

ESR 2 – NEXT STEPS TOWARDS SYSTEMS BIOLOGY: DISENTANGLING COMPLEX ECOLOGICAL NETWORKS IN MARINE MICROBES

<p>Research project</p>	<p>Biological communities are systems composed of many interacting parts that in combination constitute ecosystems. Macro-ecologists have advanced our understanding of ecosystems focusing mainly on animals and plants, generating models where species and their ecological interactions are understood as networks, which have specific characteristics that influence ecosystem functioning. In comparison, our knowledge of microbial interaction networks is rudimentary, and in most community studies, microbes are still pooled by their function (e.g. grazers), thus missing species-specific interactions. This represents a major gap in our knowledge, as microbes are key players in all ecosystems, particularly in the oceans. As such, we cannot increase our understanding of ecosystem function, which is particularly needed in a context of environmental change. Recent technological advance in microfluidics, singlecell genomics and DNA sequencing makes it now feasible to capture the most important microbes of a given community and determine their ecological interactions. Specifically, single cell genomics can provide evidence on ecological interactions such as parasitism, symbiosis or predation, following the basic premise that when a single cell is isolated, it will carry with it its symbionts, pathogens, and sometimes prey. Interaction determination will start by analysing an initial scaffold-network (soon to be available) constructed using extended Local Similarity Analysis (eLSA) and based on amplicon rDNA. Important interactions predicted by eLSA will be further analysed using single cell genomics, which will provide extra evidence on physical interactions between cells by analysing repeated taxa co-occurrences in SAGs. The latter data will be coupled, when possible, with lifestyles (e.g. free-living and parasite) and, when significant, will define the interactions to be incorporated in the scaffold network and used to construct an ecological network draft including parasitism, mbiosis and predation. Thus, the main objective of ERS2 is to determine important pairwise ecological interactions occurring in a natural marine microbial community and generate a network draft.</p>
<p>Supervisor</p>	<p><u>Name:</u> Ramiro Logares <u>Email:</u> ramiro.logares@icm.csic.es <u>Website:</u> http://www.icm.csic.es/bio/projects/icmicrobis/index.php?nom=postdocs#Ramiro</p>
<p>Host institution</p>	<p>Institute of Marine Sciences, Spanish National Research Council (CSIC-ICM) Barcelona, Spain</p>
<p>PhD program</p>	<p>To be defined according to candidate's profile</p>
<p>Expected results</p>	<p>Determine significant ecological interactions in a microbial community occurring at a well-known marine long-term microbial observatory. Specifically, interactions such as symbiosis, parasitism and predation will be determined between members of the community (microeukaryotes, bacteria and viruses) by combining single-cell genomics and metagenetics/metagenomics. The determined interactions will be used to assemble an ecological network-draft. The properties of the emerging network will be analysed.</p>
<p>Planned secondments</p>	<p>UU - Month 18 (3 m) - Improving microbial interaction detection using microfluidics CNRS-B - Month 26 (2 m) - Cross-validation of microbial interactions derived from SCG CNRS-R - Month 35 (3 m) - Exploitation of the SAG database from Tara-Oceans/Oceanomics</p>
<p>Required profile</p>	<p>Graduated in bioinformatics or molecular biology. The candidate must have demonstrable skills with R, Bash or Python.</p>