

Table. *Cryptosporidium* genotypes identified by using sequencing of partial sequences of the small subunit rRNA gene in the stool samples of immunocompetent humans, Czech Republic

Patient no.	Age, y/sex	Examination year	<i>Cryptosporidium</i> species/genotype	Infection intensity*		GenBank accession no.
				Sample 1	Sample 2	
H15	9/M	2005	<i>C. parvum</i> †	56	78	EU331237
H23	10/M	2005	<i>C. hominis</i>	77	121	EU331242
H98	10/F	2005	<i>C. parvum</i> †	43	25	EU331238
H101	11/M	2006	<i>C. parvum</i> †	11	5	EU331239
H132	8/M	2006	<i>C. parvum</i> †	150	62	EU331240
H158	11/M	2007	<i>C. parvum</i> †	26	85	EU331241
H199	29/M	2007	<i>Cryptosporidium</i> pig genotype II	38‡	27‡	EU331243

*Numbers of oocysts per 30 fields at ×1,000 magnification, unless otherwise indicated.

†Bovine genotype.

‡Numbers of oocysts per whole slide at ×1,000 magnification.

the source of both *Cryptosporidium* and *Giardia* infection in the *Cryptosporidium* pig genotype II–positive patient. The passage of oocysts can be excluded because of the number of oocysts detected in repeat samples (Table). Moreover, identification of the infection in an immunocompetent patient underlines the zoonotic potential of this pig genotype and possible presence of risk factors in rural areas with poor water treatment or inadequate biosecurity in pig units. Further evidence of the zoonotic potential of this *Cryptosporidium* genotype is needed to show its pathogenic potential in immunocompetent patients as a cause of gastroenteritis (in the absence of *Giardia* spp. and other established enteropathogens) and to demonstrate invasive tissue stages. The use of molecular techniques to identify *Cryptosporidium* spp. probably will show more zoonotic species or genotypes in humans.

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References

- Feltus DC, Giddings CW, Schneck BL, Monson T, Warshauer D, McEvoy JM. Evidence supporting zoonotic transmission of *Cryptosporidium* spp. in Wisconsin. *J Clin Microbiol*. 2006;44:4303–8. DOI: 10.1128/JCM.01067-06
- Nichols G. Epidemiology. In: Fayer R, Xiao L, editors. *Cryptosporidium* and cryptosporidiosis. Boca Raton (FL): CRC Press; 2007. p. 79–118.
- Robinson G, Elwin K, Chalmers RM. Unusual *Cryptosporidium* genotypes in human cases of diarrhea. *Emerg Infect Dis*. 2008;14:1800–2. DOI: 10.3201/eid1411.080239
- Ajjampur SS, Gladstone BP, Selvapandian D, Muliylil JP, Ward H, Kang G. Molecular and spatial epidemiology of cryptosporidiosis in children in a semiurban community in South India. *J Clin Microbiol*. 2007;45:915–20. DOI: 10.1128/JCM.01590-06
- Xiao L, Fayer R, Ryan U, Upton SJ. *Cryptosporidium* taxonomy: recent advances and implications for public health. *Clin Microbiol Rev*. 2004;17:72–97. DOI: 10.1128/CMR.17.1.72-97.2004
- Miláček P, Vítovec J. Differential staining of cryptosporidia by aniline-carbol-methyl violet and tartrazine in smears from faeces and scraping of intestinal mucosa. *Folia Parasitol (Praha)*. 1985;32:50.
- Jiang J, Alderisio KA, Xiao L. Distribution of *Cryptosporidium* genotypes in storm event water samples from three watersheds in New York. *Appl Environ Microbiol*. 2005;71:4446–54. DOI: 10.1128/AEM.71.8.4446-4454.2005
- Ryan U, Read C, Hawkins P, Warnecke M, Swanson P, Griffith M, et al. Genotypes of *Cryptosporidium* from Sydney water catchment areas. *J Appl Microbiol*. 2005;98:1221–9. DOI: 10.1111/j.1365-2672.2005.02562.x
- Xiao L, Bern C, Arrowood M, Sulaman I, Zhou L, Kawai V, et al. Identification of *Cryptosporidium* pig genotype in a human patient. *J Infect Dis*. 2002;185:1846–8. DOI: 10.1086/340841
- Langkjaer RB, Vigre H, Enemark HL, Maddox-Hyttel C. Molecular and phylogenetic characterization of *Cryptosporidium* and *Giardia* from pig and cattle in Denmark. *Parasitology*. 2007;134:339–50. DOI: 10.1017/S0031182006001533

