Funded PhD project in Integrated Structural & Cell Biology in Grenoble, France (2025-2028)

Title of the PhD project: Floral Complexes

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Host laboratories: Laboratoire de Physiologie Cellulaire et végétale (LPCV) and Institut de Biologie Structurale
Host teams: Flo_Re team (LPCV) and MEM team (IBS)
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Project summary: The LEAFY transcription factor (LFY) is a universal regulator of flower formation. It plays a central role in the development of the floral bud from its emergence to the formation of the organ whorls (sepals, petals, stamens and pistil). At the molecular level, LFY acts by activating the ABC homeotic genes, responsible for the identity of the flower's organs.

To carry out its various functions, LFY interacts with different protein partners, whose action modulates its activity in space and time. Although these partners have long been identified, their mechanisms of action remain largely unknown at the molecular and structural level. We have recently elucidated the mechanism of induction of class B genes by the complex formed by LFY and its partner UFO. We have shown that UFO enables LFY to recognize cis-elements in the B gene promoter that LFY cannot bind alone. Cryo-electron microscopy revealed the ability of UFO to interact directly with DNA and with LFY, an unexpected property for this factor.

However, the mechanisms by which LFY interacts with its partners to induce class A genes (initiation of the floral meristem) and class C genes (formation of reproductive organs) remain to be explored. The aim of FLOCOM is to elucidate the molecular role of the LFY-BOP2 complex, involved in the activation of class A genes, and the LFY-WUSCHEL complex, necessary for the induction of class C genes. We will adopt an integrative approach by combining functional analyses in Arabidopsis protoplasts, which allow rapid characterization of the targets regulated by these complexes, with biochemical and structural studies. In vitro genomics experiments will be used to identify the targeted DNA sequences, while cryo-electron microscopy will be used to reveal the architecture of the LFY-BOP2 and LFY-WUSCHEL complexes associated with DNA. This project aims to resolve fundamental questions about the molecular mechanisms that diversify the functions of LFY and to make significant advances in our understanding of floral development in angiosperms.

Preferred skills: Biochemistry (bacterial and insect cell protein expression, recombinant protein purification, biophysical protein/DNA characterization).

Student role: The PhD student will be in charge of expression experiments in protoplasts, production of proteins and characterization of protein/DNA complexes by DAP-seq, EMSA and cryo-EM. Bioinformatics analyses will be carried out in collaboration with members of the Flo_Re team (LPCV) and cryo-EM analyses in collaboration with the MEM team (IBS).

Keywords: Flower development, Transcriptional regulation, Integrative structural biology, Cryo-EM

Relevant publications of the team:

Azpeitia, E., Tichtinsky, G., Le Masson, M., Serrano-Mislata, A., Lucas, J., Gregis, V., Gimenez, C., Prunet, N., Farcot, E., Kater, M. M., et al. (2021). Cauliflower fractal forms arise from perturbations of floral gene networks. **Science.** 373:192–197.
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Rieu, P., Beretta, V. M., Caselli, F., Thévénon, E., Lucas, J., Rizk, M., Franchini, E., Caporali, E., Paleni, C., Nanao, M. H., et al. (2024). The ALOG domain defines a family of plant-specific transcription factors acting during Arabidopsis flower development**. Proc. Natl. Acad. Sci.** 121:2017.
Hugouvieux, V., Blanc-Mathieu, R., Janeau, A., Paul, M., Lucas, J., Xu, X., Ye, H., Lai, X., Le Hir, S., Guillotin, A., et al. (2024). SEPALLATA-driven MADS transcription factor tetramerization is required for inner whorl floral organ development. **Plant Cell** 36:3435–3450.
Blanc-Mathieu, R., Dumas, R., Turchi, L., Lucas, J., and Parcy, F. (2024). Plant-TFClass: a structural classification for plant transcription factors**. Trends Plant Sci.** 29:40–51.

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