



PHENOMAP

OCEAN PHYTOPLANKTON : BRIDGING THE PHENOTYPE GAP

A deluge of genomics data shows us that single-celled eukaryotes are far more diverse and complex than we had previously thought. The value of these studies is severely limited, however, as most of the sequencing does not correspond to any reference sequence associated with a phenotype or taxonomy.

Most phytoplankton (a polyphyletic group of photosynthetic microorganisms that play a central role in aquatic biogeochemical cycles) have simply not been described.

PHENOMAP seeks to bridge this 'phenotype gap' with a detailed morphogenetic description of key cryptic lineages.

The work plan integrates a suite of state-of-the-art methods that will be applied to two outstanding existing resources:

- The Roscoff Culture Collection, which is the largest and most diverse collection of marine microalgae in the world;
- The collection of 15,000 samples from the Tara Oceans expeditions between 2009 and 2018.

A targeted sampling programme at three French marine stations will complement these resources. Phenotypic analyses will include fluorescence optical and electron microscopy for live and fixed samples and pigment profiling for cultures.

The aim is to formally describe 50 new taxa and to link genotypic and phenotypic information for hundreds of known species.

The objective is to add significant value to genetic reference databases to help interpret environmental sequencing data and better understand the biology, ecology and evolution of phytoplankton.

Partners

Research centers

Sorbonne Université, site de Roscoff [Project Developer]
CNRS, Station biologique de Roscoff
IFREMER, Station marine de Concarneau

Funder

Agence Nationale de la Recherche

Labelisation

09/11/2020

Overall budget

1 101 K€