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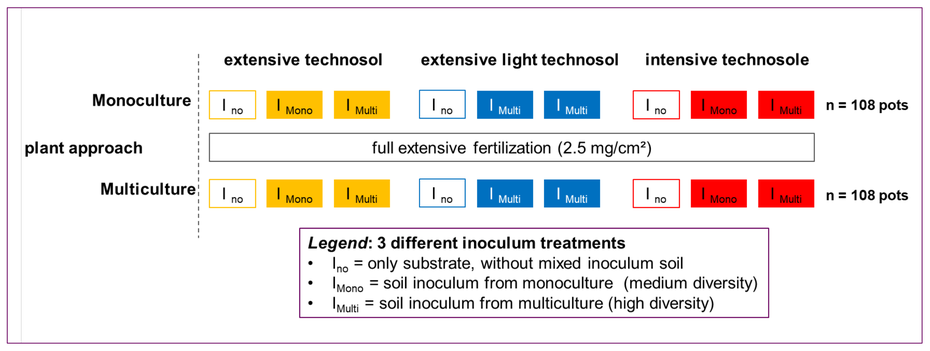
MICROBIAL TRANSPLANTS AS A TOOL TO IMPROVE SOIL QUALITY FROM TECHNICAL ORIGIN

Introduction

Aim: create space for biodiversity by restructuring already existing space, like rooftops. The there used technosols as soil-like substrate for plant growth have low microbial diversity, biomass[1] and activity resulting in poor soil quality with limited growth opportunities for plants. To increase the microbial diversity in technosols, we investigated your influence of the microbiome of different grassland soils to improve the quality of technosols in a greenhouse experiment.

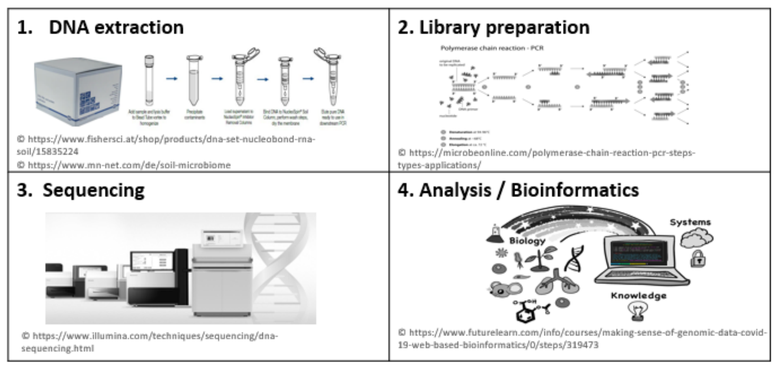


Experimental design of greenhouse experiment: plant approaches (1) monoculture (Dactylis glomerata L.) and (2) multiculture (D. glomerata L., Festuca pratensis Huds., and Trifolium pratense L.) with 3 technosols each (extensive and extensive light (n = 5) and intensive (n = 4)) and 3 inoculum treatments (no Inoculum (I_{no}), inoculum with soil from plant monoculture (I_{Mono}) and inoculum with soil from plant multiculture grassland (I_{Multi})).

Hypotheses

1. used technosols have different microbial communities
2. Inoculum increases microbial diversity - maybe soil from monoculture plot performers better because of already fitting microbial community then that from multiculture plot
3. due to the interaction relationship with the plant, the microbial abundance increases, and the functional groups differ between plant mono- and multiculture
4. the plant growth is different between the technosols and the inoculum also increases the growth

Material and Methods



0.5 g from very homogenized and sieved technosol was extracted with NucleoSpin®Soil Kit.. After quantity (Quant-iT PicoGreen dsDNA Assay Kit) and quality (Nanopore) control the sequencing library was prepared using the Earth project primers (515F and 806R (Caporasp et al., 2011)), the clean-up was done with Agencourt AMPure beads and the tacking was done with indexing primer (Nextera® XT). The library was diluted to 4 nM and sequenced with the MiSeq Reagent kit v3 (600 cycles) for paired-end sequencing.

Raw sequencing data were processed with DADA2, and taxonomy was assigned using SILVA v138. Microbial diversity, and community composition were analysed in R Studio (4.2.2) with different packages.

