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Characterization of the genetic variability of field strains of *Brucella canis* isolated in Antioquia, Colombia during 2005-2013

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Introduction: *Brucella canis*, a facultative intracellular pathogen is responsible for canine brucellosis, a zoonotic disease that affects canines causing abortions and reproductive failures, human infection may cause mild, asymptomatic or serious medical conditions. Since 2005 the presence of *Brucella canis* was demonstrated in Antioquia and the circulating strains were identified as *B. canis* type-2, besides recognizing in them the operon virB. In order to learn more about the circulating strains the entire genome of a wild strain of *Brucella canis* denoted Oliveri was sequenced, which showed insertions and deletions species-specific.

Objective: Characterize the genetic variability of field strains of *Brucella canis* isolated in Antioquia during 2005-2013.

Methods: A set of six pairs of primers that would allow identification of indels identified in the strain of *B. canis* str. *Oliveri* was designed, after this conventional PCR and sequencing of the amplified products was performed on 30 strains of *Brucella canis*, *Brucella suis* 1330 and bv. 1, *Brucella melitensis* 16M and vaccine strains of *Brucella abortus* S19 and RB51.

Results: 5 of 30 field strains studied share indels with the sequenced strain, the remaining 25 strains differ in a deletion exclusive from the Oliveri strain. Inside the deletions a related one with a critical epimerase for the synthesis of carbohydrates from the surfaces is present, which is related to the rough characteristics of the colonies like those presented by the field strains. A second deletion is related to N-acetyltransferase, which prevents the action of aminoglycosides, its absence could facilitate the action of these antibiotics in the bacteria. A third 6 bp deletions in chromosome II, is related to the ABC transporters superfamily, which perform the transport of nutrients through the membrane and it is corresponded with a unique characteristic of the species metabolism. A final deletion related to a glutamic acid tranference RNA is the only exclusive in *Oliveri* strain, this deletion may result from the adaptation of the bacteria to intracellular lifestyle more secure and stable with a constant supply of nutrients, additional we could talk about the effect of speciation and host specific adaptation or as in other *Brucella* species a possible recombination process. Inside the insertions studied, one related with an anti prophage repressor which interacts with prophage repressor genes facilitating horizontal gene transfer was presented; a second insertion evaluated as 60 bp is part of a hypothetical protein with no specific function but that facilitates differentiation of *Brucella canis* from other species.

Conclusions: The field strains isolated in Antioquia present genotypic variations from the sequenced strain *Oliveri*, indicating that this is not the only strain circulating in the region, which would be useful in future studies to determine which other strains are circulating and which one of them was responsible for the initial infection in the region.

Biography

Juana Liz Vidal Arboleda has completed her undergraduate studies in Microbiology at the University of Antioquia. She has participated as Colciencias Young Researcher of the project in the Rio Grande II Reservoir. From 2009-20013, she did specialization in Veterinary Clinical Laboratory in the UDCA (University of Applied and Environmental Sciences), currently pursuing her Master's degree in Animal Science in University of Antioquia and serves as Microbiologist and Bioanalyst in the Laboratory of Veterinary Microbiology, Faculty of Agricultural Sciences at the University of Antioquia.

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