sequences clustered within the Europe/Turkey clade. The genetic distance between the 2 strains was 1.15%, but the 2 sequences were identical at the amino acid level. Sequences from the present study showed 96.4%–98.8% similarity with respective CCHFV sequences from Bulgaria from a former study (BUL10/02 and BUL1/03) (*3*) but differed from the Kosovo 9553/2001 strain by 0.8%–2.0% and from the Greek 66/08 strain by 1.2%–2.4%.

Two additional suspected CCHF cases occurred in the same area, on March 30 and April 9 (*7*). Both persons were negative for CCHFV infection. All 119 ticks of various species (*Hyalomma marginatum*, *Dermacentor marginatus*, *Rhipicephalus bursa*, *Ixodes ricinus*) collected from the area and tested by reverse transcription–nested PCR were negative for CCHFV.

This cluster of CCHF cases has several important highlights. First, it occurred in a region that was considered to have low CCHF endemicity; however, the area is only a few kilometers from Greece, where a human fatal case was observed in June 2008 (*8*). The index case was observed earlier in the year than in previous years, and clinical manifestations of the cases were unusual (absence of craniopharyngeal syndrome and bleeding from gastrointestinal tract that are typical for CCHF patients from Bulgaria); in the fatal case, autopsy of the patient showed hemorrhages only in the lungs. Two cases were attributable to tick exposure, whereas the other 2 were most likely secondary cases attributable to contact with the index case-patient (in this regard, CCHFV sequences of the secondary cases were almost identical). Finally, the longer incubation period of the wife of the index case-patient might be associated with administration of hyperimmune gamma globulin against CCHFV.

In conclusion, CCHF emerged in southwestern Bulgaria near the border with Greece. Person-to-person transmission emphasizes the need for rapid diagnosis of CCHF, especially in cases with atypical clinical manifestations.

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## *Wohlfahrtiimonas chitiniclastica* Bacteremia in Homeless Woman

**To the Editor:** In May 2006, a 60-year-old homeless woman with a history of alcoholism was admitted to the emergency department of the Conception Hospital, Marseille, France. Firefighters had just found her in an abandoned container in the outskirts of the city, beside the body of her companion, who had died several days earlier. She described no symptoms other than fatigue. On examination, she was found to be dirty and covered with thousands of body and hair lice; dozens of insect larvae were in her hair. She was mildly febrile (38°C) and had widespread excoriations but no sign of localized bacterial infection. Head shaving exposed superficial ulcers on her scalp but no maggots. Blood analysis showed marked neutropenia

(0.44 $\times 10^9$/L), thrombocytopenia (28 $\times 10^9$/L), a marked but well-tolerated iron deficiency anemia (hemoglobin 6.8g/dL), and a C-reactive protein level of 182 mg/L. Louse infestation was treated with a single dose of ivermectin (12 mg), and the woman was hospitalized. On day 3, she was still febrile. Louse-borne borreliosis had been ruled out by a negative blood smear, and results of serologic testing and molecular screening of lice for the other 2 louse-transmitted bacteria, *Rickettsia prowazekii* and *Bartonella quintana* (*1*), were negative.

In contrast, 2 cultures of blood taken at the time of admission grew gram-negative rods susceptible to amoxicillin, ceftriaxone, imipenem, ciprofloxacin, amikacin, and trimethoprim/sulfamethoxazole. However, phenotypic tests failed to identify this bacterium with accuracy. Intravenous therapy with ceftriaxone at 2 g/d was initiated, and the patient's fever, neutropenia, and thrombocytopenia improved. Scalp wounds healed with local care. Using 16S rRNA gene amplification and sequencing as previously described (*2*), we identified the bacilli as *Wohlfahrtiimonas chitiniclastica* and determined its similarity to be 99.5% with strain E43 (GenBank accession no. AJ517825). The 16S rRNA sequence obtained from the patient's strain was deposited in GenBank under no. EU484335. The strain was deposited in the Collection de Souches de l'Unité des Rickettsies (CSUR; World Data Center for Microorganisms 875, http://ifr48.timone.univ-mrs.fr/portail2/index.php?option = com_content&task = view&id = 96&Itemid = 52) under reference CSUR P16.

*W. chitiniclastica* is a recently described γ-proteobacterium isolated from larvae of the parasitic fly *Wohlfahrtia magnifica* (*3*). Although the pathogenicity of this new species for humans is as yet undescribed, it is phylogenetically close to *Ignatzschineria larvae*, another bacterium associated with *W. magnifica* larvae (*4*), which cause severe wound myiasis in cattle (*5*). Because of its strong chitinase activity, *I. larvae* may play a role in the metamorphosis of its host fly, as has been observed for other fly symbionts, and thus may be a symbiont of *W. magnifica* flies (*6*). The bacterium was later discovered in swine waste in Quebec (*7*). In 2007, three publications renewed researchers' interest in *I. larvae*. First it was reclassified as the only species within the genus *Ignatzschineria* (*4*). Then 2 case reports demonstrated that it plays a role as a human pathogen (*8*,*9*). Both described an *I. larvae* bacteremia in adults with myiasis in southeastern France. The first patient was an elderly farmer with diabetes and myiasis of the leg, scrotum, and anus (*8*). The second patient was a middle-aged homeless man with a history of alcoholism who also had foot wound myiasis (*9*).

