

ESR 5 – DISENTANGLING THE ORIGIN OF EUKARYOTES USING PHYLOGENOMICS AND COMPARATIVE GENOMICS APPROACHES

<p>Research project</p>	<p>The majority of life on our planet is microbial in nature, and much of this remains largely uncharacterised. Studying this uncultured ‘microbial majority’ at the genomic level will allow us to gain insight in how life evolved from simple (prokaryotic) to complex (eukaryotic). According to the most recent studies, eukaryotes evolved from a complex archaeal lineage that is related to the recently discovered Lokiarchaeota (Spang et al, Nature, 2015). Yet, despite that boundaries between prokaryotes and eukaryotes are seemingly getting smaller, the gap in terms of genomic and cellular complexity towards eukaryotes is still large. Clearly, studying the vast amount of uncultured microeukaryotes should give a more resolution in the evolutionary origins of cellular complexity of eukaryotes. The main objective of this project is to gain insight in the origin and evolution of eukaryotes through comparative genomic and evolutionary analyses of single cell genome and transcriptome datasets of uncultured microeukaryotes. The data that will be generated in the larger framework of this project will be used to expand and root the eukaryotic tree of life using a variety of phylogenomic approaches. Subsequently, this tree will be used to model the evolution of eukaryotic gene content from the archaea-to-eukaryote transition. Was the first eukaryote already a complex entity, or did cellular complexity evolve gradually? Of particular interest here are the ‘prokaryotic genes’ that reside in the genomes of microeukaryotes. Are these the result of vertical or horizontal evolution, and what was the source of these genes? Endosymbiosis has been a pivotal force in eukaryotic evolution, and have given rise to mitochondria and plastids. In light of this, we will study genomic data resulting from endosymbiotic interactions, either from ancient events (plastid and mitochondrial genomes) and ongoing endosymbioses (genomes of endosymbiotic prokaryotes).</p>
<p>Supervisor</p>	<p><u>Name:</u> Thijs Ettema <u>Email:</u> thijs.ettema@icm.uu.se <u>Website:</u> www.ettemalab.org/</p>
<p>Host institution</p>	<p>Uppsala University (UU) Uppsala, Sweden</p>
<p>PhD program</p>	<p>Four year fully funded graduate training leading to a PhD in Molecular Evolution from Uppsala University</p>
<p>Expected results</p>	<p>The proposed phylogenomics and comparative genomics analysis are expected to result in (i) a high-resolution view of the eukaryotic Tree of Life based on genomic data, and (ii) a detailed overview of the evolution of eukaryotic gene repertoire, with special emphasis of those gene families that reside in prokaryotes either as part of the eukaryotic genome, or as part of organelle or endosymbiont genomes.</p>
<p>Planned secondments</p>	<p>FGT - Month 16 (2 m) - Optimization of in-chip microeukaryote capture and processing using microfluidics CNRS-P - Month 22 (3 m) - Sharing expertise on phylogenomics UOL - Month 29 (3 m) - Sharing expertise on transcriptome analysis of microbial microeukaryotes</p>
<p>Required profile</p>	<p>Graduate (MSc) in Bioinformatics, Biology, Molecular Biology (or similar).</p>
<p>Special conditions</p>	<p>The postgraduate training comprises four years of full time studies. The position can be combined with up to 20 % of teaching assistantship, which will then prolong the position accordingly. More information about postgraduate studies at Uppsala University and formal requirements are available at http://www.teknat.uu.se.</p>