Universitat Pompeu Fabra Barcelona

Master in Bioinformatics for Health Sciences

Master project 2021-2022

Personal Information

Supervisor	Silvia G. Acinas & Felipe Hernandes Coutinho
Email	sacinas@icm.csic.es
Institution	Institute of Marine Sciences (ICM), CSIC
Website	https://www.icm.csic.es/en
Group	Ecology and Genomics of Marine Microbes

Project

Computational genomics

Project Title:

Revealing novel viruses among sentinel polar prokaryotes by single cell genome analyses

Keywords:

Viruses, prokaryotes, polar regions, single cell genomics, single amplified genomes, microbial metagenomes, auxiliary metabolic genes, Arctic ocean, Antarctic ocean.

Summary:

The polar oceans are under severe threats brought by climate change. Preserving these habitats and the ecosystems therein requires an understanding of the many biological entities that reside there. Microorganisms are the main drivers of the biogeochemical cycles that sustain life in the polar oceans. In turn, viruses of microorganisms play a significant role in this process by selective killing of their hosts and by altering their metabolisms during infection. Therefore, a comprehensive understanding of the biodiversity of Arctic viruses is fundamental for the preservation of these ecosystems. Recent findings from our group revealed that members of the genus Polaribacter are sentinel species, meaning that they quickly respond to the environmental changes that threaten the Arctic (Royo et al. 2020). Yet very little is known about viruses infecting these organisms and their environmental roles. The aim of this project is to reveal novel viruses of Polaribacter through the analysis of Single-cell Amplified Genomes (SAGs). We have previously obtained a set of 91 Arctic and Antarctic Polaribacter SAGs. The project will involve using state-of-the-art bioinformatics tools to identify viruses associated with these genomes, either as prophages or free viruses. In addition, the project will focus on the genetic diversity of these viruses, specifically their repertoire of auxiliary metabolic genes that can be used to alter the host metabolism during infection. The discovered viral genomes and that of their hosts will be analysed in metagenomes from the polar oceans to determine their abundance patterns and associations with physical, chemical and biological parameters, which will shed light on how these factors, together with viruses, control the abundance of this keystone prokaryotic taxa in polar oceans. Finally, the discovery of such viruses has direct implications for the health sciences, as they are likely to encode lysins that could be engineered to be active against Flavobacterium (a close relative of Polaribacter) and other pathogens. Thus, these viruses and their lysins might represent alternatives to antibiotic therapy and are of great biotechnological potential.

References:

Marta Royo-Llonch, M, Pablo Sánchez, Clara Ruiz-González, Guillem Salazar, Carlos Pedrós-Alió, Karine Labadie, Lucas Paoli, Tara Oceans Coordinators, Samuel Chaffron, Damien Eveillard, Eric Karsenti, Shinichi Sunagawa, Patrick Wincker, Lee Karp-Boss, Chris Bowler, Silvia G Acinas. Ecogenomics of key prokaryotes in the arctic ocean. bioRxiv 2020.06.19.156794; doi: https://doi.org/10.1101/2020.06.19.156794

Expected skills::

Basic understanding of a scripting language (e.g. Python or Perl). Basic understanding of statistical analysis with R or MATLAB. Basic understanding of bacterial and viral genomics.

Possibility of funding::

To be discussed

Possible continuity with PhD: :

To be discussed

Comments:

The candidate would be integrated within the team of Dr. Acinas under the close supervision of the bioinformatician Dr. Hernandes Coutinho and the microbial ecologist Dr. Acinas. The candidate would be also interacting with other members of the Acinas' lab and other PIs of the department. The candidate would have an active scientific environment attending to lab meetings and seminars at the ICM.