



**SORBONNE  
UNIVERSITÉ**

## **CHINA SCHOLARSHIP COUNCIL**

Appel à projets

Campagne 2022

<https://www.sorbonne-universite.fr>

**Title of the research project :**

**Thesis supervisor (HDR) :**

Name :

Surname :

Title :

email :

Professional address :

*(site, dresse, bulding, office...)*

**Research Unit**

Name :

Code *(ex. UMR xxxx)* :

**Doctorate School**

Thesis supervisor's doctorate school (candidate's futur doctoral school) :

PhD student currently supervised by the thesis supervisor (number, year of the first inscription) :



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**Joint supervisor :**

Name :

Surname :

Title :

email :

Professional adress :

*(site, dresse, bulding, office...)*

**Research Unit**

Name :

Code *(ex. UMR xxxx)* :

**École doctorale**

Joint supervisor's doctorate school :

Or, if non SU :

PhD student currently supervised by the joint supervisor (number, year of the first inscription) :

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**Joint supervisor :**

Name :

Surname :

Title :

email :

Professional adress :

*(site, dresse, bulding, office...)*

**Research Unit**

Name :

Code *(ex. UMR xxxx)* :

**École doctorale**

Joint supervisor's doctorate school :

Or, if non SU :

PhD student currently supervised by the joint supervisor (number, year of the first inscription) :

## Description of the research project : Chromatin dynamics in the control of seed germination

### *Context*

Agriculture is confronted to major challenges, with unpredictable and warmer climate, but also to growing food needs due to human regulations and population increase. Climate change is expected to bring warmer temperatures, changes to rainfall patterns and frequency with an increase in heavy precipitation events and flooding in temperate regions including the possibility of coastal storms, and perhaps severity of extreme weather. In drier areas, climate models predict increased plant evapotranspiration and lower soil moisture levels (IPCC, 2007). By the end of this century, the global mean temperature could be 1.8° to 4.0°C warmer than at the end of the previous century (IPCC, 2007; Walck et al., 2011).

Since crop productions are highly dependent on climate conditions, there is an urgent need to adapt and improve agricultural productivity and thwart the negative economic aspects. Climatic changes could impact differentially and in complex ways crop production and industry: directly through changes in agronomic conditions, and indirectly by the impact on growth and distribution of incomes for agriculture demand (Schmidhuber and Tubiello, 2007). Global warming also increases water demand for agriculture whereas in parts of the world rainfall decline and water available for irrigation will become more variable leading to drought stress. Water stress during the reproductive or germination phase of crops will be particularly harmful (Hatfield et al., 2011).

Seeds are at the core of agriculture, both for plant life and as a major source of food for humans and animals. In the race of crop adaptation and yield improvement under changing environments, efficiency of germination is a strategic step on which research efforts should focus. Indeed, germination efficiency is vital for seed vigor, homogenous seedling emergence and crop yield since this is the first step in plant life for which timing strongly impacts further plant development. This is why the molecular pathways involved in germination, which integrate developmental and environmental signals, need to be better understood to adapt agriculture practices, such as seed production and sowing, to the climatic changes due to global warming.

### *Objectives and hypothesis*

Adaptation of plants to their environment mostly relies on transcriptional changes. This is also true for seeds, which have to make a decision to germinate in response to a combination of environmental and genetic factors during their imbibition. This relies on synchronized mechanisms involving the perception of environmental signals, either positive or negative, their translation into a cellular signal and an appropriate response at the transcriptomic level.

**Reactive oxygen species (ROS)** are important means for translating environmental cues into cellular signaling components. Extensive studies from Bailly's lab have shown that homeostasis of ROS during seed imbibition drives the completion of the whole germination process. ROS overproduction under stressful conditions could indicate adverse conditions for radicle protrusion and thus prevent this process as it has been demonstrated that ROS are able to reshape gene expression in specific manners (El-Maarouf-Bouteau et al. 2015, Willems et al. 2016), yet, molecular mechanisms by which ROS impact on gene expression remain poorly explored. An increasing number of studies are unveiling how transcriptional regulation is influenced by the structural context in which it occurs, and how it can be regulated by chromatin-based mechanisms in eukaryots. Chromatin organization allows structuring genomic DNA within the nucleus, and also actively participates in the regulation of gene expression in response to developmental or environmental stimuli. Controlled changes of chromatin states along the genome allows for a tight control of the genome expression program, which is continuously fine-tuned during the plant life cycle and that is subject to dramatic changes during developmental transitions. **The thesis project aims to define the chromatin-level regulatory processes impacting seed germination capacity.** Both gene-specific chromatin state

changes and higher-order chromatin rearrangements are at play during this key plant developmental switch (van Zanten et al. 2011), but the regulatory mechanisms involved and their functional significance are largely unexplored.

The thesis project proposes to combine epigenome and transcript profiling with a detailed study of ROS-mediated nuclear reorganization during seed germination in the *Arabidopsis thaliana* plant model species. To tackle this objective, the work-plan will assess more specifically how reactive oxygen species, which are major regulators of germination, impact chromatin and downstream regulatory processes. The identification of key genes influenced by chromatin-level and ROS controls in *Arabidopsis thaliana* will constitute an important step to transfer the acquired knowledge, notably defining novel molecular markers of seed vigor in species of agro-economical importance.

