

TITLE: PHYLOGENY OF BETA-RHIZOBIA FROM ROOT NODULES OF TWO ENDEMIC *Mimosa* GROWN IN CAMPOS GERAIS REGION, SOUTHERN BRAZIL

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ABSTRACT:

Fabaceae is the third largest angiosperm family traditionally divided into three subfamilies, Caesalpinoideae, Mimosoideae and Papilionoideae. However, a recent study recognized the subfamily Mimosoideae as a distinct clade in the Caesalpinoideae. Within the mimosoid clade, the pantropical *Mimosa* genus is abundant and diverse in Brazil, one of their main centers of radiation. Legumes can acquire nitrogen through the symbiotic relationships with rhizobia, a group of bacteria able to reduce atmospheric N₂ to assimilable forms by host plants in specialized structures called nodules. To date, species of *Paraburkholderia* has been reported as the main symbionts of Brazilian *Mimosa* species but the information is still limited, specially concerning to endemic species. We performed a genetic diversity study of rhizobia isolated from root nodules of two native shrubs, *M. micropteris* and *M. paranapiacabae*, endemic of South Brazil. Thirty rhizobia were isolated from plants grown in areas with acid and sandy soils, with low organic matter levels and high aluminum content. The BOX-PCR profiles indicated high genotypic variability among the strains, including five strains that presented unique profiles. The 16S rRNA phylogenetic analysis allowed the identification of all strains as *Paraburkholderia* and separated them into three clades, which didn't include any known *Paraburkholderia* species. The same evolutionary pattern was verified in the phylogram constructed with concatenated sequences of housekeeping genes *recA-gyrB*, suggesting that they may represent novel *Paraburkholderia* species. Finally, the phylogram of partial *nodC* nodulation gene supports the monophyletic origin of symbiotic genes in mimosoid-nodulating *Paraburkholderia* and a potential correlation of this nodulation gene with host plant specificity and geographical location. Our results support that *Mimosa* endemic to certain environments seems to interact with a more restricted range of symbionts, suggesting coevolution with the local microorganisms, and therefore can harbor novel lineages of rhizobia.

Keywords: Betaproteobacteria, Rhizobia, Nitrogen fixation, Phylogenetic analysis, 16S rRNA

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