Funded PhD project in Integrated Structural & Cell Biology in Grenoble, France

Title of the PhD project:
MADOF: Evolution of MADS Transcription Factors and the Origin of the Flower

PhD supervisors:
Véronique Hugouvieux veronique.hugouvieux@cea.fr

Host laboratory:
Cell & Plant Physiology Laboratory (LPCV), StrucDev team
https://www.lpcv.fr/Pages/StrucDev/Presentation.aspx

Project summary:
Since the time of Darwin, a fundamental question in plant biology is how flowering plants, or angiosperms, evolved to dominate the terrestrial landscape, quickly outcompeting their fern and cone-producing gymnosperm ancestors. Gymnosperms produce male and female organs separately, whereas angiosperms unite the male and female organs in the novel architecture of the bisexual flower. The flower is the most important reproductive innovation in the plant lineage, however the molecular origins of flower development have remained elusive. Interestingly, the transcription factors (TFs) that are responsible for organ identity in both gymnosperms and angiosperms are part of the MADS family, an ancient eukaryotic protein family that has undergone a dramatic expansion in plants. The function of the MADS family in directing the male and female organ identity programs depends on their spatially and temporally overlapping expression patterns, the specificity of the MADS TF heteromeric complexes formed and the unique DNA-binding and protein-protein interaction patterns of the resulting complexes. However, what determines the components of the MADS transcriptional complexes and how these complexes encode distinct developmental programs is still unclear. The proposed thesis project will use an integrated approach spanning the atomic to the organism level and directly address the molecular origins of the flower.

Preferred skills: Knowledge of molecular biology, biochemistry and/or plant genetics is desired. The student will be able to learn required techniques within the team.

Student role: The student will initially focus on the structure-function of the Class C MADS TFs and complexes from angiosperms and gymnosperms. These experiments include recombinant protein production and purification, biochemical characterisation and functional assays, crystallisation trials, diffraction screening and structural characterisation in collaboration with the European Synchrotron Radiation Facility. The DNA-binding activity of the purified complexes will be determined by electromobility shift assay and genome wide using sequential DNA affinity purification and sequencing, a technique developed for MADS TFs in the host laboratory. The student will perform bioinformatics analysis under the supervision of an experienced bioinformatician. In planta function will be characterized by genetic analysis in Arabidopsis. The student will have the opportunity to learn a wide variety of techniques as part of an exciting and dynamic team.

Keywords:
MADS transcription factors, evolution, flower development, protein-protein interactions, DNA binding

Relevant publications of the team:

- X. Lai, et al., **(2021)** The intervening domain is required for DNA-binding and functional identity of plant MADS transcription factors. **Nat Commun.** 6;12(1):4760.
- X. Lai, et al., **(2020)** Genome-wide binding of SEPALLATA3 and AGAMOUS complexes determined by sequential DNA-affinity purification sequencing. **Nucleic Acids Res.** 48 (17) : 19637–9648.
- X. Lai, et al., **(2019).** Structural Basis for Plant MADS Transcription Factor Oligomerization. **Comput Struct Biotechnol J.** 17:946-953.
- V. Hugouvieux et al., **(2018)** Tetramerization of MADS family transcription factors SEPALLATA3 and AGAMOUS is required for floral meristem determinacy in Arabidopsis. **Nucleic Acids Res.** 1;46(10):4966-4977.
- V.M. Conn, **(2017)**. A circRNA from SEPALLATA3 regulates splicing of its cognate mRNA through R-loop formation. **Nat Plants.** 18;3:17053.