LABEX TULIP

Symbiotic recognition, signalling and reprogramming

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Scientific objectives

Symbiotic interactions between plant roots and fungi or rhizobial bacteria help plants to efficiently cope with limitations in essential nutrients (water, phosphorus, nitrogen), while providing microbes with a privileged carbon/energy source. Endosymbiosis requires the capacity for the plant to accommodate the microbial symbiont in a microenvironment suitable for metabolic activity and exchanges between both organisms. While this capacity is widespread among terrestrial plants for endosymbioses with so-called arbuscular mycorrhizal (AM) fungi, it is mostly restricted to the legume family for rhizobial symbioses, which involve the production of a specific organ, the root nodule. These symbioses are evolutionary related and have recruited and evolved host recognition systems for the perception of structurally-related chitin-based molecules. Their intimate relationships are controlled by common genetic components, which are conserved in a wide range of non-legume plants, thereby facilitating future applications in sustainable agriculture.

We propose here to investigate how host perception systems discriminate between structurally-related microbe signalling molecules to induce host reprogramming for AM or bacterial root nodule symbioses. For this, we will study the specificity of recognition of different microbial signalling molecules by members of evolutionary conserved plant receptors in order to determine key receptors and receptor complexes involved in specific symbiotic perception. We also aim to determine how symbiotic signalling is transduced to specific downstream responses by the concomitant analyses of secondary responses (calcium signalling at the cellular level) and reprogramming of gene expression. The complementary use of the legume *Medicago truncatula* (our major model), *Brachypodium distachyon* (as a monocot model) and actinorhizal plants will also allow us to address the question of the evolutionary conservation of symbiotic signalling mechanisms and to dissect the specificities and overlaps between signalling pathways for root symbiosis, root development and plant defence.

Another important aspect is how early symbiotic signalling allows coordinated reprogramming for microbe entry (infection) and for creating a new symbiotic organ as the root nodule. We will focus on the functional characterization of key plant and bacterial regulators controlling these symbiotic programs using a variety of complementary genetic, molecular and cell imaging approaches. This includes innovative confocal imaging of symbiotic signalling *in vivo* during microbe infection and the development of tissue-specific transcriptomic approaches for determining epigenetic genome modifications or transcription reprogramming accompanying infection or nodule organogenesis.

TULIP MTR*:* Organism - Organism interactions

This project fully meets the goal defined for this MTR to explore the intimate molecular and cellular mechanisms involved in specific interactions between organisms of different species. The question of what components are shared between different symbiotic interactions or symbiotic and pathogenic interactions is also being addressed. Investigations are carried out at the molecular, genome, cellular and organ level by molecular biologists, cell biologists, biochemists and geneticists, and with the help of specialists in bioinformatics and microscopy.

ETPs involved in the project: 15 scientists, 8 technical assistants, non-permanents (post-docs and PhDs). + LIPM + FR AIB platforms in bioinformatics and microscopy.