MOL2NET, International Conference Series on Multidisciplinary Sciences
UDLABIOTECH-01: I International Biotechnology Congress,
UDLA, Quito, Ecuador, 2019

Back to the Roots: Deciphering the taxonomic and functional diversity of the root microbiome of wild and modern tomato in the Ecuadorian Andes.

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Graphical Abstract	**Abstract.**
Insert grafical abstract figure here	Ancient societies first attempted to domesticate wild plants for food production, which gave rise to present-day agriculture. Currently, more than a third of agricultural production is lost due to abiotic or biotic stress and future increases in crop yields should be achieved with fewer input of fertilizers and pesticides. These challenges have increased awareness of the importance of the plant root microbiome. Plants are colonized by a surprising number of microorganisms, revealing in most cases an intimate symbiotic relationship, but the impact of plant domestication on the functional diversity and beneficial activities of this root microbiome is still largely unknown. Recent studies showed taxonomic differences in the root microbiome between wild relatives and modern cultivars, mainly in root architecture and root exudation. This leads to the hypothesis that present-day cultivars might have lost traits to recruit and activate host-specific beneficial root microbiota.

	Our project investigates tomato species and native soils in the Andes to explore the taxonomic and functional diversity of their root microbiomes. Next generation sequencing and ‘omics technologies, combined with classic microbiological techniques are being used to obtain insight in the diversity of root-associated microbial communities of tomatoes. We hypothesize that wild tomatoes grown in their native soils harbor unique and higher frequencies of beneficial root microbiota, compared to modern cultivars.