The effect of soil types on the abundance and diversity of potato plant associated bacteria with antagonistic activity towards *Ralstonia solanacearum*

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Ralstonia solanacearum is an epidemic phytopathogenic bacterium responsible for bacterial wilt in potato and many other plant species. This pathogen can survive in the soil for several years and can spread very fast via water streams and latent infections in the tubers are particularly problematic. Endophytic biocontrol agents might be a solution as they occupy the same niches as colonized by *R. solanacearum*. The aim of this study was to assess the diversity of bacterial antagonists of *Ralstonia solanacearum* in different soil types and potato plant spheres, and to estimate the effect of soil type on the abundance and diversity of antagonistic bacteria.

The total bacterial communities from bulk soil, rhizosphere soil and from the endophytic compartments were compared by PCR-DGGE fingerprints of 16S rRNA genes amplified from total community DNA. Approximately 2000 bacterial isolates obtained from different spheres of potato plants grown in three different soils (Diluvial sand, Alluvial loam and Loess loam) were screened for in vitro antagonistic activity towards *R. solanacearum* and 200 isolates with antagonistic activity were further characterized. Using BOX-PCR fingerprints, the 200 antagonistic bacteria were compared. The biological control mode of action and the plant growth promoting potentials were investigated as well. The BOX-PCR fingerprint as well as the 16S rRNA sequences showed that some endophytic antagonistic isolates identified as *Pseudomonas umsongensis* colonized all potato plant ecto- and endospheres. The total bacterial communities denaturing gradient gel electrophoresis (DGGE) profile revealed distinct bacterial community structure associated with each plant sphere, and within each plant sphere the microbial community composition was mainly shaped by the soil type. The effect of soil type decreased in the endophytic compartments, suggesting that this endophytic compartment harbored unique indigenous bacterial communities protected from surrounding environment even so some of the endophytic antagonistic bacteria isolated from different soil types shared the same BOX-PCR fingerprints. Currently we investigate under greenhouse conditions whether endophytic bacteria can more effectively antagonize *R. solanacearum* than rhizosphere colonizing bacteria.