TITLE: MOLECULAR CHARACTERIZATION OF *Mycobacterium leprae* IN A WILD ANIMALS IN STATE OF MATO GROSSO

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ABSTRACT:
Mycobacterium leprae is a gram-positive bacillus, acidfast, obligate intracelular parasite that caused leprosy. Endemic in Brazil, prevalence of leprosy in Brazil was 1.01% per 100.000 inhabitants and in the state of Mato Grosso (MT) presented the higher prevalence (7.75% per 10.000 inhabitants). Cellular and molecular mechanisms have not yet been fully elucidated and this makes it difficult to understand the epidemiology of this microorganism. Thus, this study aimed to verify the number of TTC repeat variables that may contribute to the differentiation of lineages and to verify the distribution of genotypes among animals to better understand the epidemiology of bacillus and its role in public health. Polymerase Chain Reaction (PCR) was used to detect genetic material of *M. leprae* in 94 captive and free-ranging wild animals received by Laboratory of Microbiology and Molecular Biology. Method phenol: chloroform and glass beads were used to DNA extraction. For the amplification of 372pb of the *M. leprae* were used a set of primers (R1 5'-CGG CCG GAT CCT CGA TGC AC-3') and (R2 5'-GCA CGT AAG CTT GTC GGT GG-3'). PCR amplification visualized were purified using a GFX™ PCR DNA and Gel Band Purification kit (GE Healthcare, Piscataway, NJ, USA), sequenced using an ABI-PRISM 3500 Genetic Analyzer (Life Technologies Corporation, USA) and analyzed in the BLAST program. Posteriorly, 5 positive wild animals were submitted to the PCR based in a variable numbers of TTC repeats (TTC-A 5'-GGAC CTAAACCATCCCGTTT-3) and (TTC-B 5'-CTACAGGGGGCACTTAGCTC-3'). The PCR product was purified and sequenced. Based on the repetition of the TTC region, the analysis of the sequences in the software CLC Genomics Workbench demonstrated that the positive animals presented 12 repetitions, not having variability between the samples. In humans, this repetition had been described in other studies. Therefore, the possible contact of animals of this study, with other animals or humans can disseminate the disease. We suggest that studies related to the variability of TTC region repetition should be performed in humans in MT, and may contribute to a better understanding of the distribution of this bacillus. Thus, the detection in wild animals may be associated with endemicity in the state of MT, which makes them important sources of infection.

Keywords: genotyping, leprosy, wild animals, PCR.

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