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Rickettsia conorii

IndianTick Typhus Strain and R. slovaca in Humans, Sicily

To the Editor: Rickettsiae are vector-borne pathogens that affect humans and animals worldwide (1). Pathogens in the Rickettsia conorii complex are known to cause Mediterranean spotted fever (MSF) (R. conorii Malish strain), Astrakhan fever (R. conorii Astrakhan strain), Israeli spotted fever (R. conorii Israeli spotted fever strain), and Indian tick typhus (R. conorii Indian tick typhus strain) in the Mediterranean basin and Africa, southern Russia, the Middle East, and India and Pakistan, respectively (2). These rickettsioses share some clinical features, such as febrile illness and generalized cutaneous rash, and are transmitted to humans by Rhipicephalus spp. ticks (2).

MSF is endemic to Sicily (Italy); fatal cases occur each year, and the prevalence of R. conorii in dogs is high (3–6). Recently, R. conorii Malish strain and R. conorii Israeli spotted fever strain were confirmed in humans in Sicily in whom MSF was diagnosed (4), which suggests that other R. conorii strains might be present and diagnosed as causing MSF. The rickettsiae within the R. conorii complex, which are relevant for the study of bacterial evolution and epidemiology, can be properly identified only by appropriate genetic analyses.
We analyzed 15 blood and 19 inoculation eschar samples collected during 2005–2009 from 31 patients in Palermo Province and 2 in Catania Province, none of whom had recently traveled. None were severely ill, but all 33 had clinical manifestations and laboratory results compatible with MSF: 1-week incubation after tick bite, fever, headache, myalgia, papulonodular rash that started on the upper limbs and spread centrifugally with or without tache noire, and detection of antibody titers >180 to noire, and detection of antibody against Rickettsia conorii characterized by presence of membrane protein A (ompA) (primers Rr190.70p and 190–701 [8]), outer membrane protein B (ompB) (primers rompBSFGIF and rompBSFG/TGIR [9]), citrate synthase (gltA) (2), and 17-kDa protein (primers TZ15–19 and TZ16–20 [6]). Nucleotide sequence identity to reference strains (2), multilocus analysis by atpA–dnaK–ompA–ompB–gltA–17-kDa and ompA–ompB sequences and in silico PstI-Rsal restriction analysis of ompA sequences (8) were used to characterize Rickettsia spp. and R. conorii strains.

Results for 15 (45%) patients were positive for Rickettsia spp. Thirteen isolates were confirmed as R. conorii Malish strain (identification [ID] nos. 44, 45, 47, 49, 54, 55, 57, 59, 61, 66, 68, 92, 112) and 1 each as R. conorii Indian tick typhus strain (ID no. 58) and R. slovaca (ID no. 50). R. slovaca DNA was also found in a Dermacentor marginatus tick removed from the patient who had confirmed R. slovaca infection. R. conorii Malish strains showed 99.9%–100%, 100%, 100%, 98.7%–100%, 100%, and 97.8%–100% pairwise nt sequence identity to reference strain Malish 7 (AE006914) atpA, dnaK, ompA, ompB, gltA, and 17-kDa protein, respectively.

The R. conorii Indian tick typhus strain showed 100%, 100%, 99.4%, 100%, 100%, and 99.9% pairwise nt sequence identity to R. conorii strain Malish 7 (AE006914) atpA, dnaK, 17-kDa protein, and R. conorii Indian tick typhus reference strain ompA (U43794), ompB (AF123726), and gltA (U59730), respectively. The R. slovaca strain showed 99.4%, 97.8%, 100%, 93.7%, 99.7%, and 99.4% pairwise nt sequence identity to R. slovaca atpA (AY124734), dnaK (DQ821824), ompA (HM149286), ompB (HQ232242), gltA (AY129301), and R. conorii strain Malish 7 (AE006914) 17-kDa protein, respectively. The sequences were deposited in GeneBank under accession nos. JN182782–JN182804. Multilocus sequence analysis (Figure, panel A) and in silico PstI-Rsal restriction analysis of ompA sequences also confirmed the identity
of the Rickettsia spp. we identified. As shown (2), multilocus analysis with ompA–ompB sequences was highly informative about the phylogenetic relationship between Rickettsia spp. and R. conorii strains (Figure, panel B).

In Sicily, R. conorii Malish strain has been characterized in MSF patients (4), and R. slovaca DNA was identified in ixodid ticks (5). However, to our knowledge, R. slovaca in humans in Sicily and R. conorii Indian tick typhus strain infection in Sicily and Europe have not been reported. The only previous report outside India and Pakistan was documented in a traveler with severe clinical manifestations in France (10). Differences were not observed between R. conorii Indian tick typhus strain and R. slovaca–infected patients. Both patients had similar clinical symptoms compatible with MSF; in both, only IgM for rickettsiae was detected at hospital admission, but IgM and IgG were detected during convalescence. Tache noire were detected in the neck and right arm of patients with R. conorii Indian tick typhus strain and R. slovaca, respectively.

These results demonstrated that new rickettsiae, such as R. conorii Indian tick typhus strain, of public health relevance are emerging in Europe. The widespread distribution of tick vectors in Europe and the transstadial and transovarial transmission of the pathogen in ticks might favor transmission to humans.

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Detection of European Strain of Echinococcus multilocularis in North America

To the Editor: In 2009, an alveolar hydatid cyst, the intermediate stage of the cestode Echinococcus multilocularis, was detected in the liver of a dog from Quesnel, British Columbia (BC), Canada (1), 600 km west of the nearest known record of this parasite in central North America (Figure). Alveolar hydatid cysts normally occur in rodent intermediate hosts. However, humans can serve as aberrant intermediate hosts; cysts generally originate in the liver and, in about one third of cases, metastasize throughout the body (2). Detection of the larval stage of this pathogen in an unusual host in a new geographic region required application of multiple molecular epidemi-