

For those who develop EEEV disease, supportive care is currently the only treatment option. Elevated intracranial pressure should be watched for, monitored, and aggressively managed. Hyperosmolar therapy, external ventricular drain placement, cooling, sedation, and paralysis have been used in the management of elevated intracranial pressure for other conditions and have been used with varying degrees of success in treating EEEV disease (9,10). Further research regarding the management of EEEV disease is needed.

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The findings and conclusions in this report are those of the authors and do not necessarily represent the official position of the Centers for Disease Control and Prevention or the Arkansas Department of Health.

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Tick-Borne Relapsing Fever, Southern Spain, 2004–2015

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To the Editor: Surveillance data indicate that tick-borne diseases are substantial and increasing global public health problems (1). Various pathogens, including viruses, bacteria, protozoa, and helminthes, are transmitted from ticks to vertebrates (2). Tick-borne relapsing fever (TBRF) is a zoonosis that is enzootic in many countries (3). This illness is caused by ≥ 10 *Borrelia* species and is transmitted to humans through the bite of soft ticks of the genus *Ornithodoros* (3).

Currently, TBRF is endemic in various foci around the world. However, few TBRF cases are reported in the United States, and in most western European countries, such as Spain, TBRF occurs sporadically, usually after opportunistic infections in persons exposed to ticks (3,4). Many authors consider TBRF to be underrecognized and underreported (5). Although molecular tools such as PCR can dramatically improve diagnosis of this illness, methods used to diagnose TBRF have changed little since the discovery of the spirochete.

To evaluate the prevalence and clinical features of TBRF in a rural area of southern Spain, we retrospectively reviewed clinical data for all patients ≥ 14 years of age who sought care for TBRF during January 2004–December 2015 at Hospital de la Merced, a county hospital in Seville, Spain. We defined a case of TBRF as detection of spirochetes on thin- or thick-blood smears or in cerebrospinal fluid (CSF) samples by using conventional microscopy after Giemsa or Wright staining (Figure).

Of 75 patients, 42 (56%) were male and 33 (44%) were female. Mean age was 33 (range 14–72) years. Nine (12%)

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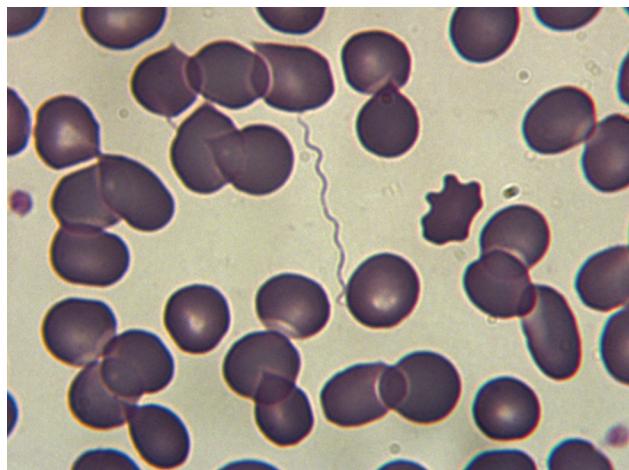


Figure. Spirochetes on a thick peripheral blood smear from a patient with tick-borne relapsing fever, southern Spain, 2004–2015. Original magnification $\times 1,000$.

patients reported tick bites. The most common symptoms were fever (64 [85.3%] patients), headache (41 [54.6%]), vomiting (26 [34.6%]), muscle ache (22 [29.3%]), and abdominal pain (21 [28%]). At the time of the hospital visit, 9 (12%) patients had signs and symptoms suggesting meningeal involvement; 3 (4%) others had clear meningeal signs. These 12 patients underwent lumbar puncture, and CSF abnormalities were found in the 3 (4%) patients with meningismus. Spirochetes were found in the CSF sample of 1 patient. Of the total 75 patients, this patient was the only 1 with spirochetes, and no patient had facial palsy or other neurologic manifestation. The main laboratory findings were elevated C-reactive protein, found in 74 (98.6%) patients; thrombocytopenia, found in 67 (89.3%); and anemia, found in 37 (49.3%).

Preferred treatment was oral doxycycline, which was used for a mean duration of 10 (range 7.3–14) days in 55 patients (73.3%). Among 3 TBRF patients with neurologic involvement, 1 was treated with penicillin G (3 million units/4 h), and 2 were treated with ceftriaxone (2 g/d for 4 d). Jarisch-Herxheimer reaction occurred in 7 (9.3%) patients, none of whom had meningitis. All patients recovered completely.

Currently, TBRF is widely distributed in various foci around the world. In much of sub-Saharan Africa, TBRF is associated with a high number of illnesses and deaths. Indeed, it is reportedly the most common bacterial infection from Senegal and is listed among the 10 leading causes of death in children <5 years of age in Tanzania (6). Elsewhere in the world, this infection is regarded as rare. Although TBRF borreliosis occurs infrequently in developed countries, our study highlights TBRF endemicity in an area of southern Spain.

Reports on TBRF in Spain are scarce. The only previous study involving numerous cases of TBRF in Spain

(7) described 230 cases and was published in the early 20th century. That research showed that, although disease caused by *B. hispanica* is less severe than that of other TBRFs, ≈5% of patients had neurologic complications. In our study, 3 (4%) patients had meningitis caused by TBRF borreliosis, a finding that accords with the previous report.

