



## PROJET CENTRAL LABEX TULIP

**Experimental evolution of phytopathogens and legume symbionts:  
insights into bacterial adaptation to the plant environment**

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**LIPM – UMR 2594 / 441**

### **Scientific objectives**

Plant-microbe interactions, either pathogenic or symbiotic (mutualistic), have a major impact on plant growth and health. Recent molecular advances in their understanding offers new opportunities for controlling plant yield in a sustainable agriculture perspective. At the same time, elucidating how these biotic interactions adapt to challenging anthropogenic or natural conditions is crucial to the long-term management of agro- and ecosystems.

Experimental evolution, *i.e.* propagation of populations over hundreds of generations in a controlled environment, allows seeing evolution in action. Experimental evolution has been predominantly used to study genetic adaptation to very simple and controlled conditions such a defined change in culture media. Although these selection experiments provide essential lessons on general evolutionary processes, they cannot mirror the complexity of natural environments, where many selective environmental forces act simultaneously. With the genomic revolution, experimental evolution coupled to NGS is becoming a fundamental of modern evolutionary biology and has now to tackle challenging complex questions such as the emergence and evolution of biotic interactions, which imposes considerably different selective pressures (immunity, nutrition, competition...).

A double experimental evolution-based project has recently emerged at the LIPM in collaboration with EDB (UMR5174): the transformation of the plant pathogen *Ralstonia solanacearum* in legume symbionts and its pathogenic adaptation to different hosts in parallel. *R. solanacearum* is ideally suited for this double approach. Its genome is completely sequenced and expert annotated and the genetic determinism of pathogenesis has been extensively studied at the LIPM. Studying the emergence of variants adapted to new plant hosts or cultivars should allow exploring and anticipating its potential of evolution as a generalist or specialist pathogen. *R. solanacearum* is phylogenetically close to some rhizobia, such as *Cupriavidus taiwanensis*. Rhizobia are phylogenetically disparate bacteria able to fix nitrogen in symbiosis with legumes. They are thought to have emerged and diversified through lateral transfer of key symbiotic genes in soil bacteria followed by adaptation of the genome recipient to the legume environment. Studying the experimental evolution of legume symbionts from a chimeric *Ralstonia* containing the symbiotic plasmid of *C. taiwanensis* (ancestor) will allow deciphering the adaptive and evolutionary mechanisms allowing the activation and optimization of the acquired symbiotic potential. In addition, it should shed light on symbiosis-pathogenesis relationships and pave the way to the experimental design of new rhizobia, *e. g.* adapted to new plants.

### **TULIP MTR**

This project is pioneer in exploring the power of experimental evolution-NGS coupling in the field of complex plant-microbe interactions (MTR2). Behind its primary scope on rhizobium-legume symbiosis and *Ralstonia*-plant pathogenic interactions, it aims at providing general insights into how bacterial genomes adapt to environmental constraints (MTR3) and at developing innovative strategies for designing plant-associated bacteria with beneficial traits in a sustainable agriculture and environment perspective.

### **ETPs involved ion rhe project**

**CBM : 2 ETPs chercheurs/an, 0,7 ETPS ITA/an, 1,5 ETPs non permanents pour 2012 et souhaités pour les années suivantes..**

**SG : 1.2 ETPs chercheurs/an, 0,2 ETPS ITA/an, 1 ETPs non permanent pour 2012 et souhaité pour les années suivantes.**