Results

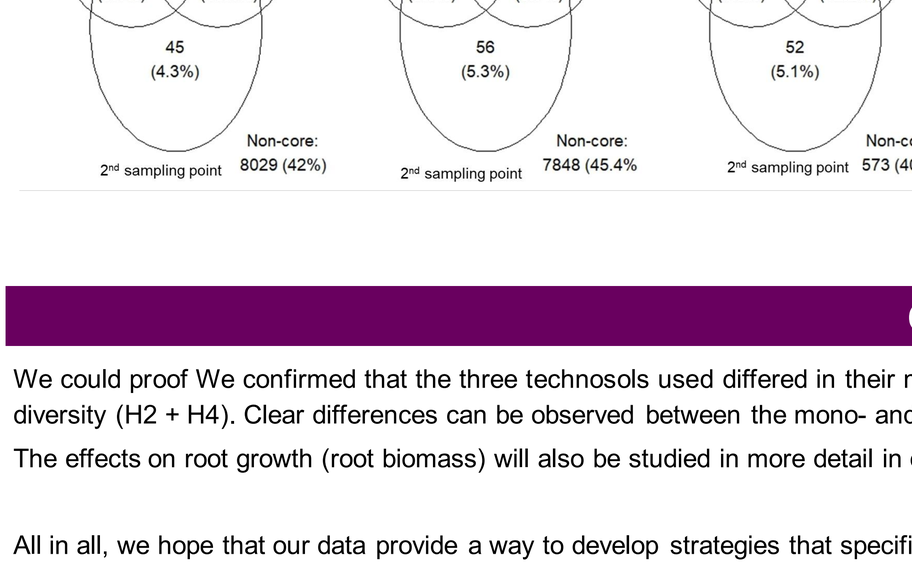


Fig. 2: Dry weight of the 3 technosols from the plant monoculture at 2 different sampling points (78 days & 136 days).

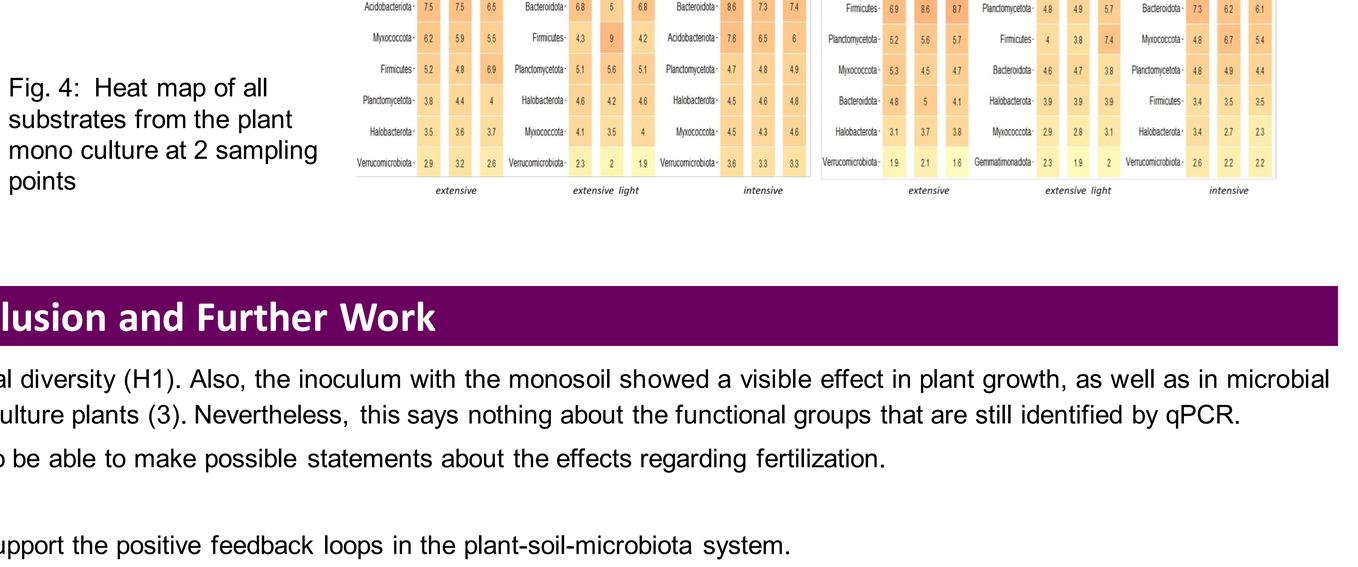


Fig. 3: Observed ASVs in the 3 technosols of the plant mono culture at 2 different time points

