

## **Environmental Mycobacterium Isolates from the Atlantic Forest Soil**

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### **Abstract:**

By far the greatest challenge of understanding the biological diversity remains in characterizing the diversity of prokaryotes. The Atlantic Forest is considered one of the richest biomes in biodiversity of the world. However, at present, less than 10% of the original covering of the Atlantic Forest is preserved. There are more than 30 thousand species of plants and animals formally described. However, there are few studies on the microbial diversity of the Atlantic Forest soil. In this study we focus on Mycobacterium isolates from the Atlantic Forest soil. Many species of the genus Mycobacterium are widely distributed in the environment, and include species that might be pathogenic to humans and animals. Environmental mycobacteria are ubiquitous, and are found in many ecosystems, such as water, dust or soil. Mycobacteria are classified into slowly growing and rapidly growing species. The rapidly growing mycobacteria (RGM) or environmental mycobacteria (EM), which require less than 7 days to produce easily seen colonies on solid media, comprise more than 50 environmental species. In order to assess the taxonomic relationships among the EM strains, belonging to the Atlantic Forest Bacteria Culture Collection (CBMA), sequence of the 16S rRNA (approximately 1500 bp) were determined. Based on nucleotide identities in the 16S rRNA gene sequences, EM from Atlantic Forest soil clustered with *M. septicum* and *M. llatzerense* species. Our results demonstrated the genetic diversity among the Mycobacterium isolates obtained from the Atlantic Forest soil, which are probably new species of the genus. In order to improve the taxonomy of this group of bacteria we are going to develop and apply Multilocus Sequence Analysis (MLSA) approach to the Mycobacterium isolates. Financial support: FAPERJ, FINEP, CNPQ, CAPES, FIOCRUZ

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