Fatal Mixed *Plasmodium* Infection in Traveler Returning to Colombia from Comoros Islands, 2024

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During 2014–2022, only *Plasmodium falciparum* malaria cases were reported in the Comoro Islands. We report a fatal case of mixed *Plasmodium* malaria infection in a traveler returning from the Comoros to Colombia in 2024, highlighting the need to strengthen laboratory detection and identification of *Plasmodium* spp. in sub-Saharan Africa.

Malaria is the most common life-threatening tropical disease associated with fever among returned travelers from sub-Saharan Africa. During 2010–2013, according to the World Malaria Report 2023, the Comoros Islands reported a total of 144,546 cases of *Plasmodium falciparum* infection and 1,571 cases of *P. vivax* infection (*1*). Nevertheless, during 2014–2022, only *P. falciparum* cases were reported, without *P. vivax* cases or mixed infections (*1*).

Data collected by the GeoSentinel Surveillance Network for 1,415 ill travelers returning from Indian Ocean islands during 1997–2010 indicated that the proportion of mosquitoborne infections (including malaria) was higher among travelers to the Comoros than among other travelers (*2*). At the same time, studies published in the past 10 years reported malaria cases exported from the Comoros to other countries during 1999–2021, mainly to territories of France (France, Réunion, and Mayotte) and 1 case to Japan; the most common etiologic agent was *P. falciparum* (≈255 cases), followed by *P. ovale* (≈19 cases) and *P. vivax* (≈11 cases) (*3*–*7*). We report a case of fatal mixed *Plasmodium* malaria infection in a man who returned to Colombia from the Comoros in 2024.

On June 14, 2024, an otherwise healthy 50-year-old male former military service member sought care at a primary care center in Bogotá (capital city of Colombia) after 7 days of fever (up to 39°C), chills, diaphoresis, myalgias, arthralgias, and headache. He reported a 2-day history of epigastric pain, loose stools, and dark urine. His illness was considered an unspecific viral infection, and he was discharged. His signs/symptoms had begun 10 days after he returned from Grande Comoroe Island, where he had stayed for 2 weeks while providing military training. Until his travel to the Comoros, he had not been in another *P. vivax*/*P. falciparum*–endemic area in the previous 5 years. On June 15, 2024, he was admitted to Hospital Militar Central, a reference military hospital in Bogotá, for a syncopal episode, disorientation, and jaundice. Physical examination revealed hypothermia, tachycardia with Kussmaul breathing, and reduced oxygen saturation. The patient was jaundiced and stuporous with no bleeding.

Laboratory tests revealed leukocytosis, anemia, severe thrombocytopenia, malarial hepatopathy, renal impairment, metabolic acidosis, and hyperlactatemia (Table). Thick and thin blood smears showed *P. falciparum* (17,840 trophozoites/μL; parasitemia of 0.35%) with gametocytes and *P. vivax* (8,320 trophozoites/μL). Severe malaria was diagnosed, and treatment with intravenous artesunate was initiated (2.4 mg/kg) in addition to fluid resuscitation and invasive mechanical ventilation support. However, the patient experienced

Table. Laboratory parameters of man with mixed *Plasmodium* malaria who had returned to Colombia from the Comoro Islands, June 15, 2024

Parameter	Value (reference range)
Leukocytes, $\times 10^9$ cells/L	28.3 (4.5–11.0)
Neutrophils, $\times 10^9$ cells/L	19.2 (2.0–8.0)
Lymphocytes, $\times 10^9$ cells/L	5.68 (0.9–4.5)
Hemoglobin, g/dl	8.3 (12.1–16.6)
Platelets, $\times 10^9$/L	12 (150–450)
Aspartate aminotransferase, U/L	109 (0–40)
Alanine aminotransferase, U/L	75 (0–41)
Total bilirubin, mg/dL	8.9 (0.01–1.1)
Conjugated bilirubin, mg/dL	7.0 (0.25–0.3)
Unconjugated bilirubin, mg/dL	1.9 (0.25–0.8)
Lactate dehydrogenase, U/L	918 (5–248)
Urobilinogen, mg/dL	8 (0.1–1.8)
Creatinine, mg/dL	2.92 (0.6–1.1)
Urea nitrogen, mg/dL	97 (8–23)
C-reactive protein, mg/dL	19.6 (0–0.5)
pH	7.03 (7.35–7.45)
Arterial partial pressure of carbon dioxide, mm Hg	13 (29–31)
Bicarbonate, mmol/L	3.4 (19–21)
Lactate, mmol/L	17 (0.36–0.75)