A recent study conducted among children in southern Spain (8) identified 9 cases of TBRF during a 10-year period. Two children, 3 and 5 years of age, had meningeal involvement but no other neurologic complication. Similar to observations in our study, Jarisch-Herxheimer reaction was infrequent, occurring in only 1 of the 9 children.

Neurologic complications are well known features of infection with 2 spirochetes, *B. burgdorferi* and *Treponema pallidum* (9). Nevertheless, little is published and known about the predilection of TBRF borreliosis to infect the nervous system. One of the few studies reviewing neurologic involvement of TBRF borreliosis reported that *B. turicatae* and *B. duttonii*, the agents of TBRF in southwestern North America and sub-Saharan Africa, respectively, cause neurologic involvement as often as *B. burgdorferi* causes Lyme disease (10).

Our study confirms that TBRF is an endemic, underreported disease in many countries and is common in southern Spain. Although the disease caused by *B. hispanica* is among the less severe illnesses caused by the relapsing fever group, serious neurologic complications can occur. With increasing globalization, physicians will likely see increased numbers of travel-related infections and will face imported and emerging TBRF cases.

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New Hepatitis E Virus Genotype in Bactrian Camels, Xinjiang, China, 2013

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To the Editor: Hepatitis E virus (HEV) is a member of the family *Hepeviridae*, genus *Orthohepevirus*, which comprises 4 species, *Orthohepevirus A–D*. *Orthohepevirus A* contains 7 genotypes (HEV1–7) (1,2). HEV1 and HEV2 infect humans only; HEV3, HEV4, and HEV7 can infect humans and other mammals; and HEV5 and HEV6 have been detected in animals only.

Worldwide, HEV is the most common cause of acute viral hepatitis in humans. The disease is generally self-limiting, but high death rates have been observed among HEV-infected pregnant women. Chronic HEV infection is a problem in immunocompromised patients, such as solid organ transplant recipients (3). Human HEV3 and HEV4 infections have been associated with consumption of undercooked pork or game meat (4).

In 2014, we described the discovery of a novel genotype of HEV in dromedaries (*Camelus dromedarius* or 1-humped camels), suggesting another possible source of human HEV infection (5). This dromedary HEV was subsequently classified as a novel *Orthohepevirus A* genotype,

HEV7 (1,2). Recently, this HEV7 genotype was also isolated from a liver transplant recipient from the Middle East with chronic HEV infection (6). The patient regularly consumed dromedary camel meat and milk, implying camel-to-human transmission of the virus (6).

Like the dromedary, the Bactrian camel (*Camelus bactrianus* or 2-humped camels) is an Old World camelid species. Thus, we hypothesize that Bactrian camels may also be reservoirs of HEV. To test this hypothesis and increase our understanding of the epidemiology of HEV in camels, we performed a molecular epidemiology study using feces samples from camels in China.

During November 2012–May 2013, we collected and tested 1 feces sample each from 205 Bactrian camels on a farm in Xinjiang, China. We performed RNA extraction and reverse transcription PCR (RT-PCR) as previously described (7). We screened for HEV by PCR amplification of a 251-bp fragment of open-reading frame (ORF) 2, using primers 5'-GTTGTCTCAGCCAATGGCGA-3' and 5'-GTAGTTGGTCATACTCAGCAGC-3'. PCR was performed, using previously described conditions (7), with the annealing temperature set at 50°C. DNA sequencing and quantitative real-time RT-PCR were performed as previously described (7). Three samples were positive for HEV; we performed complete genome sequencing of these samples as described (online Technical Appendix, <http://wwwnc.cdc.gov/EID/article/22/12/16-0979-Techapp1.pdf>) (5,7). We also performed comparative genomic analysis as previously described (1,2,8). We constructed a phylogenetic tree using the maximum-likelihood method and MEGA7 (9); bootstrap values were calculated from 1,000 trees. The optimal substitution model for each ORF was selected by MEGA7 (Figure).

RT-PCR for a 251-bp fragment in ORF2 of HEV was positive for 3 (1.5%) of the 205 fecal samples; virus loads were 1.6×10^3 , 2.1×10^3 , and 1.8×10^4 copies/mg, respectively. Whole-genome sequencing of the 3 Bactrian camel HEV (BcHEV) strains (GenBank accession nos. KX387865–7) showed genome sizes of 7,212–7,223 bp and a G + C content of 52.7%–53.1%. Overall, nucleotides in the BcHEV genome differed by >20% compared with those in all other HEVs. Genomes of the 3 BcHEV isolates contained 3 major ORFs; genome organization was typical of and characteristics were similar to those of HEVs from other *Orthohepevirus A* species. Phylogenetic trees constructed using ORF1, ORF2, ORF3, and concatenated ORF1/ORF2, excluding the hypervariable region, showed that these 3 BcHEV isolates clustered with the 2 dromedary camel HEV7 strains and the HEV7 strain from the liver-transplant recipient with chronic hepatitis (Figure; online Technical Appendix Figure 1)

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