

Plant Microbiota of Coastal Halophyte *Salicornia Ramosissima*

Authors : Isabel N. Sierra-Garcia, Maria J. Ferreira, Sandro Figueredo, Newton Gomes, Helena Silva, Angela Cunha

Abstract : Plant-associated microbial communities are considered crucial in the adaptation of halophytes to coastal environments. The plant microbiota can be horizontally acquired from the environment or vertically transmitted from generation to generation via seeds. Recruiting of the microbial communities by the plant is affected by geographical location, soil source, host genotype, and cultivation practice. There is limited knowledge reported on the microbial communities in halophytes the influence of biotic and abiotic factors. In this work, the microbiota associated with the halophyte *Salicornia ramosissima* was investigated to determine whether the structure of bacterial communities is influenced by host genotype or soil source. For this purpose, two contrasting sites where *S. ramosissima* is established in the estuarine system of the Ria de Aveiro were investigated. One site corresponds to a natural salt marsh where *S. ramosissima* plants are present (wild plants), and the other site is a former salt pan that nowadays are subjected to intensive crop production of *S. ramosissima* (crop plants). Bacterial communities from the rhizosphere, seeds and root endosphere of *S. ramosissima* from both sites were investigated by sequencing bacterial 16S rRNA gene using the Illumina MiSeq platform. The analysis of the sequences showed that the three plant-associated compartments, rhizosphere, root endosphere, and seed endosphere, harbor distinct microbiomes. However, bacterial richness and diversity were higher in seeds of wild plants, followed by rhizosphere in both sites, while seeds in the crop site had the lowest diversity. Beta diversity measures indicated that bacterial communities in root endosphere and seeds were more similar in both wild and crop plants in contrast to rhizospheres that differed by local, indicating that the recruitment of the similar bacterial communities by the plant genotype is active in regard to the site. Moreover, bacterial communities from the root endosphere and rhizosphere were phylogenetically more similar in both sites, but the phylogenetic composition of seeds in wild and crop sites was distinct. These results indicate that cultivation practices affect the seed microbiome. However, minimal vertical transmission of bacteria from seeds to adult plants is expected. Seeds from the crop site showed higher abundances of *Kushneria* and *Zunongwangia* genera. Bacterial members of the classes Alphaproteobacteria and Bacteroidia were the most ubiquitous across sites and compartments and might encompass members of the core microbiome. These findings indicate that bacterial communities associated with *S. ramosissima* are more influenced by host genotype rather than local abiotic factors or cultivation practices. This study provides a better understanding of the composition of the plant microbiota in *S. ramosissima*, which is essential to predict the interactions between plant and associated microbial communities and their effects on plant health. This knowledge is useful to the manipulations of these microbial communities to enhance the health and productivity of this commercially important plant.

Keywords : halophytes, plant microbiome, *Salicornia ramosissima*, agriculture

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