

Project Name

Acronyme du projet (8 caractères *maximum*) :

SOME : Southern Ocean Microbial Ecogenomics

PhD supervision

This 3 years PhD project will be hosted at the Lab of microbiology of extreme environments, in Brest. <https://wwz.ifremer.fr/umr6197/>

Please, send your questions regarding this project to Lois Maignien (lois.maignien@univ-brest.fr)

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Project Description

Project summary

Planktonic microorganisms are central in the carbon cycling, though the combined process of photosynthesis (CO₂ fixation), microbial loop (carbon recycling) and pump (carbon export). The comprehension of marine microorganism diversity, activity biogeography is thus of paramount importance to better understand and predict the fate of marine and atmospheric carbon globally.

Although the Southern Ocean exerts a disproportionate control on global carbon cycling, with 40% uptake of global anthropogenic CO₂ inputs, relatively little is known on the biodiversity of microorganisms living around the Antarctic continent, including their relationships with one another and with their environment. Our project will use cutting edge environmental genomics and bioinformatics tools to establish a high-resolution microbial taxonomic and genomic atlas and generate unprecedented data for this critical environment. To reach this objective, we have sampled the southern ocean during a unique Antarctic circumnavigation international expedition. This doctoral project proposes to

study the functional diversity and biogeography of microorganisms in relation to Southern Ocean biomes (polar front, polynya, open ocean, SO water masses...) and ancillary biogeochemical parameters. To reach this goal, we will use high throughput DNA sequencing of environmental DNA (metagenomics) and cutting edge bioinformatics and biostatistics to constrain microbial taxonomic and functional genes distribution around the Antarctic. This will result in a better understanding of the functioning of the Southern Ocean and its role in the global carbon budget.

Project description

The Southern Ocean (SO) has a **central role in global carbon cycling** and owing to an intense photosynthetic activity during austral summer, marine microorganisms significantly contribute to the atmospheric carbon sequestration and consequently, to climate control. However, the diversity of organisms involved in the carbon cycle and their respective contribution in the different biomes of this ocean is still unclear.

In addition, previous exploration of microbial diversity in this area has revealed unique assemblages of genes, organisms and communities due to singular conditions of temperature, light cycle and ocean circulation, thus forming a very distinct **marine ecosystem compared to other oceans**. While many studies have focused on understanding local ecosystem properties, a large-scale exploration of planktonic diversity and activity across distinct and contrasted Southern Ocean biomes is still lacking in order identify key microorganisms and metabolic pathways engaged in this original ocean's functioning.

This project aims at exploiting samples and data acquired during the ACE cruise, an international expedition that explored the Southern Ocean (SO) during the austral summer 2016/2017 in a circumpolar path from and to Cape Town, South Africa. This expedition has allowed the coordinated sampling of different Southern Ocean systems (including areas never visited by scientific expeditions before) and gathered 22 research projects providing a rich set of ancillary geochemical parameters to explore the environmental drivers of biodiversity. During ACE, PI Maignien and collaborators have collected over 1000 samples from 5-1500 m water depth of different size fractions, suitable for environmental DNA sequencing and analysis for planktonic viral, archaeal, bacterial and picoeukaryote diversity.

Thanks to the support of the Genoscope national sequencing center, samples from the ACE expedition will have their DNA sequenced using various omics approaches: 16S and 18S rRNA gene amplicon sequencing (metabarcoding) for high-resolution community structure, environmental DNA (metagenomics, the focus of this project) and RNA (metatranscriptomics) of viruses, Bacteria, Archaea and microbial Eukaryotes.

The overarching doctoral proposal is thus to (i) **better understand the ecology of SO plankton and** (ii) **its implication in the biogeochemical cycles in this ocean** based on a spatial and depth resolved analysis of bacterial, archaeal and eukaryotic taxonomic and genomic diversity in austral summer waters.

The proposed research activity will aim at achieving the following specific objectives:

Objective 1. Contribute to the census of SO microbial life, describing their diversity from taxonomy to population genome levels using metagenomics approaches.

Objective 2. Understand the ecological structure and biogeography of polar marine microbes; define core communities across major SO ecosystems (open ocean, polynia, sub-antarctic islands, coastal areas, glacier fronts, polar front) and typical SO water masses. Define depth and geographical limits of microbial populations.

Objective 3. Define the specificity of Southern Ocean microorganisms at the taxonomic, genomic, and community structure level compared to other large oceanic provinces. The

ACE data will be replaced in the context Tara Oceans, Ocean Sampling Day (OSD), and Malaspina projects.

Objective 4. Determine the abiotic controls on polar microbial community structure and function with regard to major environmental parameters compiled in the ACE metadata database.