

Molecular detection and prevalence of *Babesia bovis* in cattle of Shahreza city, the south region of Isfahan province, Iran

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Abstract

This study aimed to determine the variety of *Babesia* species among cattle of Shahreza city in the south part of Isfahan Province. A total of 253 blood samples were collected via the jugular vein from healthy cattle, randomly. The extracted DNA from blood cells was amplified by *Babesia*-all primers, which amplify an approximately 400bp DNA fragment from the region of the 18S rRNA gene from various members of the genus *Babesia*. All cattle positive samples were further analysed for the presence of *B. bigemina* and *B. bovis* by specific semi-nested PCR. *B. bigemina* and *B. bovis* were identified by specific semi-nested PCR in 0% and 65.2% of cattle blood samples, respectively. Chi-square tests were used to compare molecular prevalence values relative to Season, Farm, Type, Hygiene, Vectors, Use a disposable needle, Age, and Milk Yield. Among these factors, seasons and vectors were found to have significantly different in the prevalence. The significant major risk factors of *B. bovis* in cattle were identified as season, hygiene, and vectors by the univariate analysis. Moreover, multivariable logistic regression analysis revealed a statistically significant association of the prevalence of *B. bovis* with the season. The examination of 50 microscopic fields showed 59.39% sensitivity and 100% specificity compared to molecular examination. The Kappa coefficient between molecular and microscopy (50 fields) techniques indicated a moderate level of agreement (Kappa= 0.504). This study is the first molecular detection of *Babesia* species from cattle in the south of Isfahan Province, Iran. Further researches are needed to determine the vectors, vector-host interactions and genotypic variants that may affect the presence and distribution of *Babesia* species in Iran.

Key words: Iran, Isfahan Province, *Babesia* species, Cattle, Molecular detection

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