Detection of *Mycobacterium ulcerans* DNA in African Fruit Bats, Cameroon, 2024

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In 2024, we detected *Mycobacterium ulcerans* DNA in 2 of 46 fruit bats in Akonolinga, Cameroon, whereas 111 aquatic macroinvertebrate pools were negative for *M. ulcerans*. Broader longitudinal surveillance will be needed to clarify the role of fruit bats as a reservoir for *M. ulcerans* circulation in Cameroon and Africa.

Buruli ulcer, caused by *Mycobacterium ulcerans*, remains endemic in West and Central Africa, although case numbers have declined markedly (*1*). In Akonolinga, Cameroon, the number of Buruli ulcer cases fell by ≈80% after 2011 (Figure), and *M. ulcerans* DNA, detected in aquatic invertebrates from the Nyong River in 2008 and 2012, was undetectable at the same sites in 2024 (*2*,*3*). In Australia, possums are established mammal reservoirs of *M. ulcerans* (*4*). Experimentally infected fruit bats can also recover from *M. ulcerans* lesions (*5*). Moreover, several fruit bat lineages have altered or lost G protein–coupled receptor 84 (GPR84), which was recently linked to reduced disease severity (*6*,*7*). Those observations prompted us to investigate *M. ulcerans* in fruit bats in Akonolinga, Cameroon.

In June 2024, we sampled fruit bats and aquatic macroinvertebrates at sites along the Nyong River previously investigated for *M. ulcerans* (*2*) (Appendix Figure 1, https://wwwnc.cdc.gov/EID/article/32/12/26-1277-App1.pdf). We captured fruit bats with mist nets, identified them morphologically, and collected oral and rectal swab samples before release (Appendix Figure 2). We collected aquatic macroinvertebrates, as previously described (*2*), and pooled them according to taxonomic groups.

We extracted DNA and performed quantitative PCR, as previously described (*2*). We screened samples for insertion sequence (IS)*2404* and the ketoreductase (KR) B domain of mycolactone polyketide synthase. We considered samples to be positive when we detected both IS*2404* and KR with PCR quantification cycle (Cq) values of <36. We included extraction, amplification, and PCR inhibition controls throughout the procedures. We detailed field procedures, ethical considerations, DNA extraction protocols, assay conditions, and quality-control procedures (Appendix).

We captured 46 fruit bats comprising 5 taxa: *Eidolon helvum* (n = 24), *Epomops franqueti* (n = 10), *Micropteropus* sp. (n = 5), *Hypsignathus monstrosus* (n = 4), and *Nanonycteris* sp. (n = 3) (Table; Appendix Table 1, Figure 2). None of the bats had cutaneous lesions compatible with Buruli ulcer. Two (4.2%) bat samples tested positive for *M. ulcerans* DNA: 1 rectal swab sample from an adult female *Micropteropus* sp. bat (IS*2404* Cq = 28.8; KR Cq = 33.3) and 1 oral swab sample from a juvenile male *E. helvum* bat (IS*2404* Cq = 33.85; KR Cq = 35.76) (Table; Appendix Table 1).

We collected 413 aquatic macroinvertebrates from previously investigated sites (*2*,*3*) and grouped them into 111 taxonomically homogeneous pools as follows: 50 Heteroptera pools (179 specimens), 42 Coleoptera pools (180 specimens), 11 Araneae pools (35 specimens), and 8 Odonata pools (19 specimens) (Table; Appendix Table 2, Figure 3). All pools tested negative for *M. ulcerans* DNA (Table; Appendix Table 2), whereas previous surveys at those sites detected *M. ulcerans* DNA in ≈5%–10% of aquatic invertebrate samples (*2*,*3*). All negative controls remained negative, positive controls amplified as expected, and we did not detect PCR inhibition.

Together, *M. ulcerans* DNA detection in 2 clinically healthy fruit bats and the absence of detectable DNA in aquatic macroinvertebrates from previously positive sites (*2*,*3*) suggest a change in the ecologic context of residual Buruli ulcer transmission in Akonolinga. Our findings do not establish bats as reservoir hosts or demonstrate bacterial viability or transmission. Detection of *M. ulcerans* in oral and rectal samples could reflect transient exposure through

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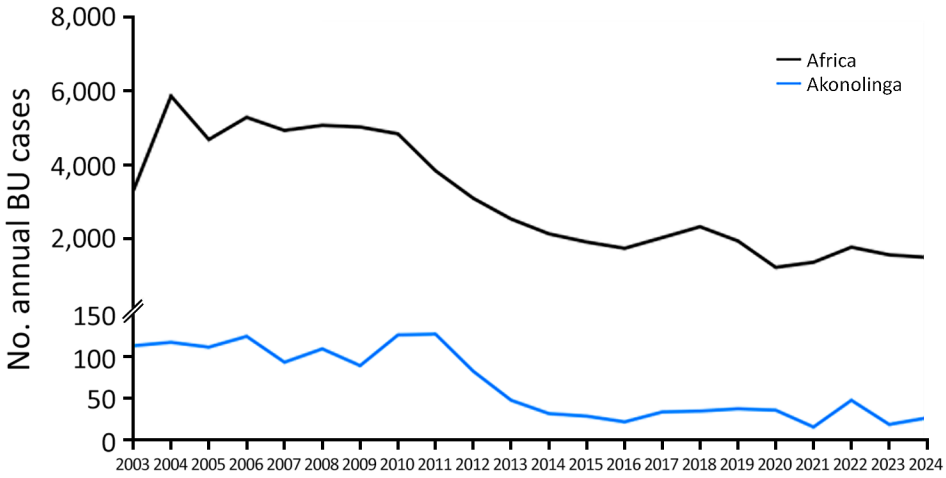


