Dengue virus (DENV) infection has been spreading widely across tropical and subtropical countries. In Africa, the incidence of dengue fever has been underestimated and underreported likely owing to the presence of other febrile illnesses such as malaria and the lack of diagnostic testing for dengue. Dengue has been reported in several African countries (1). Moreover, other reports have shown that the DENV infection has spread to African countries with unreported DENV cases; serological evidence of DENV infections has been found in Sierra Leone (2) and a case of dengue fever in Guinea (3). In Côte d'Ivoire, a case of DENV type 1 (DENV-1) infection was first reported in 1999 (4). There are no similar reports until 2008 when DENV-3 infections were confirmed in visitors to Côte d'Ivoire (5,6). Scientific research from 2011 to 2012 also identified dengue fever as a cause of febrile illness in Abidjan (7). During a 2017 outbreak in Abidjan, an imported case of DENV-2 in Japan was reported (8). We report another case of DENV-1 infection exported to Japan from Abidjan, Côte d'Ivoire, in January 2019, which was detected during the very early phase of the 2019 outbreak.

A man in his 40s visited Abidjan, Côte d'Ivoire, on business on January 12, 2019 and returned to Japan on January 27, 2019. He mainly stayed in office and denied having been bitten by a mosquito in Abidjan; Doha, Qatar; and Casablanca, Morocco, where he transited. He presented with fever, headache, joint pain, diarrhea, and fatigue on the day after his return to Japan. He visited our hospital on January 30. Physical examination revealed a body temperature of 38.3°C, hyperemic conjunctiva, and hepatomegaly approximately 2 cm below the costal margin. His blood test results showed the following: 3,010 × 10^6 leukocytes/L; hemoglobin level, 13.3 g/dL; and 126 × 10^9 thrombocytes/L. Rapid diagnostic test results for influenza (Imunoace Flu; Tauns, Shizuoka, Japan) and malaria (BinaxNOW Malaria; Alere, Waltham, MA, USA) were negative. May–Giemsa staining of a thin-coated peripheral blood smear tested negative for *Plasmodium* parasites. On performing a rapid diagnostic test for dengue (Dengue Duo NS1 Ag + Ab Combo; Alere, Waltham, MA, USA), his whole blood sample was negative for anti-DENV IgM and IgG; however, the test result for non-structural protein 1 antigen was positive. Real-time reverse transcription polymerase chain reaction was performed (9), and DENV-1 RNA was detected in the whole blood sample on January 31. The patient recovered after receiving supportive treatment for 1 week. His lowest thrombocyte count was 11 × 10^9 thrombocytes/L, but platelet transfusion was not necessary. The DENV IgM antibody tested positive on February 5, indicating seroconversion.

Sequence analysis of the envelope gene region of the DENV genome revealed that the strain detected in the patient (GenBank accession number LC462951) belonged to genotype V of DENV-1 and that it was 99.5% identical to the envelope gene of DENV-1 strains that caused the 2013–2014 dengue epidemics in Malaysia and Singapore (GenBank accession numbers KJ806860, KJ806869, KJ806862, MH680219, ...
Export of Dengue Virus Serotype 1

Fig. 1. Phylogenetic tree based on the envelope (E) gene sequence of dengue virus type 1 detected in a patient returning from Abidjan, Côte d’Ivoire, to Japan (bold arrow) with reference dengue virus strains. Virus lineages are shown on the right. The analysis was conducted on a nucleotide sequence of the genes encoding the E protein (1,485 bp), using the Maximum Likelihood method with MEGA7 software (http://megasoftware.net). Bootstrap values were calculated with 1,000 replicates (values less than 70% are omitted). Each strain is coded by the strain name (GenBank Accession number) country of detection/year of detection. Open squares indicate the strains which have 99% nucleotide sequence identity with the strain detected in the present study. Virus strains that have been previously detected in West Africa and in other parts of Africa are indicated with closed circles and open circles, respectively.
MH680191, and MH680134), and the DENV-1 strain reported in China in 2016 (GenBank accession no. KX372686), though this was an imported case from an unknown region (Fig. 1). The DENV-1 strains detected in Tanzania in 2019 (GenBank accession numbers MN923102 and LC485151) shared 98.2% and 98.1% nucleotide identity in the E protein-coding region, respectively, with the strain reported here.

Phylogenetic analysis showed that the strain detected in this patient is part of a cluster different from DENV-1 strains previously detected in Côte d’Ivoire in 1985 and 1999 (GenBank accession numbers AF425620 and AF298807, respectively), in Nigeria in 1968 (GenBank accession numbers AF425625), and in other African countries; in the Democratic Republic of Congo in 2015 and 2019 (GenBank accession numbers LC360648 and MN577472, respectively), in Angola in 2013 (GenBank accession numbers KF184975 and KM277611), and in Gabon in 2012 (GenBank accession number MG877557). Phylogenetic analysis also revealed that the strain detected in our patient belonged to a distinct cluster from that of the strains detected in Tanzania in 2019 (GenBank accession numbers LC485151 and MN923102). Written informed consent was obtained from the patient.

All 4 serotypes of DENV have been confirmed in Africa (10); DENV-2 is the most common serotype, followed by DENV-1 (1). In West Africa, DENV-3 circulation has been reported since the mid-2000s (11). Additionally, there have been reports of DENV-3 and its circulation in Côte d’Ivoire during the same period (5,7). In 2017, a dengue fever outbreak was reported in Abidjan, Côte d’Ivoire. In this outbreak, DENV-2 was the most endemic serotype, with DENV-1 accounting for only 5% of the DENV serotypes (12). Another dengue fever outbreak was reported between February and October 2019. However, during this outbreak, DENV-1 was predominant, followed by DENV-2 (13). DENV-1 was also detected in our case, indicating that it was detected in the early phase of the outbreak.

Phylogenetic analysis suggests that the DENV strain in this case is similar to the strains recently circulating in Southeast Asia while being different from previous strains detected in West Africa. This patient had traveled to Doha, Qatar, and Casablanca, Morocco, but never had been bitten by a mosquito. Before and after staying in Abidjan, he had not visited other dengue-endemic countries or regions, including Southeast Asia. Rather than being an autochthonous strain from West Africa, the endemic DENV-1 strain in Abidjan in 2019 could have been imported from Southeast Asia; however, further studies are needed to confirm this hypothesis. The present case report suggests that imported dengue fever cases could serve as an alert for outbreaks in the exporting country.

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Conflict of interest None to declare.

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