

TITLE: MOLECULAR EPIDEMIOLOGY OF *Leptospira noguchii*: IMPORTANT INSIGHTS OF AN UNDERESTIMATED PATHOGENIC BACTERIA

AUTHORS: DI AZEVEDO, M.I.^a; JAEGER, L.H.^b; LOUREIRO, A.P.^a; LILENBAUM, W.^a

INSTITUTION: ^aLaboratory of Veterinary Bacteriology, Department of Microbiology and Parasitology, Fluminense Federal University, Niterói, Rio de Janeiro, Brazil; ^bDepartment of Pharmaceutic Sciences, Faculty of Pharmacy, Federal University of Juiz de Fora, Juiz de Fora, Minas Gerais, Brazil.

ABSTRACT:

Leptospirosis is an emerging zoonosis of global importance that can affect a wide variety of hosts. It presents complex and dynamic epidemiology, including a close relationship between humans, animals and ecosystems. *Leptospira noguchii* has been reported in both wild and domestic hosts, mainly in the Americas. Human cases of leptospirosis have been associated to this agent. In addition, a correlation between the infection in animals by *L. noguchii* and the increase in the occurrence of human cases has been suggested, but remains to be elucidated. Thus, the objective of the present study was to genetically characterize *L. noguchii* strains, evaluating its genetic diversity and distribution patterns through haplotype networks, in order to better understand the epidemiology of the species, besides providing important phylogenetic inferences. Strains of *L. noguchii* (n=7) were submitted to DNA extraction, PCR and sequencing. Genetic characterization was based on *secY* gene and concatenated analysis of MLST scheme # 1 genes (*glmU*, *pntA*, *sucA*, *tpiA*, *pfkB*, *mreA*, and *caiB*). Reference sequences were cautiously selected in GenBank and MLST bank, and belonged to eight different hosts (armadillo, cow, dog, opossum, human, mangoose, pig and weasel) from nine geographical locations (Argentina, Brazil, China, Nicaragua, Panama, Peru, Trinidad and Tobago, Uruguay and USA). Descriptive analysis of the genetic diversity was performed in Arlequin v. 3.5. Phylogenetic analyzes were performed in the MEGA X software. Haplotype networks were constructed in the population genetics software PopART. Phylogenetic trees based on *secY* gene and concatenated MLST genes showed two main clusters, with sequences from the present study included in the first. In general, there was no relationship between the geographical origin of the strains and the *secY* phylogenetic clusters. Diversity indexes confirmed a high genetic variability ($H > 0.8$). This high intraspecific variation observed may be related to differences in virulence and antigenicity or even adaptability of the strains. In addition, haplotype networks clearly demonstrated the circulation of genotypes between humans and animals from different ecosystems, confirming the zoonotic potential of the species. The present study provides relevant data for the knowledge of leptospirosis in the One Health context, where human, animal, and environmental health are closely connected.

Keywords: Leptospirosis; Molecular genetics; MLST; Molecular Epidemiology; One Health

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