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Arbuscular mycorrhiza influence the occurrence of soil fluorescent pseudomonads harbouring type III secretion systems

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Introduction

Type III secretion systems (T3SS) of Gram negative bacteria mediate direct cellular interactions with eukaryotes.
Numerous Pseudomonas spp. harbouring T3SS genes have been previously encountered among rhizosphere isolates1.
This suggests a possible interaction between these bacteria and rhizosphere eukaryotes.

Objective

To evaluate the impact of arbuscular mycorrhization on the occurrence and diversity of T3SS+ pseudomonads.

Results

Frequency and occurrence of T3SS+ fluorescent pseudomonads

<table>
<thead>
<tr>
<th>Plant origin</th>
<th>Number of T3SS+ isolates</th>
</tr>
</thead>
<tbody>
<tr>
<td>root rhizoplane</td>
<td>rhizosphere</td>
</tr>
<tr>
<td>J5 Mys+</td>
<td>113 isolates</td>
</tr>
<tr>
<td>TRV48 Mys+</td>
<td>93 isolates</td>
</tr>
<tr>
<td>TRV25 Mys-</td>
<td>68 isolates</td>
</tr>
</tbody>
</table>

-No T3SS+ isolates were detected in the bulk soil.
-Distribution of T3SS+ isolates in the root/rhizoplane and in the rhizosphere was not significantly different (Chi-2=2.25; p=0.637).
-94% of the T3SS+ pseudomonads were isolated from plant mycorrhizal genotypes (J5 and TRV48).
-The representation of T3SS+ isolates among pseudomonads from both plant mycorrhizal genotypes was equivalent (Chi-2=1.34; p=0.15).

Diversity of hrcRST sequences and genotypic background of fluorescent pseudomonads

<table>
<thead>
<tr>
<th>PCR hrcRST*</th>
<th>hrcRST-RFLP genotypes</th>
<th>BOX-PCR genotypes</th>
<th>Number of isolates Mys+</th>
<th>Mys-</th>
</tr>
</thead>
<tbody>
<tr>
<td>J5 TRV48 TRV25</td>
<td>J5 100 100 50</td>
<td>TRV48 48 2 0</td>
<td>TRV25 42 10 10</td>
<td></td>
</tr>
</tbody>
</table>

-4 hrcRST-RFLP distinct genotypes were described (1, 2, 3 and 4).
- hrcRST-RFLP genotypes 1 and 2 were only described for pseudomonads isolated from mycorrhizal roots.
-No common BOX-PCR genotypes were observed between T3SS+ and T3SS- isolates.

Conclusions

Fluorescent Pseudomonas spp. harbouring T3SSs appeared preferentially associated with mycorrhizal roots of Medicago truncatula. Further studies are in progress to evaluate the role of T3SS+ pseudomonads in M. truncatula-mycorrhizal arbuscular fungi (MA) interactions.

-T3SS+ strains displayed specific genotypic backgrounds and were all associated to the P. fluorescens phylogenetic group on the basis of 16SrRNA gene identity.

-Mycorrhizal interactions observed between the hrcRST and the 16SrRNA phylogenies are compatible with previous findings made on pathogenic pseudomonads and suggesting that HGT (Horizontal Gene Transfer) is a major force in T3SS evolution.

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