Journal of Infection 91 (2025) 106544

Contents lists available at ScienceDirect

Journal of Infection

journal homepage: www.elsevier.com/locate/jinf

Letter to the Editor

Reemergence of Oropouche virus infection in Ecuador, 2024: Vectors and cases

Dear Editor,

A description of Oropouche virus (OROV) in Matanzas, Cuba, was recently published,[1] representing the first detection of the pathogen in the country in 2024. This case was detected due to the ongoing Oropouche fever epidemic that has increased OROV surveillance everywhere. In Ecuador, OROV was described at least a decade ago, with three new cases detected in 2024.[2]

OROV is a reemerging arbovirus in South America, with cases expanding beyond this region through the importation of infections in North America and Europe. In Ecuador, the presence of OROV was molecularly confirmed in 2016 in Esmeraldas province (Fig. 1). That case triggered another investigation,[3] which detected five additional cases in the same year in that province (Fig. 1). The primary recognized vector of the virus, *Culicoides paraensis*, has also been detected in some provinces of Ecuador (Fig. 1).[4] Nevertheless, no additional studies or reports of OROV were described further. In the context of the 2023–2025 Oropouche fever epidemic and due to enhanced OROV surveillance, three new OROV cases were confirmed in the country by the National Institute of Public Health Research (INSPI, in Spanish) through a retrospective analysis of dengue-negative samples (https://www.paho.org/en/documents/epidemiological-update-oropouche-americas-region-11-february-2025).

The cases involve two men, aged 45 and 62, and a 36-year-old woman. The first case is a resident of Taisha Canton, Morona Santiago Province; the second resides in Caluma Canton, Bolívar Province; and the third is from Urdaneta Canton, Los Ríos Province (Fig. 1). According to the Pan American Health Organization (PAHO) report of February 2025, none of the individuals required hospitalization and all achieved full recovery (https://www.paho.org/en/documents/epidemiological-update-oropouche-americas-region-11-february-2025). Strikingly, *Cu. paraensis* has never been detected in these provinces. Specifically, OROV's primary vector has been reported in only two provinces, in northeast Ecuador: Sucumbíos and Orellana (Fig. 1).[4] However, other *Culicoides* species have been described in the regions where OROV was detected in 2024. Specifically, *Cu. diabolicus, Cu. castillae, Cu. tetrathyris*, and *Cu. insignis* have been identified in Caluma and Echandía Cantons in Bolívar Province (Fig. 1). From them, only *Cu. insignis* has been recently considered a potential OROV vector in the Ucayali Region, Peru.[5] Other *Culicoides* have been reported across Ecuador. In Esmeraldas, *Cu. pusillus, Cu. diabolicus, Cu. ocumarensis, Cu. castillae*, and *Cu. tetrathyris* have been reported (Fig. 1). In Manabí, Santo Domingo, Pichincha, and Imbabura provinces, other species of *Culicoides* have been identified (Fig. 1).[4]

The detection of OROV in Ecuador in 2024 highlights the expanding geographic range and public health significance of this neglected arbovirus in Latin America.[6,7] More importantly, the current epidemic should serve as a warning about the lack of knowledge regarding the distribution, bioecology, and vector competence of potential *Orthobunyavirus* vectors on the continent, which should also be considered for other Culicoides-transmitted viruses, such as Orbovirus.

The actual burden of Oropouche fever in Ecuador and elsewhere may be underrecognized, as it has been seldom studied before the current ongoing epidemic. Despite that, in 2024, a total of 16,189 cases were confirmed in the Americas, with 12,312 in 2025 (up to the epidemiological week 25) in multiple countries (https://www.paho.org/es/arbo-portal/arbo-portal-oropouche), but none in Ecuador. OROV and other viruses, such as Mayaro or Venezuelan Equine Encephalitis, should be integrated into routine arboviral surveillance, especially amid overlapping syndromes with dengue, Zika, and chikungunya. Furthermore, genomic surveillance might also contribute to deriving important conclusions regarding Orthobunyavirus dynamics. For example, the 2016 Ecuadorian cases potentially seeded the first cases of OROV in Colombia, as the 2017 Colombian OROV strain showed a close genetic relationship to the 2016 Ecuadorian strains, although the specific transmission dynamics remain unclear.[8]

