

Distinct Phyllosphere Microbiome of Wild Tomato Species in Central Peru Upon Dysbiosis

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Abstract

Plants are colonized by myriads of microbes across kingdoms, which affect host development, fitness and reproduction. Hence, plant microbiomes have been explored across a broad range of host species, including model organisms, crops and trees under controlled and natural conditions. Tomato is one of the world's most important vegetable crops, however little is known about the microbiota of wild tomato species. To obtain insights into the tomato microbiota occurring in natural environments, we sampled epiphytic microbes from leaves of four tomato species, *Solanum habrochaites*, *S. corneliomulleri*, *S. peruvianum* and *S. pimpinellifolium*, from two geographical locations within the Lima region of Peru over two consecutive years. Here, a high-throughput sequencing approach was applied to investigate microbial compositions including bacteria, fungi and eukaryotes across tomato species and geographical locations. The phyllosphere microbiome composition varies between hosts and location. Yet, we identified persistent microbes across tomato species that form the tomato microbial core community. In addition, we phenotypically defined healthy and dysbiotic samples and performed a downstream analysis to reveal the impact on microbial community structures. To do so, we compared microbial diversities, unique OTUs, relative abundances of core taxa and microbial hub taxa, as well as co-occurrence network characteristics in healthy and dysbiotic tomato leaves and found that dysbiosis affects the phyllosphere microbial composition in a host species-dependent manner. Yet, overall, the present data suggests an enrichment of plant-promoting microbial taxa in healthy leaves, whereas numerous microbial taxa containing plant pathogens occurred in dysbiotic leaves.

Concluding, we identify the core phyllosphere microbiome of wild tomato species, and show that the overall phyllosphere microbiome can be impacted by sampling time point, geographical location, host genotype and plant health. Future studies in these components will help understand the microbial contribution to plant health in natural systems and can be of use in cultivated tomatoes.

Full Text

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