## ARBUSCULAR MYCORRHIZAE INFLUENCE THE OCCURRENCE OF SOIL FLUORESCENT PSEUDOMONADS HARBOURING TYPE III SECRETION SYSTEMS

Amandine Viollet, Thérèse Corberand, Agnès Robin, Christophe Mougel, Philippe Lemanceau and Sylvie Mazurier

INRA, Université de Bourgogne, UMR 1229 'Microbiologie des Sols et de l'Environnement', CMSE, 17 rue Sully, BV 86510, Dijon, France. F-21065.

Type III secretion systems (T3SS) of pathogenic and symbiotic Gram negative bacteria allow direct interactions with eukaryotic cells. Saprophytic fluorescent *Pseudomonas* spp. harbouring T3SS genes (T3SS<sup>+</sup>) have been more frequently encountered in the rhizosphere than in bulk soil, which suggests a possible interaction between these bacteria and rhizospheric eukaryotes.

Our objectives were to compare, (i) the effect of mycorrhizal and of non-mycorrhizal roots of *Medicago truncatula* on the occurrence and diversity of T3SS<sup>+</sup> fluorescent *Pseudomonas* spp. and (ii) the diversity of T3SS<sup>+</sup> and T3SS<sup>-</sup> bacterial genotypes.

Fluorescent pseudomonads from (i) the rhizosphere of mycorrhizal roots of *M. truncatula* Jemalong J5 (wild-type, Myc+ Nod+) and TRV48 (mutant Myc+ Nod-), (ii) the rhizosphere of non-mycorrhizal roots of TRV45 (mutant Myc- Nod-), and (iii) the corresponding bulk soil were isolated.

Pseudomonas spp. strains harbouring T3SS genes were identified by PCR targeting a conserved hrcRST DNA fragment. Genotypic diversity of fluorescent pseudomonads has been described by a whole cell rep-PCR fingerprinting method (BOX-PCR) and 16S rRNA sequencing. For T3SS<sup>+</sup> strains the polymorphism of hrcRST has been assessed by PCR-RFLP and sequencing.

The occurrence of T3SS<sup>+</sup> fluorescent pseudomonads was significantly higher in the rhizosphere of mycorrhizal (J5 and TRV48) than in that of non-mycorrhizal roots (TRV45) or in the bulk soil. Four distinct *lnc*RST genotypes were described, two of which were specifically described for strains associated with mycorrhizal roots. Compared to *lnc*RST negative fluorescent pseudomonads, T3SS<sup>+</sup> strains displayed specific BOX-PCR genotypes that were all ascribed to the phylogenetic group of *P. fluorescens* on the basis of 16S rRNA gene identity.

Mycorrhizal roots of *Medicago truncatula* clearly influence the population structure of root associated fluorescent pseudomonads in a different way than non-mycorrhizal roots. The occurrence of particular genotypes of fluorescent *Pseudomonas* spp. harbouring T3SS genes was highly increased in the rhizosphere of mycorrhizal roots suggesting that T3SS might be implicated in cellular interactions between fluorescent pseudomonads and arbuscular mycorrhizae.