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**Host laboratory:**

LPCV, Flo\_Re team  
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**Title of the M2 research internship:**

Molecular transcriptional complex controlling stamen and pistil development in Arabidopsis

**Project summary:**

LEAFY (LFY) is a unique transcription factor known as a master gene controlling flower development, especially through the regulation of the ABC model floral organ genes. WUSCHEL (WUS) is another transcription factor, belonging to the homeobox family, considered as the main regulator of stem cell identity in shoot and floral meristems. Surprisingly genetic data indicated that the control of stamen and pistil formation by LFY is dependent on WUS, both genes regulating the expression of the C MADS-Box gene AGAMOUS (AG) in charge of stamen and pistil identity. WUS and LFY act synergistically to induce AG expression. They bind adjacent sites on AG regulating intron but not simultaneously, which raises the question of the mechanistic of their joint action. Moreover AG activation by WUS relies on a WUS domain known to be involved in the repression of other target genes. The molecular aspects of AG regulation by WUS and LFY therefore remains very unclear. The aim of this project is to explore how LFY and WUS interact to control AG expression.

In our lab we have a large experience on LFY function at the genetic, molecular and structural level, as well as on its interaction with DNA and with different protein partners. In this project we will address the function of WUS (and of WUS sub-domains) in the LFY-joint regulation of AG using a wide range of techniques. Direct interaction between LFY and WUS will be tested by yeast 2-hybrid approaches. Their behaviour on AG regulating sequences will be assayed by EMSA using insect cells produced WUS domains and possibly visualized cryo-electron-microscopy if the complex is sufficiently purified. In parallel the functionality of AG regulation by LFY and WUS or WUS sub-domains and mutants will be followed using a protoplast gene expression system. Interest for plant development is a bonus but is not absolutely required.

**Keywords:**

DNA protein complex, transcription, plant development

**Relevant publications of the team:**

Azpeitia, E., Tichtinsky, G., Le Masson, M., Serrano-Mislata, A., Lucas, J., Gregis, V., ... & Parcy, F. (2021). Cauliflower fractal forms arise from perturbations of floral gene networks. *Science*, 373(6551), 192-197.

Lai, X., Blanc-Mathieu, R., Grandvuillemin, L., Huang, Y., Stigliani, A., Lucas, J., ... & Parcy, F. (2021). The LEAFY floral regulator displays pioneer transcription factor properties. *Molecular Plant*, 14(5), 829-837.

Grégoire, D., Gabrielle, T., Hicham, C., Sylvie, H., Irene, L. V., Christian, W., ... & François, P. (2018). Control of stem-cell niche establishment in Arabidopsis flowers by REVOLUTA and the LEAFY-RAX1 module. *bioRxiv*, 488114.

Sayou, C., Nanao, M. H., Jamin, M., Posé, D., Thévenon, E., Grégoire, L., Tichtinsky G., ... & Parcy, F. (2016). A SAM oligomerization domain shapes the genomic binding landscape of the LEAFY transcription factor. *Nature communications*, 7(1), 1-12.