

Acknowledgments

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Chikungunya Outbreak, French Polynesia, 2014

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To the Editor: Chikungunya virus (CHIKV), an arthropod-borne virus (arbovirus) of the family *Togaviridae*, genus *Alphavirus*, is transmitted by mosquitoes of the *Aedes* genus, especially *Ae. aegypti* and *Ae. albopictus* (1). The main clinical manifestations of CHIKV infections are sudden high fever, headache, back pain, myalgia, arthralgia affecting mainly the extremities, and rash.

CHIKV emerged in the Pacific region in New Caledonia in March 2011. Additional outbreaks occurred in Papua New Guinea in June 2012; Yap State (Federated States of Micronesia) in August 2013; Tonga in April 2014; and American Samoa, Samoa, and Tokelau in July 2014 (2). Phylogenetic analysis of CHIKV strains showed the existence of 3 lineages: West African, Asian, and East/Central/South African (1).

French Polynesia is a French territory in the South Pacific, with 270,000 inhabitants living on 5 archipelagoes. Arboviruses are a common cause of outbreaks in French Polynesia: the last dengue virus (DENV) outbreaks caused by DENV-1 and DENV-3 occurred in 2013 (3), and DENV-1 still circulates. French Polynesia also experienced the largest Zika virus (ZIKV) outbreak ever reported during October 2013–April 2014 (4). In May 2014, CHIKV infection was detected for the first time in French Polynesia in a traveler returning from Guadeloupe, (5) where a chikungunya outbreak was ongoing (6).

In late September 2014, an increasing number of patients with fever and rash who tested negative for DENV and ZIKV by real-time reverse transcription PCR (RT-PCR) were recorded by the French Polynesia Department of Health on the south coast of Tahiti, French Polynesia's main island. Serum samples collected from 19 of these patients were tested for CHIKV by RT-PCR using previously reported primers and a probe (7). Seven of the 19 (37%) were positive; all 7 were autochthonous. The first specimen that tested positive for CHIKV had been collected from a patient on September 25, and by October

25, a total of 318 patients were confirmed by RT-PCR to be infected by CHIKV. Nearly all districts of Tahiti were affected, and cases were reported on 4 of French Polynesia's 5 archipelagoes.

Partial sequencing of the CHIKV E1 gene of a strain isolated from a patient and collected on September 29 (strain PF14-290914-16, GenBank accession no. KM985619) was performed as previously reported (8). Phylogenetic analysis showed that French Polynesia's CHIKV strain belongs to the Asian lineage and is more closely related to a strain collected in the British Virgin Islands in 2014 (VG14/99659) and to the French Polynesian strain imported from Guadeloupe in May 2014 (PF14-270514-51impGP), with 99.9% homology, than to the strains that recently circulated in Yap State (FM13/3807), Tonga (TO14-080414-3007 and TO14-080414-3042), and New Caledonia (NC11-568) (Figure).

No cases of CHIKV infection were reported in French Polynesia within the 4 months after the imported case detected on May 25, 2014. Because of the active, ongoing circulation of CHIKV in the Pacific, introduction of this virus in French Polynesia was expected from other Pacific islands, especially from New Caledonia, because of extensive travel between the 2 French territories.

The fact that the CHIKV strain circulating in French Polynesia is closely related to the strains currently circulating in the Caribbean suggests that the French Polynesia outbreak is a result of the introduction of CHIKV from the Caribbean rather than from another Pacific island. The delay between the current outbreak and the first infected patient detected in 2014 also suggests a new introduction rather than a circulation of the strain introduced in May. However, an undetected low-level circulation of CHIKV during the cooler and drier low transmission season, simultaneously with DENV-1 circulation, cannot be excluded.

The introduction of arboviruses into French Polynesia from other French overseas territories rather than from other Pacific islands was previously reported for DENV. In 2013, DENV-3 reappeared in French Polynesia 3 months after the Solomon Islands had declared a DENV-3 outbreak. However, epidemiologic and phylogenetic investigations revealed that the DENV-3 strain that caused the outbreak in French Polynesia had been introduced by a traveler returning from French Guiana and belonged to a different genotype than the one that was circulating in the Solomon Islands (3).

Several conditions are favorable to a large chikungunya outbreak in French Polynesia. First, because CHIKV has never been previously reported in French Polynesia, the entire population is thought to be immunologically naive for CHIKV infection. Second, 2 potential vectors for CHIKV are present in French Polynesia: *Ae. aegypti* (1) and *Ae. polynesiensis* mosquitoes (9). Third, in French Polynesia the hot and rainy season that lasts from October through

