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Genetic diversity of *Burkholderia* (Proteobacteria) species from the Caatinga and Atlantic rainforest biomes in Bahia, Brazil

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ABSTRACT. The genus *Burkholderia* (β-Proteobacteria) currently comprises more than 60 species, including parasites, symbionts and free-living organisms. Several new species of *Burkholderia* have recently been described showing a great diversity of phenotypes. We examined the diversity of *Burkholderia* spp in environmental samples collected from Caatinga and Atlantic rainforest biomes of Bahia, Brazil. Legume nodules were collected from five locations, and 16S rDNA and *rec*A genes of the isolated microorganisms were analyzed. Thirty-three contigs of 16S rRNA genes and four contigs of the *rec*A gene related to the genus *Burkholderia* were obtained. The genetic dissimilarity of the strains ranged from 0 to 2.5% based on 16S rDNA analysis, indicating two main branches: one distinct branch of the dendrogram for the *B. cepacia* complex and another

branch that rendered three major groups, partially reflecting host plants and locations. A dendrogram designed with sequences of this research and those designed with sequences of *Burkholderia*-type strains and the first hit BLAST had similar topologies. A dendrogram similar to that constructed by analysis of 16S rDNA was obtained using sequences of the fragment of the *rec*A gene. The 16S rDNA sequences enabled sufficient identification of relevant similarities and groupings amongst isolates and the sequences that we obtained. Only 6 of the 33 isolates analyzed via 16S rDNA sequencing showed high similarity with the *B. cepacia* complex. Thus, over 3/4 of the isolates have potential for biotechnological applications.

Key words: 16S rDNA; *rec*A; *Inga*; *Calliandra*; *Mimosa*; Legume nodule