To enhance outbreak response, it is essential to bolster molecular diagnostic capabilities and promote active epidemiological and genomic surveillance for *Culicoides* vectors.[4,6,8] Vector control strategies must be tailored to the biology of biting midges, which differ from those of mosquitoes, requiring specific larval habitat interventions. Public health education campaigns should aim to enhance community awareness, particularly in rural or forest-fringe settings where transmission is more likely to occur.[9]

The potential resurgence of OROV in Ecuador and other regions presents a critical opportunity to strengthen surveillance systems, enhance vector mapping, and prioritize research on transmission dynamics.[10] Enhanced regional coordination and investment in field, laboratory, and bioinformatic pipelines will be pivotal in addressing this emerging public health threat.[6]

https://doi.org/10.1016/j.jinf.2025.106544

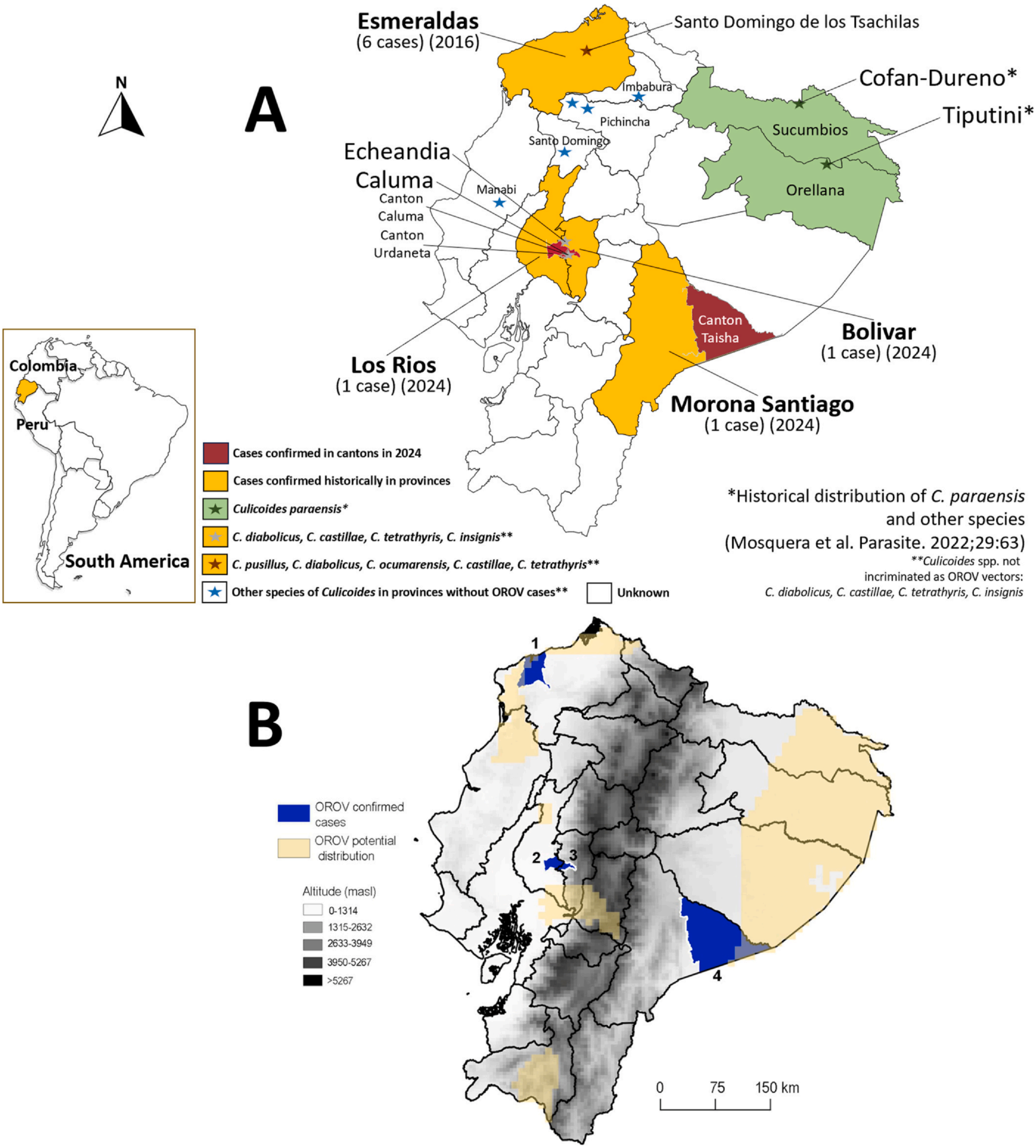

Fig. 1. OROV in Ecuador and its provinces, 2016–2024: cases and vectors (A) and OROV potential distribution developed via ecological niche modeling approaches (B). As of the end of 2024, four cantons (blue) have reported molecularly confirmed local cases of Oropouche fever, including Esmeraldas in 2016 (1) and Caluma (2), Urdaneta (3), and Taisha (4) in 2024. An ecological niche model based on human Oropouche virus (OROV) outbreaks[2,7] suggests the potential distribution of the virus in the country and potential areas for disease surveillance. masl = meters above sea level.

Funding

None.

Ethical statement

