**Master 2 internship project**

**Year 2024-2025**

**Laboratory/Institute:** LPCV CEA Grenoble **Director:** Eric Maréchal

**Team:** Structural Biology and Plant development **Head of the team:** Chloé Zubieta

**Name and status of the scientist in charge of the project:** Véronique Hugouvieux

Scénior Scientist

 **HDR: yesx no ☐**

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**Program of the Master’s degree in Biology:**

**☐** Microbiology, Infectious Diseases and Immunology **☐** Structural Biology of Pathogens

**X** Physiology, Epigenetics, Differentiation, Cancer **☐** Neurosciences and Neurobiology

**Title of the project:** Structure-function of MADS TFs in Gymnosperm and Angiosperm reproductive organs

Objectives (up to 3 lines): Our aim is to investigate the rules for MADS complex formation and function in male and female organs in Gymnosperms and compare this with Angiosperm male and female MTF complexes to understand the evolution of protein-protein interaction and function within this transcription factor family

Abstract (up to 10 lines):

MIKC-like MADS family transcription factors regulate the formation of flower organs (sepals, petals, stamens and carpel) in Angiosperms. These bind DNA in the form of dimers by binding to one site, but also in the form of tetramers capable of looping DNA by binding to two sites. The formation of tetramers requires the presence of MADS E. We have recently demonstrated the necessity of the formation of tetramers in vivo for the smooth running of flower development programs. In Gymnosperms, which produce two independent reproductive structures, male and female cones, the genes coding for the E protein do not seem to be present, but the B and C genes allowing the production of the sexual organs were identified. Our aim is to investigate the rules for MADS complex formation and function in male and female organs in Gymnosperms and compare this with Angiosperm male and female MADS complexes. The oligomerization state, ability to bind DNA (single or double site) and to regulate gene expression will be analyzed in vitro and using simplified in vivo reporter assays for gymnosperm B and C class

Methods (up to 3 lines): Experiments include recombinant protein production and purification, biochemical characterization and functional assays. Functional assays include electromobility shift assay and genome wide analysis using sequential DNA affinity purification and sequencing, and transient expression assays in protoplasts.

Up to 3 relevant publications of the team:

-Hugouvieux et l. (2024) [SEPALLATA-driven MADS transcription factor tetramerization is required for inner whorl floral organ development.](https://pubmed.ncbi.nlm.nih.gov/38771250/) ***Accepted in Plant Cell***

-Lai et al., (2020).  [Genome-wide binding of SEPALLATA3 and AGAMOUS complexes determined by sequential DNA-affinity purification sequencing.](https://pubmed.ncbi.nlm.nih.gov/32890394/) ***NAR.***25;48(17):9637-9648.

-Lai et al., (2021) [The intervening domain is required for DNA-binding and functional identity of plant MADS transcription factors.](https://pubmed.ncbi.nlm.nih.gov/34362909/) ***Nat Commun***. 6;12(1):4760

Requested domains of expertise (up to 5 keywords): MADS Transcription Factors, Evolution, Protein-Protein interaction, oligomerization