**ADDITIONAL INSIGHT IN LEPROSY TRANSMISSION IN FORTALEZA BY *MYCOBACTERIUM LEPRAE* GENOTYPING.**

AMANDA N. B. FONTES¹, LÍGIA R. F. S. KERR², LUANA N. G. C. LIMA³, CRISTIANE C. FROTA³, MAX VICTOR C. FREITAS³, MARIA ARACI A. PONTES³, HEITOR S. GONÇALVES³, CARL KENDALL⁴, EUZENIR N. SARNO⁵, PATRICK J. BRENNAN⁶, VARALAKSHMI D. VISSA⁵, PHILIP N. SUFFYS¹.

¹Laboratório de Biologia Molecular Aplicada a Micobactérias, IOC/FIOCRUZ. ²Universidade Federal do Ceará. ³Centro de Referência Nacional em Dermatologia Sanitária Dona Libânia. ⁴Tulane University; ⁵Laboratório de Hanseníase, IOC/FIOCRUZ. ⁶Colorado State University.

**Introduction:** Recently, Short Tandem Repeats (STRs) and Single Nucleotide Polymorphism (SNP) have been used in studies to understand the mechanisms of leprosy transmission. **Objectives:** Genotyping isolates of *M. leprae* from the city of Fortaleza (CE) using 16 STRs and 3 SNPs. **Methods:** About 350 newly cases are diagnosed with leprosy at Centro de Referência Nacional em Dermatologia Sanitária Dona Libânia (CDERM) during the period of September 2008 to March 2010. From 112 consented patients, biopsies of skin lesions were collected. DNA from *M. leprae* was extracted using DNeasy Blood & Tissue kit (QIAGEN) following the manufacturer’s instructions. The analysis of tandem repeats was performed by simultaneous amplification of different loci using labeled primers. The analysis of single base mutations was performed by PCR-RFLP. **Results:** 112 isolates were analyzed for 16 STRs. Three clusters composed of two samples had 100% of genetic similarity. Other 24 samples were grouped in pairs and showed genetic similarity ranging from 68,75%-93,75% differing respectively in 5 (N = 1) and only one locus (N = 3). SNP analysis showed that genotype 4 is predominant in the city of study. **Conclusions:** Although there was large allelic diversity due to the large number of isolates analyzed, we observed the formation of genetically identical or very similar groups and this could suggests a transmission relationship. Subsequent analysis of these data according to the social network of participants and other clinical information will be performed to establish the real connection between the grouped cases and eventual routes of leprosy transmission.

**Key-Words:** *Mycobacterium leprae*; STRs; SNPs.

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