Introduction

Plants form close interactions with microorganisms that are essential for their performance and survival. Thus, plant-microbe interactions are key for understanding and improving plant health and productivity, and for developing sustainable agricultural management practices. It is well-known that plants use metabolites to direct organization and growth of their associated microbial communities. However, vice versa, the plant-associated microbiome influences the metabolic activity of the plant leading to different metabolites. A significant number of plant metabolites are produced by associated microbes, or through interaction with their plant host (prominent e.g. pacitaxel). To analyze microbiome-metabolite interactions, we used the grass model Brachypodium distachyon as well as different species of medicinal plants with particularly high levels of complex constituents, including Matricaria chamomilla and Calendula officinalis. These two medicinal plants are cultivated all over the world, however with different chemical profiles. We observed a plant-specific selection of rhizospheric microbes associated with medicinal plants grown on an organically managed Egyptian desert farm. The soil microbiome comprised a high abundance of spore-forming Firmicutes (esp. Bacillus and Paenibacillus) and Actinobacteria (Streptomyces), which were linked to pathogen suppression under arid and soil conditions. The desert agro-ecosystem exhibited a higher microbial diversity and better ecosystem function for plant health in comparison to the native desert soil. Promising antagonistic counterparts to soil-borne phytopathogens were selected by a hierarchical screening for field evaluation. The priming of chamomile seedlings had a stabilizing effect on plant performance, and indigenous Bacillus and Paenibacillus strains were also able to elevate the plants’ flavonoid production. These findings suggest that a targeted bacterial treatment can influence the metabolic activity of the plant. We aim to reveal the underlying mode of action at the generic and transcriptional levels and to develop an effective biocontrol strategy on the basis of these promising antagonists.

How are the native microbial communities influenced by 30 years of organic agriculture?

Figure 1. The bacterial communities in the two different soil types. Relative abundance composition of major phyla and genera was determined by pyrosequencing of 16S rRNA from microorganisms. DNA extracted from desert and agricultural soil. Phylogenetic groups accounting for ≥1% of all quality sequences are summarized in the artificial group others.

Figure 2. Principal component analysis of OTUs identified by SSCP fingerprinting for bacterial and fungal communities. Samples were encoded using a combination of letters and numbers indicating (1) soil type or plant species (d for desert soil, s for cultivated soil, M = Matricaria chamomilla, C = Calendula officinalis, F = Solanum dulcamara). (2) replicate (1–4) and (3) microenvironment (Re = endorhiza, rhizosphere and soil have no further designation).

Figure 3. Taxonomic composition and Venn diagrams of the 16S rRNA and nifH gene communities inhabiting the rhizosphere of M. chamomilla and S. dulcamara. Both plants were cultivated in direct proximity to each other under field conditions (leamy sand soil) and were investigated in four independent replicate samples by amplicon sequencing. Singletons OTUs defined by only a single observation, were removed and not considered in both datasets.

Figure 4. Profile clustering network analysis of NHP sequences. Composition of rhizosphere samples from M. chamomilla, C. officinalis and S. dulcamara at a dissimilarity level of 8%. The abundance values for OTUs were scaled by hypergeometric between plants of more than 1% of the normalized data set were used. If the numbers of mean OTU read numbers exceed 2, the OTUs were regarded as altered and assigned to the respective profile. Node sizes ∝ OTU values corresponding to the relative abundance of the total data set; nodes matching to abundances of 0.5% and 10% were added as reference points. Distinctions between plants are displayed by widths of connection lines. Significances (p < 0.05) are indicated by colored node borders: nod node borders indicate significances between communities of all not linked profiles, green is used for significances between Matricaria and Calendula, orange for significances between Calendula and Solanum, and blue for significances between Matricaria and Solanum; nodes with black borders showing no significant differences. Black node labels indicate a similarity to the taxonomic node label (closest database match) of ≥95%, whereas grey node labels have a similarity ≤95%.

Conclusions

Figure 5. Comparison of the microbial communities of Matricaria chamomilla rhizosphere by jackknifed principal coordinate analysis. The biplot illustrates the compositional similarity between samples based on weighed UniFrac. Two coordinates are indicated by grey orls with size, as a function of relative abundance. To confine the biplot, the number of the displayed taxa was restricted to 5. The positions of the points are the averages for the jackknifed replicates generated by QIIME and are shown with ellipses representing the interquartile range (IQR) in each axis.

Figure 6. Content (%) of apigenin-7-D-glucoside in Matricaria chamomilla samples. Averages of biological replicates. HPLC-MS measurements and confidences are shown.

Figure 7. Diversity of bacterial antagonists with an activity towards pathogens. fungi isolates with activity against two pathogens were identified by partial 16S rRNA gene sequencing. Samples from rhizosphere and endorhiza include isolates from the medicinal plants M. chamomilla, C. officinalis and S. dulcamara.

Figure 8. The 16S rRNA gene copy numbers in Matricaria chamomilla plants and corresponding 16S rRNA gene sequences of antagonistic bacteria.