

## **AAP China Scholarship Council - CSC 2023 PROJET DE RECHERCHE DOCTORALE (PRD)**

**Titre du PRD : Retrograde Signalling during seed dormancy and germination**

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Ecole doctorale de rattachement : ED515 - Complexité du vivant

Nombre de doctorants actuellement encadrés : 1

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Unité de recherche : Code (ex. UMR xxx) et Intitulé : UMR 7622, IBPS, Biologie du Développement, Sorbonne Université, Paris, F-75005 France

Ecole doctorale de rattachement : ED515 - Complexité du vivant

Nombre de doctorants actuellement encadrés : 10

CO-TUTELLE INTERNATIONALE envisagée :  OUI  NON

## DESCRIPTIF du PRD :

*Ce texte sera affiché en ligne à destination des candidates et candidats chinois : il ne doit pas excéder 2 pages doit être rédigé en ANGLAIS*

Gene regulation is a dynamic process in which transcription factors (TFs) play an important role. TFs control gene expression in different cell types and tissues, by recognizing and binding short cis-regulatory DNA sequences called TF binding sites (TFBS) in their target genes. The identification of chromatin accessibility profiles and cis-regulatory elements (CREs) that fine-tune gene expression during seed germination may open new perspective for genetic engineering crops. Because of their role as master regulators of clusters of genes, TF are important targets also to ideotype new crop varieties that can enhance stress tolerance on yield under field conditions.

Reactive oxygen species (ROS) signaling is a common theme during abiotic and biotic stresses. During seed dry storage, ROS participate to dormancy release through the direct oxidation of a subset of biomolecules. Moreover, ROS are involved in the perception and transduction of environmental conditions during seed imbibition. It has also been proposed that ethylene and ROS could act in concert to control seed dormancy release (Corbineau et al., 2014). Recently in the Seed Development team, it has been shown that the effect of ethylene on seed germination requires ROS production by the mitochondrial electron transport chain. Seed response to ethylene involved a mitochondrial retrograde response (MRR) through nuclear ROS production and upregulation of several TFs (Jurdack et al. 2021).

We are interested in the regulation of ROS-related TFs and its target genes during seed dormancy and germination. A preliminary analysis has revealed the expression pattern of 27 ROS-response TFs during seed germination. During the PhD, the doctorant student will perform a screening based on seed dormancy/germination phenotypes of some TF mutants. T-DNA insertion lines or mutant alleles generated using a CRISPR/Cas9-based genome editing system will be used to characterize their seed dormancy/germination behavior.

A particular interest will be done to ANAC13 and ANAC17, two TFs strongly implicated in ROS signaling during seed germination and previously involved in MMR. Recently, a catalog of TFBS was generated on 1,812 TFs from Arabidopsis (including ANAC13 and ANAC17) using a DNA affinity purification sequencing (DAP-seq) approach (O'Malley et al., 2016). Based on this dataset, TFBS on candidate gene targets will be explored, to validate the implication of ANAC13/17 in its gene regulation. ANAC13/17 were previously reported to have a role in plant responses to environmental stresses, such as salinity, drought, heavy metals, cold, hypoxia, high light and infection by bacterial and fungal pathogens. We will explore the implication of ANAC13/17 during seed germination under different stress conditions. Moreover, the combination of this research with other axes developed in the Seed Biology team (lncRNAs associated to seed germination) may contribute to identify additional layers of gene regulation.

- a) Characterization of ROS-response TFs during seed germination using mutants and marker lines (roGFP-Orp1 addressed to different cellular compartments)
- b) Identification of targets genes and binding sites of selected TFs (ANAC13 and ANAC17)
- c) Validation of TFBS, generation of new mutants and phenotyping
- d) Integration of new genes in the MMR model during seed germination

Methodologie: We are going to implement several physiological (germination assays in various environmental conditions), biochemical (ROS chemistry, oxidative processes, metabolomics) and molecular (transcriptome, DAP-seq, CRISPR-Cas9) approaches during this internship and the following PhD project. The technology department of the IBPS provides several infrastructures (plant growth chambers, greenhouse) and methodological services (imaging, bioinformatics and proteomics) necessary to successfully perform this project. The "Seed Biology" team also has a strong background in translational biology with crop species (sunflower, barley), opens new applications to the outputs of this research project.

References :

Corbineau, F., Xia, Q., Bailly, C., El-Maarouf-Bouteau H. (2014). Ethylene, a key factor in the regulation of seed dormancy. *Front Plant Sci* 2014 Oct 10;5:539. doi: 10.3389/fpls.2014.00539. eCollection 2014.

Jurdak, R., Launay-Avon, A., Paysant-Le Roux, C. and Bailly, C. (2021). Retrograde signaling from the mitochondria to the nucleus translates the positive effect of ethylene on dormancy breaking of *Arabidopsis thaliana* seeds. *New Phytol*, 229: 2192-2205. <https://doi.org/10.1111/nph.16985>

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