Microbial footprints of tomato domestication

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Summaries

Summary

Plant domestication and breeding have substantially changed the genetic and phenotypic traits of crop species. However, the impact of domestication on the taxonomic and functional diversity of microorganisms associated with plant tissues is largely unknown. The work presented in this thesis focuses on tomato and how its domestication has shaped the diversity, structure, and functional potential of the root-associated microbiome. By examining the intricate relationships between tomato genotype, soil environment, and microbial community composition, we aim to uncover the ecological and genetic mechanisms that govern plant-microbe interactions along the domestication trajectory.

Field exploration in the native habitat of wild tomato *Solanum pimpinellifolium* in Southern Ecuador revealed a deterministic rhizosphere microbiome assembly dominated by Enterobacteriaceae and *Rhizobium*, as well as the fungal taxa *Fusarium* and *Aspergillus.* Metagenomic analysis revealed that these bacterial taxa possess traits such as motility, chemotaxis, siderophore production, and stress resistance, that may contribute to their successful establishment in the wild tomato rhizosphere under the challenging environmental conditions of their native habitat. Building on these results, controlled experiments with wild and domesticated tomato genotypes grown in Ecuadorian native and agricultural soils from the center of origin and greenhouse soil from a tomato's center of production, showed that both plant genotype and soil type shaped tomato rhizosphere microbiome composition. While the wild tomato genotypes retained similarities in microbiome composition associated with their native soil environments, the rhizosphere microbiome composition of domesticated tomato aligned with managed soil conditions. These shifts in microbiome composition suggest that domestication may unintentionally have led to a loss of beneficial microbes and microbial functions, such as motility, chemotaxis and stress response.

Further exploration revealed specific functional consequences of these changes. The results showed that in presence of its native soil microbiome, the wild tomato is better protected against herbivory by the endemic insect *Prodiplosis longifila.* Tomato plants grown in sterilized native and agricultural soils showed increased leaf damage, which was correlated with a reduced relative abundance of Actinobacteriota, particularly members of the *Actinoplanes* genus. Functional analysis of this genus revealed traits potentially involved in plant growth and stress tolerance, in particular secondary metabolite production and nutrient transport. These findings support the hypothesis that wild tomato, in contrast to its domesticated counterpart, relies on microbial partners in its native habitat for defense against herbivores. To uncover the plant's role in shaping these microbial relationships, we explored the genetic basis of microbiome assembly

using a recombinant inbred line (RIL) population derived from a cross between wild *Solanum pimpinellifolium* and domesticated tomato *S. lycopersicum* var. Moneymaker. By integrating 'microbiomics' and quantitative plant genetics, we identified genomic regions linked to the differential recruitment of *Cellvibrio* and *Streptomyces* by wild and domesticated tomato, respectively. These associations were reciprocally associated with plant traits related to nutrient uptake, stress tolerance, and metabolic functions, while corresponding microbial traits included carbon utilization, vitamin synthesis and iron acquisition.

Collectively, the results of this thesis show that domestication has reshaped not only plants traits but also the rhizosphere microbiome, changing diversity and functional traits associated with plant stress resilience. These insights highlight the importance of integrating microbiome research into plant breeding strategies, reinstating beneficial members of native microbial communities for more resilient and sustainable agricultural ecosystems.