

عنوان مقاله:

Nucleotide sequence analysis of the Second Internal Transcribed Spacer (ITS2) in *Hyalomma anatolicum anatolicum* Iran

محل انتشار:

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خلاصه مقاله:

Ticks are important acarina that infest animals. They are obligatory blood sucker arthropods which economically impact cattle industry by reducing weight gain and production. Moreover, they are important vectors of viral, bacterial, rickettsial and parasitic pathogens infecting humans and animals. In view of the importance of in pathogen transmission, including in Iran, the accurate identification of this tick is critical. Although many keys are available as aids, morphological identification of tick species such as (Koch, 1844; Hoogstral and Kaiser, 1959) is difficult and expert knowledge is required. False morphological identification at the level of species and subspecies is common, particularly for complex members which are prevalent in Iran. For example, the high similarity between and is the cause of confusion in the identification of these species. In this study, polymerase chain reaction (PCR) techniques were used for identification of based on analysis of the gene sequence of the Second Internal Transcribed Spacer (ITS2) of this tick. The ITS2 nucleotide sequence of was 963 base pairs (bp) in length and exhibited 93% homology with other GenBank registered ITS2 sequences of this subspecies (accession no: FJ593700.1). The complete ITS2 region sequence was identified in this study and registered in GenBank under accession number HQ123320

کلمات کلیدی:

Hyalomma anatolicum anatolicum.; tick; ITS2

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