ing the outbreak in French Polynesia during 2013–2014. Cases of Guillain-Barré syndrome were also recorded during the Zika outbreak in Brazil (*6*). Moreover, soon after health authorities in Brazil warned of an increase in the prevalence of microcephaly in newborns that might be associated with Zika virus infection in mothers during pregnancy, health authorities in French Polynesia confirmed that neurologic congenital abnormalities also had been observed during the Zika outbreak there (*6*).

Other lessons learned from the emergence of CHIKV and Zika virus in small tropical islands include evidence of non-vectorborne virus transmission and its associated public health implications. Perinatal transmission of Zika virus to a neonate was first described in infected pregnant women in French Polynesia, and possible transplacental transmission was further corroborated by the detection of the virus in amniotic fluid samples of 2 pregnant women in Brazil whose fetuses had been diagnosed with microcephaly (*6*). Sexual transmission of Zika virus, suggested by Foy et al. (*7*), was corroborated by detection of virus in the semen of a patient in French Polynesia (*8*). To prevent transmission of CHIKV and Zika virus by blood transfusion, local blood banks in French Polynesia and the Caribbean adjusted their algorithms for blood donation and screening of blood products during outbreaks (*9*,*10*).

When we observe the geographic distribution of DENV, CHIKV, and Zika virus over the past decade, DENV expansion appears to have been a continuous process. However, the emergence of CHIKV, first in the Indian Ocean and later in the Caribbean, and the emergence of Zika virus in the Pacific has dramatically expanded the reach of these viruses (Figure).

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Seroepidemiologic Screening for Zoonotic Viral Infections, Maputo, Mozambique

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To the Editor: In sub-Saharan Africa, febrile patients are often assumed to have, and are treated for, malaria, but when tested, many are malaria-negative. Because emerging diseases, such as chikungunya virus (CHIKV) and dengue virus (DENV) infections, cause outbreaks around the world (*1–3*), the importance of these pathogens has become more evident. However, low-income countries have limited epidemiologic data on alternative diagnoses to malaria (*4*,*5*) and poor laboratory capacity (*1*), which restrict further diagnostic investigations. An early study in Mozambique during the 1980s found antibodies to Rift Valley fever virus

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(RVFV) in 2% of pregnant women (*6*). More recently, a RVFV seroprevalence of 36.9% among cattle in the Maputo Province was shown in 2010–2011 (*7*). Furthermore, the movement of humans from rural areas to major cities, particularly to the capital of Maputo, might affect human illnesses and disease pattern of zoonotic viruses (*3*).

We conducted a pilot study on CHIKV, DENV, hantavirus, RVFV, and West Nile virus (WNV) epidemiology in Mozambique. Ethical approval (registration no. IRB00002657) was granted by the National Bioethics Committee in Mozambique and by the Regional Ethical Review Board at Karolinska Institutet, Stockholm, Sweden (permit no. 2012/974–31/3).

During 2012–2013, a total of 78 febrile patients were prospectively enrolled when they sought medical attention at the Polana Caniço Health Center and Mavalane Health Center (catchment area 4,663 km^2, estimated population 46,184 inhabitants) in the suburban area of Maputo city. All included patients answered a questionnaire and were initially screened for malaria by blood smear light microscopy; 15 were positive for malaria (Table). Patients' median age was 29 years (37 years for seropositive patients) and ranged from 5 to 78 years. Forty-six (59%) were female. Fifty-eight (74%) reported recent exposure to mosquitoes. None of these persons had a history of international travel, and none had received a yellow fever vaccination.

Sixty (77%) patients provided paired acute- and convalescent-phase blood samples, with a minimum of 14 days (median 33 days) between samples. Serum samples were sent to the Public Health Agency of Sweden and blindly screened at a titer of 1:20 for IgG to CHIKV, DENV, hantavirus, RVFV, and WNV by using in-house indirect immunofluorescence assays as described for DENV by Vene et al. (*8*). Screening for IgG were done on convalescent-phase serum samples or, when those was not available, on acute-phase serum samples. Further immunofluorescence analyses for titer increases were performed for patients for whom paired serum samples were available and screening results were positive for IgG; however, no titer increases were found. Serum from admittance were tested for DENV IgM and WNV IgM by using commercial assays according to manufacturers' instructions (Panbio Dengue IgM Capture ELISA E-DEN01M/E-DEN01M05, Standard Diagnostics, Inc., Yongin-si, South Korea; Serion ELISA classic ES-R14M West Nile Virus IgM, Institut Virion/Serion GmbH, Würzburg, Germany); 2 samples were positive for DENV IgM but none for WNV IgM. All acute serum samples were screened by using 1-step real-time reverse transcription PCR for CHIKV, RVFV, WNV (in-house validated assays), and DENV (*9*). Results were negative for viral RNA.

Twenty-three (29%) of the 78 patients had a positive serology result from acute- or convalescent-phase serum samples for ≥1 of the tested viral pathogens (Table). The main finding was CHIKV IgG in 15 (19%) patients. Ten (13%) patients had positive results for DENV, including 2 DENV IgM–positive samples.