We report *W. chitiniclastica* bacteremia also in a homeless woman from southeastern France. Although we did not test body lice for *W. chitiniclastica*, we believe that the bacteremia originated from the patient's scalp maggots. Unfortunately, as previously reported for cases of *I. larvae* bacteremia, the maggots had been rapidly discarded, permitting neither bacterial analysis nor entomologic identification. However, these larvae may have been from *W. magnifica* flies. These flies are present in southern France, and although they are not typically found at low altitude and in a semiurban environment, their distribution is known to be progressively expanding, in part because of their broad adaptation capacities. Animal hosts for *W. magnifica* flies are numerous, but humans can also be infected; >10 cases of this myiasis in humans have been reported in Europe, Asia, Morocco, and Egypt. The scalp was affected in 2 of these patients (*10*).

Among homeless persons, ectoparasitism is very common; body lice (*Pediculus humanus humanus*) are of particular interest because they transmit 3 bacterial bloodstream infections: trench fever (*B. quintana*), epidemic typhus (*R. prowazekii*), and louse-borne relapsing fever (*Borrelia recurrentis*) (*1*). Myiasis should also be considered as a relevant type of ectoparasitism in homeless and hygiene-deficient persons. In addition, like body lice, ticks, and fleas, fly larvae should also be regarded as another potential source of specific arthropod-borne bacterial systemic infections.

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# Serologic Screening for *Neospora caninum*, France

**To the Editor:** In the June 2008 issue of Emerging Infectious Diseases, McCann et al. (*1*) reported on serologic screening for *Neospora caninum* antibodies and reported a lack of serologic evidence for *Neospora* infection in humans in England, where prevalence of infection with the closely related parasite *Toxoplasma gondii* also is low. Only limited data are available on human exposure to *Neospora*. We investigated the seroprevalence of *N. caninum* in humans in France, where *Toxoplasma* spp. seroprevalence is high.

Our study comprised 500 serum samples from healthy women, followed at the Cochin–Port Royal University Hospital in 1997 within the framework of toxoplasmosis surveillance during pregnancy, and 400 serum samples from HIV-infected patients. All serum samples were submitted to anti-*Toxoplasma* antibody testing by using indirect immunofluorescence (IIF; Toxo-spot IFI; bioMérieux, Marcy l'Etoile, France) and ELISA (Platelia Toxo IgG and IgM; BioRad, Hercules, CA, USA). An in-house microplate IIF test previously validated in cattle was used for simultaneous detection of anti-*Neospora* and anti-*Toxoplasma* immunoglobulin (Ig) G on the same microplate. All samples were screened at dilutions of 1:20 and 1:80, as is usually done in anti-*Toxoplasma* IIF assays in humans. Correlation between the anti-*Toxoplasma* IIF commercial test and in-house IIF was excellent (kappa coefficient = 0.98) and allowed us to compare the antibody titers against both parasites. Forty (8%) samples from immunocompetent persons and 21 (4%) from immunocompromised persons yielded a weak fluorescence when diluted 1:20. All but 4 had significant titers of anti-*Toxoplasma* IgG (>200 IU/mL in 77% of cases), which suggests low-level cross-reactions. Whereas titers of >200 and >320 are considered sufficient to diagnose neosporosis in dogs and cattle, respectively (*2*), positivity threshold was difficult to resolve in the absence of a positive human control. We decided on a positivity threshold of 1:80, which is similar to the threshold defined by others in further studies using an indirect fluorescence antibody test in humans (*3*,*4*). None of the 500 samples from immunocompetent persons were positive for *Neospora* antibodies when assessed at a dilution of 1:80. Within the group of immunocompromised persons, 3 were positive for *Neospora* antibodies at a titer of 80, and 1 was positive at a titer of 160. Three of these 4 HIV-infected patients had high titers of anti-*Toxoplasma* IgG (>2,000 IU/mL), suggesting *Toxoplasma* serologic reactivation. We found no evidence of *Neospora* infection or exposure in immunocompetent persons but could not exclude possible *Neospora* infection associated with *Toxoplasma* infection or reactivation in immunocompromised persons.

Taken together, our data agree with data from other studies conducted in European countries (*1*,*5*), which suggest that neosporosis in healthy humans is unlikely. However, the *Neospora* spp. seropositivity of some HIV-infected patients, although weak compared with the level of seropositivity in cattle or dogs, could suggest circulation of the parasite within immunocompromised hosts, a hypothesis supported by Lobato et al. (*3*). However, our observation of a strong serologic reactivation against *T. gondii* in 3 of 4 patients with anti-*Neospora* titers >80 mostly favors cross-reactivity involving homologous antigens of both parasites and nonspecific antibody binding from polyclonal stimulation of the immune system. Finally, one should keep in mind that the positive predictive value of a serologic test used in screening in low-prevalence populations is low. Large-scale studies are needed to more precisely determine the potential role of this parasite in immunodeficient humans and to isolate the parasite or detect *Neospora* DNA in such patients.

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