Laboratory (EMBL), France's Alternative Energies and Atomic Energy Commission (CEA), the Ohio state University, University of Sorbonne, Roscoff marine station, the Ecole normale supérieure, Stazione Zoologica Anton Dohrn, Genoscope, Bremen University, Kyoto University and ETH Zurich.

DATE BEGINNING: September 2009

DATE END: December 2013

DEPARTURE PORT: Lorient (France)

ARRIVAL PORT: Lorient (France)



OBJECTIVES AND CONTEXT OF THE CRUISE

TARA OCEANS FINAL CRUISE REPORT

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The goal of Tara Oceans mission was to improve our understanding of plankton, how it evolves, how it interconnects and moves constantly from one ocean to another. How are micro-organisms distributed in the oceans and what is their biodiversity? We only know a tenth, perhaps a hundredth, of what there is to know. And what about the risks to plankton, the bacteria and the viruses? Are all these kingdoms linked and reliant on each other? In localized areas or everywhere? How many of them are there? What influence does temperature, salinity, acidity and physico-chemical parameters have on these strange creatures, and in which regions?

In 2008, to answer these questions and with the help of the Tara Ocean Foundation, Eric Karsenti, cell biologist and sailor, assembled a team of researchers with complementary skills in ocean biology and ecology, physical oceanography, cell and systems biology, genomics and imaging, around the schooner Tara and a common dream: assessing a planetary ecosystem globally, from viruses to animals, from genes to the entire community, and integrating biological data into a rich context of physico-chemical parameters.

Plankton, with its relative biological simplicity and homogeneity, the small size of all organisms from viruses to fish larvae, the constant re-organization of communities with high-turnover, and the continuous fossil record of some of its components, is arguably the best global ecosystem to achieve this dream of understanding the ecological and evolutionary principles underlying the functioning of a complex adaptive ecological system on our planet. What's more, planktonic ecosystems, at the base of the oceanic food web, have generated our oxygenic atmosphere long before terrestrial plants emerged, are still today performing ~half of the photosynthesis on our planet, and sequester massive amounts of atmospheric CO₂ into the ocean interior. Into this context the Tara Oceans project to systematically sample plankton ecosystems across the world's ocean was born.

There have been four major global cruises to map ocean plankton so far: the Challenger Expedition (1872-1876), Craig Venter's Global Ocean Survey (2003-2008), the Malaspina Expedition (2010), and the Tara Oceans expeditions (Tara Oceans, 2009-2012; Tara Oceans Polar Circle, 2012-2013). Only the latter sought to study viruses to fish larvae, organisms spanning 8 orders of magnitude in size, using the most cutting-edge molecular and imaging techniques available. During two circum-global navigations, we systematically collected eco-morpho-genetic data at 210 sites, 3 depths, covering most biogeographic provinces of the world's ocean.

The objectives of Tara oceans mission, an international, multidisciplinary project, was to get a planetary-scale understanding of the ocean ecosystem, particularly in light of climate change and to assess the complexity of ocean life across comprehensive taxonomic and spatial scales.



STATIONS OF TARA OCEANS MISSION IN THE UNITED STATES (SEE ATTACHED PRELIMINARY REPORTS)

There were 13 STATIONS CONDUCTED IN USA EEZ.

All Campaign Summary Report, Oceanographic Report, environmental and genetics data are registered on online platforms : PANGAEA and ENA.

- [Preliminary report 1](#)

Start: 28/09/2011 at 10:10 am

End: 26/10/2011 at 5:00 pm

Location: Aloha station

Subject: to study the central part of the Northern Pacific gyre and the Californian Current influence, as well as to sample in the so-called "great Pacific plastic garbage patch".

