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Biological control of potato diseases guided by plant microbiome approaches

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INTRODUCTION

Plant protection against fungal pathogens is a crucial aspect of modern agriculture and mostly relies on chemical inputs. However, phytopathogens often become resistant against conventional fungicides[1]. Additionally, the microbial diversity in agricultural soils decreases through the application of pesticides, fertilizers and the soil tillage[2]. The aim of the SusCrop – ERA-NET project 'PotatoMETAbiome' is to establish microbial consortia, which are applicable for potato cultivation to mediate the resistance against soil-borne fungal pathogens (*Verticillium dahliae* and *Rhizoctonia solani*) and support the microbial diversity in soil.

PROCEDURE OF THE PROJECT

Pre-selected microorganisms from the strain collection for antagonistic microorganisms SCAM (Institute of Environmental Biotechnology, Graz University of Technology) will be implemented. A total of 111 bacterial strains were already tested comprising the genera *Bacillus, Erwinia, Paenibacillus, Pseudomonas, Serratia, Streptomyces, Ralstonia* and several yet unidentified species. Additionally, fungi of the genus Trichoderma were assessed in terms of antagonistic effects. They will be optimized in vitro in terms of their efficiency to inhibit the target phytopathogens. The best antagonistic microorganisms will be used for consortium assemblies and their VOCs profiles will be assessed. Established consortia will then be combined with root exudates, which can act as a 'boosters' for the microorganisms. Furthermore, the consortia will be applied in greenhouse experiments and field trials. In a final step, meta-transcriptomic datasets will be obtained to analyze the interaction of the microorganisms in the consortium.

