Master 2 internship project

**Structural basis for zinc sensing in plants**

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Zinc is an essential micronutrient for all living organisms due to its presence as a structural or catalytic cofactor in proteins, with Zn-binding proteins representing nearly 10% of the proteome in eukaryotes. The risk of Zn malnutrition affects one third of the global human population, impairing cognitive development and immune function, especially in children. Zn-deficient soils account for substantial losses in crop yield and quality and micronutrient deficiencies in Europe are expected to increase with the growth in vegetarianism (Assunção et al. 2022). Enhancing Zn accumulation and Zn-use-efficiency in crops is required to improve plant nutritional value and production in nutrient-deficient soils.

To cope with low zinc availability in soils, plants activate the transcription of a suite of genes encoding transporters and enzymes that enhance zinc acquisition capacity. The team of Ana Assunçao identified the transcription factors that control this response in Arabidopsis thaliana, namely F-group basic region leucine-zipper (**F-bZIP**) transcription factors bZIP19 and bZIP23. Recently, they demonstrated that these transcription factors also act as sensors of intracellular Zn status by direct binding of Zn ions to regulate their activity (Lilay et al. 2021). The Zinc Sensing Motif (**ZSM**) in the **bZIP19/23 proteins** is rich in Cys/His amino acids and has been shown to be necessary for Zn binding. The ZSM is a new Zn binding domain unique to **F-bZIPs** but highly conserved among F-bZIP from all sequenced plants species.

The Master’s project aims at investigating the zinc binding properties of the ZSM. The conformation of a synthetic peptide (≈ 39 amino acids) encompassing the ZSM will be studied by 1H NMR spectroscopy in the absence and in the presence of a range of zinc concentrations. This will allow to determine which residues are involved in Zn binding and how zinc binding affects the conformation of the peptide in solution. To validate the results, peptides containing mutations in these residues will be tested. The affinity of the wild-type and mutant peptides for Zn will be determined by isothermal titration, a technique available at I2BC. This will allow determining whether the affinity of the ZSM for zinc falls in the range of fluctuations of intracellular free zinc concentration previously determined (Lanquar et al. 2014).

We are looking for a highly motivated student with a background in Biochemistry and or Structural Biology to engage in this interdisciplinary and international project. The project will open research perspectives that can be pursued in the context of a joint PhD between Paris Saclay and Porto Universities.

**References**

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