**Rickettsia felis Infection, Tunisia**

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We report, for the first time, serologic evidence of *Rickettsia felis* and *R. aeschlimannii* infections acquired in Tunisia from 1998 to 2003. We found that most patients with antibodies against both *R. conorii* and *R. typhi* had serologic evidence of *R. felis* infection.

Rickettsioses are arthropod-borne zoonoses with geographic distributions determined by the ecology of their vectors. The genus *Rickettsia* is divided into 2 groups, the spotted fever group (SFG) and the typhus group (TG), mainly based on their intracellular positions, optimal growth temperatures, gas chromatographic proportion (%), DNA content, clinical features, epidemiologic aspects, and antigenic characteristics. Recently, a new species of *Rickettsia* that infected humans, *R. felis*, was reported (I), and the whole genome of this species has recently been sequenced (2). The pathogenic role of *R. felis* in humans was demonstrated first in Texas (I), with subsequent reports of this “fleaborne spotted fever” confirmed in patients from Europe and South/Central America (3–5) by polymerase chain reaction (PCR), serologic tests, or both. In Tunisia, North Africa, the epidemiology of rickettsial diseases has not been documented and only 1 study concerning these diseases has been conducted. The study, conducted in 1995, confirmed that *R. conorii* and TG rickettsia were endemic in Tunisia, with estimated antibody prevalences of 9% and 3.6%, respectively (6). The aim of our study was to investigate the diversity of rickettsioses in Tunisia through the use of serologic assays.

**The Study**

Serum samples obtained from patients suspected to have clinical rickettsial infection (fever associated with an eschar or cutaneous rash) were collected from 1998 to 2003 at the Laboratory of Microbiology CHU Habib Bourguiba, Sfax, Tunisia. Acute- and convalescent-phase serum samples, when available, were stored at –80°C until they were tested in a multiple-antigen immunofluorescence assay (IFA) at the Unité des Rickettsies Marseille (7). Ten SFG rickettsial antigens were used: *R. conorii conorii* strain 7, *R. africae* strain ESF-5, *R. sibirica mon-
Conclusions

In this study, IFA and WB identified *R. felis* infection in patients from Tunisia. Serologic cross-reactions are common among *Rickettsia* species in both the SFG and TG. A difference in specific IgG or IgM antibody titers has been useful for distinguishing murine typhus from epidemic typhus (8). More sophisticated serologic methods are needed to identify the causative agent at the species level (9). WB performed on 7 of 18 serum samples with cross-reactions between SFG, *R. felis*, and *R. typhi* confirmed the diagnosis of *R. felis* in 5 patients and TG rickettsia in 1 patient; the diagnosis remained undetermined in 1 patient. Recently, the whole genome of *R. felis* has been sequenced and demonstrated genetic similarity with *R. typhi* but showed some genes missing from the *R. conorii* genome (2). Thus, *R. felis* may be the major cause of cross-reactions between *R. typhi* and *R. conorii* or other tick-borne spotted fever agents. Cross-reactions between the 2 groups of *Rickettsia* have been puzzling because this activity is not reported in experimentally infected guinea pigs and mice (10). In fact, we speculate that many of the reactions with both *R. typhi* and *R. conorii* are caused by *R. felis* infection. This hypothesis is supported by our findings of cross-reactivity in serum specimens from 5 of 7 patients with confirmed *R. felis* infection. Indeed, when antigens are not available, this cross-reactivity should be a good screening method for *R. felis* infection. Alternatively, all serum specimens exhibiting cross-reactivity between *R. typhi* and *R. felis* only were considered to be TG rickettsia infection after WB.

To the best of our knowledge, this is the first report of patients with *R. felis* and *R. aeschlimannii* infections in Tunisia. In Morocco, similar results have been reported (11). Several cases of SFG rickettsioses have been reported from North Africa, including 1 patient with *R. aeschlimannii* infection from Morocco (12) and 1 patient with *R. sibirica mongolitimonae* infection from Algeria (13). These results are not surprising since vectors of *R. felis* and *R. aeschlimannii* are present in North Africa (14). Indeed, *R. aeschlimannii* has been isolated from *Hyalomma marginatum* ticks collected from camels in Morocco (15), and *R. felis*–infected fleas in Algeria have been recently reported (14). Since *R. felis* has a worldwide distribution and infestation with these fleas is very common, *R. felis* and fleaborne spotted fever may occur worldwide.

Only a few human cases of *R. felis* infection diagnosed by serologic tests or PCR have been reported: 1 case from the United States (Texas) (1), 3 from Mexico (3), 2 from France, 2 from Brazil (4), and 2 from Germany (5). In the
Texas case (1), the patient had clinical features similar to those associated with murine typhus. However, patients with *R. felis* and central nervous system and pulmonary involvement have been reported from Mexico (3). In our study, 1 of the patients with *R. felis* infection had pulmonary involvement and 2 had adenopathy. Although none had an eschar or a history of flea bite, 3 patients had contact with animals.

Our findings indicate the need for further studies to determine the distribution of *R. felis* and the prevalence of this agent and associated infection. These results suggest that fleaborne spotted fever, as well as other SFG rickettsioses, are common in Tunisia.

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References


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