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Crimean-Congo Hemorrhagic Fever, Southwestern Bulgaria

To the Editor: Crimean-Congo hemorrhagic fever virus (CCHFV) causes a severe multisystem disease characterized by profuse bleeding with a case-fatality rate as high as 30%. The infection is endemic to the Balkans (1,2). In Bulgaria, most cases are reported from the central and eastern parts of the country (3,4). We report a cluster of cases observed in early spring 2008 in southwestern Bulgaria, an area considered at low risk for CCHF outbreaks.

The index case-patient was a 49-year-old man in whom fever, severe myalgia and joint pain, diarrhea for 1 day, cough, and weakness developed on March 20. Three days before, while not using hand protection, he removed ticks from cows. On March 25, severe epistaxis developed and he was hospitalized. His condition rapidly deteriorated; leukopenia, thrombocytopenia, and elevated levels of liver enzymes developed, and he died on March 26. The autopsy found hemorrhages in the lungs but not in the hypophysis or gastrointestinal tract. Immunoglobulin (Ig) M antibodies against CCHFV were detected in the serum sample.

The second case-patient was a 34-year-old man who had removed ticks from cows from the same herd as the index case-patient. Symptoms developed on March 23 and he was hospitalized on March 26 with fever, diarrhea, and bloody sputum. Laboratory findings showed moderate leukopenia and thrombocytopenia. His condition improved within 1 week. IgM antibodies against CCHFV were detected in a serum sample collected during the acute phase of the disease.

The third confirmed case-patient was a 52-year-old woman (nurse) who cared for the index case-patient after his hospital admission. Although she reported wearing gloves, she was extensively exposed to the patient's blood and vomit and received immunoprophylaxis (specific hyperimmune gamma globulins). On March 28, a mild disease characterized by fever, headache, weakness, and maculopapular rash with petechiae developed; she was hospitalized on April 2. She had leukopenia, thrombocytopenia, and normal levels of liver enzymes. The serum sample collected during the acute phase of the disease was IgM positive, and a 4-fold increase was present in the IgG titer in a sample collected during the convalescent phase (from 160 to 640). Blood and serum samples taken during the acute phase of the disease were positive for CCH-

FV by real-time PCR (5) and reverse transcription-nested PCR (6). Purified PCR product was sequenced; the nucleotide sequence was submitted to GenBank (accession no. FJ160262). Viral load was 3.88×10^7 copies/mL.

The fourth confirmed case-patient was a 50-year-old woman, the wife of the index case-patient. She was hospitalized April 10 with fever, headache, myalgia, weakness, stomach pain, and nausea. She reported exposure to her husband's blood before hospital admission. Thus, hyperimmune gam-

ma globulins against CCHFV were administered. She had leukopenia, thrombocytopenia, and elevated levels of aspartate aminotransferase and alanine aminotransferase. The symptoms lasted only 7 days. CCHFV was detected by both PCRs (5,6) in a serum sample taken on day 3 of the disease; sequence of the PCR products was submitted to GenBank (accession no. FJ445749).

A phylogenetic tree including sequences from the third and fourth cases was constructed (Figure). The 2