### **Project organization**

#### **1. Involvement of ROS production in response to water stress**

ROS homeostasis in *Arabidopsis* seeds in the presence of water or under water stress conditions will be investigated by confocal microscopy. ROS production will be assessed using ro-GFP reporter lines, specific for various subcellular compartments: mitochondrial ro-GFP, nucleic ro-GFP and cytoplasmic ro-GFP. Additionally, the functional role of ROS during the germination response to water stress will be assessed using mutants in the Col background showing altered ROS production (RESPIRATORY BURST OXIDASE HOMOLOG (*rboh*) D, *rbohB*, *rbohBD*) or scavenging (catalase, *cat2-1*; Vitamin E, *vte1-1*).

#### **2. Transcriptome adaptation of *Arabidopsis* seeds germinating under water stress conditions**

To gain insights into the effect of ROS homeostasis on gene expression, the transcriptome of WT seeds and selected mutants will be analysed. RNA-seq analysis of WT seeds treated with H<sub>2</sub>O<sub>2</sub>, which will constitute a direct and positive control for the oxidative response of gene expression to ROS will be performed. The results of RNA-Seq will allow identifying gene regulatory networks activated by ROS in the context of seed germination.

#### **3. Role of histone variants and post-translational modifications in gene expression**

Germination efficiency under normal, water stress and H<sub>2</sub>O<sub>2</sub> treatment conditions for mutants in histone variants will be assessed. For single mutant lines or mutant combinations with the most prominent alterations in germination efficiency, mRNA-seq under normal and water stress conditions will be performed to investigate the impact of stress on the transcriptome of germinating seeds.

#### **4. Chromatin state variations during germination in a genome wide manner**

To investigate the direct influence of histone variants on the epigenome, we will profile tagged histone variants and their modified forms as well as RNA Pol II in WT and mutant plants. This will allow identifying changes in chromatin states and activity during germination. For histone modifications, ChIP-seq analyses will be performed with Reference Exogenous genome experiments (ChIP-Rx) (Orlando et al 2014). These experiments will be complemented by cell-specific analyses of histone variants and modifications using immunolocalization in whole tissues.

#### **5. Impact of ROS homeostasis on chromatin organization.**

Here, the influence of ROS homeostasis on global nuclear organization in individual cells will be assessed. Cytogenetical analyses of higher order chromatin organization in embryonic axis cells under different stress conditions will be performed. Nuclear morphology and heterochromatin condensation will be determined by DAPI DNA-staining of nuclei and 3D imaging of fixed cells, or after DNA Fluorescence *In Situ* Hybridization (FISH) probing heterochromatic repeats. This approach will allow revealing possible changes in nuclear size and shape (e.g. sphericity) or in the distribution of the different chromatin states (e.g. heterochromatin condensation and distribution) within the embryo nuclei, and its potential variations in response to imbalanced ROS homeostasis.

Combined together, the expected results will bring a unique set of novel findings and concepts on the role of chromatin organization during seed germination. They should unravel how ROS-mediated signaling to chromatin-level regulation contributes to cellular adaptations and to efficient seed germination under environmental stress conditions, and further lead to the identification of genes

targeted by these mechanisms. The project is expected to give rise to high impact publications, and to owing to numerous approaches used in this project, experimental training at Sorbonne Université and ENS should give the PhD student a solid background in plant and molecular biology,.

### **Profile of the applicant**

We are seeking an outstanding young scientist who has recently received a M.Sc. degree in Plant Molecular Biology. Applicants should have a demonstrated background and interest in cell signaling and/or molecular physiology. Communication skills, aptitude for collaborative work and fluent English are mandatory. Applicants should fulfill requirements for being eligible for CSC fellowships.

### **Roles of supervisors and 3 of their recent publications related to the subject**

**C. Bailly**, Thesis director, specialist of Seed Biology and ROS metabolism

(<https://scholar.google.com/citations?user=8xmBf7EAAAAJ&hl=fr&oi=ao>)

Jurdak R, Launay-Avon A, Roux CP-L, Bailly C (2021) Retrograde signalling from the mitochondria to the nucleus translates the positive effect of ethylene on dormancy breaking of Arabidopsis thaliana seeds. *New Phytologist* 229, 2192-2205.

Layat E, Bourcy M, Cotterell S, Zdzieszńska J, Desset S, Duc C, Tatout C, Bailly C, Probst AV (2021) The Histone Chaperone HIRA Is a Positive Regulator of Seed Germination. *International Journal of Molecular Sciences* 22: 4031

Bailly C (2019) The signalling role of ROS in the regulation of seed germination and dormancy. *Biochemical Journal*, 476, 3019–3032.

