

LEGUME TASTERS: THE PANOPLY OF SYMBIOTIC RHIZOBIA HOST PREFERENCE

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Mutualistic interactions have great importance in biology and are key to either macro- and micro-ecosystems functioning, from biogeochemical cycles to the animal and plant microbiome. Many studies have been performed to investigate the molecular aspects of mutualism, however, the genetic repertoire needed for efficient association with host by the microbial symbionts is still poorly understood. Several studies highlighted that the expression of the desired phenotype in the host resides in species-specific, even genotype-specific interactions between the symbiotic partners. Consequently, there is a need to dissect such an intimate level of interaction, aiming to identify the main genetic components in both partners playing a role in symbiotic differences/host preferences [1]. The rhizobia are an exemplary model of microbial mutualist. They are facultative mutualist partners of leguminous plants, with which they establish nitrogen-fixing symbioses.

By applying complementary approaches spanning from computational reconstruction of metabolic interactions to transcriptomic and comparative genomic analyses, we dissected genotype-by-genotype interactions in the model symbiotic partnership between the rhizobium *Sinorhizobium meliloti* and the host plant (*Medicago* spp.).

Results from integrated rhizobium-plant genome-scale metabolic model [2], genome-wide association [3] and comparative transcriptomic analyses [4] of late and early stages of symbiosis will be presented and discussed in the light of explaining and exploiting the large genomic diversity rhizobial symbiont populations in the perspective of improving microbial inoculants formulations in sustainable agriculture practices.

References

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