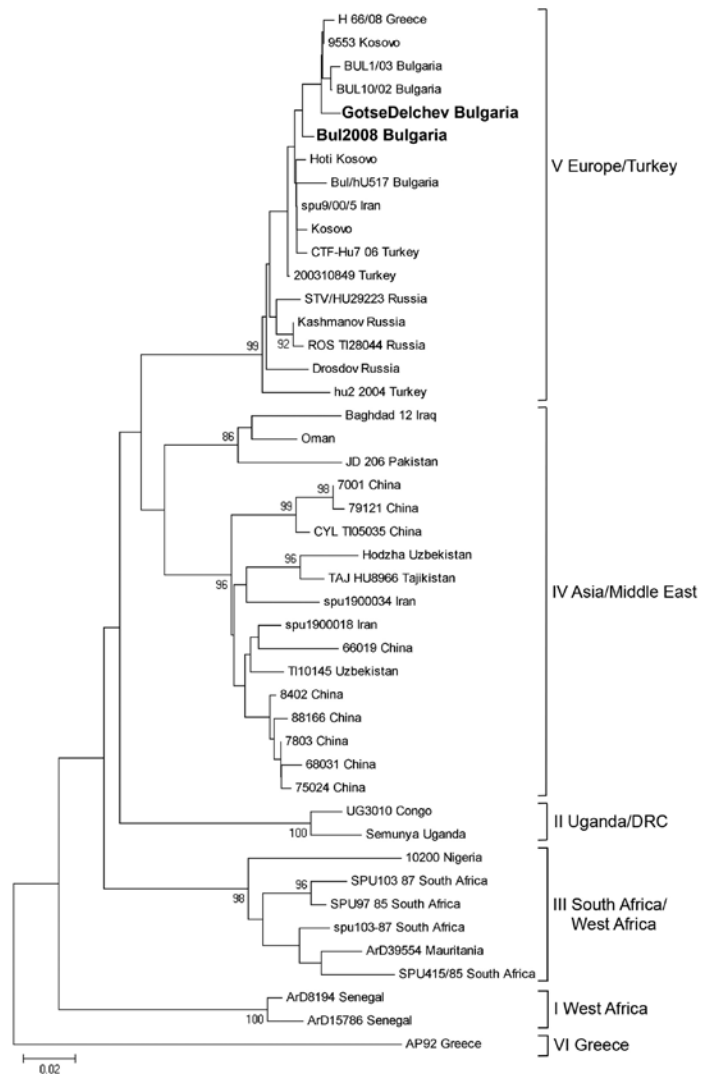


Figure. Phylogenetic tree of partial sequence (256 bp) of Crimean-Congo hemorrhagic fever (CCHF) virus nucleoprotein gene. CCHF virus sequences are listed as viral strain name and country of origin. Sequence of case 3 is designated in the tree as "Gotse Delchev Bulgaria," and sequence of case 4 is designated as "Bul 2008 Bulgaria" (in boldface). Strain AP92, Greece, was used as an outgroup. Numbers at the nodes represent bootstrap values. Scale bar indicates number of nucleotide substitutions per site.

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 cranio-pharyngeal 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 trans-

mission emphasizes the need for rapid diagnosis of CCHF, especially in cases with atypical clinical manifestations.

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References

- Ergonul O, Whitehouse CA. Crimean-Congo hemorrhagic fever, a global perspective. New York: Springer; 2007.
- Ergonul O. Crimean-Congo haemorrhagic fever. *Lancet Infect Dis*. 2006;6:203–14. DOI: 10.1016/S1473-3099(06)70435-2
- Papa A, Christova I, Papadimitriou E, Antoniadis A. Crimean-Congo hemorrhagic fever in Bulgaria. *Emerg Infect Dis*. 2004;10:1465–7.
- Monev V, Dikov I, Kamarinchev B. Crimean-Congo-haemorrhagic fever. In: Serbezov V and Kalvatchev Z, editors. Arbovirus infections viral haemorrhagic fevers and bioterrorism [in Bulgarian]. Sofia; 2005. p. 130–42.
- Papa A, Drosten C, Bino S, Papadimitriou E, Panning M, Velo E, et al. Viral load in Crimean-Congo hemorrhagic fever. *Emerg Infect Dis*. 2007;13:805–6.
- Rodriguez LL, Maupin GO, Ksiazek TG, Rollin PE, Khan AS, Schwarz TF, et al. Molecular investigation of a multisource outbreak of Crimean-Congo hemorrhagic fever in the United Arab Emirates. *Am J Trop Med Hyg*. 1997;57:512–8.
- Kunchev A, Kojouharova M. Probable cases of Crimean-Congo-haemorrhagic fever in Bulgaria: a preliminary report. *Euro Surveill*. 2008;13. pii: 18845.
- Papa A, Maltezou HC, Tsiodras S, Dalla VG, Papadimitriou T, Pierroutsakos I, et al. A case of Crimean-Congo haemorrhagic fever in Greece, June 2008. *Euro Surveill*. 2008;13. pii: 18952.

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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