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Summary

Chitin is the second most abundant polymer in nature. In aquatic ecosystems, chitin is mainly present as part of the exoskeleton of arthropods; in soil, chitin is mainly present as component of fungal cell walls. The main enzymes involved in the breakdown of chitin are chitinases. Chitinases are produced by both fungi and bacteria. Chitinases of soil-borne bacteria can decompose chitin of dead fungal hyphae and other resources, but they may also play a role in antagonistic activities against fungi by destroying the chitin in the fungal cell walls. In the research described in this thesis, I tested the hypothesis that bacterial chitinases may perform different functions in different environments and under different circumstances, while the genetic composition and function of bacterial chitinases vary between different habitats.

Different approaches were applied in the current Ph D project including “in silico” genomic comparison of bacterial chitinolytic system as well as experiments. The results of genomic comparison of the chitinolytic system of terrestrial and aquatic bacteria in chapter 2 showed that terrestrial bacteria have more complex chitinolytic systems than aquatic bacteria which may be the result of adaptation to more complex functioning of chitinases in terrestrial habitats. In terrestrial ecosystems, bacterial chitinases may be involved in the degradation of chitinous material and in antifungal activity whereas in aquatic ecosystems chitinases mainly function as chitin degrading agents because in these systems the fungal biomass is generally low. In correspondence with these findings we observed more diverse chitin binding domains within the chitinase complex of terrestrial bacteria. Besides, I found a higher fraction of chitin binding proteins and other proteins that may be involved in antifungal activity within the genomes of terrestrial chitinolytic bacteria.

In chapter 3, a fungi-bacteria confrontation experiment using 13 different bacteria was conducted in order to investigate the effect of chitinase numbers
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and morphological properties of bacteria on their chitin degradation capability and antifungal activity. Remarkably, we found that the number of chitin binding proteins within bacteria was significantly correlated with the capability to degrade crystal chitin. On the contrary, chitinase numbers and morphological properties of bacteria (hyphal structure versus single cells) were not correlated with any chitin source degradation or antifungal activity. This confirmed the importance of chitin binding proteins in crystal chitin degradation.

In order to find out if different bacterial communities are selected by different chitin sources, I added four different chitin resources including crystal chitin, two different types of fungal cell walls and cuticles from mealworm as substrates to two soils. Pyrosequencing of 16S rRNA of bacteria and of the catalytic domain of the bacterial chiA gene was applied to identify chitin-degrading bacteria containing chitinases. Both the composition of the total bacterial community and of the chitinolytic bacterial community was significantly affected by soil, chitin sources and time of incubation. However, the richness and diversity of the chitinolytic bacterial community were not different between chitin resources indicating that the chitin content of the material does not have a major effect on the relevant bacterial community as long as the chitin has an equivalent structure.

I also tested the chiA gene diversity and abundance, as well as the dynamics of the chitinolytic bacterial community in response to the dynamics of the saprotrophic fungal biomass in the potato rhizosphere in order to test the function of bacterial chitinases as tool in the competition with fungi. The results showed that an increase of the fungal biomass in the potato rhizosphere caused an increase of chiA copy numbers, an increasing relative abundance of beta- and gamma- Proteobacteria, and a decreasing abundance of Actinobacteria, indicating that chitinases do play a role in bacteria-fungi interactions in soil.

The results obtained in this study have contributed to a better understanding of the ecological functions of bacterial chitinases. New insights in the composition of the bacterial chitinolytic system and the importance of its components were
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obtained. The potential ecological functions of the bacterial chitinase complex were explored and the role of chitinases in bacteria-fungi interactions, which are vital to the functioning of terrestrial ecosystems, was revealed further.