**Scientific project**

This project is part of HAPAR ANR (Head L. Guillou), in collaboration with the ABiMS [1] platform (Analysis and Bioinformatics for Marine Science) and the University of Ghent (S. Rombauts, Y. Van de Peer)

Microalgae can produce harmful and / or toxic blooms. These microalgae have many pathogens, especially roughly specialist eukaryotic microparasites. In cultures or in the field, these parasitoids are able to limit the growth of their host and thus to limit the impact of these blooms. These parasitoids, harmless to humans, are close to many human pathogens such as Plasmodium falciparum, the malaria agent. In the ANR project HAPAR (2014-2019), we focus on the molecular mechanisms related to the specialization of these parasites.

As part of this work a full analysis of the genomes of two parasitic dinoflagellates will be realized, one specific of a genus and one that can infect two different genus. The sequencing of these two genomes was performed and RNAseq data is already available for the annotation of these genomes, RADseq and proteomic data will also be available soon. These studies will highlight process (and products of metabolism) involved during host invasion.

**Context**

The Marine Station provides to the scientific community a bioinformatics platform, ABiMS, in which the research will be conducted. The Ghent site on its side provides the ORCAE genome curation platform that will be used during the project. The postdoc will be under the responsibility of the head of the ABiMS platform with the co supervision of L. Guillou (UMR7144). He / she will interact with the different partners of the projects: the Ghent university and the Genoscope.

**Missions**

The postdoc will be in charge of the genome, RADseq and RNAseq data analyses. From the first results of automatic annotation of these genomes produced by Genoscope, the postdoc will work on the improvement of the structural and functional annotation using NGS data. The study of the phylogenetic evolution of some gene families and species delineation will also be considered. Pipelines in place for the analysis will be deployed under the Galaxy platform for a valuation to the community.

**Skills**

- Good experience of eukaryote genome annotation

- Strong knowledge of NGS analysis tools and methods, and particularly in RNAseq and/or RADseq analysis

- Good knowledge of phylogeny

- Good knowledge of statistical analysis

- Advanced knowledge of scripting languages (Perl, Python,…)

- Basic knowledge of Linux and Unix

- Global knowledge in genetics and molecular biology

- Ability to work and integrate a team

- Autonomy, rigor and openness

**The salary is currently 1880 up to 2100 euros / month**

**Contract starting : as soon as possible**

**Location :** Roscoff / France

**Limited term contract with funding available for 15 months (could be extended to 24 months)**

**Send CV and cover letter to** [corre@sb-roscoff.fr](mailto:corre@sb-roscoff.fr), before 15 of January 2016