Key factors influencing fate and activity of bacterial inoculants and their effect on the indigenous microbial community in the rhizosphere

Susanne Schreiter[1], Ute Zimmerling[1], Petra Zocher[2], Rita Grosch[2], Kornelia Smalla[1]
[1]Julius Kühn-Institut, Institute for Epidemiology and Pathogen Diagnostics
[2]Leibniz-Institute of Vegetable and Ornamental Crops Großbeeren/Erfurt e.V
susanne.schreiter@jki.bund.de

Rhizoctonia solani is a soil-borne plant pathogen which causes bottom rot disease and leads to a massive loss of lettuce and potato every year. The lack of effective fungicides makes it difficult to control this and other plant pathogens (WELLER *et al.*, 2002). So it is necessary to find alternative strategies. A promising approach is the use of natural antagonists of the plant pathogen. Under laboratory and greenhouse conditions two isolates, *Pseudomonas jessenii* RU47 and *Serratia plymuthica* 3Re4-18, showed the ability to reduce disease symptoms (ADESINA *et al.*, 2007). But the efficiency of biocontrol agents was reported as very variable and the reason for this variability is largely unknown (ROBINSON-BOYER *et al.*, 2009). Therefore, a better understanding of the interaction of the microbial community, the plant rhizosphere and the soil is required for a successful exploitation of this antagonistic potential. Within the frame of a DFG-Project a field experiment has been set up with a unique experimental plot system in Großbeeren comparing three different soil types. This made it possible to analyze the influence of the soil type independently from other factors such as climate and cropping history. Each soil type came under six different treatments with four replicates each: 1. water control, 2. pathogen control, 3. inoculation with *P. jessenii* RU47, 4. inoculation with *S. plymuthica* 3Re4-18, 5. inoculation with *P. jessenii* RU47 and *R. solani*, and 6. inoculation with *S. plymuthica* 3Re4-18 and *R. solani*. From the extracted total community-DNA 16S rRNA gene fragments were amplified and run in a DGGE-Gel to give insights into the structural diversity of microbes in the rhizosphere (SMALLA *et al.*, 2001). This molecular fingerprint technique and the following statistical analysis showed a clear difference between the three different soil types. These results revealed that the soil type is the driving factor for the composition of the microbial community while the treatment with the biocontrol agents was of minor influence.

ADESINA, M.F., A. LEMBKE, R. COSTA, A. SPEKSNIJDER and K. SMALLA, 2007: Screening of bacterial isolates from various European soils for in vitro antagonistic activity towards *Rhizoctonia solani* and *Fusarium oxysporum*: Site-dependent composition and diversity revealed. Soil Biol. Biochem **39**, 2818-2828.

ROBINSON-BOYER, L., M. J. JEGER, X.-M. XU and P. JEFFRIES, 2009.: Management of strawberry grey mould using mixtures of biocontrol agents with different mechanisms of action. Biocontrol Sci. Techn. **19**, 1051-1065.

SMALLA, K., G. WIELAND, A. BUCHNER, A. ZOCK, J. PARZY, S. KAISER, N. ROSKOT, H. HEUER and G. BERG, 2001: Bulk and rhizosphere soil bacterial communities studied by denaturing gradient gel electrophoresis: Plant-dependent enrichment and seasonal shifts revealed. Appl. Environ. Microb. **67**, 4742-4751.

WELLER, D. M., J. M. RAAIJMAKERS, B. B. M. GARDENER and L. S. THOMASHOW, 2002: Microbial populations responsible for specific soil suppressiveness to plant pathogens. Annu. Rev. Phytopathol. **40**, 309-348.