

Post-Doc Position: algae omic data analysis

Context: A post-doctoral researcher position is open at Le Mans University (France) and University Laval (Québec, Canada) for a duration of one year from the 1st of October. The first 6th months will take place in France and the last 6 months in Canada. The aim of the research project is to analyse omic data (genomes and transcriptomes) from different strains and species of the genus *Haslea*, already available in partner laboratories. The exploitation of these data will have important outputs at both fundamental and application levels (for instance in blue biotechnology).

Problematic and objectives: Diatoms from the genus Haslea are marine, mostly benthic or epiphytic organisms. The type species of the genus, *H. ostrearia* (Gaillon) Simonsen, produces the very specific blue pigment marennine, responsible for the greening of marine invertebrates, especially bivalves. So far, the genus Haslea encompasses ca. 40 taxa as listed in AlgaeBase (Guiry & Guiry 2021) distributed all over the world, mostly in temperate, waters, but also tropical as well as polar species. Less than 20% of these species produce marennine-like blue pigments. Therefore, Haslea is a good model for exploring evolutionarily relevant ecological adaptations of diatoms in general, as well as adaptation with polar and temperate distributions. Currently, six Haslea species, including two arctic ones, have been sequenced by both laboratories, some of them using a combination of long and short reads (ONT and Illumina). These sequencing efforts have revealed relatively small genomes, from 60 to 100Mb, with probable high density gene content and high level of repeats. The aim of this project is to exploit all available genomic data of Haslea species in order to comprehend adaptation in different benthic and pseudo-benthic environments, in particular between temperate and polar regions. This will have important outputs both for fundamental research (diatom genome evolution, specific biosynthesis pathways) and biotech applications (strain selection, added value and bioactive compounds).

Expertise required: The candidate must have a bioinformatic background oriented in omic data analyses: genome assembly using long and short reads, annotation, comparative genomics (pan genome, polymorphism, selection). Knowledge in ecology and molecular evolution will be appreciated. The candidate must be familiar with UNIX environment and different langages (Bash, Python). Moreover, he/she must be rigorous, autonomous and curious.

Contact:

French coordinators are Dr. Myriam Badawi and Pr. Jean-Luc Mouget from the laboratory of Interactions of Organisms, Stress, Health and Environment (BIOSSE, former MMS EA 2160, Le Mans). Canadian coordinator is Pr. Connie Lovejoy from the Institute of Integrative Biology and System (IBIS, Laval, Québec).

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