Station n° 131

Date: 29/9/2011 Location: North Pacific Ocean

Mean Longitude: -158.0013° Mean Latitude: 22.7519°

Station n° 133

Date: 18/10/2011 Location: North Pacific Ocean

Mean Longitude: -127.3227° Mean Latitude: 35.0127°

Station n° 134

Date: 22/10/2011 Location: North Pacific Ocean

Mean Longitude: -121.9884° Mean Latitude: 32.6714°

Station n° 135

Date: 23/10/2011 Location: North Pacific Ocean

Mean Longitude: -121.386° Mean Latitude: 33.0171°

- [Preliminary report 2](#)

Start: 30/12/2011

End: 10/01/2011

Location: Panama canal

Subject: to trace the waters of the Western Boundary Current system of the Western North Atlantic as they circulate from the Caribbean Sea to the Gulf Stream

Station n° 143

Date: 16/01/2012 Location: North Pacific Ocean

Mean Longitude -79.7981° Mean Latitude 30.3437°

- [Preliminary report 3](#)

Start: 26/01/2011

End: 5/02/2011

Location: inside the Gulf Stream and also north of it in the cold waters.

Subject: to characterize the Gulf Stream systems in terms of plankton diversity at surface as well as at depth.

Station n° 144

Date 28/1/2012 Location North Pacific Ocean

Mean Longitude -73.6278° Mean Latitude 35.818°

Station n° 145

Date 2/2/2012 Location North Pacific Ocean

Mean Longitude -70.0565° Mean Latitude 39.1839°

- [Preliminary report 4](#)

Start: 07/09/2013 at 12:00 am

End: 18/09/2013 at 8 8:00 pm

Location: Barrow Canyon and Beaufort Sea

Subject: to sample the Pacific waters coming through the Bering Straits into the Arctic and sample both near and away from the ice pack.

Station n° 194

Date 11/9/2013 Location Polar Circle

Mean Longitude -168.4486° Mean Latitude 73.3509°

Station n° 195

Date 13/9/2013 Location Polar Circle
Mean Longitude -159.6714° Mean Latitude 72.2182°

Station n° 196

Date 14/9/2013 Location Polar Circle
Mean Longitude -154.9125° Mean Latitude 71.8834°

Station n° 197

Date 15/9/2013 Location Polar Circle Mean
Longitude -148.6484° Mean Latitude 71.3331°

Station n° 198

Date 16/9/2013 Location Polar Circle
Mean Longitude -141.8666° Mean Latitude 71.4773°

Station n° 199

Date 17/9/2013 Location Polar Circle
Mean Longitude -140.2461° Mean Latitude 70.3851°

RESULTS

On board the schooner *Tara*, Tara Oceans' team sampled plankton at 210 globally distributed sites at depths down to 1,000m. We describe publicly available resources of molecular, morphological and environmental data, and discuss how an ecosystems biology approach has expanded our understanding of plankton diversity and ecology in the ocean as a planetary, interconnected ecosystem. These efforts illustrate how global-scale concepts and data can help to integrate biological complexity into models and serve as a baseline for assessing ecosystem changes and the future habitability of our planet in the Anthropocene epoch.

Tara Oceans mission came back with a treasure-trove of ~40,000 standardized plankton samples embedded into a rich context of physico-chemical parameters. Thanks to the French 'Investissement d'Avenir' grant OCEANOMICS and France-Genomics, we could generate, organize, and start analyzing data generated from these samples: >250 billion paired DNA reads (or >50 Terabases of raw DNA data) and >6 million images of single plankton (>30 Terabytes of raw data), obtained across 11 organismal size-fractions (>8 500 plankton subcommunities) with a combination of innovative approaches in multi-omics technologies and automated imaging. This represents today by far the most comprehensive, publicly available, description of a planetary biome, and a critical base line to assess Earth-system changes.

This report briefly synthesizes the Tara Oceans 'omics', 'imaging' and 'ecological' data, their integration in European permanent and public databases, their use to provide a new view of plankton ecosystems, within each domain of life (viruses, prokaryotes, protists, and metazoans) and across kingdoms and oceanic provinces; and their use to improve ocean policy and ethics, and inform the world's citizens, from children to decision makers, about the complex equilibrium of our symbiotic planet. A list of deliverables, including the 120 publications produced so far, with 9 papers in *Science* and *Nature* (and 3 additional articles in revision in *Nature* in 2017), is also included.

