

Proposition de Stage

1. Equipe d'Accueil :

- Equipe Morphogenèse Florale, RDP-ENS-Lyon
- Responsable de l'équipe : Mohammed Bendahmane
- Responsable de l'encadrement : Annick Dubois
- Tél : 04 72 72 89 84 ; 04 72 72 86 10
- Courrier électronique : mbendahm@ens-lyon.fr / adubois@ens-lyon.fr
- Adresse Internet de l'équipe : <http://www.ens-lyon.fr/RDP/spip.php?rubrique23&lang=en>

2. Thème du stage: « Caractérisation d'un mutant de morphogenèse florale chez la rose »

Our general objective is to contribute to the understanding of the molecular control of flower architecture in roses. In particular, we aim at identifying how floral organ initiation is controlled, both in organ number and positioning, and how floral organs acquire their identity in roses.

One of the most well known floral abnormality in roses is the “double-flowered” characteristic, which groups all varieties of flowers that develop extra petals. We demonstrated that the restriction of *RhAG* (C-function gene ortholog of *AGAMOUS*) expression domain towards the center of the floral meristem is at the origin of the double flowers phenotype in roses (Dubois et al., 2010). This trait was selected independently during early agricultural days following rose domestication in two distinct domestication areas, *i.e.* China and the Middle East/ Peri-Mediterranean zone. The Master student will address in more details the genetic and molecular basis by which *RhAG* expression domain can be modified in the rose floral meristem, allowing more or fewer petals to form. For this purpose, he/she will study a reversion of the mutation from a 20 petals rose to a single flower rose (5 petals phenotype).

The goal of the Master internship is to identify the molecular mechanism by which this mutation occurred. The student will first perform a fine phenotypic characterization of the 5 petal mutant plant. Recently, we performed RNA-seq experiment in which we compared “simple flower” and “double flower” roses. Data analyses permitted to identify a gene pathway that is shedding light on the mechanisms by which double flowers have been selected. In a second study, the Master student will participate to RNA-seq data validation using high throughput cDNA and DNA quantification methods (such as QPCR, HRM). In parallel he/she will test gene expression modifications of chosen candidate genes and its relation with the double flower phenotype in roses.

3. Publications en relation avec le projet

- Bendahmane M, Dubois A, Raymond O, Le Bris M (2013) Genetics and genomics of flower initiation and development in roses. *J. Exp. Bot* Feb;64(4):847-57
- Dubois A, Carrere S, Raymond O, Pouvreau B, Cottret L, Roccia A, Onesto JP, Sakr S, Atanassova R, Baudino S, Foucher F, Le Bris M, Gouzy J, Bendahmane M. (2012) Transcriptome database resource and gene expression atlas for the rose. *BMC Genomics* 13:638
- Dubois A, Remay A, Raymond O, Balzergue S, Chauvet A, Maene M, Pécrix Y, Yang SH, Jeauffre J, Thouroude T, Boltz V, Martin-Magniette M-L, Janczarski S, Legeai F, Renou JP, Vergne P, Le Bris M, Foucher F, Bendahmane M (2011). Genomic Approach to Study Floral Development Genes in *Rosa* sp. *PLoS ONE* 6(12): e28455.
- Dubois A, Raymond O, Maene M, Baudino S, Langlade NB, Boltz V, Vergne P and Bendahmane M (2010) Tinkering with the C-function: A molecular frame for the selection of double flowers in cultivated roses. *PLoS ONE* 5(2): e9288.
- Scalliet G, Piola F, Douady CJ, Réty S, Raymond O, Baudino S, Bordji K, Bendahmane M, Dumas C, Cock JM, Huguency P (2008) Scent evolution in Chinese roses. *Proc Natl Acad Sci USA* 105: 5927–5932.