Summary of the DVM thesis No 14772 , Faculty of Veterinary Medicine, Urmia University .
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Genomic detection of *Bartonella* genus in blood samples of dogs in Urmia using the PCR method

Summary

The aim of this study is to determine the genomic detection and prevalence of *Bartonella* genus and *B. henselae* species in blood samples of dogs referred to the clinic of the Faculty of Veterinary Medicine of Urmia university veterinary clinic and small animals clinics in Urmia city. One hundred blood samples were collected on August and December 2022. DNA was extracted from all blood samples. Then PCR method was used to identify the *Bartonella* genus based on *16SrRNA* gene primers with a fragment length of 522 bp. In the next step, *gltA* specific primers with a fragment length of 130 bp and Nested-PCR method were used to identify *B. henselae* species. . In this study, software (AmplifiX, made in France) was used to design primers. The results showed that four samples (4%) of the blood samples, based on the genus primers, were positive for *Bartonella* infection. Additionally, the results showed that out of the four positive samples, three samples with species-specific primers were infected with *B. henselae*. It was concluded that due to the difficult growth of *Bartonella* bacteria, PCR technique can be a suitable method for diagnosing this bacterium at the genus and species levels due to its high speed, accuracy, and sensitivity. Although the level of contamination was not significant, the low level of contamination can be even worrying in terms of public health due to the zoonotic nature of this bacterium.

Key words: *Bartonella*, PCR, Dogs, Urmia