

ESR 10 – NEW TOOLS FOR GENOME ANNOTATION IN UNKNOWN MICROEUKARYOTE LINEAGES

Research project	<p>With the advent of next generation genome sequencing, the number of sequenced microeukaryote genomes and transcriptomes is rapidly growing. However, apart from browsing sequence data from a single species, integrating and exploring complete genome or transcriptome information from multiple species remains a major challenge. Here, we will obtain an overview of computational methodological strategies for analysing gene content from culture derived versus single cell derived microeukaryote genomes. Furthermore, we will develop tools to systematically perform functional annotation and integrate different types of microeukaryote sequence data through a comparative genomics framework. This will shed light on the origin and evolution of gene content and species/clade-specific gene families. Finally, we will further develop online resources and tools (see e.g. pico-PLAZA and TRAPID) for the analysis and dissemination of single cell genomics.</p>
Supervisor	<p><u>Name:</u> Klaas Vandepoele <u>Email:</u> vandepoele@psb.vib-ugent.be <u>Website:</u> http://www.vib.be/en/Pages/default.aspx</p>
Host institution	<p>Ghent University (VIB) Ghent, Belgium</p>
PhD program	<p>PhD program, Ghent University</p>
Expected results	<p>Integrative resources for the comparative and functional analysis of complete and incomplete genome and transcriptomics data. Application of newly developed methods and resources to phytoplankton datasets, including the analysis of gene family evolution (core and species/clade-specific gene families), HGT and gene functions/pathways.</p>
Planned secondments	<p>CNRS-B - Month 14 (4 m) - Sharing expertise on microeukaryote biodiversity UU - Month 24 (3 m) - Sharing expertise on detection horizontal gene transfer ASC - Month 35 (2 m) - Transcriptome annotation to multiple databases</p>
Required profile	<p>Master in computational sciences, preferably with some experience in biological data analysis Experience with Unix and command-line usage Good programming skills (Python, or Java/C++) Experience with relational databases (mySQL), PHP and webdesign/JavaScript is a plus Excellent English communication skills A passion for science and driven to decode the mysteries of life</p>