

PhD subject at Evo-Eco-Paleo lab

University: University of Lille (France)

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Host laboratory: Evolution, Ecology and Paleontology, UMR CNRS 8198

Website: http://eep.univ-lille.fr/en/research/group_CP

Funding: 100% University of Lille (requested)

Title of the project:

Evolution of the micro-RNA/mRNA targets regulatory network in the *Arabidopsis* genus

Background:

Micro-RNAs (miRNAs) are central regulators of gene expression playing a role in many fundamental processes particularly during the development of organisms. They act on the messenger RNAs (mRNAs) of their target genes, forming a regulatory network whose modes of emergence, functional role and fine-scale evolutionary processes are still poorly understood in plants.

Objectives:

The central objective of this project is to study the evolution of these regulatory networks at a fine phylogenetic scale by combining high-throughput sequencing approaches and bioinformatics analyses. The project will focus mainly on two closely related plant species, *Arabidopsis halleri* and *A. lyrata* (Brassicaceae), which diverged about one million years ago, but will also extend to more distant lineages. The main objectives of the PhD project will be to 1) study the mechanisms by which the regulatory network arises: how do novel miRNAs appear in genomes and how do they acquire their targets? 2) compare the strength of natural selection on the different elements of the network, in particular according to whether the miRNAs are conserved at a large phylogenetic scale or have emerged more recently within specific lineages? 3) study the joint evolution of interacting partners of the network: can co-evolution between network elements be detected, indicating that mutations in the sequence of some elements may compensate for mutations in others?

This project is based on an ongoing interdisciplinary collaboration with the bioinformatics team of the CRISTAL lab (UMR 9189), an active national collaboration network (Genoscope, CNRS Perpignan, ENS Paris), and intensive use of the regional bioinformatics platform BiLille. The student will gain skills in molecular biology and bioinformatics and will follow the training courses offered by the bioinformatics platform BiLille. Data for the project have been or will be acquired in the frame of two ongoing projects (ANR TE-Moma and ERC consolidator NOVEL).

Requested skills: A degree in Biological sciences with good knowledge of Evolutionary Biology, Population Genetics or Molecular Biology. Bioinformatic skills would be appreciated but can be acquired in the course of the project.

Keywords: micro-RNAs, evolutionary biology, gene regulatory networks, bioinformatics.

Relevant publication of the host laboratory related to the project:

Durand, E., Méheust, R., Soucaze, M., Goubet, P.M., Gallina, S., Poux, C., Fobis-Loisy, I., Guillon, E., Gaude, T., Sarazin, A., Figeac, M., Prat, E., Marande, W., Bergès, H., Vekemans, X., Billiard, S., Castric, V., 2014. Dominance hierarchy arising from the evolution of a complex small RNA regulatory network. *Science* 346, 1200–1205.

Guigon, I., Legrand, S., Berthelot, J.-F., Bini, S., Lanselle, D., Benmounah, M., Touzet, H., 2019. miRkwood: a tool for the reliable identification of microRNAs in plant genomes. *BMC Genomics* 20, 532.

Legrand S, Caron T, Maumus F, Schwartzman S, Quadrana L, Durand E, Gallina S, Pauwels M, Mazoyer C, Huyghe L, Colot V, Hanikenne M, Castric V. 2019. Differential retention of transposable element-derived sequences in outcrossing *Arabidopsis* genomes. *Mobile DNA*. 10:30.