

## Molecular Survey and Genetic Diversity of Bartonella henselae Strains Infecting Stray Cats from Algeria

**Authors :** Naouelle Azzag, Nadia Haddad, Benoit Durand, Elisabeth Petit, Ali Ammouche, Bruno Chomel, Henri J. Boulouis

**Abstract :** Bartonella henselae is a small, gram negative, arthropod-borne bacterium that has been shown to cause multiple clinical manifestations in humans including cat scratch disease, bacillary angiomatosis, endocarditis, and bacteremia. In this research, we report the results of a cross sectional study of Bartonella henselae bacteremia in stray cats from Algiers. Whole blood of 227 stray cats from Algiers was tested for the presence of Bartonella species by culture and for the evaluation of the genetic diversity of B. henselae strains by multi-locus variable number of tandem repeats assay (MLVA). Bacteremia prevalence was 17% and only B. henselae was identified. Type I was the predominant type (64%). MLVA typing of 259 strains from 30 bacteremic cats revealed 52 different profiles. 51 of these profiles were specific to Algerian cats/identified for the first time. 20/30 cats (67%) harbored 2 to 7 MLVA profiles simultaneously. The similarity of MLVA profiles obtained from the same cat, neighbor-joining clustering and structure-neighbor clustering showed that such a diversity likely results from two different mechanisms occurring either independently or simultaneously independent infections and genetic drift from a primary strain.

**Keywords :** Bartonella, cat, MLVA, genetic

**Conference Title :** ICAVLS 2020 : International Conference on Agriculture, Veterinary and Life Sciences

**Conference Location :** Dublin, Ireland

**Conference Dates :** October 22-23, 2020