

TITLE: THE SAME STRAIN LEADING TO DIFFERENT CLINICAL OUTCOMES: THE ENIGMA BEHIND CANINE LEPTOSPIROSIS

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ABSTRACT:

Canine leptospirosis is a worldwide zoonosis, varying from asymptomatic and chronic infections to clinical acute disease characterized by fever, anorexia, vomiting, severe jaundice, renal and hepatic injury, systemic and pulmonary hemorrhage and death, depending on the virulence of the strain. In many parts of the world *Leptospira interrogans* serogroup Icterohaemorrhagiae strains have great epidemiological importance, being the most prevalent on dogs. It is consensual that, while anicteric disease is usually associated with other serovars, including Canicola, the highly virulent serovars of the Icterohaemorrhagiae serogroup tend to be more commonly associated with clinical acute disease. In this context, the present study aims to characterize and compare strains/sequences belonging to the serogroup Icterohaemorrhagiae recovered from clinically ill and asymptomatic dogs, and to discuss the agent-host-environment relationship as well as the intriguing similarities of the bacterium regardless the clinical condition of the host. Based on *secY* gene sequences of *L. interrogans* serovar Icterohaemorrhagiae, we have studied genetic diversity of strains obtained from 13 dogs, including dogs with clinical signs of acute leptospirosis (n=4), asymptomatic dogs (n=7) and animals with chronic kidney disease (n=2), all of them from the same geographical area, the state of Rio de Janeiro, Brazil. Genetic distance was $K2P=0.00$, i.e., they were all 100% similar to *L. interrogans* serovar Icterohaemorrhagiae, reference strain L1-130. This could also be observed on phylogenetic tree, that clearly demonstrates a homogeneous well supported group (bootstrap = 93%) including all studied sequences. Moreover, no significant associations were observed between clinical status and age, sex or vaccinal status. Concluding, the same strain leads to different clinical outcomes on canine leptospirosis. The answer for this fact will rise from deep studies regarding whole genomic sequencing of the strains, as well as proteomics. Those studies may provide key information for understanding of the clinical manifestation of the disease.

Keywords: *Leptospira* sp.; PCR; *secY*; sequencing.

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