

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

To be completed and returned to the following address: helene.marche@ibs.fr or labex-gral@univ-grenoble-alpes.fr

Supervisor:

Name : Christel CARLES

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Host laboratory:

Lab : Laboratoire de Physiologie Cellulaire et Végétale (LPCV)

Host group/team:

ChromDev: Chromatin dynamics and Developmental Transitions

<https://www.lpcv.fr/en/ChromDev>

Title of the M2 research internship:

Characterization of the interactions between chromatin modifiers in Arabidopsis

Project summary:

In multicellular eukaryotes, body patterning, developmental transitions and cell fate highly depend on the dynamics of antagonistic chromatin marks, in particular those that correspond to the trimethylation of Histone H3 at Lysine 27 (H3K27me₃, repressive mark) and of H3 at Lysine 36 (H3K36me₃, active mark). In the team, we study chromatin modifying complexes that are key in deposition of H3K27me₃ and removal of H3K36me₃. Our working hypothesis is that they may cooperatively contribute to the switch of several developmental genes from an active to a repressed state. By generating different mutant combinations for these chromatin modifiers in the model plant *Arabidopsis thaliana*, we revealed striking phenotypes including shifts in reproductive transition and de-differentiation of tissue of embryonic origin. **The goal of this Master thesis project** will be to (i) **further characterize the developmental defects of these mutants** - that we are currently introgressing into fluorescent markers lines, and (ii) **assess the underlying molecular regulations**, with transcriptomic and epigenomic approaches - for which starting material will have been prepared. **The candidate** should have a strong interest in epigenetic regulation of development and some expertise in chromatin biology and molecular genetics. Prior experience with the Arabidopsis plant model could be a plus but is not required.

Keywords:

Cell fate, Gene expression, Chromatin modifiers, Histone marks, Polycomb complex
Epifluorescence microscopy, RNA-seq, ChIP

Relevant publications of the team:

Geshkovski V, Engelhorn J, Izquierdo J-B, Laroussi H, Thouly C, Turchi L, Le Masson M, Thévenon E, Petitalot A, Simon L, Desset S, Michl-Holzinger P, Parrinello H, Grasser KD, Probst A, Margueron R, Vachon G, Kadlec J, Carles CC* (2024). The dual trxG/PcG protein ULTRAPETALA1 modulates H3K27me₃ and directly enhances POLYCOMB REPRESSIVE COMPLEX 2 activity for fine-tuned reproductive transitions (2024). *BioRxiv* 2024.10.21.619451; doi: 10.1101/2024.10.21.619451.

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, 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* 238:1085–1100. doi:10.1111/nph.18666.

W. Yan, D. Chen, C. Smaczniak, J. Engelhorn, H. Liu, W. Yang, A. Graf, C.C. Carles, D.X. Zhou, K. Kaufmann* (2018). Dynamic and spatial restriction of Polycomb activity by plant histone demethylases. *Nature Plants* 4(9):681-689. doi: 10.1038/s41477-018-0219-5.

J. 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.

F. Moreau, E. Thevenon, R. Blanvillain, I. Lopez-Vidriero, J.M. Franco-Zorrilla, R. Dumas, F. Parcy, P. Morel, C. Trehin and C.C. Carles* (2016). The Myb-domain protein ULTRAPETALA1 INTERACTING FACTOR 1 controls floral meristem activities in *Arabidopsis*. *Development*, 143(7):1108-19. doi:10.1242/dev.127365.