- **OMICS**

We used high-throughput DNA/RNA sequencing to assess the genetic complexity of Tara Oceans plankton samples. Multi-marker DNA metabarcoding (metaB) provided a primary vision of the diversity and abundance of prokaryotic and eukaryotic taxa inhabiting the ocean globally. Metagenomics (metaG) and metatranscriptomics (metaT) revealed the gene content and functional potential of viruses, prokaryotes and eukaryotes, generating large databases that can be leveraged to provide insights into population structure, gene evolution and mutation pressure across the three kingdoms of Life.

In addition, metaT provide information about gene expression in natural conditions for both eukaryotes and prokaryotes. These efforts have led to the creation of large metabarcode and gene collections, annotated for their taxonomic and functional content, as well as their abundance in the ocean, a unique resource not only for marine biology and ecology, but also for other disciplines.

In total, the current sequencing effort has produced >250 billion DNA paired reads out of >4 300 size-fractionated plankton communities, being by far the largest homogeneous multi-omics data set for any biome (>50 Terabases of raw data). Finally, metagenetics catalogs were produced for viruses, prokaryotes, and eukaryotes, using new bioinformatics pipelines adapted to each kingdom of Life, allowing gene-centric analyses to be performed, and paving the way toward genome-based meta-analyses.

- **IMAGING**

On top of our multi-omics approach to assess ocean genomes and genes, we used a series of innovative, automated imaging tools to identify the concentration, taxonomic composition, and morphological characteristics of plankton and non-living suspended particles across organismal size-fractions.

These included Underwater Video Profiler (UVP), Zooscan, FlowCAM, Imaging FlowCytobot (IFCB), Flow Cytometry, and a brand-new high content screening 3D-microscopy workflow, together encompassing a comprehensive organismal size range, from pico-plankton to large gelatinous zooplankton and marine snow, across different taxonomic and trophic groups, and generating 11 different datasets. More classical imaging techniques were also used to generate smaller datasets at higher resolution, including confocal (3D-CSLM) and electron (SEM and TEM) microscopy (Table 2). The full strategy was used from surface to 1000 m depth, with a current production of >6 million images of single plankton from >9,200 size-fractionated plankton communities (>30 Terabytes).

In the absence of an international framework to share and annotate environmental images (the equivalent of GenBank for DNA sequences), we developed a web- based application, EcoTaxa (<http://ecotaxa.sb-roscoff.fr/>), which allows for the first time online archiving, exploration and collaborative annotation of plankton images by experts worldwide. EcoTaxa also provides tools for computer-assisted image recognition (including deep learning algorithms) to accelerate time consuming taxonomic assignation by experts. The taxonomy implemented in EcoTaxa corresponds to the universal eukaryotic framework developed online with the world community of expert taxonomists in the UniEuk effort, allowing future cross-comparison between imaging and DNA sequencing data.

- **VIRUSES**

In 2009, the baseline knowledge of ocean virus diversity and ecological genomics was incredibly low. This is because viruses have until very recently been near impossible to study due to the lack of experimental and informatics tools to 'access' viruses in nature. Tara Oceans transformed all that. We now know that there are tens of thousands of viral 'types' in the oceans, most of which were captured in the Global Ocean Virome dataset and are now incorporated into a novel network-based taxonomy that is currently serving as the best tool to explore the 'dark matter' that dominates the virosphere. Novel analytical approaches have also linked many of these viruses to ecologically important marine prokaryotic hosts, and advanced our understanding of how viruses metabolically reprogram their hosts during infection by directly modulating key metabolic genes.

