low SAFV detection rate remains thereby difficult to explain.

The outcome can be explained by a short duration of virus excretion in stool, which, however, is unlikely for an infection spreading by the fecal–oral route. Alternatively, it may be that the virus is unstable in stool and rapidly degrades, such that fecal samples are inadequate for diagnosis of the infection. Other specimens, however, such as respiratory samples, yielded also low numbers of positive findings (*4*). Remarkably, the study with a high prevalence of positive stool samples made use of primers selected in a conserved region of 2C helicase (*5*), whereas other studies used primers in the 5′ noncoding region (*3*,*4*). Hence, a difference in sensitivity between the different PCRs may be responsible for the discrepancy between seroepidemiology and the low diagnostic yield by PCR. This discrepancy, however, awaits further investigation.

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References

1. Jones MS, Lukashov VV, Ganac RD, Schnurr DP. Discovery of a novel human picornavirus in a stool sample from a pedriatric patient presenting with fever of unknown origin. J Clin Microbiol. 2007;45:2144–50. doi:10.1128/JCM.00174-07
2. Abed Y, Boivin G. New Saffold cardioviruses in 3 children, Canada. Emerg Infect Dis. 2008;14:834–6.
3. Drexler JF, de Souza Luna LK, Stöcker A, Silva Almeida P, Medrado Ribeiro TC, Petersen N, et al. Circulation of three lineages of a novel Saffold cardiovirus in humans. Emerg Infect Dis. 2008;14:1398–405. doi:10.3201/eid1409.080570
4. Chiu CY, Greninger AL, Kanada K, Kwok T, Fischer KF, Runckel C, et al. Identification of cardioviruses related to Theiler's murine encephalomyelitis virus in human infections. Proc Natl Acad Sci U S A. 2008;105:14124–9. doi:10.1073/pnas.0805968105
5. Blinkova O, Kapoor A, Victoria J, Naeem A, Shaukat S, Sharif S, et al. Cardioviruses are genetically diverse and common enteric infections in South Asian children. J Virol. 2009;83:4631–41. doi:10.1128/JVI.02085-08
6. Zoll J, Erkens Hulshof S, Lanke K, Verduyn Lunel F, Melchers WJ, Schoondermark-van de Ven E, et al. Saffold virus, a human Theiler's-like cardiovirus, is ubiquitous and causes infection early in life. PLoS Pathog. 2009;5:e1000416. doi:10.1371/journal.ppat.1000416
7. Itagaki T, Abiko C, Aoki Y, Ikeda T, Mizuta K, Noda M, et al. Saffold cardiovirus infection in children associated with respiratory disease and its similarity to Coxsackievirus infection. Ped Infect Dis J. 2011 Mar 7; [Epub ahead of print].
8. Chiu CY, Greninger AL, Chen EC, Haggerty TD, Personnet J, Delwart E, et al. Cultivation and serological characterization of the human Theiler's-like cardiovirus associated with diarrheal disease. J Virol. 2010;84:4407–14. doi:10.1128/JVI.02536-09
9. Viskari H, Ludvigsson J, Uibo R, Salur L, Marciulionyte D, Hermann R, et al. Relationship between the incidence of type 1 diabetes and maternal enterovirus antibodies: time trends and geographical variation. Diabetologia. 2005;48:1280–7. doi:10.1007/s00125-005-1780-9
10. Benschop K, Thomas X, Serpenti C, Molenkamp R, Wolthers K. High prevalence of human parechovirus (HPeV) genotypes in the Amsterdam region and identification of specific HPeV variants by direct genotyping of stool samples. J Clin Microbiol. 2008;46:3965–70. doi:10.1128/JCM.01379-08

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Alkhurma Hemorrhagic Fever in Travelers Returning from Egypt, 2010

To the Editor: The report of 2 visitors from Italy being infected by Alkhurma hemorrhagic fever virus (AHFV) in southeastern Egypt near the border with Sudan (*1*) provides useful data to help clarify the evolutionary origin of these tick-borne flaviviruses. AHFV was first isolated in Saudi Arabia and is associated with camel ticks (*2*). It is a genetically close relative of Kyasanur Forest disease virus, which was first isolated in India in 1957. Following the original isolation of Kyasanur Forest disease virus, there was no clear explanation for its apparent isolation in the Indian forests. Indeed, its subsequent discovery in southern China (*3*) suggested that migratory birds might carry the infected ticks to or from that region.