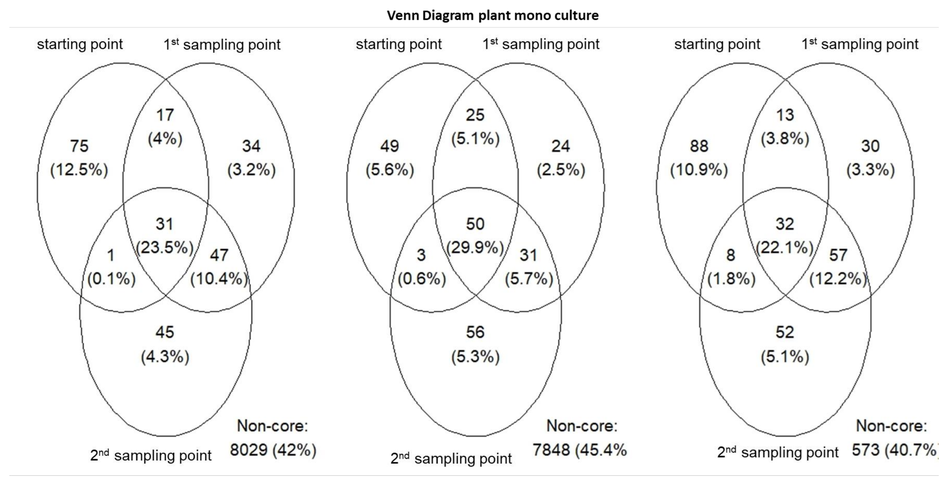


Fig. 4: Venn diagram of the overlapping ASVs from the starting point (T0), the first sampling point (T78) and the second sampling point (T136)

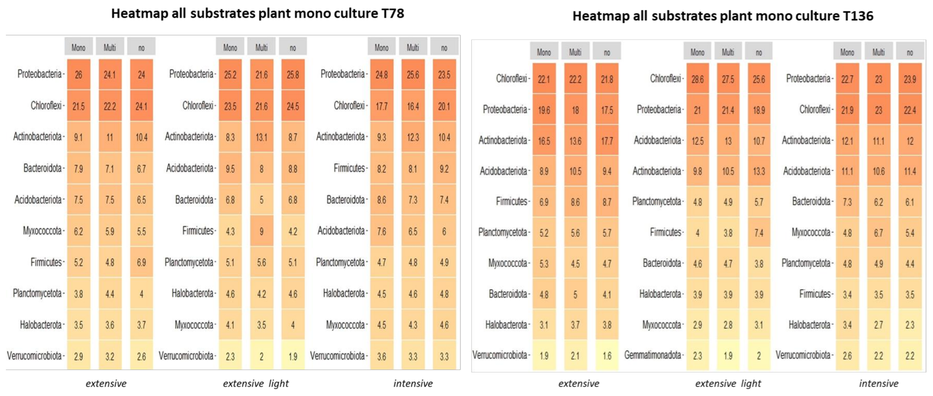


Fig. 4: Heat map of all substrates from the plant mono culture at 2 sampling points

Conclusion and Further Work

We could proof We confirmed that the three technosols used differed in their microbial diversity (H1). Also, the inoculum with the monosoil showed a visible effect in plant growth, as well as in microbial diversity (H2 + H4). Clear differences can be observed between the mono- and multiculture plants (3). Nevertheless, this says nothing about the functional groups that are still identified by qPCR.

The effects on root growth (root biomass) will also be studied in more detail in order to be able to make possible statements about the effects regarding fertilization.

All in all, we hope that our data provide a way to develop strategies that specifically support the positive feedback loops in the plant-soil-microbiota system.

ECOLOPES

Technical University of Munich