



Genome-based approach to optimize the performance of biocontrol agents towards *Rhizoctonia solani*

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Abstract

An antagonistic cocktail containing endophytic and rhizobacteria (*Pseudomonas fluorescens* L13-6-12, *P. poae* RE*1-1-14, *Serratia plymuthica* 3Re4-18) was selected following an extended screening. To fortify aspects in biological control of *R. solani*, the screening based on issues regarding sugar beet root colonization, plant growth promotion, and human safety. Additionally, the genome of the endophyte *P. poae* RE*1-1-14 was sequenced and functionally analysed.

Phylogenetic alignments revealed a high similarity to the sugar beet-associated, antagonistic *P. fluorescens* SBW25. However, 555 of the 4797 genes were specific for *P. poae* RE*1-1-14. Many of them have importance in general stress response by the production of antioxidants or detoxification but also for plant association. The unique genes represent a source for the identification of genes enabling endophytic lifestyle as well as biocontrol and plant promotion activity. Surprisingly, *P. poae* RE*1-1-14 appears to be endophytic only in specific sugar beet cultivars. The *Rhizoctonia* tolerant cultivar (JENNA KWS) showed a better colonisation with *P. poae* RE*1-1-14 than the *Rhizoctonia* susceptible cultivar (BERETTA). In long-term field trials, all bacterial strains were applied to seeds and showed positive effects by suppressing the pathogen *R. solani* and increasing the number of healthy beets.

By the application of 'omic'-technologies for the sequenced model strain, essential genes and regulatory processes involved in mechanisms necessary for rhizosphere competence and antagonistic activities will be identified and implications in agricultural applications will be accessed.