

TITLE: MOLECULAR DETECTION OF *Mycobacterium leprae* IN A FREE-RANGING MONKEY, *Sapajus apella* (Primates: Cebidae)

Mycobacterium leprae IN A FREE-RANGING MONKEY, *Sapajus apella* (Primates: Cebidae)

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ABSTRACT

Endemic in Brazil, Leprosy is a chronic disease caused by *Mycobacterium leprae*, of great importance to public health. Prevalence of leprosy in Brazil was 1.01% per 100.000 inhabitants and there were more than 10.000 new cases detected in 2016. Among the Brazilian states, Mato Grosso (MT) presented the higher prevalence (7.75% per 10.000 inhabitants). The epidemiologic comprehension and the early diagnosis and treatment are crucial in the control of leprosy disease. Wild animals can be considered disease reservoirs. In Brazil, only armadillos (*Dasypus novemcinctus* and *Euphractus sexcinctus*) leprosy were described with *M. leprae*. The aim of this study was to verify the occurrence of leprosy in wild mammals in Mato Grosso State, Brazil. Polymerase chain reaction (PCR) was used to detect genetic material of *M. leprae* in 27 nasal swabs of captive and free-ranging wild animals received by Laboratory of Microbiology and Molecular Biology. Phenol:chloroform and glass beads techniques were used for DNA extraction. For the amplification of *M. leprae* DNA, a set of primers 5'-CGG CCGGATCCTCGATGCAC-3' and 5'-GCACGTAAGCTTGTCGGTGG-3' were used. Amplifications were visualized in agarose gel (1.5%), purified, sequenced and analyzed in the BLAST program. As results, 27 nasal samples were analysed and only one was positive (3.7%) from *Sapajus apella* was positive. Non-human primates are known to be experimental models for *M. leprae*, due to their phylogenetic proximity to humans. Chimpanzee (*Pan troglodytes*), Sooty mangabeys (*Cercocebus atys*) monkeys and cynomolgus macaque (*Macaca fascicularis*) have been described with leprosy in Africa. However, this is the first report of natural infection in species *Sapajus apella* with *M. leprae*, showing the capacity of infecting different hosts. The PCR contributes to the identification of subclinical infections, exposure and transport of the bacteria. The detection of *M. leprae* in a new host supports the hypothesis of finding new environmental reservoirs, and the monkey may be involved in the epidemiological chain of this disease, becoming a possible perpetrator of leprosy. Despite this microorganism being studied for a long time, the mechanism is not fully elucidated. Therefore, in order to comprehend the endemic in distinct regions, it is necessary to understand the environment around that infected humans or animals, the route of infection and the mode of transmission.

Keywords: Leprosy, Primates, PCR.