



## Master project 2021-2022

### Personal Information

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### Project

## Computational genomics

#### Project Title:

The Microeukaryotic Virome

#### Keywords:

Virome, Giant Viruses, Microeukaryotes, Viral Endogenization

#### Summary:

The laboratory The del Campo Lab is based at the Institut de Biologia Evolutiva (UPF-CSIC) in Barcelona. The research at the del Campo Lab is focused on the study of host-associated microbes and the effect of global warming on the microbiomes of benthic and planktonic marine animals. We have a wet and dry lab, to perform experiments and bioinformatics analysis, enabling the broadest possible goals. The ongoing climate change and its effects on the environment, such as rising sea temperature, has strong impacts on free-living marine microbial communities. However, the effects of global warming have not been properly studied on host-associated microbiomes. Microbiomes (both prokaryotic and eukaryotic) associated with host organisms have a strong influence on host evolution, physiology, and ecological functions. We study how environmental changes resulting from global warming affect the composition and function of the microbiomes in key members of the marine fauna and consequently how these changes affect the hosts. Currently, our study focuses on these impacts on corals, teleost fish, and zooplankton. To tackle this novel research topic, we use a combination of molecular biology, ecophysiology, and bioinformatics. The proposed project Virus have been reported as a significant component of the nuclear genomes of different microeukaryotes from algae to heterotrophic protists. These viruses have been proved to be relevant for different aspects of microeukaryotic biology, shaping the genome of their algal host or protecting the host from other viral infections. The number of viruses described from microeukaryotes is relatively low compared to those infecting bacteria or macroorganisms. The microeukaryotic virome is a source of novel viral diversity, particularly of giant viruses. The aim of this project in collaboration with Professor Richard A. White from the University of North Caroline Charlotte is to characterize the viral landscape of the unicellular eukaryotes. Initially we will build a comprehensive database of microeukaryotic genomes and transcriptomes. Using this dataset, we will proceed to extract the viral signal from the different organisms' genome and proceed to their characterization using phylogenetic trees. We expect in this project to unveil a significant amount of viral diversity. As a byproduct of it we will also generate a comprehensive microeukaryotic genomic database.

#### References:

Fischer, M. G. et al. (2016) Host genome integration and giant virus-induced reactivation of the virophage mavirus. *Nature* 540, 288–291 Moniruzzaman, M. et al. (2020) Widespread endogenization of giant viruses shapes genomes of green algae. *Nature* 588, 141-145

#### Expected skills::

R, Python, Genome Analysis, Phylogenies, Database Management

#### Possibility of funding::

No

**Possible continuity with PhD :**

To be discussed

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