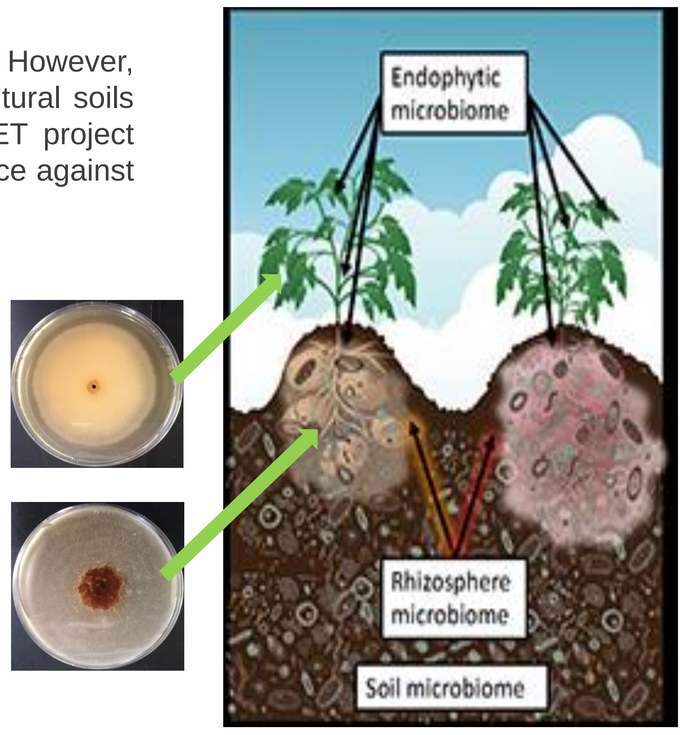
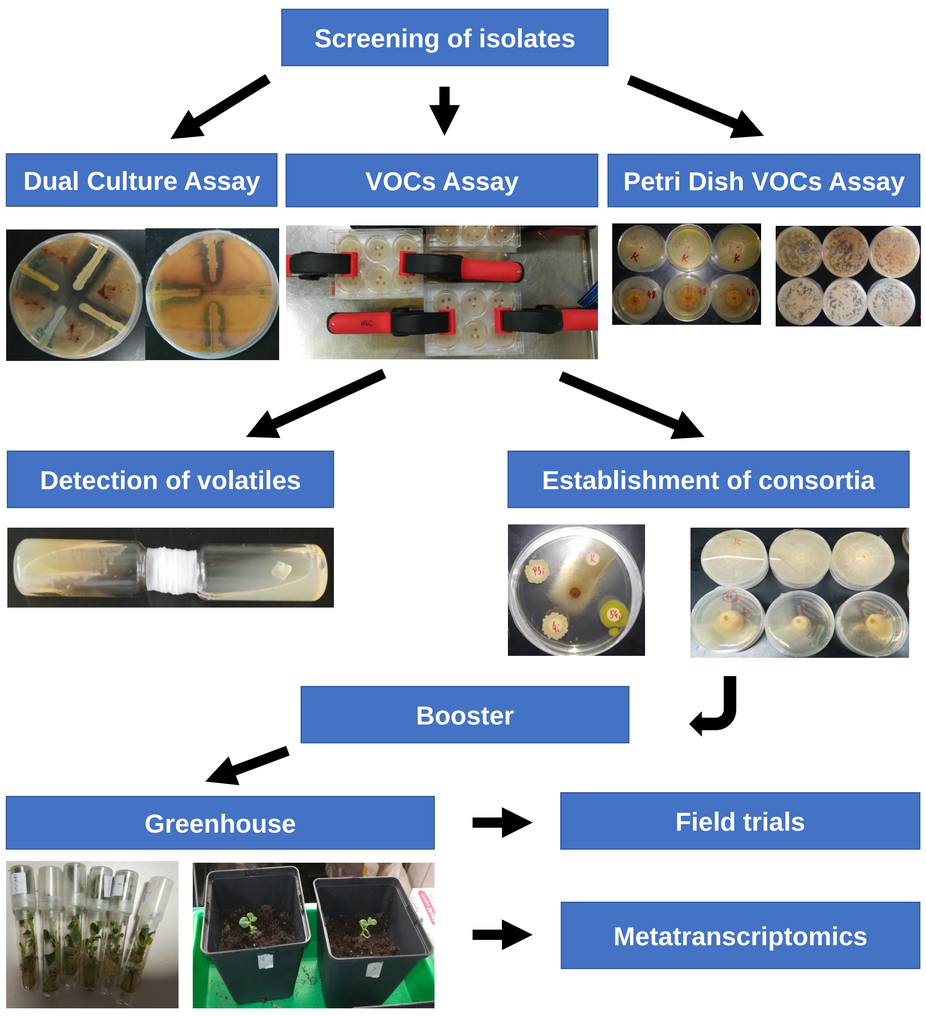


Figure 1: ***Solanum tuberosum; (above) Verticillium*** **wilt disease** ***(Verticillium dahliae); (below)*** **Root rot disease** ***(Rhizoctonia solani)***

STRATEGY



RESULTS

The isolates with the highest *in vitro* antagonistic activity against *R. solani AG-3* and *V. dahliae ELV-16* included the genera *Bacillus, Pseudomonas, Serratia, Trichoderma* and *Ralstonia*. Growth inhibition of volatiles up to 60% (*R. solani*) and 75% (*V. dahliae*) are achieved by using bacterial consortia (Fig. 2). The best *in vitro* combination of bacterial consortia includes the species *P. corrugata, P. chlororaphis, B. subtilis* and *T. gamsii*. Combinations of isolates with the lowest antagonistic activity were even tested. One of these combinations exposes high antagonistic activity.

