



TULIP LabEx

Application form to the “Young Scientists for the Future” Call 2016

- **Research Unit of the PhD student: LIPM**
- **Thesis supervisor: Fabrice ROUX**
- **Co-Supervisor: Dominique ROBY**

Number of post-docs and PhDs currently supervised : Fabrice Roux : 2 x 0.5 PhD - Dominique Roby: 1post-doc, 0.5 PhD

- **Thesis project title: The genetics of plant – plant cooperation in the model plant species *Arabidopsis thaliana***
- **Thesis project description (1.5 page maximum) (Scientific context, Previous results, Project description, References)**

Scientific context. Studying the mechanisms underlying plant-plant interactions is essential to understand the structure and functioning of communities, which may in turn help to predict ecosystem responses to global change (Martorell & Freckleton 2014). It is also of primary importance for the optimization of breeding programs based on crop mixtures (Litrico & Violle 2015). While this exciting challenge calls for a multidisciplinary approach **at the frontier between evolutionary ecology and functional genomics** (Whitham *et al.* 2006; Hendry 2013), we are still at the beginnings of the genetic analysis of plant-plant interactions underlying the adaptive dynamics of plant communities (Bailey *et al.* 2006; Genung *et al.* 2011). In particular, to our knowledge, only two studies have been so far designed to identify Quantitative Trait Loci (QTLs) associated with natural variation of plant-plant interactions, both in the model plant species *A. thaliana*. Although *A. thaliana* has the current status of a pioneer species with low competitive abilities, recent studies have challenged this view by revealing extensive genetic diversity for the response to intra- and interspecific competitive ability (reviewed in Roux & Bergelson 2016).

One of the two studies (Baron *et al.* 2015) has been published by the host team of Fabrice Roux. In this study, based on a local mapping population of *A. thaliana* phenotyped for its competitive ability in presence of four competitor species (*i.e.* *Poa annua*, *Stellaria media*, *Trifolium repens* and *Veronica arvensis*), we found that the response to interspecific competition largely differs among the accessions, suggesting a **biotic specialization** of each accession to a specific competitor species. In addition, based on a Genome Wide Association (GWA) mapping approach, we demonstrated that the QTLs (and the corresponding candidate genes) of competitive ability were dependent on the identity of the competitor species. These results constitute the basis for the understanding of species coexistence and the identification of the molecular mechanisms involved in competitive ability.

This study focused on plant-plant interactions at the interspecific level. In a complementary approach, the next challenge will be to identify the genetic bases associated with plant-plant interactions at the intra-specific level. In particular, studying the genetic diversity and the underlying molecular mechanisms associated with cooperation between genotypes will help to understand **how plants can perceive and discriminate between self, non-self and kin** (Williams 2013).



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Previous results. We recently conducted a GWA mapping study in *A. thaliana* to fine map QTLs associated with natural variation of plant-plant interactions at the intra-specific level. To do so, 192 target accessions of a local mapping population of *A. thaliana* were grown alone or in presence of each of three other partner accessions from the same population. Above-ground vegetative growth of the target and partner plants was estimated showing that competition for resources led in most cases to a reduced growth for one or both interacting plants. Interestingly, we also observed a cooperative strategy for a significant portion of pairwise interactions (between 6.5% and 11.7%, depending on the partner accession) for which an increased growth has been detected for both interacting plants. We identified neat peaks of associations that are clearly different between the three partner accessions, suggesting a biotic specialization between the 192 focal accessions for each of the three partner accessions. **This study is certainly the first one that reports the identification of QTLs associated with natural variation of cooperation.** Preliminary work on the identity of the genes underlying these major QTLs has identified gene involved in functions related to root growth and basal plant defence.

Project description. The objectives of the project will be to elucidate the genetic and molecular bases of cooperation at the intra-specific level in the model plant *A. thaliana*, and will include three main steps:

- (i) To functionally validate the gene(s) underlying the QTL(s) associated with cooperation. This will be performed by phenotyping of (i) mutants affected in this/these candidate gene(s), (ii) complemented mutant lines, and (iii) candidate gene overexpressing lines. This last point will be envisaged according to the candidate gene function.
- (ii) To study the genetic diversity and the selective forces (selective sweeps vs balancing selection...) acting on the functionally validated genes.
- (iii) To study the link between genetic diversity and the degree of intra-specific competition monitored since 2014 in 168 natural populations of *A. thaliana* located in the South-West of France.

Given the absence of genes identified in plant-plant interactions, this project will be a major break-through in the understanding of the molecular mechanisms underlying major interactions in the **social network of plants**.

References.

- Bailey *et al.* 2006 *Ecology Letters* 9: 78–85.
Baron *et al.* 2015 *Functional Ecology* 29: 1361-1370.
Genung *et al.* 2011 *Functional Ecology* 25: 408–419.
Hendry 2013 *Heredity* 111: 456-466.
Lictrico & Violle 2015 *Trends in Plant Science* 20(10): 604-613
Martorell & Freckleton 2014 *Journal of Ecology* 102: 74–85.
Roux & Bergelson 2016 *Current Topics in Developmental Biology* 119: 111-156.
Whitham *et al.* 2006 *Nature* 7: 510-523.
Williams 2013 *Plant Cell* doi/10.1105/tpc.110.tt0310



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- **Project summary (200 words) :**

Plant-plant interactions have been recognized for years as a major factor responsible for plant community dynamics and for productivity and stability of agro-ecosystems. Surprisingly, the dissection of the genetic and molecular mechanisms underlying plant-plant interactions is still in its infancy. In particular, only two studies have been so far designed to identify QTLs associated with natural variation of plant-plant interactions, both in the model plant species *A. thaliana*. By combining cutting edge expertise in genetics, plant molecular and cell biology, and evolutionary ecology, the objective of this project is to identify the genetic and molecular bases of plant-plant interactions at the intra-specific level, notably cooperation where two genotypes grow better in interaction than alone. Based on a GWA mapping approach, we already fine mapped (~20-30kb) three QTLs associated with plant-plant cooperation in *A. thaliana*. This project is based on three main steps: (i) functional validation of the gene(s) underlying the QTL(s) associated with cooperation, (ii) study of the genetic diversity and the selective forces acting on the functionally validated genes, and (iii) study of the link between genetic diversity and the degree of intra-specific competition monitored in natural populations of *A. thaliana*.