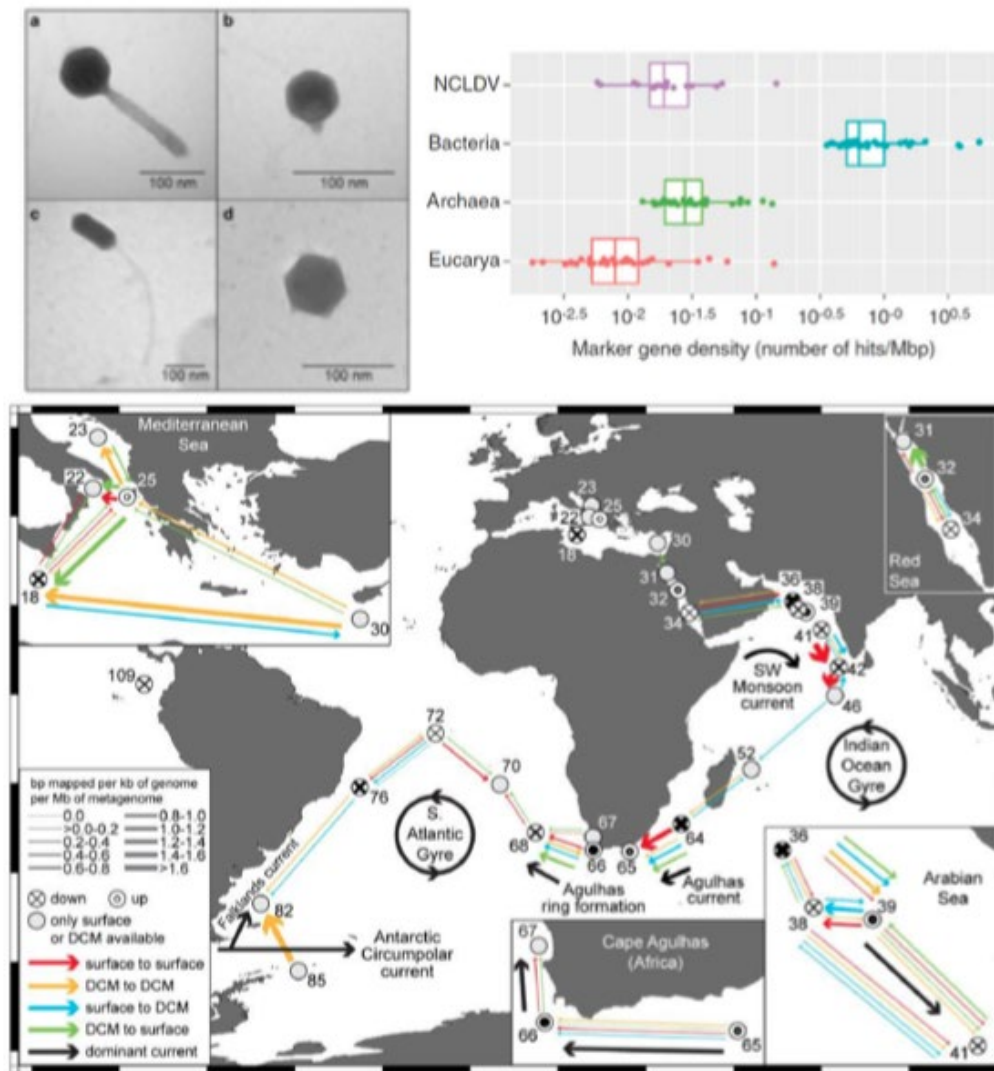


Figure 3. Tara Oceans virus morpho-genetic study. **Upper left:** Morphologies of prokaryote-infecting viruses observed in Tara Oceans samples: (a) myovirus; (b) podovirus; (c) siphovirus; (d) non-tailed virus. The understudied non-tailed viruses emerged as being the most representative in our meta-omics datasets. **Upper right:** taxonomy marker genes suggest that the abundance of giant DNA viruses (NCLDV) infecting eukaryotes exceed the abundance of their host by one order of magnitude, a pattern reminiscent of the 1 to 10 ratio between the abundance of bacteria and phages. **Bottom panel:** (f) Our first global virome analysis indicated that viral communities were passively transported by oceanic currents and locally structured by environmental conditions that affect host community structure.

