TITEL: GENOTYPING OF *Mycobacterium leprae* PRESENT ON ZIEHL-NEELSEN-STAINED MICROSCOPIC SLIDES FROM LEPROSY PATIENTS IN STATES MATO GROSSO, MIDWESTERN BRAZIL

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ABSTRACT:

Mycobacterium leprae (M. leprae) is an intracellular pathogen of global distribution that causes public health problems in developing countries, especially in those with a tropical climate like Brazil. Infection in humans occurs mainly by inhalation of infectious aerosols released by untreated cases with the multibacillary (MB) clinical form of the disease. According to the World Health Organization (WHO), leprosy occupies the second place with the largest endemic cases of the disease, with 26,395 cases (13%), which is still the only country in the world that has not reached the WHO target of <1 new case per 10,000 population. The State of Mato Grosso, located in the Midwestern region of Brazil, has an incidence of more than 7 cases per 10,000 registered inhabitants. Due to the lack of data on the genotypes of *M. leprae*, this work aimed to verify the occurrence of *M. leprae* genotypes based on variable numbers of repeat polymorphism (TTC). A total of 240 suspected clinical leprosy specimens from Ziehl-Neelsen (Z-N) stained blades were analyzed. The Polymerase Chain Reaction (PCR) technique was used to verify the presence of the genetic material of *M. leprae* (rLep) and after that screening the TTC replicate protocol was performed. PCR positive for Rlep were 175 (72,9%), of which 88 were PCR positive for TTC. Ten different genotypes with repeats varying from 7 to 16, with a high prevalence of genotype 11 (17.04%) and 12 (45.45%). Studies in other countries suggests a wide variation in the number of copies of TTC repeats ranging from 7-18, 20-21, 24-25, 28, 34 and 37, that could explain different infectious source among patients even in those who are contactors. In this study, *M. leprae* genotypes had a great variability but with a high frequency of genotypes 11 and 12, which indicated that this genotype could be geographically related to Midwestern region.

Keywords: molecular diagnosis, leprosy, genotyping, humans, Mato Grosso

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