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**Diversity of bacteria isolated from legume nodules cultivated in soils from a tropical mountain ecosystem**

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Tropical mountain ecosystems cover 25% of the Earth's surface and are known for their high degree of endemism and plant species richness. In Brazil, these ecosystems exist in different biomes, but little is known about them, especially regarding soil microorganisms and their functions and interactions.

The aim of this study was to assess the diversity of bacteria isolated from legumes nodules from different habitats that compose rupestrian fields (quartz gravel field, sandy bogs, peat bogs, rocky outcrop and cerrado), an important environment type located in tropical mountains from Serra do Cipó, Minas Gerais, Brazil. To capture legume nodulating bacteria (LNB) - two trap plants species (*Macropodium atropurpureum* and *Mimosa tenuiflora*) were grown in a mixture of soil inoculum and sterile substrate. After 90 days, the nodules were collected, and the isolated bacteria were characterized by culturing. In total, 381 isolates were characterized, which were mostly fast-growing and culture medium 79-acidifying bacteria with colonies of up to 1 mm in diameter.

A total of 90 distinct culture groups were found, indicating high phenotypic diversity of the bacteria isolated from legumes nodules in rupestrian fields. We partially sequenced 16S rRNA from strains representing 55 culture groups. Most isolates belonged to the alpha- and beta-classes of proteobacteria, with a predominance of the *Rhizobium* and *Burkholderia* genera, respectively. The use of more than one trap plant belonging to distinct subfamilies (Faboideae and Mimosoideae) was essential for capturing greater LNB diversity. The high diversity of LNB cultures found in rupestrian fields did not correlate to a specific habitat or to the occurrence of legumes (present in the different habitats).

However, the greatest genetic and culture group diversity was found in the cerrado habitat, and there is evidence that this diversity is important in maintaining the bacterial diversity in other habitats.

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