

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

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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

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