The most likely explanation for these outbreaks of hemorrhagic disease now begins to fit a pattern that can be interpreted in terms of the diseases' evolutionary origin in Africa. Thousands of animals are annually transported from Africa and other countries to Mecca, Saudi Arabia, to meet the human demand for food and transport during the Hajj. Many of these animals, including camels, are infested with ticks that may carry AHFV and thus provide the source of this human infectious agent. Phylogenetic evidence had previously suggested that the tick-borne encephalitic flavivirus serocomplex originated in Africa and gradually evolved and dispersed across the Northern Hemisphere of the Old World (*4*,*5*). This concept is totally consistent with the discoveries of AHFV in Saudi Arabia and now in southeastern Egypt. Thus, Africa is a likely source of infected ticks that are regularly moved between Africa

and Saudi Arabia. This concept of an African evolutionary origin for these viruses could readily be tested by serologic investigation of humans and animals and also by analysis of ticks from this region of Africa.

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References

1. Carletti F, Castilletti C, Di Caro A, Capobianchi MR, Nisii C, Suter F, et al. Alkhurma hemorrhagic fever in travelers returning from Egypt, 2010. Emerg Infect Dis. 2010;16:1979–82.
2. Charrel RN, Zaki AM, Attoui H, Fakeeh M, Billoir F, Yousef AI, et al. Complete coding sequence of the Alkhurma virus, a tick-borne flavivirus causing severe hemorrhagic fever in humans in Saudi Arabia. Biochem Biophys Res Commun. 2001;287:455–61. doi:10.1006/bbrc.2001.5610
3. Wang J, Zhang H, Fu S, Wang H, Ni D, Nasci R, et al. Isolation of Kyasanur Forest disease virus from febrile patient, Yunnan, China. Emerg Infect Dis. 2009;15:326–8. doi:10.3201/eid1502.080979
4. Gould EA, de Lamballerie X, Zanotto PM, Holmes EC. Evolution, epidemiology, and dispersal of flaviviruses revealed by molecular phylogenies. Adv Virus Res. 2001;57:71–103. doi:10.1016/S0065-3527(01)57001-3
5. Gould EA, de Lamballerie X, Zanotto PM, Holmes EC. Origins, evolution, and vector/host coadaptations within the genus *Flavivirus.* Adv Virus Res. 2003;59:277–314. doi:10.1016/S0065-3527(03)59008-X

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In Response: The concept suggested by Charrel and Gould (*1*) of an African evolutionary origin for these tick-borne flaviviruses and their dispersal across the Northern Hemisphere raises concerns over possible spread of a new potentially dangerous infection outside its country of origin. This awareness should alert physicians in Western countries to pathogens that cause unspecific, unusual, or totally unknown clinical signs. We agree that more research is needed in human and animal health, as well as in entomologic and environmental studies, especially in light of the recent data suggesting a nonexclusive role of ticks as vectors for human infection with Alkhurma virus and the hypothesis of human-to-human transmission (*2*).

Past experience with emerging diseases in travelers (Crimean-Congo hemorrhagic fever, Lassa fever, Marburg hemorrhagic fever) or with autochthonous spread of imported diseases (chikungunya, West Nile virus disease, malaria) indicates a consistent delay in the diagnosis of first or sporadic cases, leading to inappropriate or untimely treatment of some of the patients. To confront the problem of unusual and emerging pathogens, Western countries must invest in evidence-based and integrated strategies of preparedness and response.

First, the frontline physicians' ability to recognize, diagnose, and treat illnesses caused by unusual pathogens should be improved through training covering rare and tropical diseases. Second, a system of timely information and alerts about threats posed by new infectious diseases should be set up. Third, concentrating clinical samples in virology laboratories with proven experience in detecting emerging pathogens is crucial for comprehensive and rapid differential diagnosis. It must be also remembered that no commercial tests are available for serologic or molecular detection of many rare pathogens or for differential diagnosis. And, finally, laboratory diagnosis is often made difficult by antibody cross-reactivity, as documented in our article (*3*).

For Alkhurma virus, further research is needed in the animal setting because little is known about length and severity of illness, duration of viremia, and modes of animal-to-animal and animal-to-human transmission; we need to better understand the role of vectors to limit the spread of the disease.

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References

1. Charrel RN, Gould EA. Alkhurma hemorrhagic fever in travelers returning from Egypt, 2010 [letter]. Emerg Infect Dis. 2011;17:1573–4.
2. Madani TA, Azhar EI, Abuelzein el-TM, Kao M, Al-Bar HM, Abu-Araki H, et al. Alkhumra (Alkhurma) virus outbreak in Najran, Saudi Arabia: epidemiological, clinical, and laboratory characteristics. J Infect. 2011;62:67–76. Epub 2010 Oct 15. doi:10.1016/j.jinf.2010.09.032
3. Carletti F, Castilletti C, Di Caro A, Capobianchi MR, Nisii C, Suter F, et al. Alkhurma hemorrhagic fever in travelers returning from Egypt, 2010. Emerg Infect Dis. 2010;16:1979–82.

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