

## ESR 3 – UNCULTURED OPISTHOKONTS AND THE ORIGIN OF METAZOAN MULTICELLULARITYS

<b>Research project</b>	<p>The origin of multicellular animals (metazoans) from their unicellular ancestor remains a long-standing evolutionary question. Recent genome data from unicellular opisthokont lineages (i.e., choanoflagellates, ichthyosporean, and filasterean) have shown that the unicellular ancestor of metazoans already was genetically more complex than previously thought. However, there are additional unicellular lineages closely related to Metazoans that remain unsampled due to the lack of cultures. These taxa might be key to fully pinpoint the evolutionary history of genes involved in multicellularity. Thus, the objective of this ESR is to obtain genome or transcriptomic data from several SAGs of novel opisthokont taxa. We will focus on novel ichthyosporeans, choanoflagellates, filastereans, representatives of the still unsampled “marine opisthokonta” clade, or novel opisthokonts. By using comparative genomic analyses we will analyse the presence of genes and pathways involved in cell adhesion, cell signalling and transcriptional regulation. We will also analyse the repertoire of genes involved in filopodia and flagellar apparatus to enable inferences of the morphology of the target groups. Finally, we will use this data to perform taxon-rich phylogenomic analyses of the opisthokonts. The data generated will be important to the question of multicellularity origins, but also in the phylogeny of the opisthokonts and into our understanding of cell evolution across the eukaryotes.</p>
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<b>Host institution</b>	<p>Institute of Evolutionary Biology (CSIC-UPF) Barcelona, Spain</p>
<b>PhD program</b>	<p>Biomedicine, Universitat Pompeu Fabra</p>
<b>Expected results</b>	<p>The new genome/transcriptomic data from uncultured opisthokont taxa will result in a better understanding of 1) the origin and evolution of genes involved in multicellularity, 2) opisthokont diversity and evolution, and 3) the phylogenetic relationships of the opisthokonts.</p>
<b>Planned secondments</b>	<p>UU - Month 17 (3 m) - SAGs from cultured and uncultured taxa CRG-CNAG - Month 24 (3 m) - Assembly and annotation of SAGs CNRS-P - Month 35 (3 m) - Phylogenomics</p>
<b>Required profile</b>	<p>Graduate in Biology, Bioinformatics, Biotechnonology, Biodiversity or Molecular Biology</p>