



H2020 MSCA-ITN-2015-ETN 675752 Promoting SINgle cell GEnomics to explore the ecology and evolution of hidden microeuKaryotes

ESR 6 – DEVELOPMENT OF METHODOLOGY FOR SINGLE CELL ORGANISM GENOME ANALYSIS

Research project	Much improvement and technical quality checks are still needed to reach the full potential of SCG for microbial eukaryotes, especially along critical steps of high-throughput sequencing and preliminary bioinformatic analysis. Indeed, eukaryotes have much more complex genomes than prokaryotes, and optimal solutions for all these steps are fundamental to obtain meaningful genome assemblies that can be readily exploited for addressing unsolved scientific questions. The main objective of this ESR is the establishment of methodology for single cell whole organism genome characterization. This will consist of implementing the best laboratory procedures for single cell handling, isolation by Fluorescence Activated Cell sorting directly into microtitre plates, lysis procedures, improving DNA accessibility, DNA amplification, RNA handling, library preparation, process automation, sequencing, process quality control, and data analysis procedures for do novo assembly of the obtained genomes. All these steps still need fine refining, and all of them are fundamental for a good success of the methods and science proposed in SINGEK.
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Host institution	National Centre for Genomic Analysis, Centre for Genomic Regulation (CNAG-CRG) Barcelona, Spain
PhD program	Biomedicine, Universitat Pompeu Fabra
Expected results	Procedures and data analysis methodology for single cell studies of species for which no reference genome sequences exist. Methodology establishment of homogeneous DNA amplification from single cells, de novo genome assembly, RNA analysis, de novo transcriptome assembly.
Planned secondments	UU - Month 16 (3 m) - Sharing expertise on single cell sorting procedures CEA - Month 24 (3 m) - Sharing expertise in high-throughput sequencing VIB - Mont 33 (3 months) - Sharing expertise in bioinformatic pipelines
Required profile	Graduate in Biology or Molecular Biology, bioinformatic skills.