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Station Biologique
RoscoffTARA
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2 PhD positions available @SBR - Station Biologique de Roscoff

EPEP Team - *Evolution des Protistes et des Ecosystèmes Pélagiques*CNRS, UMR7144 - AD²M, Adaptation et Diversité en Milieu Marin

Fall 2016

1. **SYMBIOME: an eco-systemic approach to eukaryotic symbioses in global photic plankton**
2. **Exploring the Ocean's biological dark matter using single eukaryotic cell genomics & transcriptomics applied to world meta-omics datasets.**

Key Words:

Tara-Oceans; plankton systems ecology; diversity, ecology, & evolution of marine planktonic protists; marine protist symbioses; single-cell -omics

Context:

Over the last 7 years, the EPEP team @SBR, France, has been coordinating global oceans sampling and analyses of marine planktonic protists in the *Tara*-Oceans/OCEANOMICS expeditions and project. For the first time in ecology, a small but highly interdisciplinary consortium has assembled a **holistic, standardized eco-morpho-genetic dataset across a planetary biome**, comprising >30,000 biological samples and associated contextual data from 220 sites, 3 depths, and 11 organismal size-fractions from viruses to small animals (Karsenti et al. 2011, Bork et al. 2015). We have then generated the largest meta-omics dataset available to date (>40 Terabases!), including >1,000 viral, prokaryotic, and eukaryotic-enriched metagenomes and metatranscriptomes, as well >4 billion eukaryotic and prokaryotic metabarcodes from >3,000 size-fractionated, worldwide plankton communities. This dataset covering global geographic and taxonomic scales represents today a unique opportunity to explore the boundaries of a planetary ecosystem at the crossroad between biodiversity, ecology, and evolution. The first wave of *Tara* Oceans analyses, based on a fraction of the current dataset, was published in 8 papers in *Science* and *Nature* in 2015 and 2016.

In particular, the *Tara* Oceans DNA metabarcoding data (de Vargas et al. 2015) have revealed **the phenomenal hidden diversity of protists (mostly symbiotic, mixo/heterotrophic) in plankton systems**, which is significantly greater than the one of viruses (Brum et al. 2015) or bacteria (Sunagawa et al. 2015). Automated *in situ* imaging data further demonstrate the **great prominence of photosymbiotic groups** such as the Collodarians, whose biomass (Biard et al. 2016, de Vargas et al. 2015) and biodiversity (de Vargas et al. 2015) can surpass the ones of zooplankton (animals)! Co-occurrence graph techniques applied to -omics data have confirmed the **central and multifaceted position of protists in biotic interaction networks**, which appear to structure plankton communities more than abiotic or physical environmental forcing (Lima-Mendez et al. 2015, Guidi et al. 2016).

The 2 PhD projects proposed here aims at further **exploring the symbiotic/mixotrophic structure of protistan diversity across Life's kingdoms and global oceans biogeography and hydrography**, as well as understanding the **acclimation and adaptation patterns of the key protist players** in these ecosystems which cover 71% of our planet and generate half its oxygen. Both students will apply innovative protocols combining **eco-bioinformatics, single-cell -omics, and advanced imaging**. They will integrate the *Tara* Oceans/Oceanomics international consortium (<http://oceans.taraexpeditions.org/en/>; <http://www.oceanomics.eu/>), and benefit from the great and long-standing pluridisciplinary expertise developed over the last 7 years in the collaborative network.

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- de Vargas, C., S. Audic, N. Henry, J. Decelle, F. Mahé, ... , P. Wincker, and E. Karsenti. 2015: Eukaryotic plankton diversity in the sunlit ocean. **Science** 348:DOI:10.1126/science.1261605.
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- Karsenti, E., S.G. Acinas, P. Bork, C. Bowler, C. de Vargas, ... , the *Tara* Oceans consortium. 2011. A holistic approach to marine eco-systems biology. **Plos Biology** 9(10): e1001177. doi:10.1371/journal.pbio.1001177
- Lima-Mendez, G., K. Faust, N. Henry, ... , C. Bowler, C. de Vargas, and J. Raes. 2015: Determinants of community structure in the global plankton interactome. **Science** 348:1262073.
- Sunagawa, S., L. P. Coelho, S. Chaffron, ... , C. de Vargas, G. Gorsky, ... , S. G. Acinas, and P. Bork. 2015: Structure and Function of the Global Ocean Microbiome. **Science** 348:1261359.

