

TITLE: GENETIC CHARACTERIZATION OF ANTIGENS IN *LEPTOSPIRA* SP. STRAINS OF CATTLE FROM BRAZIL: ARE WE CLOSE TO A VACCINAL CANDIDATE?

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ABSTRACT:

Leptospirosis is a bacterial zoonotic disease caused by *Leptospira* spp. In bovines, it is commonly associated to chronic reproductive disease, as abortion and subfertility, resulting in economic losses in animal production. To minimize these losses, disease control can be done through environmental management, antibiotic therapy and vaccination. The latter still has limitations in terms of effectiveness, since vaccine is serogroup specific and the genus present high serological diversity. Therefore, greater knowledge about the antigenic diversity of local strains is essential. Thus, the aim of the present study is to evaluate the genetic variability of antigens from *Leptospira* sp. obtained from cattle in the state of Rio de Janeiro for evaluation of vaccine candidates for veterinary use. Strains of *Leptospira* spp. (n=24) used were originated from the culture bank of the Laboratory of Veterinary Bacteriology-UFF (LaBV-UFF). Isolates selected were from circulating pathogenic species - *Leptospira interrogans*, *L. santarosai* and *L. borgpetersenii* – and from the most common serogroups associated with chronic diseases in cattle in Brazil- Sejroe, Icterohaemorrhagiae and Pomona. Nine antigenicity genes (*lipL21*, *lipL32*, *loa22*, *ompL37*, *lemA*, *ligA*, *lipL45*, *ompL1* and *ligB*) were amplified and sequenced. Genetic variability (nucleotides and amino acids) was analyzed together with sequences available in GenBank, using bioinformatics tools (BioEdit, ClustaW and MegaX). Based on the genetic distances of the aligned sequences of amino acids of the studied genes, the following similarity degrees were obtained: LigB – 76%; ompL1-91%; LipL45 - 92%; LigA-92%; LemA - 95%; OmpL37 - 96%; Loa22 - 96%; lipL32 - 98%; lipL21 - 99%. Therefore, the gene with the minimum genetic distance at amino acid level was *lipL21*, being considered the best vaccine candidate for bovine leptospirosis in the Brazilian Southeast region, since it is presumed to be more conserved in these strains. Importantly, it will be the target of further studies based on reverse vaccinology.

Keywords: animal leptospirosis; PCR; bovine; gene sequencing.

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