

Supervisor(s):

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Host laboratory:

LPCV, ChromDev team

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

Title of the M2 research internship:

Epigenome editing effect on chromatin and gene regulation in plants

Project summary:

Considerable advances have been made in identifying epigenetic regulators but so far, studies of epigenomes have mainly derived correlations between chromatin contexts and development. To convert correlation-based findings into mechanistic principles, a challenge in functional epigenomics is to develop and use tools for precise modification of epigenetic marks. The global aim of the project is to use such tools for addressing the functionality of histone marks on the regulation of genes that control plant development and architecture. In the team, we have developed transgenic lines that allow controlling the deposition or removal of histone post-translational modifications (so-called histone marks). In particular, we have obtained proof-of-concept data for the epigenetic edition of the repressive trimethyl mark on Lysine 27 of Histone 3 (H3K27me3), using the dCas9 technology coupled to a demethylase activity: Removal of H3K27me3 was effective in ectopically de-repressing the organ frontier-specific CUC3 gene, and inducing characteristic developmental phenotypes. The next step is to analyse the mechanistic through which a change in the H3K27me3 histone mark induces CUC3 de-repression. For this, the Master student will contribute to follow the dynamics of nucleus and chromatin structure, as well as gene transcription, using in cyto labelling approaches coupled to microscopy imaging, as well as chromatin immuno-precipitation techniques.

We are seeking candidates with a strong interest in epigenetics regulation of development and with some expertise in chromatin biology and molecular genetics. Knowledge on the *Arabidopsis thaliana* plant model isn't a pre-requisite.

Keywords:

histone mark editing, dCas9-based technology, gene expression

Relevant publications of the team:

K. Fal, D. Tomkova, G. Vachon, M-E. Chabouté, A. Berr and C. Carles* (2020). Chromatin manipulation and editing in plants: Challenges, approaches and new technologies. *International Journal of Molecular Sciences* 22(2):512. doi: 10.3390/ijms22020512

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. *Nat Plants*. 4(9):681-689. doi: 10.1038/s41477-018-0219-5

Yan W, Chen D*, Schumacher J, Durantini D, Engelhorn J, Chen M, Carles C, Kaufmann K. (2019). Dynamic control of enhancer activity drives stage-specific gene expression during flower morphogenesis. *Nature Com*, 10(1):1705. doi: 10.1038/s41467-019-09513-2

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