Thesis #1

SYMBIOME: an eco-systemic approach to eukaryotic symbioses in global photic plankton

- collaboration SBRoscoff CNRS /Genoscope CEA -

Description: This project aims at unveiling the overall diversity and main ecological structure of eukaryotic symbioses in the world photic oceans. Eukaryotic symbioses are still poorly known in marine plankton, as compared to terrestrial (e.g. mycorrhiza) or coastal marine (e.g. coral reefs) ecosystems. Their knowledge is still largely descriptive and based on initial microscopy observations made by former marine biologists. SYMBIOME proposes a **radically new, systemic (*sensu* 'systems biology', without *a priori*) approach to plankton eukaryotic symbioses**, driven by the novel *Tara*-Oceans eco-morpho-genetic datasets that cover comprehensive spatial, taxonomic, and eco-systemic (genes, organisms, environment) scales in the world oceans. In a first phase, we will **combine bioinformatics and co-occurrence graph techniques on the *Tara* Oceans global metabarcoding and metatranscriptomics/genomics size-fractionated datasets to detect the main eukaryotic holobionts** and their symbiotic partners (eukaryotes, prokaryotes, and/or viruses). In parallel, **light and fluorescent microscopy** (to detect in particular the eukaryotic and prokaryotic photosymbionts) will allow **isolation of single symbiotic protists** (holobionts) from the collection of *Tara* Oceans plankton samples preserved in Roscoff (<http://tara-oceanomics-roscoff.fr/>), followed by systematic *Illumina* sequencing of eukaryotic and prokaryotic metabarcodes in order to validate and/or improve the purely bioinformatics inferences described above to detect eukaryotic symbioses. In a second phase, we will **assess the biogeographic and ecological patterns of the most abundant eukaryotic holobionts in the world oceans, via the distribution of the rDNA OTUs and the expression of the genes** (co-occurrence patterns in metatranscriptomes) **of both symbiotic partners across the 5 organismal size-fractions sampled in *Tara* Oceans**. Global oceanic distributions of symbiotic protists will be compared to those of non-symbiotic, sister taxa in order to understand the impact of symbiosis on the fundamental and realized ecological niches. We will also try to assess which ecological conditions trigger the free-living or symbiotic phases of the interaction cycles, and which genes/genes' networks are expressed in the various phases, and why. Overall, this work will not only unveil the main symbiotic associations in eukaryotic plankton, but also appreciate their biogeographic and ecological distributions across the world oceans, and interpret their genomic advantages and potentials for acclimation/adaptation.

A more detailed plan of the project is given, in French, in Annex 1 (pp. 4-6 of this document).

Qualifications & Experience: graduate in Bioinformatics or Cell/Molecular Biology; demonstrable skills with R and biostatistics, Python or Perl programming, in a Unix /Linux framework. Theoretical and technical skills in molecular biology/ecology will be an advantage.

Supervisors: This PhD Thesis will be co-supervised by Colombar de Vargas (EPEP team leader, plankton systems biology/evolution) and Stéphane Audic (bioinformatics and statistics) at CNRS-Roscoff, as well as Eric Pelletier (bio/systems-informatics) at GENOSCOPE (UMR 8030, Génomique Métabolique (CEA-CNRS-Université d'Evry Val d'Essonne)).

Work environment: The student will integrate the *Tara* Oceans/Oceanomics international consortium (<http://oceans.taraexpeditions.org/en/> ; <http://www.oceanomics.eu/>), and benefit from the great and long-standing pluridisciplinary expertise developed over the last 7 years in the collaborative network. She/He will be based in Roscoff (<http://www.sb-roscoff.fr/>), with regular working period at Genoscope (<http://www.genoscope.cns.fr/>), or inversely.

PhD program: ED227, National Museum of Natural History/University Pierre et Marie Curie (<http://www.mnhn.fr/fr/enseignement-formation/enseignement-superieur/ecole-doctorale>).

Application process: Please send an email to C. de Vargas (vargas@sb-roscoff.fr) and Eric Pelletier (ericp@genoscope.cns.fr) including: (i) your detailed CV, including your academic record and research experience; (ii) a motivation statement (why you are interested in this project, max. 500 words); and (iii) a short essay commenting a paper you have recently read and that changed your vision of science (max. 300 words).