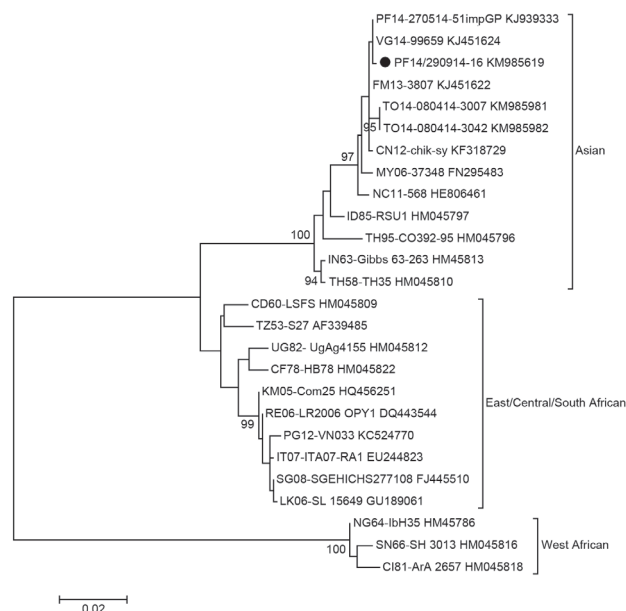


Figure. Phylogenetic analysis of chikungunya virus strain isolated in French Polynesia on September 29, 2014. The evolutionary history was inferred by using the maximum-likelihood method based on the Kimura 2-parameter model. The percentage of trees in which the associated taxa clustered together is shown for values >90 next to the branches (1,000 replicates). Evolutionary analyses were conducted in MEGA6 (<http://www.megasoftware.net/mega.php>). Each strain is labeled by country (iso country code, 2-letter) and date of origin/strain name/GenBank accession number. The chikungunya virus strain isolated in French Polynesia on September 2014 is marked with a black circle. Scale bar indicates nucleotide substitutions per site.

March is conducive to the proliferation of mosquitoes. We have the experience of the French Polynesian ZIKV outbreak that started with the same favorable conditions in October 2013 and was responsible for 28,000 estimated symptomatic cases from October 2013 through April 2014 (10). This new outbreak corroborates the recent observation that the expansion of arboviruses in the Pacific is ongoing and inevitable (2).

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Influenza A and B Viruses but Not MERS-CoV in Hajj Pilgrims, Austria, 2014

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To the Editor: The World Health Organization recommends that persons who return from pilgrimages to the Middle East with acute severe respiratory infections be tested to determine the cause of infection; the aim is to identify infections with the Middle East respiratory syndrome coronavirus (MERS-CoV), which have been occurring in Saudi Arabia since 2012. Each year, >2.5 million persons from >180 countries, including 240,000 pilgrims from Europe, participate in Hajj, the Muslim pilgrimage to Mecca, Saudi Arabia. The gathering of mass numbers of persons during the Hajj increases the risk for the spread of respiratory infections among participants, and this risk has raised global concern that travelers returning from this pilgrimage could contribute to the international spread of MERS-CoV. During the 2012 and 2013 Hajj and Umrah

(a minor pilgrimage) pilgrimages, no MERS cases in pilgrims were reported (1,2). However, in 2014, cases of MERS-CoV infection were confirmed in 2 returning pilgrims in the Netherlands (3). The International Health Regulations Emergency Committee advised all countries to improve awareness about MERS-CoV among pilgrims and to conduct surveillance for MERS-CoV among pilgrims during and after Hajj (4).

According to data from the International Air Transport Association, Austria received an estimated 68,000 air travelers from Saudi Arabia, Jordan, Qatar, and the United Arab Emirates during June–November 2012 (a period encompassing 1 month before Ramadan and 1 month after the Hajj) (5); of these travelers, 1,000 were pilgrims performing the Hajj. Relatively constant travel volumes to Austria on commercial flights out of these countries during 2010–July 2014 have been confirmed by an analysis of air traffic statistics for Austria (A. Herndler, M. Rudolf, pers. comm.). We report on the investigation of illness among Austrian residents just after their return home from the 2014 Hajj pilgrimage, which ended in early October.

As of October 27, 2014, a total of 7 Hajj pilgrims from Austria had sought medical care in different Austrian hospitals/medical centers just after returning from Saudi Arabia. The patients had fever and/or respiratory symptoms. A summary of the patients' characteristics is presented in the Table. Of the 7 patients, 4 had cough, 1 had dyspnea, and 4 had fever. Patients 1, 2, and 7 had an acute febrile illness and clinical and/or radiologic evidence of pulmonary parenchymal disease. Patient 1 had sought medical care in Saudi Arabia, and patient 2 had been hospitalized for 10 days in Saudi Arabia.

For the diagnosis of viral infection, a serum sample and a sputum, throat swab, or bronchoalveolar lavage sample were collected and sent to the Department of Virology, Medical University of Vienna, Austria, for analysis. All samples were tested for MERS-CoV by using reverse transcription PCR targeting regions upstream of the envelope gene (6). Respiratory and serum samples from all 7 patients were negative for MERS-CoV. The respiratory samples were also tested for influenza A and B viruses and for rhinoviruses, as previously described (7–9). Of the 7 patients, 3 were positive for influenza B virus, 2 for influenza A(H3N2) virus, and 2 for rhinoviruses (Table). Subsequent phylogenetic analysis showed that the influenza A(H3N2) strains belonged to the A/Hong Kong/146/2013-like viruses and the influenza B strains belonged to the B/Phuket/3073/2013-like viruses of the Yamagata lineage, both of which are subtype H3N2 and B strains included in the 2014–15 seasonal influenza vaccine for the Northern Hemisphere.

Our results showed that MERS-CoV was not detected in any of these patients, and our findings support those from reports investigating illness among 2013 Hajj