Characterizing the Microbiome of *Citrullus colocynthis* using Metabarcoding and Whole-Genome Sequencing.

Abstract content:

Plants growing in arid ecosystems, such as *Citrullus colocynthis* (L.) Schrad., exhibit exceptional adaptability to harsh conditions such as drought, high temperatures, and nutrient scarcity. Apart from the plant's morphological and physiological characteristics, plant associated microbiota emerges as a critical aspect underlying plant's survival in such conditions. This study investigates the diversity, composition, and functional potential of bacterial communities inhabiting the shoots, roots, and rhizosphere of *C. colocynthis*, using 16S rRNA gene metabarcoding and whole-genome sequencing.

Metabarcoding analysis revealed a rich and compartment-specific microbiome, dominated by members of Pseudomonadota (47.1%), Actinomycetota (21.8%), and Bacillota (13.2%). Significant differences in taxonomic composition were observed across plant compartments at the phylum level ($p = 0.001$), while environmental variables such as potassium ($p = 0.002$) and total nitrogen ($p = 0.027$) were identified as key drivers of community structure.

Whole-genome analysis of isolated endophytes uncovered a wide range of plant growth-promoting traits. Most strains carried genes involved in phosphorus solubilization, siderophore production, phytohormone biosynthesis, and tolerance to salinity and pH stress.

These findings highlight the functional versatility of *C. colocynthis* associated endophytes and their potential roles in enhancing plant nutrition and stress tolerance in nutrient-poor, arid soils. The study emphasizes the value of locally adapted microbial communities for developing sustainable, ecologically grounded agricultural strategies in dryland systems.

Keywords: *Citrillus colocynthis*, Microbiome, Whole genome sequencing, Metabarcoding.