



***In silico* analysis of the 16S rRNA gene of endophytic bacteria, isolated from the aerial parts and seeds of important agricultural crops**

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ABSTRACT. Because of human population growth, increased food production and alternatives to conventional methods of biocontrol and development of plants such as the use of endophytic bacteria and fungi are required. One of the methods used to study microorganism diversity is sequencing of the 16S rRNA gene, which has several advantages, including universality, size, and availability of databases for comparison. The objective of this study was to analyze endophytic bacterial diversity in agricultural crops using published papers, sequence databases, and phylogenetic analysis. Fourteen papers were selected in which the ribosomal 16S rRNA gene was used to identify endophytic bacteria, in important agricultural crops, such as coffee, sugar cane, beans, corn, soybean, tomatoes, and grapes, located in different geographical regions (America, Europe, and Asia). The corresponding 16S rRNA

gene sequences were selected from the NCBI database, aligned using the Mega 5.2 program, and phylogenetic analysis was undertaken. The most common orders present in the analyzed cultures were Bacillales, Enterobacteriales, and Actinomycetales and the most frequently observed genera were *Bacillus*, *Pseudomonas*, and *Microbacterium*. Phylogenetic analysis showed that only approximately 1.56% of the total sequences were not properly grouped, demonstrating reliability in the identification of microorganisms. This study identified the main genera found in endophytic bacterial cultures from plants, providing data for future studies on improving plant agriculture, biotechnology, endophytic bacterium prospecting, and to help understand relationships between endophytic bacteria and their interactions with plants.

Key words: Endophytic bacteria; 16S rRNA gene; Agronomic crops; Phylogenetic analysis; Biotechnology; Bioprospection