The foretold Oropouche fever epidemic

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Since October, 2023, Oropouche virus (OROV) has caused a large outbreak of Oropouche fever in the Americas, exposing yet again the vulnerabilities of infectious disease surveillance systems. These weaknesses are far from a uniquely Latin American problem and might apply to other understudied pathogens lurking elsewhere in the Americas or globally.[1]

Approximately 20 000 cases of Oropouche fever have been reported as of the end of January, 2025. Between 2020 and 2023, detection of molecular and serological traces of OROV in French Guiana and Haiti[3] and modelling of OROV's potential ecological suitability across the continent[4] suggested regional endemicity of the virus and wide circulation before the ongoing epidemic started. In their Article,[2] Carlo Fischer and colleagues report an average OROV IgG antibody detection rate of 6·3% in 9420 serum samples collected between 2001 and 2022 from six Latin American countries. The study's age-correlated detection of OROV-specific IgG supports the endemicity of OROV in Latin America, and the author's serological findings provide the first evidence of the virus in Costa Rica.[2]

Even though OROV circulation and expansion was clearly happening over the past 25 years, research on the topic only exploded during the current epidemic (as happened, for example, during the 2016 Ebola virus disease outbreak). This trajectory follows a classic pattern: a rise in cases is followed by an increase in the public visibility of a pathogen, which fosters research (ie, academic publishing) that subsides with time.[5] Despite the pledge for One Health studies on primary pandemic prevention,[1] in reality, research reacts to epidemics instead of anticipating them or detecting them sooner to enable mitigation. The knowledge gaps in our understanding of OROV's natural history have unfortunately been neglected and need further investigation despite the fact that the virus was discovered 70 years ago. We still need to disentangle the role of known and unknown reservoirs in OROV transmission,[3] establish whether *Culex quinquefasciatus* and *Culicoides paraensis* are the best transmitting vectors,[3] perform in-situ studies to corroborate the role of deforestation in OROV outbreaks,[4] and study which pathogenic pathways lead to Oropouche fever, meningoencephalitis, and miscarriage.[3]

The reach of the current OROV outbreak might be driven by a combination of virus, vector, and host parameters. Specifically, a recent OROV reassortant, detected for the first time in Tefé in the Amazon state of Brazil in 2015, is causing the majority of new Oropouche fever cases across Latin America. The reassortant has genomic segments from Brazilian and non-Brazilian clades.[6] This genetic arrangement might influence OROV antigenic expression and viral features such as transmissibility. The presence of extreme climatic events, plus the ongoing dengue epidemic and the possible involvement of *Culex quinquefasciatus* as a transmitting vector in urban settlements, might be allowing the virus to reach previously unaffected regions.[7] Even if human populations have been exposed to OROV before, the new reassortant might be immunologically different enough to cause the large incidences detected across Brazil, or the emergent epidemics of Oropouche fever in Cuba and Panama.[8] More research is needed to establish whether immune evasion or increased virulence are changing the risk of OROV spread. The reassortant might account for proposed OROV vertical transmission and fetal malformations, or even the deaths attributable to the disease[9]—hypotheses that need to be tested.

Species distribution models are elegant tools for suggesting areas at risk of infectious disease emergence or spread.[10] Accordingly, Fischer and colleagues used a species distribution model framework to show that climate variables, rather than landscape alteration, might be driving OROV expansion.[2] However, as in the case of any modelling experiment, empirical tests are needed to corroborate and complement their effort before causal inference can be declared. As with other pathogens, knowledge of OROV's true distribution in the region and how it might expand to other locales[4] is key to aiding public health specialists in raising local awareness of Oropouche fever and, hopefully, allocating resources for improving surveillance and targeting research.

We expect that the ongoing epidemic will foster research to fill OROV and Oropouche fever knowledge gaps. It should also motivate improved research on arthropod-borne viruses across the region. Tragically, questions regarding the ecology, biology, and virology of Mayaro virus, Eastern Equine Encephalitis virus, and

West Nile virus, among many other pathogens currently circulating in Latin America, will only begin to be answered after the next epidemic.

We declare no competing interests.

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1. Plowright RK, Ahmed AN, Coulson T, et al. Ecological countermeasures to preventpathogen spillover and subsequent pandemics. *Nat Commun* 2024; **15:** 2577.
2. Fischer C, Frühauf A, Inchauste L, et al. The spatiotemporal ecology of Oropouche virus across Latin America: a multidisciplinary, laboratory-based, modelling study. *Lancet Infect Dis* 2025; published online April 14. https://doi.org/10.1016/S1473-3099(25)00110-0.
3. Navarro J-C, Romero-Alvarez D, Escobar L, et al. Oropouche fever: a growing threat in Latin America. In: Pujol FH, Paniz-Mondolfi AE, eds. Emerging viruses in Latin America. Switzerland: Springer Nature, 2024: 161–73.
4. Romero-Alvarez D, Escobar LE, Auguste AJ, Del Valle SY, Manore CA. Transmission risk of Oropouche fever across the Americas. *Infect Dis Poverty* 2023; **12:** 47.
5. Medley GF, Vassall A. When an emerging disease becomes endemic. *Science* 2017; **357:** 156–58.
6. Naveca FG, Almeida TAP, Souza V, et al. Human outbreaks of a novel reassortant Oropouche virus in the Brazilian Amazon region. *Nat Med* 2024; **30:** 3509–21.
7. Benitez AJ, Alvarez M, Perez L, et al. Oropouche fever, Cuba, May 2024. *Emerg Infect Dis* 2024; **30:** 2155–59.
8. Pan American Health Organization. Epidemiological update Oropouche in the Americas region—11 February 2025. Pan American Health Organization, 2025. https://www.paho.org/en/documents/epidemiological-update-oropouche-americas-region-11-february-2025 (accessed Feb 28, 2025).
9. Sah R, Srivastava S, Mehta R, et al. Oropouche fever fatalities and vertical transmission in South America: implications of a potential new mode of transmission. *Lancet Reg Health Am* 2024; **38:** 100896.
10. Peterson AT. Mapping disease transmission risk: enriching models using biogeography and ecology. Baltimore: Johns Hopkins University Press, 2014.