Marburgvirus in Egyptian Fruit Bats, Zambia


We detected Marburg virus genome in Egyptian fruit bats (Rousettus aegyptiacus) captured in Zambia in September 2018. The virus was closely related phylogenetically to the viruses that previously caused Marburg outbreaks in the Democratic Republic of the Congo. This finding demonstrates that Zambia is at risk for Marburg virus disease.

The genus Marburgvirus, like Ebola, belongs to the family Filoviridae and consists of virus species that cause severe hemorrhagic fever in humans and non-human primates. Marburgvirus contains 1 species, Marburgvirus, and 2 viruses, Marburg virus (MARV) and Ravn virus (RAVV) (hereafter referred to as Marburgviruses) (1). Marburgvirus disease (MVD) has occurred most frequently in central Africa countries such as Uganda and the Democratic Republic of the Congo (DRC) (2). Sporadic outbreaks including imported cases have also been reported in Angola, Kenya, and South Africa (2).

Epidemiologic evidence strongly suggests that Egyptian fruit bats (Rousettus aegyptiacus) are the primary natural reservoir of Marburgviruses. Entry into caves and mines inhabited by Egyptian fruit bats has frequently been linked to MVD outbreaks (3). Cave-dwelling Egyptian fruit bats in Uganda have been shown to maintain genetically diverse Marburgviruses for at least several years (4–6). However, key findings on Marburgvirus ecology have been obtained mainly through epidemiologic studies in endemic countries such as Uganda and the DRC. Although Egyptian fruit bats are widely distributed from Africa to the Middle East, northern India, and Pakistan (7), it remains elusive whether these bats outside endemic areas also harbor Marburgviruses.

Because a traveler who had visited Zimbabwe developed MVD in South Africa in 1975 (3), it has been suggested that countries in southern Africa are also at risk for MVD. Indeed, Angola has had the largest MVD outbreak, in 2004–2005 (2). To estimate the risk of MVD in Zambia, which has had recognized human cases, we conducted an epidemiologic study of infection of Egyptian fruit bats with Marburgviruses in this country since 2014. Previously, we reported a high serorevalence of Marburgvirus infection (43.8%) in the Egyptian fruit bat population in Zambia (8). Peaks of serorevalence were repeatedly observed in November to December of each year, strongly suggesting the seasonality of infection in the Egyptian fruit bat colony in Zambia. However, neither infectious Marburgvirus nor its RNA genome had been detected in Egyptian fruit bats as of September 2018 (8).

In 2018, we captured 71 cave-dwelling Egyptian fruit bats in Lusaka Province, Zambia, as part of the research project Molecular and Serological Surveillance of Viral Zoonoses in Zambia (DNPW8/27/1), approved by the Department of National Parks and Wildlife, Ministry of Tourism and Arts of the Republic of Zambia (act no. 14 of 2015). We sampled lung, liver, kidney, spleen, and colon tissues from 22 bats in February and 25 bats in September (Table 1). In November, we collected oral and rectal swab samples from 24 bats. We extracted total RNA from pooled tissue homogenates (lung, liver, kidney, and spleen), colon homogenates, and pooled swab samples, as described previously (8). Subsequently, we tested RNA samples by reverse transcription PCR with panfilovirus nucleoprotein (NP) (9), Marburgvirus NP, viral protein (VP) 35 (6), and RNA-dependent RNA polymerase (L) gene primer sets (10).

We obtained all the expected PCR products from the RNA samples of an Egyptian fruit bat (ZB18-36) captured in September (Table 2). By Sanger sequencing of the PCR products and subsequent BLAST searches (https://blast.ncbi.nlm.nih.gov/Blast.cgi), we confirmed detection of Marburgvirus NP, VP35, and L genes (GenBank accession nos. LC465155–7). We also detected the NP gene in the pooled tissue RNA of another bat (ZB18-55) (GenBank...
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Moreover, further research is needed to elucidate the ecology of Marburgviruses in the entire African region and to estimate potential risks of MVD outbreaks in previously nonendemic countries. In particular, more extensive information is needed on Marburgviruses in the Egyptian fruit bat population, including the genetic diversity of the viruses, the distribution and migratory behavior of the bats, and the seasonal pattern of virus infection prevalence.

Figure. Phylogenetic trees showing evolutionary relationships of Marburgviruses from Egyptian fruit bats (Rousettus aegyptiacus), Zambia, 2018 (boldface), and reference viruses. The trees were constructed based on nucleotide sequences of 440 nt for the nucleoprotein gene (A), 296 nt for the viral protein 35 gene (B), and 238 nt for the RNA-dependent RNA polymerase gene (C) by using the maximum-likelihood method in MEGA7 (11). Nucleotide sequences of representative Marburgvirus strains were obtained from GenBank; accession numbers are shown with strain names. Bootstrap values >80 are shown near the branch nodes. Scale bars indicate nucleotide substitutions per site.
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References

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