We confirm that the manuscript has been read and approved by all named authors and that no other persons have satisfied the criteria for authorship but are not listed. We further confirm that all have approved the order of authors listed in the manuscript. The material is original and has not been previously published elsewhere. Furthermore, we confirmed that no generative artificial intelligence (AI) or AI-assisted technologies were used in the writing process. As the data is retrospective, additional ethical approvals were not required.

Author contributions

JCN: Data curation, Investigation, Writing – original draft, writing – review & editing. APM: Data curation, Investigation, Writing – original draft, Writing – review & editing. DAFP: Formal analysis, Investigation, Writing – original draft, Writing – review & editing. DRA: Formal analysis, Investigation, Writing – original draft, Writing – review & editing. LNL: Formal analysis, Investigation, Writing – original draft, Writing – review & editing. JAS: Formal analysis, Investigation, Writing – original draft, Writing – review & editing. AJRM: Conceptualization, Data curation, Formal analysis, Investigation, Methodology, Project administration, Resources, Software, Supervision, Validation, Visualization, Writing – original draft, Writing – review & editing.

Data availability

Data is available upon reasonable request.

Declaration of Competing Interest

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.

Acknowledgments

This article has been registered in the Research Proposal Registration of the Coordination of Scientific Integrity and Surveillance of Universidad Cientifica del Sur, Lima, Peru, under the number PI-50-2025-0463.

