to BLAST analyses (https://blast.ncbi.nlm.nih.gov/Blast.cgi). The YFV Uganda 2016 strain envelope sequence was aligned with reference YFV genomes by using MAFFT through the EMBL-EBI server (http://www.ebi.ac.uk), and phylogenies were generated with BEAST 1.8.4 (*9*), as previously described (*7*).

BLAST analyses determined that the highest percentage identity (95%) is shared between the Uganda 2016 strain and strains from South Sudan 2003 in the envelope region (the only region for which data from the Sudan strain are available) versus 83% with Angola 2016 strains from the same region. Furthermore, the Uganda 2016 sequences corresponding to the NS genes NS3 and NS5 have the highest percentage identities (94% and 95%, respectively) with a Uganda 1948 strain relative to 85% and 84% with the Angola 2016 strains in the same regions. Together these BLAST analyses indicate that the Uganda 2016 YFV is most similar to strains in the East African genotype. Phylogenetic analyses confirm the BLAST analyses and place the Uganda 2016 YFV in a well-supported clade along with these East African genotype strains, whereas the Angola 2016 strains group with an Angola 1971 YFV (Figure), indicating that the Uganda outbreak in 2016 was not seeded by the Angola outbreak.

These findings reiterate the endemicity of YFV throughout the tropical regions of Africa because at least 2 concurrent yellow fever outbreaks of independent origins were identified in 2016. Our findings also highlight the importance of assessing the molecular epidemiology of the virus in outbreak investigations. These data improve our understanding of YFV epidemiology in Africa and support the previous studies of Mutebi and colleagues (*2*). In addition, removal of contaminating ribosomal RNA proved to be an effective method for unbiased enrichment of viral RNA in degraded samples to enhance sequencing sensitivity.

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LETTERS

Visceral Leishmaniasis in Traveler to Guyana Caused by *Leishmania siamensis*, London, UK

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To the Editor: In a case report of visceral leishmaniasis in a traveler returning from Guyana, Polley et al. identified *Leishmania siamensis* as the causative agent (*1*). However, we believe that the parasite responsible for this infection has been misidentified. Classification of parasites formerly identified as *L. siamensis* has recently been revisited (*2*) after description of a new species

(*L. martiniquensis*) from the West Indies (*3*). All previously described *L. siamensis* strains, except 1, are now reported as *L. martiniquensis*. Their rDNA internal transcribed spacer 1 sequences are still deposited in GenBank under the name *L. siamensis*. The exception, reported from Thailand (GenBank accession no. JX195640), is the only known *L. siamensis* sample to date.

New analysis of *Leishmania* (*Mundinia*) sequences available in GenBank and of *L. infantum* showed no variability in *L. martiniquensis*, including the sequence (GenBank accession no. LT577674) reported by Polley et al. (*1*), and sequence divergence when compared with *L. siamensis* (32.4%), a *Leishmania* sp. from Ghana (32.3%) (*4*), *L. enrietti* (30.6%), and *L. infantum* (43.6%). *L. martiniquensis* has been reported worldwide (Florida, West Indies, central Europe, and Southeast Asia). However, *L. siamensis* has been reported only once (in Thailand).

If one considers possible quiescence of the parasite, and that the patient was from Guyana, migrated to the United Kingdom in 1967, and had a relevant travel history, including visits to France (2003), Ghana (2005), Caribbean Grenada (2012), and Guyana (2012 and 2013), the geographic origin of this infection is unknown. Moreover, the mode of transmission of *L. martiniquensis* is not yet clearly defined. In contrast to the report of Polley et al. (*1*), although the genus *Sergentomyia* could play a role in some foci of leishmaniasis, it has never been recorded in the Americas (*5*).

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Visceral Leishmaniasis in Traveler to Guyana Caused by *Leishmania siamensis*, London, UK

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To the Editor: Polley et al. reported a case of *Leishmania siamensis* infection outside Thailand (*1*). In Thailand, 2 *Leishmania* species, *L. siamensis* (MON-324, World Health Organization code MHOM/TH/2010/TR) and *L. martiniquensis* (MON-229, World Health Organization codes MHOM/TH/2011/PG and MHOM/MQ/92/MAR1), are sporadically reported in immunocompetent and immunocompromised patients and cause cutaneous and visceral leishmaniasis (*2*). Cases of asymptomatic visceral leishmaniasis caused by both species were also detected in HIV-infected patients in Thailand (*3*).

Before 2017, *L. siamensis* was described as having 2 lineages: PG and TR. Additional information from zymodeme and genetic analysis indicated that these 2 lineages are different species (i.e., lineage PG is *L. martiniquensis* and lineage TR is *L. siamensis*) (*2*). A review of leishmaniasis cases in Thailand during 1999–2016 (*2*) summarized the biological characteristics of *L. martiniquensis* and *L. siamensis* and clarified *Leishmania* species reported in humans (Thailand and Myanmar), animals (Thailand, Germany, Switzerland, and the United States), and sand flies (Thailand).

Polley et al. (*1*) reported phylogenetic analysis of internal transcribed spacer 1 sequences of 8 isolates of *L. siamensis* (GenBank accession nos. EF200012, JX195637, GQ281279, GQ226034, JQ866907, JQ617283, JQ001751, and GQ293226) against reference sequences of other *Leishmania* species. Their results confirmed that these sequences clustered with *L. siamensis* sequences as a monophyletic group, supported by bootstrap values of 100%.

However, 7 of these sequences (GenBank accession nos. EF200012, JX195637, GQ281279, GQ226034, JQ866907, JQ001751, and JQ617283) are *L. martiniquensis* sequences (MON-229), as reported in our article (*2*). Thus, we have revised and updated our sequences submitted to GenBank regarding the species of *L. martiniquensis* (MON-229) and *L. siamensis* (MON-324) for future analysis.

The patient had a history of traveling to Caribbean Grenada, which is in the same geographic area where *L. martiniquensis* was first reported (*4*). Thus, we believe