

Master 2 research internship in Integrated Structural & Cell Biology in Grenoble

Supervisor(s):

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Host laboratory:

Lab : LPCV, <https://www.lpcv.fr/en>

Host group/team:

ChromDev: Chromatin Dynamics and Developmental Transitions, <https://www.lpcv.fr/en/ChromDev>

Title of the M2 research internship:

Epigenetic control of flowering time by Polycomb complexes

Project summary:

In plants, flowering is a critical developmental transition that marks the onset of the reproductive phase, leading to flower and seed formation. The timing of flowering is tightly regulated by a module of two transcription factors with opposing functions: FLOWERING LOCUS C (FLC) acts as a key repressor by inhibiting the expression of FLOWERING LOCUS T (FT), a central activator of flowering.

Epigenetic regulators from the Polycomb Repressive Complex 2 (PRC2) modulate the expression of *FLC* and *FT* in a differential manner, thereby influencing the balance between repression and activation and ultimately determining the flowering decision.

The Master's student will contribute to investigating the differential regulation of *FLC* and *FT* by PRC2, using molecular genetics approaches to understand the conditions under which repression overrides activation, and vice versa.

To achieve this, the student will analyze a set of plant lines (combining gain- and loss-of-function mutants, including some CRISPR-induced) by:

- Characterizing developmental phenotypes, particularly flowering time
- Measuring *FLC* and *FT* gene expression using RT-qPCR
- Examining the chromatin landscape of *FLC* and *FT* loci using ChIP-qPCR (to assess PRC2 binding and epigenetic marks such as H3K27me3, H3K27ac, and H3K36me3) and ATAC-seq

We are looking for candidates with a strong interest in epigenetic regulation of development and some expertise in chromatin biology and molecular genetics. Prior experience with the *Arabidopsis thaliana* model is not required.

Keywords:

Cell fate

Gene expression

Chromatin complexes and histone marks

Relevant publications of the team:

Vangeli Geshkovski, Julia Engelhorn, Jean-Baptiste Izquierdo, Hamida Laroussi, Caroline Thouly, Laura Turchi, Marie Le Masson, Emmanuel Thévenon, Ambre Petitalot, Lauriane Simon, Sophie Desset, Philipp Michl-Holzinger, Hugues Parrinello, Klaus D. Grasser, Aline Probst, Raphaël Margueron, Gilles Vachon, Jan Kadlec, Cristel C. Carles (2024). The dual trxG/PcG protein ULTRAPETALA1 modulates H3K27me3 and directly enhances POLYCOMB REPRESSIVE COMPLEX 2 activity for fine-tuned reproductive transitions. *BioRxiv* 2024; doi: <https://doi.org/10.1101/2024.10.21.619451>

K. Fal*, S. El Khoury, M. Le Masson, A. Berr, C.C. Carles (2025). CRISPR/dCas9-targeted H3K27me3 demethylation at the *CUC3* boundary gene triggers ectopic transcription and impacts plant development. In press at *iScience* and available on *BioRxiv* 2024; <https://doi.org/10.1101/2024.03.18.585636>

K. Fal, A. Berr, M. Le Masson, A. Faigenboim, E. Pano, N. Ishkhneli, N-L. Moyal, C. Villette, D. Tomkova, M-E. Chabouté, L. Eshed Williams and C. C. Carles (2023). Lysine 27 of histone H3.3 is a fine modulator of developmental gene expression and stands as an epigenetic checkpoint for lignin biosynthesis in Arabidopsis. *New Phytologist*. <https://doi.org/10.1111/nph.18666>

C. Thouly, M. Le Masson, X. Lai, C.C. Carles, G. Vachon (2020). Unwinding BRAHMA Functions in Plants. *Genes*, 11(1):E90

G. Vachon, J. Engelhorn, C.C. Carles (2018). Interactions between transcription factors and chromatin regulators in the control of flower development. Flowering Newsletter Review, *Journal of Experimental Botany*, 69:2461-2471

Engelhorn, R. Blanvillain, C. Kröner, H. Parrinello, M. Rohmer, D. Pose, F. Ott, M. Schmid, C.C. Carles (2017). Dynamics of H3K4me3 chromatin marks prevails over H3K27me3 for gene regulation during flower morphogenesis in Arabidopsis thaliana. *Epigenomes*, 1(2), 8. doi:10.3390/epigenomes1020008