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Application of single-nucleotide polymorphism analyses to clinical *Mycobacterium tuberculosis* isolates from a region of high TB endemicity; Salvador, Bahia, Brazil

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Current genotyping techniques used to study the epidemiology of MTB isolates are based on repetitive genetic elements. Studies have revealed that single nucleotide polymorphisms (SNP) are valuable phylogenetically informative markers. SNP has been used to differentiate between clinical isolates, because recombination events that could occur independently within repetitive sequences are avoided. Also, availability of reliable, non labor-intensive and high-throughput genotyping methods is of foremost importance to improve our understanding of MTB transmission dynamics. SNP genotyping was used to investigate the discriminatory power of this methodology. 90 SNP previously identified through genomic comparisons of the H37Rv, CDC1551, and *M. bovis* genomes were examined. Then, clustered nodes in the tree were assigned to individual genetic groups or subgroups. The SNP genotyping and the MTB strains clustering framework strategy presented here are a very high performing system to discriminate MTB clinical isolates in regions of high TB endemicity.

Biography

Tonya Duarte, Science Doctor, has completed her PhD from Federal University of Rio de Janeiro, School of Medicine. She got her BSc in Veterinary Medicine, Specialist in Teaching Methodology in Higher Education, MSc in Experimental Pathology. In 2005, she got successful experiences award from Municipal Health Department of Salvador. In 2010/2011, she was member of the Collectives Dynamics Group at Gulbenkian Institute of Science. Nowadays, she is a Professor of Microbiology in Federal University of Bahia, Institute of Health Sciences, and guest Researcher of the NB3 Laboratory at Oswaldo Cruz Foundation. Recently, she has published paper in reputed journal (*Tuberculosis*), about innate immune response in tuberculosis. Currently, her researches focus on immunomodulatory effects of the intercellular communication during tuberculosis infection and molecular biology of *Mycobacterium tuberculosis*.

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