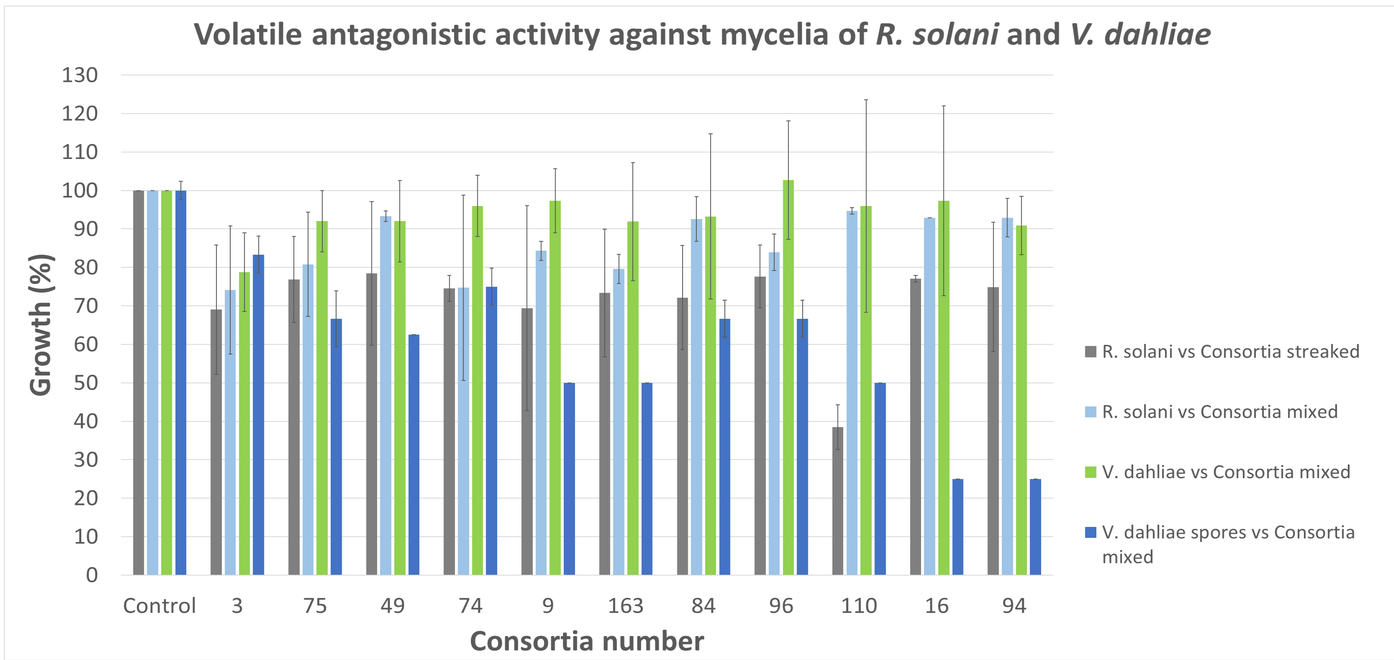


Figure 2: Antagonistic assay of microbial consortia against mycelia of ***R. solani AG-3*** **and** ***V. dahliae ELV-16*****, and spores of** ***V. dahliae ELV-16.*** Petri Dish VOCs Assay and VOCs Assay (against *V. dahliae*) are used for exploring the volatile antagonistic activity of consortia against the pathogens. The consortia are cultivated on NA agar and the pathogen on PDA agar.

Conclusions

- The antagonistic activity of the bacterial consortia depends on its composition.
- Consortia containing isolates with low antagonistic activity can even expose antagonistic activity.
- It is important to stabilize the consortia to get continuous antagonistic effects.
- Greenhouse and field trials can show different antagonistic effects of the consortia, because of different conditions (e.g. nutrition, plant interactions)

Objectives

- ✓ Growth inhibition of fungal pathogens by using microbial consortia
- ✓ Resilience against biotic and abiotic stresses
- ✓ Decline the usage of fertilizers and pesticides
- ✓ Increase microbial diversity in soil for enhancing plant health
- ✓ Ecological friendly plant treatment
- ✓ Understand interactions between microbial consortia and the potato plant

[1] Oerke, E. C. (2006) 'Crop losses to pests', Journal of Agricultural Science. doi:10.1017/S0021859605005708
[2] Matson et al (1997) 'Agricultural Intensification and Ecosystem Properties'. Science 25 Jul 1997: Vol. 277, Issue 5325, pp. 504-509 doi: 10.1126/science.277.5325.504