

TITLE: THE MICROBIOME OF THE HALOPHYTE *ATRIPLEX NUMMULARIA* (OLD MAN SALTBUSH) IN NORTHEASTERN BRAZIL

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ABSTRACT:

Atriplex nummularia, popularly known as old man saltbush (or *erva-sal*, in Portuguese), is one of the most promising species for phytoremediation of salt affected soils. However, little is known about its endophytic microbiome and how this community is affected by salt content in soil. To characterize the bacterial community associated to this plant, we performed 16S rRNA gene sequencing of DNA extracted from leaves, roots and rhizospheric soil of 30 different *A. nummularia* bushes from the Northeast of Brazil. The plants were collected from plantations in the cities of Caruaru (CA), Ibimirim (IB) and Serra Talhada (ST), located in the state of Pernambuco. We performed alpha diversity, beta diversity, network, indicator species and core analysis to describe and detect differences among plant habitats (leaf, root and rhizospheric soil) and sites (CA, IB and ST). OTU richness and Shannon index were higher in soil, with no differences among plant parts (root and leaf). Sites did not differ on alpha diversity, and almost no differences between sites in abundances of the main bacterial phyla and classes were detected in leaves and roots. In beta diversity, all plant habitats were different among themselves, while for the sites, CA was different from IB and ST, especially due to heterogeneity in soil communities. Leaf and root communities as well showed a high similarity in beta diversity among sites in ordinations. Networks helped define OTUs with a high degree of interaction inside each habitat (soils, roots and leaves). Core analysis (OTUs with 90-100% and 80-90% occurrence in samples) showed a higher diversity of OTUs in roots than leaves, being leaves core apparently a subset of the roots core. These results describe the microbiome of *A. nummularia* in northeastern Brazil and show that the selection of the endophytic community is highly influenced by the plant itself, since communities from a same habitat were very alike regardless of the sampled site. Also, this knowledge helps selecting potential plant growth promoting bacteria (PGPB) for halophytic plants involved in phytoremediation initiatives and also expand what is known about plant-microorganisms' interactions in extreme environments.

Keywords: halophytes, *Atriplex nummularia*, endophytes, plant microbiome, salt affected soils

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