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SHORT NOTE

Detection of Rickettsia aeschlimannii and Rickettsia sibirica mongolitimonae in Hyalomma marginatum (Acari: Ixodidae) ticks from Turkey

Adem Keskin* and Ahmet Bursali

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Department of Biology, Gaziosmanpasa University, Faculty of Science and Art, 60250 Tokat, Turkey.
ademkeskin@yahoo.com (*Corresponding author); bursali383@yahoo.com

ABSTRACT — A total of 784 (626♀, 158♂) Hyalomma marginatum Koch, 1844 ticks collected from humans in Turkey were tested for the presence of spotted fever group rickettsiae using polymerase chain reaction (PCR) targeting the citrate synthase (gltA= 381 bp) and the outer membrane protein A (ompA= 532 bp) genes, followed by sequencing analysis. Of the ticks tested, 39 were infected by Rickettsia aeschlimannii while 2 were infected by Rickettsia sibirica mongolitimonae. To our knowledge, this is the first report of R. sibirica mongolitimonae in H. marginatum ticks.

KEYWORDS — Hyalomma marginatum, Lymphangitis-associated rickettsioses, Rickettsia aeschlimannii, Rickettsia sibirica mongolitimonae, PCR

The rickettsiae are a group of obligate intracellular gram-negative bacteria responsible for serious human diseases, such as Lymphangitis-associated rickettsioses (LAR), and Mediterranean spotted fever (Parola et al. 2013; Portillo et al. 2015). Rickettsial infections are one of the oldest known vector borne diseases, and infections are mainly spread through fleas, mites (chiggers), lice, or ticks (Portillo et al. 2015). To date, 10 spotted fever group (SFG) rickettsiae, namely Candidatus Rickettsia vini, R. aeschlimannii, R. africae, R. conorii, R. felis, R. helvetica, R. hoogstraalii, R. monacensis, R. raoultii and R. slovaca, have been molecularly detected in ticks mainly collected from humans in Turkey (Gargili et al. 2012; Orkun et al. 2014; Keskin et al. 2014, 2016).

In the present study, a total of 784 (626♂, 158♀) Hyalomma marginatum Koch, 1844 ticks were collected from humans by health personnel under aseptic conditions in Tokat province, Turkey. Ticks were stored in 70 % alcohol and morphologically identified using the key and descriptions of Apanaskevich and Horak (2005). Total DNA was extracted from individual ticks by a genomic DNA Isolation Kit developed by our laboratory (Turkuaz Genomic DNA Isolation Kit, Tokat, Turkey). DNA isolation procedures were described in our previous studies (Keskin et al. 2014, 2016). DNA quantity and
quality was evaluated with a spectrophotometer (Eppendorf Biophotometer, Eppendorf, Hamburg, Germany) and gel electrophoresis in 1 % agarose. It should be noted that no specific test of DNA quality using a tick target was performed due to the large number of tested tick samples; prevalence may therefore be underestimated if DNA varied greatly in quality.

Primers aimed at the rickettsial citrate synthase gene (gltA) and outer membrane protein A (ompA) gene, previously described by Regnery et al. (1991), were used to detect the presence of rickettsiae in ticks and evaluate their diversity. Firstly, rickettsial DNA was screened by PCR using primers RpCS.877p (5'-GGGGACCTGCTACGGCGG-3') and RpCS.1258n, (5'-ATTGCAAAAAGTACAGGAA-3') which is a 381-bp fragment of the gltA gene. Each gltA positive sample was then screened with primer pairs RpCS.877p (5'-GGGGACCTGCTACGGCGG-3') and RpCS.1258n, (5'-ATTGCAAAAAGTACAGGAA-3') targeting a 532-bp portion of the gltA gene. Each gltA positive sample was then screened with primer pairs Rr190.602n (5'-AGTGCAGCATTCGCTCCCTG-3') and Rr190.700p (5'-ATGGCGAATATTTCTCCAAAA-3') for both primers were as follows: denaturation at 95 °C for 5 min, then 35 cycles of 30 s at 95 °C, 60 s at 48 °C, and 30 s at 72 °C, followed by 5 min at 72 °C. Agarose (1 %) electrophoresis was used to visualize rickettsial DNA positive samples on a gel documentation system (UVP, Upland, CA, USA). PCR conditions for both primers were as follows: denaturation at 95 °C for 5 min, then 35 cycles of 30 s at 95 °C, 60 s at 48 °C, and 30 s at 72 °C, followed by 5 min at 72 °C. Agarose (1 %) electrophoresis was used to visualize rickettsial DNA positive samples on a gel documentation system (UVP, Upland, CA, USA). Distilled water and Rickettsia slovaca DNA (obtained from a previous study) were used as negative and positive controls, respectively.

