

INTERNSHIP PROPOSAL

Institute and Group: BIG/LPCV/Regulators of flower development

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Research project title: Deciphering the structure and function of the master floral complex

5 Keywords to describe the project: Flower development, transcriptional protein complex, ubiquitination, biotechnology

Description of the project (aims, experimental techniques, recommended background):

10 to 15 lines:

Flowering plants are the most successful group of plants. Flowers are the basis for fruits and seeds used for human and animal consumption. The architecture of the structure bearing the flowers (the inflorescence) has aesthetic importance, but also a strong influence on yield or harvest mode. Key regulators of floral development are known. Among them, the LEAFY transcription factor stands out as THE cardinal actor orchestrating this process. However, as shown in many species, LFY activity highly depends on its physical interaction with the UFO protein, a subunit of an ubiquitin ligase complex. Strikingly, a variant of UFO is sufficient to trigger flower development onto the surface of leaves. The goal of the project is double: engineer an artificial regulator based on LFY and UFO to trigger flower development from any plant tissue and understand the LFY-UFO interaction at the structural and functional levels.

Justification that the internship's subject fits with the general theme of GRAL (3 lines):

This is an integrated structural biology project comprising i) experiments in planta (creating a tool to induce flowers and analyse post-translational modifications of a master floral regulator)

ii) an in vitro study of the LFY-UFO regulatory complex that we will analyse at the biochemical and structural levels to provide a molecular description of their interaction as well as novel tools to precisely disrupt this interaction in plants.

Relevant publications of the team (3 max):

[1] Denay, G., Chahtane, H., Tichtinsky, G. and Parcy, F*. 2017. A flower is born: an update on Arabidopsis floral meristem formation. **Current Opinion in Plant Biology**. 35, 15–22.

[2] Sayou, C., Monniaux, M., Nanao, M.H., Moyroud, E., Brockington, S.F., Thévenon, E., Chahtane, H., Warthmann, N., Melkonian, M., Zhang, Y., Wong, G.K.-S., Weigel, D., Parcy, F*. and Dumas, R. 2014. A promiscuous intermediate underlies the evolution of LEAFY DNA binding specificity. **Science**. 343, 645–8.



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[3] Sayou, C., Nanao, M.H., Jamin, M., Posé, D., Thévenon, E., Grégoire, L., Tichtinsky, G., Denay, G., Ott, F., Peirats Llobet, M., Schmid, M., Dumas, R. and Parcy, F*. 2016. A SAM oligomerization domain shapes the genomic binding landscape of the LEAFY transcription factor. **Nature communications**. 7, 11222.