Investigating the methylome of grape and oak under water stress

Project coordinator: Philippe Gallusci

Host Institution: INRA

Duration: 12 months with possible extension of 18 additional months.

Fixed start date: 1st july 2019

Description:

Global climate changes that includes several environmental constraints including drought, is a major concern that affects plant survival both in agro-systems and forest ecosystems. Indeed plants have evolved a wide range of mechanisms to cope with adverse environmental conditions that often lead to rapid and integrated reprogramming of gene expression patterns. Recent works have evidenced that epigenetic regulations, including DNA methylation, are essential to the responses of plants to environmental constraints, and may contribute to their long term adaptation to adverse conditions. In this context the METDRY project addresses the question of the potential involvement of genomic DNA methylation in the adaptation and responses to drought in woody perennial plants using grape and oak as representatives of cultivated plants and forest ecosystems respectively. It is based on the comparative analysis of methylomes, transcriptomes and small RNA populations in a drought sensitive and drought tolerant species in grapevine and oak and aims at identifying differentially methylated regions (DMRs) and gene expression profiles linked to long term adaptation to drought.

The main objectives of the project are:
1. To analyze the genome wide distribution of 5mC in a drought sensitive and tolerant species in oak and grapevine, and determine similarities and differences between these contrasted phenotypes in each genus.
2. To determine changes in DNA methylation landscape induced by drought in the sensitive and tolerant species in each genus.
3. To investigate if DNA methylation contributes in a similar way to the responses to drought stress and to long term adaptation to drought in plants from natural population (oak), and in plants that have been selected by breeders over several generation (grapevine).
4. To implement a robust bioinformatics data analysis pipeline for BS-seq data and integrative approaches including BS-Seq, RNA seq, and Small RNA seq data.

Applicants should be highly motivated and have a PhD with expertise in bioinfomatic and strong background in (epi)genomics . Knowledge in plant sciences is strongly recommended.

Qualifications: We seek a bright, highly motivated, and enthusiastic bioinformatician with a background in epigenomics or genomics and an interest for plant biology. However, candidates with other backgrounds such as molecular biology, with a strong interest in bioinformatics, are also encouraged to apply. Experience with NGS technologies and pipeline development is required. Applicants should have demonstrated abilities to work in a Linux environment and have experience in handling NGS data. Programming (Python, Perl, etc.) is required and knowledge of biostatistics is appreciated. A high standard of spoken and written English is appreciated, as are good communication skills. Ability to work autonomously, as well as part of a team, and to interact with scientist from different background including molecular biologist, plant physiologist and bioinformaticians is necessary. Applicants will have to share their time between three different laboratories.

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Links:

UMR EGFV: https://www6.bordeaux-aquitaine.inra.fr/egfv/

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