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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References

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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...
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

References
3. Desbois N, Pratlong F, Quist D, Dedet JP. 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).
4. 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).

Let’s break down the key points of this letter:

- **Visceral Leishmaniasis in Traveler to Guyana**
  - The authors discuss a case of leishmaniasis caused by Leishmania siamensis in a traveler to Guyana.
  - The traveler had a history of traveling to Caribbean Grenada, which is in the same geographic area where L. martiniquensis was first reported.

- **Phylogenetic Analysis**
  - Polley et al. (2018) reported a phylogenetic analysis of internal transcribed spacer 1 sequences of 8 isolates of L. siamensis.
  - Their results confirmed that these sequences clustered with L. siamensis sequences as a monophyletic group, supported by bootstrap values of 100%.

- **Revised Sequences**
  - The authors revised and updated their sequences submitted to GenBank, clarifying the species of L. martiniquensis (MON-229) and L. siamensis (MON-324) for future analysis.

- **Geographic Considerations**
  - The geographic origin of the infection is unknown, and the mode of transmission of L. martiniquensis is not yet clearly defined.

- **Travel History**
  - The patient had a history of traveling to various locations, including France, Ghana, Caribbean Grenada, and Guyana.

- **Species Comparison**
  - L. siamensis has been reported only once (in Thailand), while L. martiniquensis has been reported worldwide.

This letter highlights the importance of considering the patient's travel history and the need for ongoing research on the transmission and geographic distribution of Leishmania species.