

THE RHIZOBIA-LEGUMES INTERACTION IN THE GENOMIC ERA

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The symbiosis between legumes and N₂-fixing bacteria (rhizobia) is of huge agronomic benefit, allowing many crops to be grown without N fertilizer. It is a sophisticated example of coupled development between bacteria and higher plants, culminating in the organogenesis of root nodules. This host-bacteria interaction is apparently mutualistic and was possibly developed through a coevolution process, thus suggesting a strong interdependence of the two partners.

The mechanisms of the symbiotic process are well known and many molecular aspects are now elucidated; more recently, the sequencing of the complete genomes of at least four rhizobium species and the sequencing projects for some legumes, accompanied by several EST libraries, allowed genomic and post-genomic tools to be applied to this important interaction.

Among the several specific symbioses of rhizobia and legumes, that of *Sinorhizobium meliloti* with plant of the genus *Medicago*, is probably the most intensely studied and the best known. These studies demonstrated that natural *Sinorhizobium* populations are extremely variable and this variability reflects on the nodulation specificity toward the 83 species of *Medicago* that host them; moreover the genetic diversity of *Sinorhizobium* allowed this genus to colonize several different environment including some very specialized and stressful.

In order to study the origin of that diversity, a microarray-based comparative genomic approach was applied to assess which functional genes are the most variable in *S. meliloti* strains isolated from different geographical areas and ecological contexts. Results obtained showed that a large part of the genomic variation resided within the symbiosis-required plasmid pSymA. To investigate the evolutionary meaning of such results, the pattern of gene expression under plant root exudates treatment, the very preliminary phase of symbiotic interaction, was analysed on the same strains. Actually, evidences are accumulating of a major role of differential gene expression as one of the main causes for phenotypic (and adaptive) evolution in both plants and animal systems and in microorganisms. The assessment of the extent of transcriptomic variation in *S. meliloti* natural strain is a key step for providing insights into which genes are 'important' for plant-bacteria interaction in an evolutionary perspective. Results obtained so far indicate the presence of transcriptomic variation among different strains which is due to several genes of already known and of unknown function which could likely play a role in the symbiotic process and in strain competitions and adaptation.