Investigation of *Babesia microti* parasite by PCR method and determining the sequence of 18S rDNA gene in Ixodidae in Khuzestan province

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Abstract

Babesiosis is a tick-borne disease in domestic and wild animals worldwide. This disease is caused by different species Babesia, including Babesia microti, which is zoonotic and can be transmit between humans and animals due to their ability to be transmitted from blood. Limited information is available regarding the presence of Babesia microti in ticks in Iran. The aim of this study was to investigate the presence of Babesia microti in ticks of Khuzestan province and to determine their molecular and genotypic characteristics. The present study was a field-descriptive-cross-sectional study that was conducted for 16 months from June 2017 to September 2018 in Khuzestan province. The ticks (No = 620) were collected from cows, sheep, goats and horses in Khuzestan province and their characteristics were determined using valid keys. The presence of Babesia microti infection and its genotype in collected ticks were investigated by polymerase chain reaction (PCR) using 18S rDNA gene, amplifying a PCR product of 149 bp in length. A total of 620 salivary gland samples collected from ticks included Rhipicephalus turanicus (150), Rhipicephalus sanguinus (60), Hyalomma anatolicum (310) and Hyalomma exquavatum (100). Ten samples were pooled as one sample for DNA extraction. The results of PCR showed that the infection rate of Babesia microti in Hyalomma anatolicum species is 64%. The results of the sequencing of 4 PCR positive samples of Babesia microti from 4 regions of Khuzestan province (Ahvaz, Behbahan, Elahaye and Lali) showed that there are 2 mutations at position (A>G) 465 and (A>C) 517 in Ahvaz isolate. The results of this study also showed the presence of Babesia microti infection in the ticks of domestic animals in Khuzestan province, which should be considered in terms of transmission to humans.

Key words: Phylogeny, Babesia microti, 18S rDNA, Ixodidae

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