The seroepidemiologic findings in this pilot study in Maputo strongly suggest possible and neglected alternative causes of febrile illness in Mozambique. Antibodies to CHIKV were found in 19% of the patients, which was a novel finding for Mozambique but corresponded well with other reports on the spread of CHIKV in tropical and subtropical areas of the world (*2*,*3*). DENV antibodies were present in 13% of the study population, representing a new finding in southern Mozambique; previous outbreaks have been reported from the northern part of the country (*5*). The median age of the seropositive patients (37 years) was higher than for the group as a whole (29 years), which might reflect increased exposure to zoonotic viruses over time. One patient was IgG positive for RVFV, a potentially emerging cause of fever in Mozambique, especially in view of recent reports of RVFV in cattle (*7*). The samples positive for both DENV and WNV IgG could represent previous independent infections with these viruses, co-infection, or cross-reactivity, which are common for flavivirus IgG (*10*).

Overall, results indicate that exposure to vectorborne viruses in persons living in suburban areas of Maputo city is frequent, suggesting that infections with CHIKV, DENV, and RVFV infection should be considered as alternative diagnoses for patients with febrile illness in these settings. On the basis of these results, more extensive research is planned on the epidemiology of zoonotic viral infections in Mozambique.

Table. Results of screening for viral antibodies and malaria parasites in 78 febrile patients, Maputo, Mozambique, 2012–2013*

Organism	No. (%) positive†
Chikungunya virus	15 (19.2)
Dengue virus	10 (12.8)‡
Hantavirus	0
Rift Valley fever virus	1 (1.3)
West Nile virus	3 (3.8)
Malaria parasites	15 (19.2)§

*Viral antibody–positive patients had positive IgG or IgM response for ≥1 of the zoonotic viruses in acute- or convalescent-phase serum samples. The overall malaria screening results for the study cohort is also presented
†Three of the 23 serology-positive patients were positive for dengue virus and West Nile virus IgG, of whom 2 were also positive for chikungunya virus IgG and 1 for Rift Valley fever virus IgG.
‡Including 2 dengue virus IgM-positive samples.
§Three of 15 malaria-positive patients had a positive serologic finding (2 for dengue virus IgG and 1 for chikungunya IgG).

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Hemorrhagic Diathesis in *Borrelia recurrentis* Infection Imported to Germany

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To the Editor: Relapsing fevers are paroxysmal bloodstream infections caused by spirochetes of the genus *Borrelia*. Louseborne relapsing fever (LBRF; i.e., epidemic relapsing fever) is caused by *B. recurrentis* and transmitted by the human body louse (*Pediculus humanus*). Soft ticks of the Argasidae family (e.g., *Ornithodorus moubata*) are vectors for tickborne relapsing fever (TBRF) borreliae, which encompass several human-pathogenic species. In Europe, LBRF was epidemic in the early 20th century but is now rarely seen. We report an infection with *B. recurrentis* imported to Germany by a Somalian refugee who had high fever and hemoptysis and describe the process of molecular diagnosis.

In August 2015, an 18-year-old man sought asylum in Germany after travel through Somalia, Ethiopia, Sudan, Libya, and Italy. He reported general weakness and fever while in Libya, ≈16 days before seeking care, and started coughing up blood after arriving in Italy. At hospital admission in Germany, he had a temperature up to 40.4°C, cough, and hemoptysis; his suspected diagnosis was tuberculosis. No ectoparasites were reported or found on physical examination. Abnormal laboratory findings included relative neutrophilia (91% [reference 39%–77%]), thrombocytopenia (platelets 112×10^3/mL [reference $160–385 \times 10^3$/mL]), and prolonged activated partial thromboplastin time (APTT) (Figure, panel A). Because of highly elevated levels of C-reactive protein (250 mg/L [reference <5 mg/L]) and procalcitonin (16.4 μg/L [reference <0.5 μg/L]), the patient was treated with ceftriaxone (2g/d intravenously), metronidazole (500 mg/d intravenously), and paracetamol (acetaminophen). Repeated examinations of Giemsa-stained thick and thin blood slides were negative for malaria parasites. Blood cultures, tests for tuberculosis, and PCRs for Rift Valley fever, yellow fever, dengue, and chikungunya viruses also were negative. With antimicrobial therapy, the patient's fever declined within 12 hours, but platelet counts further decreased and APTT continued to increase (Figure, panel A).

The patient's symptoms and travel history raised suspicion of a spirochete infection. A plasma sample from his second day in the hospital tested positive for *Borrelia* spp. 16S DNA by real-time PCR (*1*). Retrospective microscopy revealed a low number of extracellular spirochetes in thin blood smears (Figure, panel B). The antimicrobial regimen was changed to doxycycline (100 mg 2×/d) on day 7 after admission and, because species identification had not been completed, continued for 10 days. No signs of a Jarisch-Herxheimer reaction were seen. During days 4–9 after admission, APTT, platelet counts (Figure, panel A), and C-reactive protein values returned to normal, and the patient was discharged.

For species identification, we amplified the entire coding sequence of *glpQ* (glycerophosphodiester phosphodiesterase) with newly designed primers (online Technical Appendix, http://wwwnc.cdc.gov/EID/article/22/5/15-1557-Techapp1.pdf). The amplicon was 100% (1,002/1,002 bp)