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Microbial footprints of tomato domestication

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Stellingen
Behorende bij het proefschrift

Microbial footprints of tomato domestication

1. While domestication improved tomato phenotype, it simultaneously disrupted microbial partnerships. Restoring beneficial microbe-plant alliances could be key to building resilient agriculture (this thesis).
2. The native microbiome of wild crop relatives in the center of origin is the most underexplored genetic bank in agriculture (this thesis).
3. *Enterobacter*, *Rhizobium*, *Actinoplanes*, *Streptomyces*, *Cellvibrio*, *Bacillus*, *Sphingomonas*, Cyanobacteria, *Pseudomonas*, and *Massilia* are not merely soil inhabitants, they represent functional microbial genera that have co-evolved with their tomato host plant (this thesis).
4. The microbial footprints of tomato domestication are imprinted in the rhizosphere, encompassing a shift from microbial genera supporting stress resilience of wild tomato plants to erosion of beneficial microbial alliances of domesticated tomato cultivars (this thesis).
5. The rhizosphere is not only a microbial niche, but also it is an evolutionary record of plant-microbe co-adaptation.
6. The rhizosphere microbiome represents a legacy of the soil microbiome, shaped by thousands of years of natural and human selection.
7. Rewilding the microbiome is not a return to the past, but it is a forward-looking strategy for sustainable agriculture.
8. Future crop breeding depends on selecting invisible microbial beneficial traits.
9. Feeding humanity in the future requires collaboration across soil, plant, and microbial sciences.

Stalin Wladimir Sarango Flores
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