References

1. Bello-Rodríguez BM, Vega-Jiménez J, Cañete R, Rodriguez-Morales AJ. *Emergence of Oropouche virus infection in Matanzas, Cuba, 2024. J Infect* 2025;**90**(4):106470.
2. Navarro J-C, Romero-Alvarez D, Escobar L, Aguilar PV. *Oropouche fever: A growing threat in Latin America.* In: Pujol FH, Paniz-Mondolfi AE, editors. Emerging Viruses in Latin America: Contemporary Virology. Cham: Springer Nature Switzerland; 2024. p. 161–73.
3. Wise EL, Márquez S, Mellors J, Paz V, Atkinson B, Gutierrez B, et al. *Oropouche virus cases identified in Ecuador using an optimised qRT-PCR informed by metagenomic sequencing. PLoS Negl Trop Dis* 2020;**14**(1):e0007897. https://doi.org/10.1371/journal.pntd.0007897
4. Mosquera JD, Zapata S, Spinelli G, Gualapuro M, León R, Augot D. *An updated list of the Culicoides (Diptera, Ceratopogonidae) fauna from Ecuador. Parasite* 2022;**29**:63.
5. Requena-Zúñiga E, Palomino-Salcedo M, García-Mendoza MP, Figueroa-Romero MD, Merino-Sarmiento NS, Escalante-Maldonado O, et al. *First detection of Oropouche virus in Culicoides insignis in the Ucayali region, Peru: Evidence of a possible new vector. medRxiv* 2024. https://doi.org/10.1101/2024.12.06.24318268
6. Rodriguez-Morales AJ, Drexler JF. *Re-emergence of Oropouche virus in Brazil and Latin America. Lancet Infect Dis* 2025;**25**(2):137–9.
7. 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**(1):47.
8. Gómez-Camargo DE, Egurrola-Pedraza JA, Cruz CD, Popuche D, Ochoa-Díaz MM, Guevara C, et al. *Evidence of Oropouche Orthobunyavirus Infection, Colombia, 2017. Emerg Infect Dis* 2021;**27**(6):1756–8. https://doi.org/10.3201/eid2706.204405
9. Rodriguez-Morales AJ, Navarro J-C, Paniz-Mondolfi A, Forero-Peña DA, Romero-Alvarez D, Naranjo-Lara L, et al. *Reemergence of Oropouche virus infection in Venezuela, 2025. N Microbes N Infect* 2025;**65**:101583. https://doi.org/10.1016/j.nmni.2025.101583
10. Culquichicón C, Cardona-Ospina JA, Patiño-Barbosa AM, Rodriguez-Morales AJ. *Bibliometric analysis of Oropouche research: impact on the surveillance of emerging arboviruses in Latin America. F1000Res* 2017;**6**:194.

Alfonso J. Rodriguez-Morales [a,b,*]
[a] *Faculty of Health Sciences, Universidad Científica del Sur, Lima, Peru*
[b] *Grupo de Investigación Biomedicina, Faculty of Medicine, Fundación Universitaria Autónoma de las Américas-Institución Universitaria Visión de las Américas, Pereira, Colombia*

Juan-Carlos Navarro
Grupo de Enfermedades Emergentes y Ecoepidemiología, Universidad Internacional SEK, Campus Miguel de Cervantes, Calle Albert Einstein s/n, Carcelén, 170120 Quito, Ecuador
Instituto de Zoología Tropical, Facultad de Ciencias, Universidad Central de Venezuela, Caracas, Venezuela

Daniel Romero-Alvarez
Grupo de Enfermedades Emergentes y Ecoepidemiología, Universidad Internacional SEK, Campus Miguel de Cervantes, Calle Albert Einstein s/n, Carcelén, 170120 Quito, Ecuador
Instituto Nacional de Biodiversidad (INABIO), Quito, Ecuador

Alberto Paniz-Mondolfi
Icahn School of Medicine at Mount Sinai, New York, NY, USA

David A. Forero-Peña
Faculty of Medicine, Universidad Central de Venezuela, Caracas, Venezuela
Biomedical Research and Therapeutic Vaccines Institute, Ciudad Bolivar, Venezuela

Laura Naranjo-Lara, Jose A. Suárez
Sistema Nacional de Investigación-SENACYT, Panama, Panama
Infectotropico, Panama, Panama

[*]Corresponding author at: Faculty of Health Sciences, Universidad Científica del Sur, Lima, Peru.
E-mail addresses: arodriguezmo@cientifica.edu.pe (A. Rodriguez-Morales), juancarlos.navarro@uisek.edu.ec (J.-C. Navarro), daniel.romero@uisek.edu.ec (D. Romero-Alvarez), Alberto.Paniz-mondolfi@mountsinai.org (A. Paniz-Mondolfi), vacter.cv@gmail.com (D. Forero-Peña), naranjo.laura1@gmail.com (L. Naranjo-Lara), jasuarez05@gmail.com (J. Suárez).