

# Microbiomes of Velloziaceae from phosphorus-impooverished soils of the campos rupestres, a biodiversity hotspot

Antônio Pedro de Castello Branco da Rocha Camargo, Rafael Soares Correa de Souza, Paulo Arruda, Marcelo Falsarella Carazzolle

*Universidade Estadual de Campinas*

## Abstract

The rocky, seasonally-dry and nutrient-impooverished soils of the Brazilian campos rupestres impose severe growth-limiting conditions on plants. Species of a dominant plant family, Velloziaceae, are highly specialized to low-nutrient conditions and seasonal water availability of this environment, where phosphorus (P) is the key limiting nutrient. Despite plant-microbe associations playing critical roles in stressful ecosystems, the contribution of these interactions in the campos rupestres remains poorly studied. We generated and investigated the first microbiome sequencing data of Velloziaceae spp. thriving in contrasting substrates of campos rupestres. We assessed the microbiomes of *Vellozia epidendroides*, which occupies shallow patches of soil, and *Barbacenia macrantha*, growing on exposed rocks. The prokaryotic and fungal profiles were assessed by rRNA barcode sequencing (16S V4 and ITS2) of epiphytic and endophytic compartments of roots, stems, leaves and surrounding soil/rocks. Through this data, we found that there is a large quantity of as-yet-unknown microorganisms thriving in the campos rupestres environment. When contrasting the microbiomes of the two plants, we observed major differences regarding the community composition, diversity and colonization profiles. Interestingly, we also noticed that there are several highly abundant microorganisms that associate with both *V. epidendroides* and *B. Macrantha*, suggesting a shared core microbiome in this environment. Shotgun sequencing of total DNA extracted from microbial samples of rhizosphere and substrate was performed to investigate the functional landscape of the campos rupestres microbiomes. The samples were individually assembled and annotated, generating a median number of 9,907 noncoding genes and 2,544,611 protein-coding genes. The comparison between metabolic profiles of communities associated with the substrates and the rhizospheres of the two plants revealed major functional differences between the two microbiomes. We foresee that these data will contribute to decipher how the microbiome contributes to plant functioning in the campos rupestres, and to unravel new strategies for improved crop productivity in stressful environments.

Funding: FAPESP