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Assemblage and functioning of bacterial communities in soil and rhizosphere

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Summary

Soil biodiversity is huge and determines largely the functioning of terrestrial ecosystems both at the ‘macro’ and the ‘micro’ level. Despite the general acceptance of the large impact of land use and other human activities on species loss in terrestrial ecosystems, their effects on microbial species reduction and the consequences are largely unknown. A major reason is the scarcity of experimental approaches to assess the relevance of soil microbial diversity for the functioning of soil ecosystems. The main goal of the study described in this thesis was to obtain better understanding of the diversity, structuring and functioning of bacterial communities in soil and rhizosphere. With that purpose, we initially applied the rather old dilution approach to manipulate the diversity of microbial communities in soil by inoculation and subsequent incubation of more or less diluted soil suspensions in pre-sterilized soils.

In order to evaluate the potentials provided by the dilution approach to manipulate bacterial species diversity I combined this approach with next generation sequencing and advanced bioinformatics and statistical procedures. In Chapter 2, I revisited this approach and shed more light on the assemblage processes of bacterial communities in soil. The results presented in Chapters 2 and 3, showed the overriding impact of soil on the assemblage of bacterial communities from suspensions with different diversities. The dilution approach reduced dramatically the community diversity at the species or OTU level of the suspensions at the species or OTU level. Both composition and diversity of the regrown bacterial communities were altered dramatically compared to the original suspension. This indicates the soil’s selective power during the assemblage of bacterial communities in terrestrial ecosystems. Remarkably, rare bacterial species could not be separated from abundant members as unique OTU’s were detected in the most diluted suspensions and the soil communities that developed from these most diluted suspensions.

I also assessed the bacterial community assemblage in the rhizosphere as well as the functionality of the communities formed after inoculation of suspensions with communities with different diversities (Chapter 4). The bacterial diversity as well the composition of the community and functionality were significantly different between soil and rhizosphere. Network analysis revealed stronger interactions among bacterial OTU’s in the rhizosphere than in

the soil. The enrichment processes in the rhizosphere selected microbes with particular functional genes mainly related to transporters, Embden-Meyerhof-Parnas, EMP, pathway and hydrogen metabolism. This selection was not random across bacteria with these functional traits, but specific for particular groups of bacteria containing these functions. Hence, I concluded that the selection processes in the rhizosphere are mainly driven by the functionality of the bacteria.

The potential effects of the bacterial communities in the rhizosphere on plant growth were further investigated in detail in Chapter 5. Plant biomass was on average the lowest and showed the highest variation in soils inoculated with the undiluted suspension harboring the most diverse community. A combination of unsupervised multivariate statistics and partial correlations showed that *Arthrobacter* was the taxonomical group that was most strongly related to plant biomass. A similar analysis showed that ‘transporters’ genes were the functional genes that were most strongly correlated to plant biomass. The frequency of ‘transporters’ genes was higher in *Arthrobacter* than in other components of the bacterial community. Partial correlation indicated further that the frequency of ‘transporters’ genes was more important than the frequency of *Arthrobacter* species to explain the effects on plant biomass production. Based on the results presented in Chapters 4 and 5, it can be concluded that plants select for specific bacterial species in the rhizosphere based on their functional properties, which benefit plant growth.