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Molecular Identification of Camel Tick and Investigation of Its Natural Infection by Rickettsia and Borrelia in Saudi Arabia

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Abstract : Hard ticks Hyalomma spp. (family: Ixodidae) are obligate ectoparasite in their all life stages on some domestic animals mainly camels and cattle. Ticks may lead to many economic and public health problems because of their blood feeding behavior. Also, they act as vectors for many bacterial, viral and protozoan agents which may cause serious diseases such as tick-born encephalitis, Rocky-mountain spotted fever, Q-fever and Lyme disease which can affect human and/or animals. In the present study, molecular identification of ticks that attack camels in Riyadh region, Saudi Arabia based on the partial sequence of mitochondrial 16s rRNA gene was applied. Also, the present study aims to detect natural infections of collected camel ticks with Rickessia spp. and Borelia spp. using PCR/hybridization of Citrate synthase encoding gene present in bacterial cells. Hard ticks infesting camels were collected from different camels located in a farm in Riyadh region, Saudi Arabia. Results of the present study showed that the collected specimens belong to two species: Hyalomma dromedari represent 99% of the identified specimens and Hyalomma marginatum which account for 1 % of identified ticks. The molecular identification was made through blasting the obtained sequence of this study with sequences already present and identified in GeneBank. All obtained sequences of H. dromedarii specimens showed 97-100% identity with the same gene sequence of the same species (Accession # L34306.1) which was used as a reference. Meanwhile, no intraspecific variations of H. marginatum mesured because only one specimen was collected. Results also had shown that the intraspecific variability between individuals of H. dromedarii obtained in 92 % of samples ranging from 0.2- 6.6%, while the remaining 7 % of the total samples of H. dromedarii showed about 10.3 % individual differences. However, the interspecific variability between H. dromedarii and H. marginatum was approximately 18.3 %. On the other hand, by using the technique of PCR/hybridization, we could detect natural infection of camel ticks with Rickettsia spp. and Borrelia spp. Results revealed the natural presence of both bacteria in collected ticks. Rickettsial spp. infection present in 29% of collected ticks, while 35% of collected specimen were infected with Borrelia spp. The valuable results obtained from the present study are a new record for the molecular identification of camel ticks in Riyadh, Saudi Arabia and their natural infection with both Rickettsia spp. and Borrelia spp. These results may help scientists to provide a good and direct control strategy of ticks in order to protect one of the most important economic animals which are camels. Also results of this project spotlight on the disease that might be transmitted by ticks to put out a direct protective plan to prevent spreading of these dangerous agents. Further molecular studies are needed to confirm the results of the present study by using other mitochondrial and nuclear genes for tick identification.

Keywords : Camel ticks, Rickessia spp. , Borelia spp. , mitochondrial 16s rRNA gene
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