**F. Barneche**, co-director, expert in epigenetics and chromatin organization

(<https://scholar.google.com/citations?hl=fr&user=xjP-VXAAAAAJ>)

Bourbousse C, Barneche F, Laloi C (2020) Plant Chromatin Catches the Sun. *Frontiers in Plant Science* 10: 1728

Fiorucci A-S, Bourbousse C, Concia L, Rougée M, Deton-Cabanillas A-F, Zabulon G, Layat E, Latrasse D, Kim SK, et al F Barneche (2019) Arabidopsis S2Lb links AtCOMPASS-like and SDG2 activity in H3K4me3 independently from histone H2B monoubiquitination. *Genome Biology* 20: 100

Nassrallah A, Rougee M, Bourbousse C, Drevensek S, Fonseca S, Iniesto E, Ait-Mohamed O, Deton-Cabanillas AF, Zabulon G, Ahmed I, Stroebel D, Masson V, Lombard B, Eeckhout D, Gevaert K, Loew D, Genovesio A, Breyton C, de Jaeger G, Bowler C, Rubio V and F Barneche. (2018) DET1-mediated degradation of a SAGA-like deubiquitination module controls H2Bub homeostasis. *eLife* e37892.

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### **References cited**

**El-Maarouf-Bouteau, H., Sajjad, Y., Bazin, J., Langlade, N., Cristescu, S., Balzergue, S., Baudouin, E., and Bailly, C.** (2015) Reactive oxygen species, abscisic acid and ethylene interact to regulate sunflower seed germination. *Plant Cell Env.* **38**: 364-374.

**Hatfield JL, Boote KJ, Kimball BA, Ziska LH, and Al, E** (2011) Climate impacts on agriculture: implications for crop production. *Agron. J.* **103**:351–370

**IPCC** (2007) Bilan 2007 des changements climatiques : Rapport de synthèse. *Change.* doi: 10.1256/004316502320517344

**Orlando, D.A., Chen, M.W., Brown, V.E., Solanki, S., Choi, Y.J., Olson, E.R., Fritz, C.C., Bradner, J.E., and Guenther, M.G.** (2014). Quantitative ChIP-Seq Normalization Reveals Global Modulation of the Epigenome. *Cell Reports* **9**: 1163–1170.

**Schmidhuber, J, and Tubiello, FN** (2007) Global food security under climate change. *Proc Natl Acad Sci U S A* **104**: 19703–19708

**van Zanten, M, Koini, MA, Geyer, R, Liu, Y, Brambilla, V, Bartels, D, Koornneef, M, Fransz, P, and Soppe WJJ** (2011) Seed maturation in Arabidopsis thaliana is characterized by nuclear size reduction and increased chromatin condensation. *Proc. Natl. Acad. Sci. U.S.A.* **108**: 20219–24

**Walck, JL, Hidayati, SN, Dixon, KW, Thompson, K, and Poschlod, P** (2011) Climate change and plant regeneration from seed. *Glob. Chang. Biol.* **17**: 2145–2161

**Willems, P., Mhamdi, A., Stael, S., Storme, V., Kerchev, P., Noctor, G., Gevaert, K., and Van Breusegem, F.** (2016) The ROS Wheel: Refining ROS Transcriptional Footprints. *Plant Physiol.* **171**: 1720–1733.



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### CALENDRIER DE LA CAMPAGNE

#### 26 juillet

Lancement de la campagne

Diffusion de l'appel à projets par les écoles doctorales auprès de leurs encadrantes et encadrants.

#### Jusqu'au 17 septembre

Les chercheurs/enseignants-chercheurs et chercheuses/enseignantes-chercheuses de Sorbonne Université soumettent des propositions de projets de recherche doctoraux à leur directeur et directrice d'école doctorale (en utilisant le formulaire joint) et à l'adresse suivante :

<https://inscriptions.sorbonne-universite.fr/lime25/index.php/344242?lang=fr>

#### Jusqu'au 24 septembre

Les écoles doctorales valident le cas échéant les projets et notifie le collège doctoral de leur décision à l'adresse suivante : [csc-su@listes.upmc.fr](mailto:csc-su@listes.upmc.fr)

#### 1er octobre

Mise en ligne des projets validés sur le site web de Sorbonne Université et ouverture des candidatures

<https://www.sorbonne-universite.fr>

Les candidats chinois prennent contact avec les porteurs et porteuses de projets et leur envoient un dossier de candidature.

Les candidates et les candidats déposent leur dossier à l'adresse suivante :

<https://inscriptions.sorbonne-universite.fr/lime25/index.php/383154?newtest=Y&lang=fr>

#### 31 janvier

Fermeture des candidatures

Les porteurs et porteuses de projet ont transmis la candidature retenue après audition des candidates et candidats à leur école doctorale

#### Jusqu'au 21 février

Après examen, les écoles doctorales envoient les lettres de pré-admission signées et tamponnées des candidats et candidates retenues au collège doctoral

#### 28 février

Le collège doctoral envoie les lettres de pré-admission aux candidates et candidats

#### Jusqu'au 31 mars

Les candidates et candidats retenus par Sorbonne Université candidate sur le site internet du CSC

#### 31 mai

Diffusion des résultats par le CSC auprès de SU

Envoi résultats aux candidates et candidats ainsi qu'aux porteurs et porteuses de projet