

The Institute of Evolutionary Biology seeks a: Research technician

The Institute of Evolutionary Biology (IBE) is a joint Institute of the Spanish National Research Council (CSIC) and the Pompeu Fabra University (UPF) located in Barcelona city. IBE research is focused on the processes and mechanisms that generate biodiversity and on understanding the genetic basis of evolution. The IBE is a center member of Barcelona Biomedical Research Park (PRBB).

Description Group/Unit

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.

Effects of ocean warming on the microbiomes of benthic and planktonic marine animals. 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 eukaryotic microbiome. Unlike the study of the bacterial fraction of the microbiome, the study of the micro-eukaryotes associated with animals has largely been restricted to visual identification or molecular targeting of particular groups. The application of high-throughput sequencing approaches, such as those used to look at bacteria, has been limited because the barcode gene we use to study microeukaryotes ecology and distribution in the environment, the 18S rRNA gene, is also present in the host animals. As a result, when host-associated microbial eukaryotes are analyzed, the retrieved sequences are dominated by the host. Stemming from my work on coral-associated microeukaryotes, we successfully implemented an approach that avoids the amplification of metazoan host genes, which allows us to use high throughput methods to study the microeukaryotic communities of animals. This approach opens the door to the study of diversity and distribution of microeukaryotes in a myriad of environments, from the coral surface to the human gut.

Project description

Heat stress-causing coral bleaching and necrosis is one of the main threats' corals are facing in the current context of climate change. Genomics, in particular transcriptomics, are useful tools to help us understand biological processes. In recent years biomedical transcriptomic studies have been moving to the use of single-cell approaches. These single-cell transcriptomic strategies are being incorporated gradually into other fields of biology such as evolutionary and developmental biology. However, little has been done so far to use this approach to understand ecologically relevant processes, such as the impact of heat stress in corals. Currently, all transcriptomic studies on reef coral holobionts have focused on either the symbiotic algae or the coral, sometimes as a function of which algal symbiont is hosted. However, seldom have the transcriptional states of

different members of the holobiont been characterized at the same time, and never have comparisons among cell types been made. Furthermore, zooxanthellae are not the only symbionts within the coral holobiont, and there are currently no transcriptomic studies characterizing the response of other microeukaryotes or prokaryotes, either individually or at the community level, and little is known regarding how the microbiome changes during bleaching and necrosis induced by heat stress and how this corresponds to functional response. Here we propose to contribute in-depth understanding of the granular diversity of the corals holobiont transcriptome and its differential response to heat stress and, in so doing, provide more powerful tools to develop potential interventions in the future. Our proposed project will generate for the first time an integrated and detailed transcriptomic map of the coral holobiont under heat stress. We will describe at the single-cell level the transcriptomic response of the different coral cell types and for its representative microbial symbiont, both prokaryotic and eukaryotic. This granular and expanded approach to study the coral holobiont transcriptome will increase and improve our knowledge of the functional genomics of corals and the necrosis processes associated with heat stress. This project will also generate one of the first calcifying coral and the first azooxanthellate coral single-cell transcriptomics dataset. Furthermore, a genomic characterization of the heat stress response using single-cell transcriptomics will represent a valuable opportunity to study interactions among all the members of the holobiont, gaining granularity by generating thousands of individual cellular transcriptomes instead of a bulky whole organism metatranscriptome. Because this approach targets neither the coral nor its zooxanthellae specifically we will also capture the transcriptomes of other symbionts that are rarely or never characterized (such as bacteria, or the recently described corallicolids). Finally, this work will represent one of the first studies to combine microbiome data and functional transcriptomics data, in a way that helps inform previous and future coral microbiome studies by identifying which members of the holobiont are correlated with the differential gene expression patterns that we will observe in the single-cell transcriptomes. Our results are not only expected to fundamentally advance the field of coral ecology but will have parallel broad and positive impacts in other fields of the biological sciences.

Duties: We are looking for a motivated, curious, organized research technician to perform the key laboratory steps of this project. The candidate's tasks will involve:

- Collection of coral samples.
- Processing of coral tissues to obtain single cells.
- Cell sorting using FACS.
- Single-Cell RNA seq data analysis.
- Symbiont Isolation.
- Symbiont nucleic acids extraction.

Candidate requisites

- Degree in Genetics.
- Experience with coral single-cell RNA transcriptomics.
- Experience on the use of flow cytometry.
- Experience on the use of shell and R.

We will value

- Diving license.
- Outreach experience.

What do we offer?

- A full-time contract for one year (with possible extension to two)
- Starting September 2022
- Salary around 25.000 €/annual gross
- Location in Barcelona (Passeig Marítim de la Barceloneta, 37 – 49)

Application process

Interested candidates please send a full CV to jdelcampo@ibe.upf-csic.es before July 18, 2022.