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**Abstract**

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**EJEMPLO:**

**P1 The rhizosphere microbiome of wild tomato in the Andean mountains**

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**Abstract**

Domestication and breeding have substantially changed the genetic and phenotypic traits of plant species. How domestication affected the taxonomic and functional diversity of microorganisms living on and inside plant tissues is largely unknown for most species. To investigate if domestication of plants impacted the association with specific microbial taxa and beneficial microbial traits, we took a BackToRoots approach to first determine the taxonomic and functional composition of wild tomato plants growing in the arid lowlands of the Andes depression region between southern Ecuador and northern Peru, the center of origin of tomato. We specifically focused on taxonomic profiling of bacteria and fungi associated with tomato roots in three areas in the Low Andes. Three sites in Loja province (South of Ecuador) from 1400 to 200 masl (meters above sea level) were selected for sampling wild tomatoes. The sites resulted to be significantly different based on their environmental parameters which were clustered in a Principal Component Analysis-PCA (PERMANOVA sites: r2 = 0.18048, p = 0.0112). The beta diversity analysis showed that for all three sites, the rhizosphere microbiome was significant different from that of the bulk soils both in bacteria (PERMANOVA soil type: r2 = 0.09567, p = 0.0001) and fungi (PERMANOVA soil type: r2 = 0.08384, p = 0.0001).

On the other hand, the latitude, percent organic matter and magnesium content of the soils were determinative factors in rhizobacterial and fungal community assembly. The differential abundance analysis on the microbial composition revealed that wild tomato rhizosphere is dominated by *Enterobacter*, *Lactococcus*, *Lechevalieria*, unidentified fungi, *Acrocalymma*, *Aspergillus* and *Fusarium*. To further reveal the functional diversity of the rhizosphere microbiome of wild tomatoes, we have initiated a metagenomic analysis. These and culture-based analyses will be conducted to resolve if the rhizosphere of wild tomato harbors yet unclassified microbial genera and microbial traits that were lost during domestication.

**Keywords:** Domestication**,** microorganisms, Ecuador, Peru, rhizosphere microbiome, rhizobacterial and fungal community.