been associated with HLA-DQ/DR variants (4). Although most persons lack susceptibility, high nasal carriage rates in disease-endemic areas and living conditions associated with poverty further increase infection risk for susceptible persons because acquisition is facilitated by malnutrition, overcrowding, and poor sanitation (5).

Leprosy treatment is determined according to disease severity. The Ridley-Jopling system assesses lesion quantity, neurologic involvement, and bacterial load, and the current World Health Organization system simplifies this system to facilitate clinical classification, defining paucibacillary leprosy as ≤5 skin lesions and multibacillary leprosy as ≥6 lesions (6).

Combination drug regimens for 6–24 months are highly effective. Together with efforts of the World Health Organization toward eradication, combination therapy has dramatically reduced the prevalence to current levels from previously stable levels of 10–12 million in the 1960s–1980s (7). Typical regimens include dapsone and rifampin, and clofazimine is available in the United States by investigational new drug application for multibacillary disease.

Patients undergoing treatment must be monitored for immunologic complications, such as cell-mediated reversal reaction (type 1 reaction) or interferon-α–mediated erythema nodosum leprosum (type 2 reaction). Reversal reactions may be especially severe and require urgent immunosuppression to avoid neurologic and vascular complications.

Leprosy is extremely rare in the United States (150 annual cases). Because transmission by prolonged close contact is more common than by casual contact, it is likely that the infection in this patient may have been acquired during childhood in a disease-endemic area, which represents the upper limit of incubation time. However, rare cases have been reported among military members, which makes it difficult to exclude the question of acquisition during military service in disease-endemic areas (8–10). Therefore, in patients with geographically appropriate foreign service or prolonged travel history, leprosy must be considered in the differential diagnosis of progressive skin lesions, particularly when lesional anesthesia is present.

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Address for correspondence: Catherine M. Berjohn, Division of Infectious Diseases, Naval Medical Center San Diego, Bldg 1, 2nd Deck, 34800 Bob Wilson Dr, San Diego, CA 92134, USA; email: catherine.berjohn@med.navy.mil

Tickborne Relapsing Fever in Southern Iran, 2011–2013

Saied Reza Naddaf, Behnaz Ghazinazhed, Mohammad Mehdi Sedaghat, Hossein Masoumi Asl, Sally Jane Cutler

Author affiliations: Pasteur Institute of Iran, Tehran, Iran (S.R. Naddaf, B. Ghazinazhed); Tehran University of Sciences, Tehran (M.M. Sedaghat); Ministry of Health and Medical Education, Tehran (H.M. Asl); University of East London, London, United Kingdom (S.J. Cutler)

DOI: http://dx.doi.org/10.3201/eid2106.141715

To the Editor: Tickborne relapsing fever (TBRF) is endemic in Iran; >1,400 cases were confirmed in 19 provinces during 1997–2006 (1). In the western, northwestern, and foothill regions of the Alborz Mountains, the Argasid soft tick *Ornithodoros tholozani* is commonplace and accounts for ≈60% of TBRF cases attributed to *Borrelia persica*. However, in central and western Iran, *O. tholozani* and *B. microti*–infected *O. erraticus* ticks coexist (1,2). Two other *Borrelia* species, *B. latyschewii* and *B. baltazardi*, have also been described in northeastern and northwestern Iran (3,4), but no recent human infections with these species have been documented. Cases of TBRF occurring in southern Iran have presumably been caused by *B. microti* because its tick vector, *O. erraticus*, predominates in this region.

Relapsing fever infections in Hormozgan Province in southern Iran are commonly identified during routine checks for malaria. During 2011–2013, blood samples were obtained from 14 febrile patients referred to medical centers in Jask and Rodan in Hormozgan Province.
strain may not be apart from other strain (B. microti eastern Africa, highest homology (97%) with relapsing fever agents from IGS analysis revealed that spirochetes in our analysis had tholozani are limited to 2 isolates of (frequently recovered from rodents' burrows in the region Iran, but ticks that transmit B. microti –infected O. erraticus ticks, respectively (B. persica and B. microti are not seen in southern Iran and those from borreliae in Africa have a close phylogenetic similarity, they have different virulence levels and abilities to infect vector and host species. Consequently, deciphering the evolutionary links for these Borrelia spp.

Thick and thin blood smears were prepared from blood samples, stained with Giemsa, and examined. None showed malaria parasites; however, spirochetes were observed in thick or thin smears from 3 patients (online Technical Appendix Table). Patients whose samples tested positive by microscopy were treated with 500 mg tetracycline every 6 hours for 10 days and became afebrile.

DNA was extracted from patients’ serum samples by using the Miniprep DNA kit (QIAGEN, Hilden, Germany) and screened for borrelia DNA by using real-time PCR; negative and positive control DNA from B. microti or B. persica was also screened. Borrelia spp. DNA was detected in 5 (36%) of 14 serum samples (online Technical Appendix Table). Of these 5 samples, 2 were also positive by nested PCR that targeted the intergenic spacer (IGS) region (5). The 2 IGS regions were sequenced (ABI-3130XL sequencer; Applied Biosystems, Foster City, CA, USA) in both directions at the Pasteur Institute of Iran. The resulting 539- and 527-bp IGS sequences (GenBank accession nos. KM271987 and KM271988, respectively) were 97% homologous with B. recurrentis and B. duttonii from Africa (GenBank accession nos. CP000993 and DQ000280, respectively); 96% homologous with B. microti from Iran (GenBank accession no. JQ436580); and 92% homologous with B. crocidurae from Africa (GenBank accession no. GU350723). A neighbor-joining phylogenetic tree was constructed by using MEGA6 (http://www.megasoftware.net); the 2 IGS sequences clustered into a distinct group separate from B. microti, B. duttonii, and B. recurrentis genotypes (Figure).