• PROKARYOTES

In Tara Oceans, we generated the largest ocean microbial sequencing data set available to date and developed new bioinformatics approaches to explore the frontiers of global ocean microbial diversity. We found a minimum boundary of 35,000 prokaryotic 'species' in the pelagic realm, whose community structure appears to be essentially driven by seawater temperature in surface oceans. Analysis of the >200 metagenomes resulted in the first Ocean Microbial Reference Gene Catalogue comprising >40 million non-redundant genes, which now serves as a treasure for biologists and marine scientists.

The OM-RGC improved our understanding of biogeography and microbial functional capabilities across oceanic regions and ecosystems. A notable derivative was the inference of the first world ocean "interactome" uncovering organismal interactions across all domains of life including viruses, and showing the predominance of biotic relations in shaping the global plankton network. We further used the power of Tara Oceans' multi-omics and morphological data to unveil the functional and ecological significance of critical nitrogen-fixing cyanobacteria-haptophyte symbioses in the euphotic zone worldwide. A better understanding of the genetic capacity for mixotrophy and the factors controlling the biogeographic distribution of the two most abundant and widespread phototrophs on Earth (*Prochlorococcus* and *Synechococcus*) was established.

- **PROTISTS**

In Tara Oceans, we focused >45% of the morpho-genetic sampling effort on protists. We then applied the full power of our multi-omics and automated imaging (see 'Omics' and 'Imaging' sections above) workflow to generate ~170 billion DNA paired-reads and >1.5 million images from ~1,000 plankton communities in 4 organismal size- fractions from pico- to micro-plankton. This is by far the largest consistent morpho-genetic dataset of protist biocomplexity from a single biome, which we leveraged by creating a series of new metaB transcriptomes, and single-cell genomes - reference databases for annotating taxonomically and functionally the deluge of new environmental data. We are also building a universal taxonomic framework for eukaryotes implemented at EBI, in order to unite the complex phen-omics protist data under a single ontology.

Our primary large-scale DNA metabarcoding analysis revealed ~150,000 eukaryotic genera in the euphotic zone, >85% of which are protists, essentially heterotrophic taxa, including many uncharacterized parasites and symbionts, in addition to the better known components of plankton ecosystems such as diatoms and ciliates. Reconstruction of a global plankton interactome and plankton sub-networks confirmed the central role of parasitic and photosymbiotic protists as keystone taxa increasing the connectivity of plankton food-webs and the flux of carbon to deeper layers of the ocean. Underwater video-profiling reinforced the abundance of giant photosymbiotic rhizarian protists whose biomass exceeds that of all zooplankton in (sub)tropical oceans.

Tara Oceans enable to make protists emerge today as the richest biotic compartment in the world plankton, their fundamentally symbiotic nature increasing the complexity and connectivity of ecosystems.

- **METAZOANS**

In Tara Oceans, we used five different types of nets to collect a unique collection of ~1 500 standardized zooplankton samples from surface to a few hundred meters depth across the world ocean. Imaging and 'omics' tools were then used to assess the morpho-genetic complexity of zooplankton communities in well-defined oceanographic provinces.

In terms of imaging, all zooplankton samples have now been analyzed and their great majority validated by experts using EcoTaxa (>6 million images on <http://ecotaxa.sb-roscoff.fr/>). Images were used to assess the mechanisms contributing to the limited dispersal of Indian Ocean plankton populations into the Atlantic. In the Indian Ocean, combined imaging datasets have shown the absence of metazoan plankton in the Oxygen Minimum Zone, and its effect on carbon flux. Based on in situ video profiling (UVP) performed at each Tara Oceans station, we demonstrated that the biomass of rhizarian protists, undersampled by nets because of their fragility, may in fact be equivalent to that of all other mesozooplankton in the oligotrophic inter-tropical open oceans. On the 'omics' front, Tara Oceans samples were used to reconstruct the macro- evolutionary history of sea snails (Thecosomata) using a combination of morphological and molecular data.

However, these studies are just scratching the tip of the iceberg of morphogenetic information hidden in the Tara Oceans comprehensive zooplankton collection, and efforts to sequence metabarcodes and genomes of the main players and correlate genetic to imaging information is needed.

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