Comparison of the genetic structure and diversity of bacteria associated with mycorrhized and non-mycorrhized roots of Medicago truncatula

Pierre Offre, Barbara Pivato, Sylvie S. Mazurier, Séverine S. Siblot, Thérèse Corberand, Graziella Berta, Christophe Mougel, Philippe P. Lemanceau

P-684

Comparison of the genetic structure and diversity of bacteria associated with mycorrhized and non-mycorrhized roots of Medicago truncatula

Offre P [1], Pivato B [2], Mazurier S [1], Siblot S [1], Corberand T [1], Berta G [2], Mougel C [1], Lemanceau Philippe [1]

[1] INRA SPE UMR MSE 17; rue Sully BP 86510 21065 Dijon France
[2] Università del Piemonte Orientale, DISAV, Alessandria, Italy

Arbuscular mycorrhizae (AM) are ancient symbiosis (400 millions years) between Glomeromycetes and roots of 80% of terrestrial plant families. AM are known to be non-specific associations. However, the plant community is affected by the diversity of AM fungi (van der Heijden et al., 1998), and reciprocally we have recently shown that the genetic diversity of AM fungi differ according to the plant species. These observations are consistent by the long joint evolution of plants and AM fungi. This evolution is expected to not have occurred independently from the rhizosphere microflora.
To test this hypothesis, we have compared the genetic structure of bacterial communities associated with Medicago truncatula J5 (Myc+/Nod+) and its symbiosis-defective mutants TRV48 (Myc+/Nod-) and TRV25 (Myc-/Nod-). DNA was extracted from the corresponding rhizospheres and its polymorphism was assessed by A-RISA DNA fingerprint. Based on Principal Component Analysis of the corresponding fingerprints, markers explaining the differences of structure between the communities associated with M. truncatula genotypes were sequenced and identified. These markers were further used to design probes used to screen isolates from mycorrhized roots that belonged to the corresponding microbial groups. The diversity of these isolates was characterized by BOX-PCR.
The genetic structure of bacterial communities associated with mycorrhized and non-mycorrhized plants differed significantly. Phylogenetic analysis of the molecular markers explaining these differences indicated that they belong to Comamonadaceae, Oxalobacteriaceae, and Rubrivivax sub-group. The isolates harboring sequences highly homologous to that of markers affiliated to these microbial groups were clustered in 25 groups on the basis of their BOX-PCR fingerprints, indicating a high diversity of these isolates. The distribution of the isolates in the different BOX-PCR groups differed significantly upon their origin (mycorrhized/non-mycorrhized roots). The effects of isolates representative of the genetic diversity described here above is currently being evaluated to test the value of our initial hypothesis.

Offre P., Pivato B., Siblot S., Gamalero E., Corberand T., Lemanceau P., Mougel C. 2007. Appl. Environ. Microbiol. 73: 913-921.