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Impact of plant domestication on spermosphere and rhizosphere microbiome composition

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Summary

Plants rely, in part, on the association with microbes for a number of life-support functions including nutrient acquisition, tolerance to biotic and abiotic stresses and immune regulation. In my thesis, I hypothesized that modern cultivars of crop plants have lost some of the traits needed to recruit host-specific microbiota as compared to their wild relatives, which are genetically more diverse and adapted to pre-agricultural soils. The research presented in this thesis assessed the impact of domestication of common bean (*Phaseolus vulgaris*) and habitat expansion on spermosphere and rhizosphere microbiome composition. For this, the microbiome composition of the spermosphere and the rhizosphere of wild and modern bean accessions grown in an agricultural and a native soil from Colombia, one of the centres of common bean diversification, was characterized by metagenomics and cultivation-dependent approaches.

A higher relative abundance of Bacteroidetes, mainly *Chitinophagaceae* and *Cytophagaceae*, was observed in the rhizosphere of wild bean accessions while an increase in relative abundance of Actinobacteria and Proteobacteria was observed in the rhizosphere of modern bean accessions. These divergences in rhizobacterial community composition between wild and modern bean accessions associated with differences in root morphological traits. In particular the specific root length (SRL) explained a significant portion of the variability in the abundance of families from the phylum Bacteroidetes. Using 16S-rDNA data from several other studies revealed that also wild relatives of other crop plant species presented higher relative abundances of members of the Bacteroidetes. The reason behind the higher relative abundance of Bacteroidetes in the root and rhizosphere compartments of wild relatives of various plant species is yet unknown but may be related to their ability to metabolize more complex polymers in the root exudates.

Plant domestication not only comes with changes in plant traits, but is also accompanied by progressive changes in the habitat and crop management practices. Hence, the transition from native habitats to agricultural soils may have led to a loss of plant-associated microbes thereby affecting specific, co-evolved beneficial functions of the plant microbiome. To begin to understand how these domestication factors affect the rhizosphere microbiome, the bean accessions were grown in a native and an agricultural soil from the Colombian highlands. The results showed that this transition of common bean from a native soil to an agricultural soil led to a gain of rhizobacterial diversity and led to a stronger bean genotype-dependent effect on rhizosphere microbiome assembly. A core rhizosphere microbiome was identified for common bean which mainly consisted of bacterial genera with nitrogen fixing capabilities, an important feature of microbes associated with leguminous plant species. However, also for other non-leguminous plant species, these bacterial genera are members of the core rhizosphere microbiome, suggesting a homogenization of rhizobacterial diversity of plants grown in different agricultural landscapes. Co-occurrence analyses further showed a reduction in complexity of the interactions going from native to agricultural soil which may indicate that rhizobacterial community assembly for common bean grown in agricultural soil is more modular than for common bean in native soil, making it relatively more easy for bacteria and other microorganisms to invade and establish in the rhizosphere of bean plants grown in agricultural soils.

The results of this thesis also showed that already during seed imbibition and germination, small but significant differences were detected between the spermosphere microbiomes of wild and modern bean accessions. These results suggest a domestication effect on microbiome assembly already at this early developmental stage. Exudation profiles showed that the spermosphere of a modern bean accession contained higher levels of

glutamate and glutamine as compared to a wild bean accession. Although a strong impact on microbiome composition was observed, a clear trend towards specific bacterial taxa consistently enriched in vitro by this amino acid was not observed. These results suggested that more complex mixtures of different exudate constituents are needed to mimic in vitro the selection occurring in situ in the bean spermosphere.

In conclusion, the research presented in this thesis showed that domestication of common bean had a significant effect on the composition of the rhizosphere and spermosphere microbiome. The higher abundance of Bacteroidetes in the rhizosphere of wild relatives of common bean and other crop species as well as the higher abundance of Actinobacterial families in the rhizosphere of modern crop cultivars provide new research directions to unravel the chemical cross-talk between plants and microbes, and to investigate the functional impact of these microbiome shifts on plant growth, development and health.

