

Global Veterinary Microbiology and Veterinary Medicine Summit

October 17-18, 2016 Chicago, USA

Phylogenetic analysis of the *Brucella canis* str. *Oliveri* isolated in Antioquia, Colombia

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Introduction: *Brucellosis* is an infectious disease caused by a facultative intracellular pathogen of the genus *Brucella*. Ten species are recognized and exhibit different host preference; comparative analysis of this genus have show a close genetic relationship between species. To study the evolution of these species have developed multiple phylogenetic analyzes on which consensus has been separated into a clade *B. melitensis* and *B. abortus*, in another clade marine species and one species consisting of *B. suis* and *B. canis*, recognizing *Brucella ovis* as the ancestral species, suggesting that the initial contact to pigs, goats and cattles occurred from contact with infected sheep.

Objective: To establish the phylogenetic relationships and the time of divergence of *Brucella canis* strain *Oliveri*.

Methods: Concatenated sequences of these genes were used: *glK*, *trpE*, *cobQ*, *aroA*, *dnaK*, *rpoB*, *gap*, *gyrB*, *Omp2a*, *Omp2b*, *Omp25* and *Omp3* in 24 species of *Brucella*, including *Brucella canis* str. *Oliveri*. Using the Mega 6 program phylogenetic analysis was performed by the method of neighbor joining with the substitution model Tamura-Nei and 10000 Bootstraps repetititons. The molecular clock hypothesis among *Brucella* species was tested and the test of relative rates of Tajima between *Brucella canis* str. *Oliveri* and *Brucella canis* ATCC was performed.

Results: Phylogenetic analysis including *O. anthropi* as out group indicate that *Brucella ovis* was the first lineage split is the most basal species. The clade with greater genetic diversity is formed by *B. suis* where it will also find strains of *B. canis* suggesting a recent divergence. *B. abortus* and *B. melitensis* appear as sister species, being each one monophyletic. Aquatic species *B. ceti* and *B. pinnipedialis* are part of the same clade but separate from the terrestrial strain. Within *B. canis* all strains present a simultaneous divergence since they split from their common ancestor, corroborating the result of the test of relative rates of Tajima with $P=0.31731$. The molecular clock hypothesis is rejected between species indicating that the rate of evolution of all species of *Brucella* is not the same.

Conclusions: The strain of *Brucella canis* str. *Oliveri* like others *canis* species diverged from *Brucella suis*. The *Brucella canis* species had a similar rate of evolution and a genetic distance, so is not possible define which diverged first.

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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