



How genetic pressure of [*Medicago trunculata*] acts on the molecular selection and population pattern of its favourite symbiotic bacteria, [*Sinorhizobium*] sp.?

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► Oral presentations

O-738 How genetic pressure of *Medicago truncatula* acts on the molecular selection and population pattern of its favourite symbiotic bacteria, *Sinorhizobium* sp.?Rangin Cécile¹, Béna Gilles¹, Brunel Brigitte¹, Perrineau Marie-Mathilde¹, Mauré Lucette¹, Mougél Christophe², Cleyet-Marel Jean-Claude¹¹ LSTN TA A-82/J, Campus International de Baillarguet 34398 Montpellier cedex 5, France² UMR Microbiologie et géochimie des sols, Inra Dijon, 17 rue Sully BP 86510, 21065 Dijon cedex, France

Nitrogen-fixing *Sinorhizobium* sp. bacteria interact with *Medicago truncatula* plants, forming root nodules in this nitrogen fixation symbiosis. When rhizobia colonize the rhizosphere of legumes, symbiotic specificity is expressed at two levels, among-species for nodulation ability and within-species for nodulation competitiveness.

We investigated the genetic diversity of 223 *Sinorhizobium* sp. strains isolated from nodules sampled from four *Medicago truncatula* fixed lines, each issued from distinct geographic areas, and cultivated on the same French soil. The DNA molecular polymorphism of isolates was analyzed by CE-SSCP and RFLP on 5 loci chosen either for species characterization or for their involvement in symbiosis and effectors translocation pathways.

Although more than 90% of the sample bacteria belonged to *Sinorhizobium medicae* (others belonging to *S. meliloti*), statistical tests showed a significant differentiation among *M. truncatula* lines for bacterial species proportion. Conversely, on the basis of the four other loci analysed, we could not detect any significant among-lines population differentiation, for each bacterial species. Nevertheless, several rare strains isolated were specific from a single plant line. Thus, we compared the nodulation ability and the fixation efficiency of these isolates on the different *M. truncatula* lines used for trapping. Moreover, to enlighten the role played by bacterial genetic diversity on nodulation competitiveness, intraspecific competition assays were performed with genetically different strains on 80 plants. Hence, SNP molecular genotyping of 200 nodules allowed the choice of the most competitive strain for each of the two *Sinorhizobium* species. Therefore, those two strains were tested for their ability to compete in the formation of nodules on the four *Medicago truncatula* lines, with inoculation of strains at different ratios (90/10, 50/50 and 10/90 proportions) on 30 plants each. Results led us to formulate hypotheses explaining the *S. medicae* versus *S. meliloti* proportions found initially in this bacterial trapping.

This work outlines the influence of the genetic diversity of the host plant on the distribution of symbiotic genotypes in rhizospheric bacterial populations, and allows a better understanding of bacterial selection in natural and cultivated ecosystems.

O-517 Effects of systemically induced resistance on the indigenous rhizosphere and phyllosphere microflora of *Arabidopsis thaliana*

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Pathogen-induced Systemic Acquired Resistance (SAR) and Induced Systemic Resistance (ISR) mediated by non-pathogenic rhizosphere bacteria are phenotypically similar in that upon challenge inoculation disease severity is reduced and the growth and/or activity of the challenging pathogen is reduced. In how far SAR or ISR affect the non-pathogenic microflora in the rhizosphere and phyllosphere is as yet unknown. To study possible effects on the indigenous microflora we used the model plant *Arabidopsis thaliana*, of which constitutive expressors of induced resistance and mutants impaired in expression of SAR and/or ISR are available. Changes in population density and diversity of the resident microflora were studied by selective plating and by denaturing gradient gel electrophoresis (DGGE) of PCR amplicons of the small subunit rRNA genes, using primers specific for various microbial groups, including eubacteria and *Pseudomonas* spp.

Qualitative analysis using DGGE did not demonstrate differences in the rhizosphere microflora between any of the *A. thaliana* lines tested. However, a quantitative analysis using selective plating revealed significant differences in bacterial numbers of both the rhizosphere and phyllosphere of several salicylic acid-signaling mutants compared to the wild-type Col-0 plants. Effects of induced resistance on the biodiversity of the indigenous rhizosphere and phyllosphere microflora are currently under investigation.