Brill-Zinsser Disease in Moroccan Man, France, 2011

To the Editor: Epidemic typhus is caused by Rickettsia prowazekii and transmitted by human body lice. For centuries, it has been associated with overcrowding, cold weather, and poor hygiene. Brill-Zinsser disease is a recurrent form of epidemic typhus that is unrelated to louse infestation and develops sporadically years after the primary illness. Clinical features are similar to, but milder than, those of epidemic typhus (1). We report a case of Brill-Zinsser disease in a patient who was born in Morocco and had no history of epidemic typhus.

A 69-year-old man living in France sought care from his general practitioner on March 7, 2011, after 2 days of high-grade fever (40°C) associated with headache, myalgia, fatigue, and mild cough. Amoxicillin was prescribed for a putative diagnosis of acute respiratory infection.

He was admitted to hospital on March 9 for persistent fever. Physical examination results were unremarkable. Blood test results were as follows: C-reactive protein 111 mg/L (reference 0–8 mg/L); procalcitonin 0.49 ng/mL (reference 0.1–0.4 ng/mL), lymphocyte count 0.7 × 10^3 cells/μL (reference 1–4 × 10^3 cells/μL), platelet count 92 × 10^3 cells/μL (reference 150–450 × 10^3 cells/μL), and lactate dehydrogenase 376 U/L (reference 94–246 U/L). Chest radiograph results were normal. Results of 5 blood cultures and a urine culture were normal. Because the patient lived near a goat farm, Q fever and tularemia were considered plausible hypotheses, and oral doxycycline was introduced on March 13. The patient became afebrile on March 15, and he was discharged from the hospital and remained well.

On the basis of serologic results, the following diagnoses could be ruled out: viral infections (HIV, cytomegalovirus, Epstein-Barr virus); tularemia; Q fever; leptospirosis; salmonellosis; and Legionella, Mycoplasma, and Chlamydia spp. infections. Acute-phase and convalescent-phase serum samples were positive for typhus-group rickettsiae by the microimmunofluorescence assay at the World Health Organization Collaborative Center for Rickettsioses and Other Arthropod-Borne Bacterial Diseases (Marseille, France). A microimmunofluorescence assay showed titers of 100 for IgM and 6,400 for IgG. Western blot analyses and cross-adsorption studies strongly suggested R. prowazekii as the cause of the man’s illness. Quantitative PCR result on DNA extracted from the acute-phase serum was negative (2).

The patient had been raised in Morocco. At 19 years of age, he emigrated to France, where he lived in a urban area. He subsequently traveled every 3 years to Morocco for 1-month summer holidays, always in urban areas. He had most recently traveled to Morocco in 2008. He denied any history of hospitalization for a severe febrile illness and any exposure to louse bites. In the weeks before disease onset, he had not taken any new drug. He had no immunoglobulin deficiency.

On the basis of serologic analysis with Western blot, we confirmed R. prowazekii infection in a patient with no recent travel and no contact with lice or flying squirrels. R. prowazekii infection may occur rarely in France; it was found in Marseille in 2002 in an asymptomatic homeless person (3). In contrast, the patient in our report was living in a hygienic environment, and an autochthonous infection is therefore highly unlikely.

Epidemic typhus was endemic to North Africa until the 1970s (4). Subsequently, this region was thought to be free from epidemic typhus, but 2 cases have been reported since 1999 in Algeria, where 1 case of Brill-Zinsser disease was observed in a man who had had epidemic typhus in 1960 during the Algerian civil war (5–7). Few published data exist about the seroprevalence of R. prowazekii infections in North Africa (4). In Tunisia, no epidemic typhus was found in 2005 among 47 febrile patients (8). However, a seroepidemiologic survey performed in blood donors and hospitalized patients in the Aures, Algeria, found a prevalence of 2% (4). This finding suggests that R. prowazekii infection might have occurred in this population more often than suspected. No recent published data are available from Morocco.

Since 1970, reports of only 8 cases of Brill-Zinsser disease have been published (9,10). In all cases, known risk factors were present (overcrowding, poor hygiene, or contact with flying squirrels). Brill and Zinsser described that stress or waning immunity could reactivate R. prowazekii infection (2). Corticosteroids can trigger recurrence of R. prowazekii in mice (2), but no such observations were made in humans. In the case presented here, we found no stress factor, no immunosuppression, and no medical history of epidemic typhus.

Brill-Zinsser disease can develop >40 years after acute infection. The mechanism of R. prowazekii latency has not been established. A recently explored reservoir for silent forms of R. prowazekii infection is adipose tissue because it contains endothelial cells, which are the target cells for R. prowazekii infection, and because of its wide distribution throughout the body (2). Brill-Zinsser disease should be considered as a possible diagnosis for acute fever in any patient who has lived in an area where epidemic typhus is endemic.
LETTERS

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References


Temperate Climate Niche for Cryptococcus gattii in Northern Europe

To the Editor: Cryptococcus gattii was considered to be geographically restricted to countries with tropical and subtropical climates until 1999, when an outbreak of cryptococcosis in humans and animals occurred in the temperate climate of Vancouver Island, British Columbia, Canada (1). Montagna et al. reported the first environmental C. gattii in Europe from the Mediterranean region of Italy; these authors isolated it from 11 (4.3%) of 255 samples of plant detritus of Carob, Ceratonia siliqua, in Spain (2). These observations were recently substantiated by the isolation of C. gattii from plant debris of trees belonging to C. gattii in Apulia (2). These observations were recently substantiated by the isolation of C. gattii from plant debris of trees belonging to Ceratonia siliqua (carob), Pinus halepensis (stone pine), and E. camaldulensis in Spain (3). We report environmental isolation of the primary pathogenic fungus C. gattii from a forest in Berg en Dal, the Netherlands, which extends its geographic distribution to the temperate climate of northern Europe.

We investigated 112 decayed wood samples collected from inside trunk hollows of 52 living trees belonging to 5 families during April–May 2011 in Nijmegen, the Netherlands. The trees sampled were chestnut (Castanea sativa, n = 24), Douglas fir (Pseudotsuga menziesii, n = 17), oak (Quercus macranthera, n = 6), walnut (Juglans regia, n = 3), and mulberry (Morus alba, n = 2). The main criterion in selecting a tree for sampling was advanced age and presence of large trunk hollows variably sheltered from sunlight. The sampled sites had no bird nests and were apparently free from avian excreta. The decayed wood samples were collected with an in-house swabbing technique by using simplified Staib niger seed agar as described (4). The plates were incubated at 30°C and periodically observed up to 7 days for isolation of C. gattii and C. neoformans. Suspected colonies of Cryptococcus spp. were purified by dilution plating and identified by their morphologic and biochemical profiles, including development of blue color on l-canavanine-glycine-bromothymol blue medium.

Identity of the isolates was confirmed by sequencing the internal transcribed spacer and D1/ D2 regions, and they were genotyped by using amplified fragment-length polymorphism (AFLP) fingerprinting and multilocus sequence typing (MLST). The MLST loci CAP10, CAP59, GPD1, IGS, LAC1, MPD1, PLB1, SOD1, TEF1α, and URA5 of the environmental C. gattii isolates were amplified and sequenced, and data were compared with MLST data from a large C. gattii population study (5) and with a recently published set of clinical, animal, and environmental C. gattii isolates from Mediterranean Europe and the Netherlands (Figure) (3,6,7). In addition, the mating type was determined with PCR by using mating type–specific primers for the STE12α and α alleles (8).