Figure. Number of annual human BU cases in study of *Mycobacterium ulcerans* DNA in African fruit bats, Cameroon, 2024. Graph indicates the temporal evolution of Buruli ulcer incidence in Africa and the Akonolinga Health District in Cameroon during 2003–2024. BU, Buruli ulcer.

food or water, digestive passage, or more persistent carriage. Because both *M. ulcerans*–positive bats belonged to frugivorous taxa, the ingestion of contaminated fruits or other plant material cannot be excluded. That possibility is biologically plausible, because plant-derived carbohydrates, particularly glucose polymers, can stimulate *M. ulcerans* growth in vitro (*8*). Longitudinal fecal sampling, together with investigation of dietary and environmental sources, could help distinguish exposure from carriage.

M. ulcerans DNA has been detected in lesions from terrestrial mammals in West Africa (*9*). The absence of visible lesions in fruit bats from Akonolinga is compatible with experimental observations showing that fruit bats can recover from *M. ulcerans* lesions (*5*). The absence of lesions is also consistent with our recent findings showing that GPR84 influences disease outcome and is consistent with reports that several fruit bat lineages have altered or lost that receptor (*6*,*7*). Those observations provide a biologic rationale for investigating fruit bats as potential permissive hosts, although a role for GPR84 in natural carriage has not been demonstrated.

If fruit bats contribute to *M. ulcerans* carriage, their high mobility could promote bacterial dissemination among distant environments. That possibility is consistent with a molecular epidemiologic study that reported identical or closely related *M. ulcerans* genotypes across geographically separated disease endemic regions (*10*).

An epidemiologic and ecologic shift similar to our findings was recently observed in Benin; ≈80% decline in Buruli ulcer incidence and aging of the affected population coincided with the disappearance of *M. ulcerans* DNA from previously positive aquatic environments (*1*). The changing profile resembles that observed in Australia, where Buruli ulcer predominantly affects adults, and mammals are clearly implicated in *M. ulcerans* ecology. The contributions of aquatic and nonaquatic ecologic compartments to *M. ulcerans* persistence in Akonolinga appear to change over time. Therefore, broader longitudinal

Table. PCR results for fruit bats and aquatic macroinvertebrates in study of *Mycobacterium ulcerans* DNA in African fruit bats, Cameroon, 2024*

Taxa	No. animals	No. swab or pooled samples	Positive animals, no. (%)
Fruit bats†			
Eidolon helvum	24	48 swabs	1 (4.2)‡
Epomops franqueti	10	20 swabs	0
Micropteropus sp.	5	10 swabs	1 (20.0)§
Hypsignathus monstrosus	4	8 swabs	0
Nanonycteris sp.	3	6 swabs	0
Totals	46	92 swabs	2 (4.3)
Aquatic macroinvertebrates¶			
Heteroptera	179	50 pools	0
Coleoptera	180	42 pools	0
Araneae	35	11 pools	0
Odonata	19	8 pools	0
Totals	413	111 pools	0

*Cq, quantification cycle; IS*2404*, insertion sequence *2404*; KR, ketoreductase B domain of the mycolactone polyketide synthase gene.
†Both oral and rectal swab samples were analyzed from each animal; positivity was calculated per animal.
‡Positive oral swab sample from *Eidolon helvum* bat (IS*2404* Cq = 33.9; KR Cq = 35.8).
§Positive rectal swab sample from *Micropteropus sp*. bat (IS*2404* Cq = 28.8; KR Cq = 33.3).
¶Animal specimens were analyzed in taxonomically homogeneous pools; positivity was calculated per pool.

surveillance of *M. ulcerans* circulation in Cameroon and Africa will be needed.

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Human Discovertebral Infection Caused by *Camelimonas* Species Bacteria, France, 2025

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We describe a case of human *Camelimonas* species infection, highlighting this bacterium as a potential emerging zoonotic pathogen with bone tropism. Diagnosis required repeated biopsies and genome sequencing. The isolate was susceptible to trimethoprim/sulfamethoxazole and doxycycline; clinical improvement followed prolonged therapy. Our findings support this bacterium's pathogenic role in humans.

Discovertebral infection (DVI) is the most common hematogenous osteomyelitis in persons >50 years of age and typically involves intervertebral disks and adjacent vertebral bodies. Diagnosis relies on clinical,

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