

First detection of *Rickettsia aeschlimannii* in *Hyalomma aegyptium* from Algeria

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INTRODUCTION

Tick-borne spotted fever group (SFG) rickettsioses are zoonoses caused by obligate intracellular Gram-negative bacteria belonging to the genus *Rickettsia* [1]. In Algeria, three species of SFG rickettsia transmitted by ticks are known to occur, including *Rickettsia conorii conorii* (the agent of Mediterranean spotted fever), transmitted by *Rhipicephalus sanguineus*, *Rickettsia aeschlimannii*, an emerging pathogen transmitted by *Hyalomma marginatum marginatum*, and *Rickettsia massiliae*, another emerging pathogen transmitted by *Rh. sanguineus* and *Rhipicephalus turanicus* [2]. We report here the detection of SFG rickettsiae in *Hyalomma aegyptium* ticks collected in Algeria.

MATERIALS AND METHODS

Seven *Testudo mauritanicum* tortoises were collected in Sidi Ferruch, located above 40 km north-east of Algiers, the capital of Algeria (36°46'N, 3°02'E). In total, 17 ticks were found attached to these tortoises. The ticks were removed, and kept in absolute ethanol until they were transported to Marseille France, where DNA was extracted from each arthropod. Each sample was tested by PCR using the primers CS.409p and CS.1258n, which amplify a 750-bp fragment of the citrate synthase gene (*gltA*) of *Rickettsia*. Additionally, all PCR-positive samples were tested for the *ompA* gene of *Rickettsia*, using the primers Rr. 190.70 and Rr. 190.701 [2]. For all PCR procedures, negative controls consisted of distilled water and DNA extracted from an uninfected tick from the *R. sanguineus* colonies of the Unité des Rickettsies that were added to the PCR master mix instead of the tick's DNA. Molecular

identification of ticks was performed for all ticks found to be positive by PCR by amplifying and sequencing the partial 12S RNA gene of ticks [3].

RESULTS

Using the *gltA* primers, PCR products of rickettsial DNA were detected in nine of 17 *H. aegyptium* ticks and from the positive controls (Fig. 1). No nucleic acids were amplified from the negative controls. All ticks were also shown to be positive on the second PCR screening using *ompA* primers. When the sequences of the *gltA* and *ompA* amplified fragments were obtained, they were shown to correspond to *Rickettsia aeschlimannii* for all samples (98.81% and 100% similarity with GenBank accession numbers AY259084 and AY259083 for *gltA* and *ompA*, respectively).

DISCUSSION

Rickettsia aeschlimannii is an emerging pathogen that has been associated with ticks, particularly *H. marginatum marginatum* and *H. marginatum rufipes* ticks, in southern Europe and Africa [1,2], and also detected in a single study in *Rhipicephalus appendiculatus* in South Africa. To date, only two cases of *Rickettsia aeschlimannii* infection have been described, including one in a patient bitten in Morocco, and one in South Africa [1]. The clinical signs of *Rickettsia aeschlimannii* infection seem to be similar to those of Mediterranean spotted fever caused by *Rickettsia conorii conorii*.

This is the first report of *Rickettsia aeschlimannii* in the tortoise tick *H. aegyptium*. These ticks have a typical three-host life cycle, and infect mainly tortoises and other reptiles. *H. aegyptium* ticks are found in south-west and central Asia, northern and southern Africa, southern Europe, and the Middle East. Tortoises of the genus *Testudo* are the

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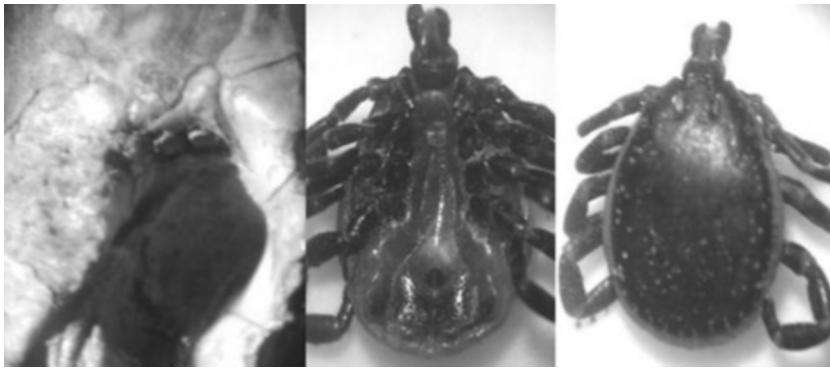


Fig. 1. Left: *Hyalomma aegyptium* attached to a *Testudo mauritanicum* tortoise in Algeria. Middle: ventral view of a male of *H. aegyptium*. Right: dorsal view of a male of *H. aegyptium*.

principal hosts of adult stages of *H. aegyptium*, although *H. aegyptium* may infest lizards, partridges, hares, hedgehogs, some rodents, and also humans. However, the role of *H. aegyptium*, which had been associated in 2003 with a *Borrelia* sp. in Turkey, in the transmission of *Rickettsia aeschlimannii* remains unclear [4].

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