

Agricultural management influences barley rhizomicrobiota and plant immune response

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Agricultural management practices are assumed to shape soil microbial communities. We hypothesize that the rhizomicrobiota of barley grown in soils under different long-term soil management or fertilization treatment will harbor different prokaryotic communities. Therefore, barley rhizosphere (BBCH55) and bulk soil was sampled from a long term field experiment (LTE) in Bernburg, Germany, with four different agricultural managements (mouldboard plough (MP) and conservation cultivator tillage (CT) with standard N-fertilization and pesticide application (I) or reduced N-fertilization without pesticides (E)). Rhizosphere and bulk soil was investigated by amplicon sequencing of 16S rRNA gene fragments amplified from total community (TC)-DNA. The soil managements MP and CT revealed significant differences in the prokaryotic community composition. However, the fertilization treatments did not show any differences.

In order to test our hypothesis, a greenhouse experiment was conducted with the barley cultivar Golden Promise grown in the four differently managed soils from LTE Bernburg. Additionally, a standard greenhouse substrate was

used as control. The plants were grown until BBCH13 and subsequently infected with model pathogen *Blumeria graminis* f. sp. *hordei*. Relative gene expression profiles of the defense-related genes *PR1b* and *PR17b* were determined in barley leaves before and 24 h after infection. The relative gene expression tended to be higher in all infected samples compared to the uninfected samples, with a significant difference for plants grown in MP-I soil. The amount of *B. graminis* fungal hyphae was determined in a detached leaf assay. No differences were revealed for plants grown in field soil which all had significantly lower infection rates compared to the plants grown in standard substrate. Our results indicate that the rhizomicrobiota of barley grown under field conditions was shaped by the agricultural soil management. Whether management dependent differences under greenhouse conditions were less pronounced is presently investigated by amplicon sequencing of 16S rRNA gene fragments obtained from TC-DNA of rhizosphere and bulk soil and will be presented at the meeting. Managing soil microbiomes could be a new approach to enhance crop resistance.