

## ESR 1 – GENOME BASIS FOR ECOLOGICAL DIFFERENTIATION AMONG RELATED UNCULTURED LINEAGES

<b>Research project</b>	Biodiversity studies of marine microbial eukaryotes have revealed a large diversity of taxonomic lineages, especially within the smaller size classes of heterotrophic cells. In addition, these studies have also unveiled the presence of novel and uncultured groups, which have defied scientific scrutiny until very recently. The objective of this ESR is first to obtain an overview of the biodiversity of heterotrophic microeukaryotes using the phylogenetic affiliation of single cells from marine assemblages. For this general overview, large collections of SAGs will be analysed at the 18S rDNA level to obtain a biodiversity inventory, and to identify a set of related uncultured lineages potentially occupying a similar ecological niche (i.e. bacterivory) as ascertained by their phylogenetic placement. A set of SAGs from these will be sequenced, assembled, and gene annotated in order to identify functional genes related to ecological adaptations within these novel and uncultured clades. Then a comparison between the genome-based ecological adaptations of different and related clades will be performed in order to explain niche differentiation. We expect that this genomic level study will contribute to linking functional diversity and phylogenetic diversity within the dominant bacterial grazers in the oceans.
<b>Supervisor</b>	<u>Name:</u> Ramon Massana <u>Email:</u> <a href="mailto:ramonm@icm.csic.es">ramonm@icm.csic.es</a> <u>Website:</u> <a href="http://www.icm.csic.es/bio/projects/icmicrobis/?nom=massana">www.icm.csic.es/bio/projects/icmicrobis/?nom=massana</a>
<b>Host institution</b>	Institute of Marine Sciences, Spanish National Research Council (CSIC-ICM) Barcelona, Spain
<b>PhD program</b>	Marine Sciences, Universitat Politècnica de Catalunya
<b>Expected results</b>	A single cell study of marine microeukaryotic biodiversity. Detection of gene repertoires related to ecological functions (phagocytosis, organic matter degradation, membrane transporters, meiosis) in different lineages of heterotrophic microeukaryotes. Ecological preferences of given clades derived from comparative genomics.
<b>Planned secondments</b>	LU - Month 18 (3 m) - Overview of population genetics for environmental studies UNEXE - Month 26 (4 m) - Gene annotation and functions derived from genome analyses ASC - Month 40 (2 m) - SAG databases and tools for genome screening
<b>Required profile</b>	Graduate in Biology, Bioinformatics, or Molecular Biology