

INTERNSHIP PROPOSAL

Institute and Group: BIG, group LPCV

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Research project title: *In vitro* and *in planta* characterisation of the transcription factor, SEPALLATA3, and ATPase remodeller complexes

5 Keywords to describe the project: transcription factor, ATPase remodeller, chromatin, gene regulation, flower development

Description of the project (aims, experimental techniques, recommended background):

Unlike animals, plants maintain a pool of stem cells in order to produce new organs such as flowers throughout their life cycle. The development of new floral organs (sepals, petals, stamen and carpels) is tightly controlled and requires an exquisite balance between stem cell proliferation and termination. We have recently shown that two splice variants of SEPALLATA3, SEP3.2 and SEP3.3, determine whether stem cell termination occurs (SEP3.2) during flower development or whether stem cells are allowed to proliferate (SEP3.3) resulting in a flower within a flower phenotype (Hugouvioux, in preparation). *We hypothesize that this activity is due to differences in SEP3.3 and*

SEP3.2 recruitment of the ATPase chromatin remodeller, BRM, necessary for the activation of downstream targets. The proposed project will determine the molecular mechanisms of SEP3.2 and SEP3.3 interactions with BRM in vitro and in planta. The student will 1) map the interactions between SEP3.2/3.3 and BRM using yeast two-hybrid experiments 2) express and purify core SEP3/BRM complexes for structural studies and 3) probe the role of SEP3.2/3.3-BRM interactions *in planta* using our available 35S:SEP3.3 and 35S:SEP3.2 overexpression and *brm* knock-out lines. These experiments will define the atomic and molecular mechanisms important for SEP3-BRM interactions and show the physiological *in vivo* role of this complex in stem cell termination and plant development. Knowledge in molecular biology and protein biochemistry would be a desirable.

Relevant publications of the team (3 max): (team members in bold)

1. **Puranik, S.**, Acajjaoui, S., **Conn, S.**, Costa, L., **Conn, V.**, Vial, A., **Marcellin, R.**, Melzer, R., Brown, E., Hart, D., Theissen, G., **Silva, C. S.**, Parcy, F., Dumas, R., Nanao, M. & **Zubieta, C.** (2014). Structural Basis for the Oligomerization of the MADS Domain Transcription Factor SEPALLATA3 in Arabidopsis. *Plant Cell* **26**(9): 3603-3615.
2. Westfall, C.S., Sherp, A.M., **Zubieta, C.**, Alvarez, S., Schraft, E., **Marcellin, R.**, Ramirez, L., Jez, J.M. (2016). Arabidopsis thaliana GH3.5 Acyl Acid Amido Synthetase Mediates Metabolic Crosstalk in Auxin and Salicylic Homeostasis. *Proc. Natl. Acad. Sci.*, accepted.
3. **Silva, C. S.**, **Puranik, S.**, Round, A., Brennich, M., **Jourdain, A.**, Parcy, F., **Hugouvioux, V.** & **Zubieta, C.** (2016). Evolution of the Plant Reproduction Master Regulators LFY and the MADS Transcription Factors: The Role of Protein Structure in the Evolutionary Development of the Flower. *Front Plant Sci* **6**, 1193.



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