TITLE: Genomic analyses from plant growth-promoting rhizobacteria isolated from fruit trees

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ABSTRACT:

The food production relies in the use of industrial agricultural inputs from non-renewable resources. The growing demand for fertilizers, associated with its high costs and environmental impacts points to the need of mitigatory technologies. Biological inputs possess potential to substitute at least part of conventional fertilizers. The plant growth-promoting rhizobacteria (PGPR) in the bioinoculant form represents a biological input. PGPR can stimulate plant growth by several mechanisms, and the most important mechanisms are: biological nitrogen fixation; auxin and cytokinin secretion; production of the enzyme 1-aminocyclopropane-1-carboxylate (ACC) deaminase (inhibitor of ethylene, phytohormone that prevents plant growth); soil nutrient solubilization and; antibiotics production and other mechanisms of biological disease control. Two rhizobacteria strains, isolated from passion fruit (*Burkholderia* sp.) and pineapple (*Azospirillum* sp.), with plant growth-promoting potential were identified by the marker rRNA16S and had their genomes sequenced by UENF research groups. The goal of this work is to identify the genetic bases related to plant growth promotion and other ecophysiological processes for both strains. The genome sequencing raw reads were assembled by several genome *de novo* assemblers, and the assemblies with best metrics were selected. Automatic and manual annotations were performed to access the possible metabolites produced by these rhizobacteria. Both annotations pointed the biological nitrogen fixation genes (*nif* genes), ACC deaminase (*acds*), cytokinin activation enzyme *LOG*, genes involved in the metabolism of several carbon sources, antibiotics production and resistance genes. The *Burkholderia* sp. strain presented the phosphate solubilization involved gene *gabY* and one gene from the final step of the auxin production pathway indole-3-acetamide hydrolase (*iaaH*). The *Azospirillum* sp. strain presented the PQQ genes, involved in phosphate solubilization, and genes from Calvin-Benson-Brassam cycle, indicating that in the absence of soil carbon sources this strain can behave as autotrophic.

Keywords: Genomics, Microbiology, Biological Inputs

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