

DE662 - Doenças endêmicas negligenciadas

[854] **MOLECULAR CHARACTERIZATION OF LEPTOSPIRA ISOLATES DURING ANNUAL EPIDEMICS IN SALVADOR, BRAZIL 1996-2008.**

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**Resumo:**

Introduction: Leptospirosis is a spirochaetal zoonotic disease that has emerged as an important public health problem due to annual rodent-borne epidemics associated with high mortality in urban slum populations. Although there are more than 200 *Leptospira* serovars, urban outbreaks in Brazil appear to be due to a single serovar, *L. interrogans* serovar Copenhageni. Clinical manifestations associated with urban outbreaks are diverse and include a mild self-limiting illness to severe manifestations such as Weil's Disease and pulmonary hemorrhage syndrome. We hypothesize that differences in the strain's virulence characteristics may be responsible for different clinical severity and outcomes that are observed after infection. Objective: Ahmed et al developed a multilocus sequence typing (MLST) method which discriminated serovar Copenhageni strains from a reference collection of isolates collected worldwide. The objective of this study was to apply this method to determine whether genotype of serovar Copenhageni isolates from Salvador, Brazil was associated with clinical phenotype. Methods: We randomly selected 26 serovar Copenhageni strains among 120 isolates which were isolated from leptospirosis patients in the Salvador area from 1996-1998 (7 of 72 isolates) and 2006-2008 (19 of 48 isolates). Isolates were obtained from patients with different clinical manifestations, including four individuals with severe pulmonary hemorrhage syndrome. Genomic DNA was extracted from isolates and we used PCR to amplify three loci, *icdA* (Isocitrate dehydrogenase), *LipL41* (outer membrane Lipoprotein 41) and *rrs2* (16S rRNA). An ABI 3100 DNA sequencer was used to sequence amplified products. Mega 4 software system was used to analyse concatenated sequences. Results: DNA sequence analysis identified that all 26 isolates had 100% homology with the *L. interrogans* serovar Copenhageni strain Fiocruz L1-130, which was an isolate whose genome was sequenced as part of a national sequence project. Discussion: Our results indicate that there is a single clonal group of *Leptospira* that has been the agent for severe leptospirosis in Salvador since 1998. This study supports the findings of other studies in Rio de Janeiro and Salvador that there is limited diversity among *Leptospira* which are the cause of urban epidemics. Alternatively, the MLST method may have had low discriminatory power in differentiating serovar Copenhageni isolates. Whole genome sequencing of these isolates is needed to determine whether the causal agent is truly clonal and if not, to identify specific polymorphic markers that would aid the identification of pathogen-related determinants involved in producing severe clinical manifestations and outcomes.