The rickettsia positive PCR products were sequenced with their corresponding PCR primers at a commercial facility (RefGen, Ankara, Turkey). The consensus sequences were prepared using BioEdit 7.0.4.1 (Hall 1999) and compared with other rickettsial sequences in the NCBI GenBank database. All sequences obtained were submitted to GenBank and the corresponding accession numbers were obtained.

According to sequence analyses, 41 of the 784 H. marginatum ticks were found to be positive for rickettsial DNA. GltA (KU574125) and ompA (KU574126) gene sequences obtained from two H. marginatum ticks were 100 % identical to sequences of R. sibirica mongolitimonae obtained from human patients (gltA: DQ423368, ompA: HQ728352).

This pathogenic rickettsia was first isolated in Hyalomma asiaticum Schulze & Schlottke, 1930 collected from Inner Mongolia (China) (Yu et al. 1993). Afterwards, R. sibirica mongolitimonae was detected in H. excavatum Koch, 1844 (Greece and Cyprus), Hyalomma sp. (Israel), H. truncatum Koch, 1844 (Niger), Rhipicephalus pusillus Gil Collado, 1936 (France, Portugal, and Spain) and R. bursa Canestrini & Fanzago, 1878 (Spain) (Parola et al. 2001, 2013; Harrus et al. 2011). To our knowledge, this is the first report of R. sibirica mongolitimonae in H. marginatum.

R. sibirica mongolitimonae, etiological agent of Lymphangitis-associated rickettsioses (LAR), is a member of Rickettsia sibirica species complex within the spotted fever group (SFG) of rickettsiae (Edouard et al. 2013; Parola et al. 2013). Maculopapular rash, fever, and multiple eschars are basic clinical signs and symptoms of R. sibirica mongolitimonae infection (Ramos et al. 2013; Portillo et al. 2015). The first human infection caused by R. sibirica mongolitimonae was reported in France in 1996 (Raoult et al. 1996). Since then, more than 25 R. sibirica mongolitimonae cases in humans have been reported in Europe (France, Greece, Portugal and Spain) and Africa (Algeria, Egypt, and South Africa) (Preterius et al. 2004; Parola et al. 2013; Portillo et al. 2015). Although R. sibirica mongolitimonae was detected in Asian ticks (H. asiaticum in Inner Mongolia, China), there is currently no report of R. sibirica mongolitimonae infection in humans in Asia (Portillo et al. 2015).

In addition to infection by R. sibirica mongolitimonae, 39 H. marginatum ticks were found to be infected with R. aeschlimannii (Genbank similarity = 100%), which has been reported in previous studies (Gargili et al. 2012; Orkun et al. 2014; Keskin et al. 2016). R. aeschlimannii is broadly distributed in the Mediterranean where H. marginatum is common (Portillo et al. 2015). However, only a single case of R. aeschlimannii has been reported in Europe (Eastern Crete, Greece) to date (Germanakis et al. 2013).
Congo hemorrhagic fever virus is the most frequently encountered tick species on humans in Turkey (Keskin et al. 2015, 2016). In addition, other tick-borne pathogens such as *R. aeschlimannii* and *Borrelia burgdorferi* sensu stricto have been detected in *H. marginatum* ticks in Turkey (Gargili et al. 2012; Orkun et al. 2014). In Turkey, the most common rickettsial infections in humans are considered to be Mediterranean spotted fever, caused by *R. conorii* (Kuloglu et al. 2012). However, we suggest that *H. marginatum* and *R. sibirica mongolitimonae* could also be involved in the transmission of *R. aeschlimannii* and *R. sibirica mongolitimonae* in this region. Further studies on the prevalence of rickettsiae found in ticks are now required.

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