

GRAL MSc RESEARCH SCHOLARSHIP 2020-2021 RESEARCH INTERNSHIP PROPOSAL

Institute / Group

IRIG / PCV - ChromDev

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Research Project Title

Impact of epigenome editing on gene expression and cell fate in Plants

Description of the project

How do higher plants deploy flexible and adjustable developmental programs?

Considerable advances have been made in identifying genetic and epigenetic regulators, but so far, studies of plant 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 tools for precise modification of epigenetic marks. The aim of the project is to use such tools for addressing the functionality of histone marks on plant architecture. The tools, developed in plant transgenic lines, allow inducing deposition or removal of histone post-translational modifications (so-called histone marks), thanks to novel molecular technologies (nanobody or dCas9-driven), in a controlled manner. By analysing developmental phenotypes, cell fates (in situ imaging) and gene expression, the student will follow the effects of induced chromatin dynamics on plant morphogenesis. This internship project should bring a stepping-stone to discoveries of epigenetic determinants for plant plasticity.

We are seeking candidates with a background in DNA technologies and molecular genetics, and showing a strong interest in chromatin biology and development; knowledge on Arabidopsis thaliana plant model isn't a pre-requisite.

Keywords

Chromatin Biology, Histone marks, Polycomb, trithorax, stem cell fate

Relevant publications of the team

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

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