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MICROBIAL COMMUNITIES ASSOCIATED WITH NATIVE SHRUB SPECIES IN DEGRADED DRYLAND SOIL OF ARGENTINA

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In Patagonia, Argentina, restoration projects are being implemented in areas impacted by hydrocarbon exploitation within the Monte Desert ecoregion. These arid regions undergo substantial soil modifications due to oil drilling activities and once abandoned, provide a unique opportunity to study microbial succession and ecologic restoration. We aim to integrate plant-soil-microbiome criteria into drylands restoration by including microbiological parameters in the selection of plant species for revegetation, focusing on their ability to recruit beneficial microorganisms essential for establishment and survival, while also assessing microbial diversity recovery. We selected three plant species that spontaneously colonized our study sites: *Larrea divaricata*, *Neltuma flexuosa* and *Junellia crithmifolia*. Soil samples were collected from two contexts: the selected reference ecosystem (RE) and the degraded site (DS) in an abandoned oil field. Within each context, bulk soil was sampled both without vegetation and under the canopy of the selected plant species. Samples were analysed for physical and chemical parameters such as organic carbon (OC), nitrogen, and phosphorus, among others. After DNA extraction using a commercial kit, and 16S rRNA gene fragments sequencing, Amplicon Sequence Variants were classified using DADA2 and analysed with phyloseq and microViz packages in R to describe bacterial communities. RE samples exhibited greater richness and diversity than DS samples, even in areas without vegetation, revealing a decline in diversity due to soil degradation, including under shrub canopies. Beta diversity analysis revealed that the primary factor differentiating bacterial communities was the site, followed by vegetation type. Soil characterization showed distinct clustering of RE and DS samples, with OC as a key differentiator. Correlation heatmaps suggested more complex interactions among bacterial genera in RE samples compared to DS. Bacterial communities

associated with the same plant species shared certain taxa across different site conditions. For instance, *L. divaricata* recruited both in RE and DS beneficial bacteria involved in carbon and nitrogen cycles, and plant growth promotion genera, such as *Microvirga* and *Streptomyces*. Assessing bacterial diversity in the RE underscores the crucial role of native vegetation in biodiversity recovery. The beta diversity analyses highlight the impact of abiotic factors on bacterial communities, with OC being a significant factor. Despite the varying complexity of communities in DS and RE, the ability of certain plant species to recruit beneficial microorganisms across varying site conditions suggests their potential as candidates for restoration actions. Future studies will focus on comparing plant species' capacity to recruit beneficial microorganisms, thus enhancing dryland restoration strategies.

Palabras clave: Dryland restoration – Native vegetation – Bacterial diversity