Various Rhizobacteria Species that Support Plant Growth

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ABSTRACT

Rhizobacteria that encourage plant growth are a crucial part of the intricate rhizosphere microbiome. It is frequently stated that the Pgpr community of various plant species is chosen by their rhizosphere, which favour the growth of some more than others. We evaluated the Pgpr community in the rhizosphere of significant plant species, including two cultivars and one landrace, in this greenhouse study utilizing the same agricultural soil. The landrace, cultivars, and rhizosphere all have different Pgpr community structures, although having comparable community structures. Exclusive Pgpr groups, which are implicated in plant resistance and stress tolerance, were found in the rhizosphere of the lima bean. Similar relative abundances of Bacillus and Paenibacillus, two groups engaged in promoting plant growth through the generation of antibiotics and biological N fixation, were found in the rhizosphere of both cultivars. Additionally, compared to landraces, cultivars showed a higher number of specialized microorganisms and more complicated community interactions. The results of this study add to our understanding of the Pgpr community in various plant species and support the importance of landraces and cultivars in determining the rhizobacteria community.

Keywords: Agricultural, Soil, Rhizosphere, and Plant Growth

INTRODUCTION

Rhizobacteria that promote plant growth are a significant group of bacteria that inhabit the rhizosphere and influence plant growth through a variety of methods, including biological N2 fixation, the generation of plant hormones, and antibiotic production. The rhizosphere community is influenced by the soil's characteristics, the genotypes of the plants, and their stage of development. However, little is understood about the make-up, organization, and variety of the native community that inhabits the rhizosphere of many plant species. The properties of each plant species' root exudates affect the recruitment of the native PGPR community. The rhizosphere community is shaped by a range of metabolites that are released from the roots of various plant species. For instance, wheat recruits Pseudomonas and Rhizobium while the rhizosphere of soybean recruits.

Sinorhizobium and Bradyrhizobium.

Comparing cultivars and landraces, however, can reveal differences in the rhizosphere recruitment of microorganisms. In the rhizosphere of landraces and cultivars of common bean, for instance, Pérez-Jaramillo analyzed the bacterial community and discovered different bacterial species inhabiting each plant group. Recently, Albuquerque evaluated the rhizobacterial population by contrasting cowpea cultivars that were wild and those that were modern, and they discovered differing recruitment patterns for certain rhizobacterial groups and keystone species.

Although the rhizosphere of many plant species, cultivars, and landraces contained a diverse bacterial community, nothing is known about the natural pgpr community that inhabited the rhizosphere of these plants. Particularly significant plant species grown in Northeastern Brazil include maize, cowpea, and lima beans. Additionally, maize and cowpea are recent cultivars, while lima beans are landraces. Therefore, these variations may influence how the pgpr community of plants growing in the same soil and environment colonise the rhizosphere. In this study, it was expected that variations in maize, cowpea, and lima bean could have an impact on the pgpr population in each plant's rhizosphere. By sequencing the 16 S rRNAs gene from the rhizosphere of maize, cowpea, and lima bean, this study examined the pgpr community.

MATERIAL AND METHODS

The research was done in a greenhouse that belonged to the Agricultural Science Center of the Brazilian university Federal do Piau. Tropical dry climate is defined as 1000 mm or less of annual precipitation and 30 °C. The primary characteristics of the agricultural soil used were that pH was 6.4, P 4.3 mg kg1 and K 42.1 mg kg1 base saturation, and V 62%.

RESULTS AND DISCUSSION

In this study, using 16 S rRNAs amplicon sequencing to compare the rhizosphere of maize, cowpea, and lima bean, we evaluated the composition, structure, and diversity of native pgpr. The pgpr community generally showed differences when comparing landrace lima beans, maize, and cowpeas, which is partially consistent with the study's hypothesis.

CONCLUSION

In this work, we compared the pgpr community in various plant species, including landrace Lima bean, maize cultivars, and cowpea and cow cultivars. Overall, the findings demonstrated that cultivars and landraces differed in the organization of the pgpr communities, with particular bacterial genera exhibiting differential abundances in each species' rhizosphere. Comparing the cultivars to the landrace lima bean, the cultivars showed a higher proportion of specialized microorganisms and a more complex community.