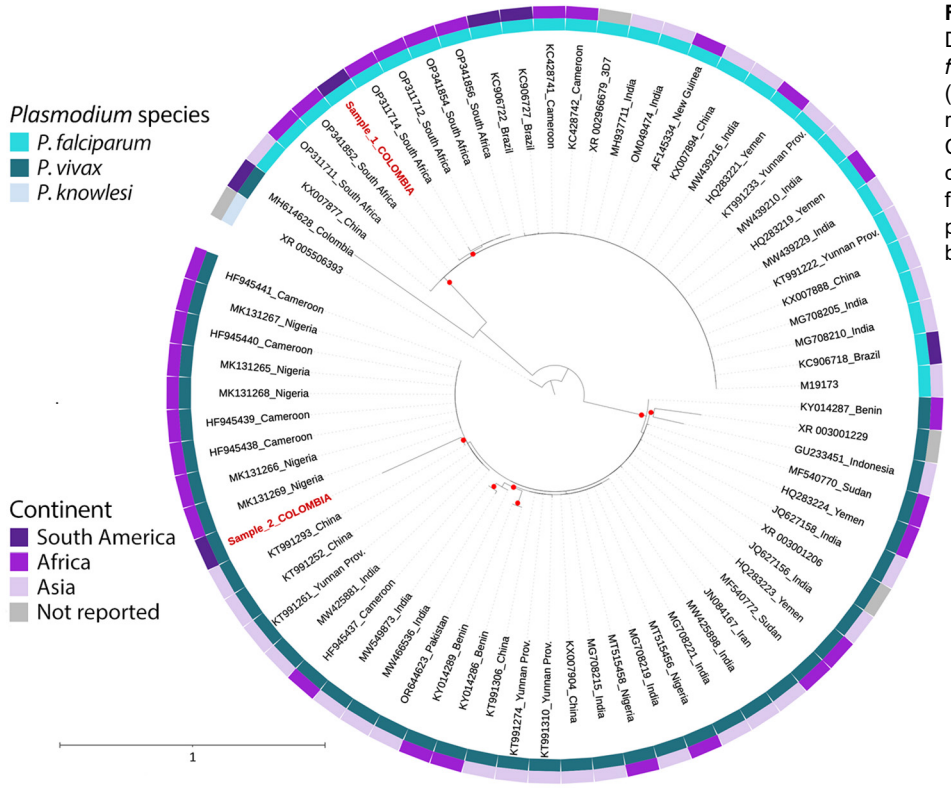

Figure. Phylogenetic tree of the DNA sequences of *Plasmodium falciparum* and *Plasmodium vivax* (red text) isolated from traveler returning to Colombia from the Comoros Islands, 2024, and compared with sequences reported from other countries. The red points on the tree represent bootstraps >80%.

2 episodes of cardiopulmonary arrest and died. Autopsy and histopathologic examination of heart and brain samples revealed multiple parasitic structures compatible with *Plasmodium* trophozoites (Appendix Figures 1, 2, https://wwwnc.cdc.gov/EID/article/31/1/24-1491-App1.pdf). PCR performed on blood smears confirmed the presence of *P. falciparum* and *P. vivax* (Appendix). DNA gene fragments from the small subunit rRNA 18S gene were sequenced from the positive specimens, and phylogenetic analyses positioned the obtained sequences in the same subclade as *P. falciparum* sequences detected in South Africa and as *P. vivax* sequences detected in Cameroon, Nigeria, China, and India (Figure; Appendix). Sequences were deposited in GenBank (*P. falciparum* accession no. PQ408861, *P. vivax* accession no. PQ408862).

In the most recent study that used PCR to assess the distribution of *Plasmodium* spp. on Grande Comore Island, among 159 positive samples collected during 2012–2013, nearly all (98.11%) were positive for *P. falciparum* and only 1.25% were positive for *P. vivax* (*8*). At that time, the authors indicated that routinely, without PCR testing, the rapid diagnostic tests used in the Comoros were able to identify *P. falciparum* but no other *Plasmodium* spp. (*8*), which is in accordance with a recent published editorial that discusses the contemporary concern with regard to the need to re-evaluate the spread of *P. vivax* in sub-Saharan Africa (*9*). The editorial mentioned that during 2017–2021, among 1.57 billion malaria rapid diagnostic tests purchased for use by sub-Saharan Africa national malaria control programs, 79.4% were focused on identifying *P. falciparum* and the remainder were combination tests lacking *P. vivax* specificity; thus, the predominant approach for malaria diagnosis across Africa was unable to specifically detect *P. vivax* (*9*). Our report highlights the value of strengthening laboratory diagnostic tools with good performance for detecting and accurately identifying *Plasmodium* spp. in clinical settings and of conducting more genetic-epidemiologic studies in the Comoros and other sub-Saharan Africa countries.

Because the patient died, written consent inform for publication of this article was obtained from the patient's wife.

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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Dr. Medina-Lozano is an internal medicine physician at Hospital Militar Central in Bogotá, Colombia. His research interests primarily focus on tropical infectious diseases.

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Equine Encephalomyelitis Outbreak, Uruguay, 2023–2024

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We report the genomic analysis from early equine cases of the Western equine encephalitis virus outbreak during 2023–2024 in Uruguay. Sequences are related to a viral isolate from an outbreak in 1958 in Argentina. A viral origin from South America or continuous enzootic circulation with infrequent spillover is possible.

In November 2023, multiple outbreaks of equine encephalomyelitis were reported in the central Argentina provinces of Corrientes and Santa Fe and then in western Uruguay (Pan American Health Organization, pers. comm., email, 2023 Dec 19). On December 5, 2023, Western equine encephalitis virus (WEEV) was confirmed as the causative agent of an equine death from Salto Department, in northwestern Uruguay (Figure 1). Through March 2024, this outbreak has extended across Uruguay and affected 1,086 equines. We report the diagnosis and preliminary genomic analysis of WEEV on the basis of partial sequencing of the nonstructural protein (NSP) 4 gene that was conducted in the first case of the outbreak (November 28, 2023) and 7 additional cases during December 2023–February 16, 2024.

We collected equine brain tissue samples from 5 departments: Salto, Paysandú, Rio Negro, San José,

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