Grand Programme de Recherche
BPS | Sciences des Plantes
Bordeaux
université
de BORDEAUX

PostDoc in Plant Sciences :

Analysis of stress epigenetic memory in perennials

Starting Date: may 2022
Duration: 18 months
Location: UMR EGFV / UMR BIOGECO
Proportion of work: full-time
Salary: 31k€ yearly before-tax salary (approx. 25k€ net)
Desired level of education: PhD
Experience required: PhD + 3 years max of research experience

A 18 months position supported by Bordeaux Plant Science (BPS) research program is available in UMR Ecophysiology and Grape Functional Genomics (EGFV) and in UMR Biodiversity, Genes and Communities (BIOGECO) in Bordeaux, France. This post-doc position is one of 19 offered positions as part of Bordeaux University excellence BPS program, which will provide access to many scientific events and resources.

The successful candidate will be integrated into the Tepimemory project, which focuses on short and long term epigenetic memory induced by abiotic stress and which is structured around the following four major tasks:

Task 1: To analyze the epigenetic response to combined stresses in perennial plants and short-term memory effects.
Task 2: To explore the long-term effects of epigenetic memory using wood tissue.
Task 3: Molecular mechanisms underlying the epigenetic response and its memory effects. This will be the main work of the post-doctoral student recruited, who will be involved in the establishment of transgenic lines in grapevine and oaks (pilot study) and their analysis.
Task 4: Data management and analysis of results.

Job description: The post-doctoral researcher recruited to the project will mainly be involved in task 3, which aims to elucidate the molecular mechanisms underlying the memory effects in grapevine and oak, and task 4, which focuses on the analysis of omics data, in particular RNA seq and Whole Genome Bisulfite Sequencing (WGBS) data on oak, grapevine and apricot.
The postdoc will (1) focus on the study of the molecular mechanisms involved in epigenetic regulation and its memory effects using reverse genetic approaches (2) participate in the analysis of the "omics" data generated by the study of the response to combined stresses in grapevine, apricot and oak.

(1) In order to determine the mechanisms underlying the epigenetic response and its short- and/or long-term memory effects in response to abiotic stresses, grapevine will be used as a model in which reverse genetic approaches have already been developed. To this end, among the various genes involved in both the control of the distribution and the level of DNA methylation, we will select those that participate in the establishment of the marks analyzed in task 1. These will include genes coding for DNA methylase 1 (MET1) and chromomethylase 3 (CMT3), which are involved in the maintenance of CG, CHG and CHH methylation respectively. We will also analyze genes involved in the decrease of

DNA methylation such as DDM1 and/or DNA demethylases, which are key genes to reset methylation marks. The main task of the postdoc will be to produce the transgenic lines for all the listed genes and to characterize them in terms of phenotype, molecular and epigenetic responses. The transformed genotypes will be analyzed under water-limited and water-free conditions. For the different sampling points, we will investiagte the transcriptome and epigenome for each line produced. This approach should allow, (a) determining the role the genes involved in the regulation of methylation on the topology of the gene networks involved in the response to stresses and, (b), to formulate hypotheses on the molecular mechanisms underlying the epigenetic response and its short and/or long-term memory effects in the response of plants to a changing environment.

(2) He will participate in the analysis of data generated by RNA seq and WGBS of plants (oak, grapevine, apricot) grown under control conditions or subjected to combined stress (I;E; fusarium andwater stress). In particular, after sequence trimming, alignment of on reference genomes (oak, grapevine, apricot), data will be used to determine, differentially expressed genes (DEGs) between the conditions tested and, parts of the genome whose methylation varies according to the growth conditions of the plants. Finally, we will determine which of the DEGs are likely controlled by their methylation level. In addition, these data will be used to investigate the consequences of growth conditions on transposons (expression mobility) and their possible impact on nearby genes.

Environment: The project takes place at the INRAE sites of Grande Ferrade, in Villenave D'ornon, and Pierroton, and will require regular travel between these two work sites. It is placed under the responsibility of Dr G. Le Provost (UMR BIOGECO) and Pr P. Gallusci (UMR EGFV); the two UMRs are recognised for their expertise in genetics, epigenetics, molecular biology and physiology of perennial plants (vine and oak) and have developed the necessary expertise in bioinformatics for "omics" analyses. Both sites have all the equipment necessary for molecular biology, in vitro culture and plant cultivation.

Bordeaux is an easy-going and enjoyable UNESCO world heritage city with many cultural, social, sportive events, famous for its vineyards and only one hour away from marvellous sand beaches.

Skills: The recruited person should have expertise in the field of molecular biology and epigenetics, combined with a good knowledge of perennial plants (grapevine, oak, other). A first experience in in vitro plant culture and in the manipulation of transgenic plants is desirable, if possible including a knowledge of transgenesis systems related to grapevine and/or other perennial plants and of cloning methodologies.

The candidate should also have previous experience in the analysis of omics data, at least RNA-seq data, but a first experience in the analysis of Whole Genome Bisulfite Sequence data would be also highly appreciated. Knowledge of R is desirable. The person should be able to work independently and have the ability to interact with several partners located on different sites in Bordeaux. A good knowledge of English is required, as well as writing and good communication skills.

Selection process: Candidates will submit their application, consisting of a cover letter (2 pages maximum) and a CV (including list of publications, if applicable), to Grégoire Le Provost (UMR BIOGECO) and Philippe Gallusci (UMR EGFV) **before the 2022/04/30**.

Team/lab website:
https://www6.bordeaux-aquitaine.inrae.fr/egfv/
https://www6.bordeaux-aquitaine.inrae.fr/biogeco

Selected publications:

📌 Plomion C., Aury J.-M., Amselem J., Leroy T., Murat F., Duplessis S., Faye S., Francillonne N., Labadie K., **Le Provost G**., Salse J. (2018). Oak genome reveals facets of long lifespan. *Nature Plants*, 4 (7), 440-452.

📌 Sow M. D., Allona I., Ambroise C., Conde D., Fichot R., Gribkova S., Jorge V., **Le Provost G**., Pâques L., Plomion C., Salse J., Sanchez Rodriguez L., Segura V., Tost J., Maury S. (2018). Epigenetics in Forest Trees: State of the Art and Potential Implications for Breeding and Management in a Context of Climate Change, *Epigenetics Coming of Age for Breeding Applications*. Academic press, Elsevier, 454 p.

📌 B. Rubio, L. Stammitti, S. J. Cookson, E. Teyssier, **P. Gallusci**. Small RNA populations reflect the complex dialogue established between heterograft partners in grapevine, *Horticulture Research*, Volume 9, 2022, uhab067, https://doi.org/10.1093/hr/uhab067.

📌 **P. Gallusci**, Z. Dai, M. Génard, A. Gauffretau, N. Leblanc-Fournier, S. Brunel-Muguet. Epigenetics for plant improvement: current knowledge and modeling avenues, (2017) *Trends in plant science* 22 (7), 610-623.

📌 Fortes A.M. and **Gallusci P**., Plant Stress Responses and Phenotypic Plasticity in the Epigenomics Era: Perspectives on the Grapevine Scenario, a Model for Perennial Crop Plants. (2017) *Front. Plant Sci.* 8:82. doi: 10.3389/fpls.2017.00082.

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