Thesis #2

Exploring the Ocean's biological dark matter using single eukaryotic cell genomics & transcriptomics applied to world meta-omics datasets.

This project is part of **SINGEK**, a EU H2020 Marie-Sklodowska Curie Innovative Training Network (MSCA-ITN) project aimed at providing a unique and structured training programme to 15 Early Stage Researchers (ESRs) to study microeukaryotes at the single-cell level.



Description: Microbial eukaryotes (protists) appear to be the dark matter of oceans' Life, and are particularly prominent in planktonic ecosystems where they play the role of plants in terrestrial systems and allow organic matter transfer from the smallest microbes (prokaryotes and viruses) to animals (zooplankton). Over the last 7 years, 2 major circumglobal scientific expeditions, *Tara Oceans* (2009-2014) and *Malaspina* (2010-2011), have collected holistic plankton samples for high-throughput sequencing and imaging technologies, from viruses to fish larvae, across the world oceans from surface waters to meso- and bathy-pelagic layers. Hundreds of meta-genomes and meta-transcriptomes have been generated from these projects, in particular across the organismal size-fractions corresponding to eukaryotic cells (from 1 to >1,000 μm). If meta-omics data from prokaryotic or viral size-fractions are reaching saturation and are relatively well annotated (taxonomically and functionally), **the genes and contigs from eukaryotic meta-omics data are far from saturation and unknown for the great majority, pointing out the huge gap in reference gen(ome)s of marine protists and leaving us with a massive amount of orphan genes and senseless environmental data.** The PhD candidate will generate new Single-Amplified Transcriptomes (SATs) from key planktonic protists, as well as use the Single-Amplified Genomes/Transcriptomes (SAG/Ts) generated by other ETN partner teams (ESR1 and ESR7 among others) and within the *Tara Oceans* consortium, in order to recruit meta-omics reads from the *Tara Oceans* and *Malaspina* datasets. This will allow to **(i) annotate and assemble, taxonomically, a significant part of global oceans eukaryotic meta-omics data; (ii) assess the genomic and phylogenomic variability around key eukaryotic plankton taxa; and (iii) understand which genes are co-triggered by specific environmental conditions for key plankton taxa.** In particular, the functional and evolutionary hypotheses generated by ESR 1, ESR2, ESR9 and ESR11 will be tested in the real world across global ecological and geographical scales. A focus will be given on one of the most important but poorly understood ecological function in oceanic plankton: mixotrophy or the capacity that most if not all eukaryotic phytoplankton have to both photosynthesize and feed by endo/phago-cytosis.

Expected results: Taxonomic annotation of massive amount of orphan meta-omics data from global oceans. Assessment of genomic variability over global biogeographic scales for key eukaryotic ecological players (adaptation). Understanding of acclimation process for key ecological players at the genic expression level. Assessment of mixotrophic genomes expression over large geographic and ecological scales.

Qualifications & Experience: graduate in Bioinformatics or Cell/Molecular Biology; demonstrable skills with R and biostatistics, Python or Perl programming, in a Unix /Linux framework. Theoretical and technical skills in molecular biology/ecology will be an advantage.

Supervisors: Colombari de Vargas (CNRS-Roscoff, EPEP team leader, plankton systems biology/evolution); (CNRS-Roscoff, EPEP); Olivier Jaillon (GENOSCOPE CNRS/CEA; genomics, bio bioinformatics and statistics); Ramiro Logares (ICM-Barcelona, eco-informatics and marine microbes).

Work environment: This position is part of the European ITN (Innovative Training Network) **SINGEK** - *Promoting SINGle cell GENomics to explore the ecology and evolution of hidden microeuKaryotes*, which provides a unique and structured training program to a new generation of **15 excellent PhD students** in environmental eukaryotic single cells - omics (see <http://www.singek.eu/>).

PhD program: ED227, National Museum of Natural History/University Pierre et Marie Curie (<http://www.mnhn.fr/fr/enseignement-formation/enseignement-superieur/ecole-doctorale>).

Application process: Please send asap an email to C. de Vargas (vargas@sb-roscoff.fr) with a strong statement of interest and your CV + follow the instructions @: <http://www.singek.eu/registration-form/>