B. microti was expected to be found because O. tholozani ticks that transmit B. persica are not seen in southern Iran, but B. microti–infected O. erraticus ticks have been frequently recovered from rodents' burrows in the region (6). Current molecular data from TBRF borreliae from Iran are limited to 2 isolates of B. persica and B. microti from O. tholozani and O. erraticus ticks, respectively (5,7,8). In situ IGS analysis revealed that spirochetes in our analysis had highest homology (97%) with relapsing fever agents from eastern Africa, B. duttonii and B. recurrentis, followed by B. microti (96%) from Iran (8). B. microti clustered with 1 strain (B. duttonii; GenBank accession no. GU350721) and apart from other B. duttonii IGS strains, suggesting that this strain may not be B. duttonii. The phylogenetic tree separated B. duttonii into 4 clades, 2 of which also contained B. recurrentis, confirming previous observations (9) and providing further support that B. recurrentis represents an ecotype of B. duttonii rather than a species (10). Furthermore, the high level of phylogenetic similarity among borreliae from eastern Africa and Iran indicates that the borreliae in our study might represent ecotype-adapted strains. More sequencing of different genomic markers is required to substantiate or refute this possibility. Lack of GenBank data for the remaining borreliae from Iran, B. latachewii and B. baltazardi, prevent exclusion of these species.

Although relapsing fever spirochetes from southern Iran and those from borreliae in Africa have a close phylogenetic similarity, they have different virulence levels and abilities to infect vector and host species. Consequently, deciphering the evolutionary links for these Borrelia spp.

![Figure](https://www.cdc.gov/eid/article/21/6/14-1715-Techapp1.pdf)
is of paramount importance and might provide valuable insights into host–microbe interactions.

Our report confirms a novel Borrelia IGS sequence type detected in situ from 2 relapsing fever patients. This species showed greatest homology with the relapsing fever borreliae from Africa, B. recurrentis and B. duttonii, but not with B. microti, which is transmitted by O. erratius ticks, previously believed to be the only soft tick species in this region. These findings challenge the assumption that TBRF in Iran is attributed to only B. persica or B. microti.

Acknowledgment

We thank Gholam Mohseni, the late technical supervisor at Bandar Abbas Health Research Station, Tehran University of Medical Sciences, for his contributions to this study.

This study was partially funded by the Pasteur Institute of Iran and by the Center for Disease Control, Ministry of Health and Medical Education, Tehran, Iran (grant no. 749).

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Address for correspondence: Sally Jane Cutler, School of Health, Sport, and Bioscience, University of East London, Water Lane, Stratford, London E15 4LZ, UK; email: s.cutler@uel.ac.uk

Reducing the Risk for Waterborne Nosocomial Neonatal Legionellosis

Joseph S. Cervia

Author affiliation: Hofstra–North Shore/Long Island Jewish Health System School of Medicine, Hempstead, New York, USA

DOI: http://dx.doi.org/10.3201/eid2106.141779

To the Editor: I read with interest the report by Wei et al. (1) regarding 2 cases of neonatal legionellosis associated with infant formula prepared with hospital tap water. Two hospitals were involved, and water samples from both were positive for Legionella pneumophila bacteria that had molecular profiles indistinguishable from those for bacteria from the infected neonates. As Wei et al. (1) and others have established, control of waterborne pathogens, such as Legionella spp., in health care institutions remains a work in progress.

Recently, leading medical centers have recognized the efficacy and cost-effectiveness of performing certain measures to ensure the safety of hospital water. These measures include routine microbial analyses of tap water and use of waterborne pathogen prevention and control measures such as hot water flushing of plumbing; use of chlorination, chlorine dioxide, monochloramine, copper–silver ionization, or ultraviolet light; ozonation; and point-of-use water filtration. Each method has advantages and disadvantages related to ease of implementation, cost, maintenance issues, and short- and long-term effectiveness. Randomized controlled trials comparing the efficacy of these strategies are lacking, but the availability of guidance for using waterborne pathogen prevention and control strategies has resulted in substantial declines in health care–associated legionellosis (2). Efforts at waterborne pathogen detection and control are complicated by the role of biofilm, comprising microbes embedded in the polymeric matrix attached to internal plumbing surfaces, which protects waterborne pathogens from adverse environmental conditions, including antimicrobial agents and systemic controls (e.g., ultraviolet light, metals, acid pH) (2,3).

Prevention of legionellosis in health care settings offers a clinically beneficial and cost-effective alternative to intermittent case detection and outbreak control. For example, it has been demonstrated that, even in the absence of a recognized outbreak, hospital units caring