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Letter to the Editor

Reemergence of Oropouche virus infection in Venezuela, 2025

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As of March 2025, Oropouche virus (OROV) has expanded beyond the Amazon, with cases in Brazil, Bolivia, Colombia, Cuba, Ecuador, Guyana, Panama, and Peru since late 2022 [1]. By 2024, 16,128 cases were confirmed in the Americas, including four deaths (https://www. paho.org/es/arbo-portal/oropouche), notably with cases among international travelers in North America and Europe. In 2025 (EW 13), 6939 cases have been confirmed. OROV is mainly transmitted by biting midges, particularly *Culicoides paraensis* [2], and secondarily by *Culex quinquefasciatus, Coquillettidia venezuelensis, Mansonia venezuelensis*, and *Aedes serratus*, causing symptoms similar to those of dengue [3]. Severe cases resulted in deaths and potential congenital anomalies due to vertical transmission. The Pan American Health Organization (PAHO) emphasises the need for enhanced surveillance and preventive measures to curb its spread.

Previous studies in Venezuela documented the isolation of an *Orthobunyavirus oropoucheense* reassortant, Madre de Dios virus (MDDV), from a sick monkey during a 2010 epizootic in Anzoátegui State (Fig. 1) [4], underscoring the role of sylvatic cycles in local virus evolution and potential spillover to humans. In the context of the recent OROV epidemics in the Americas and the recommended OROV surveillance by PAHO, OROV was confirmed in Venezuela in March 2025. Here, we analysed the situation, historically reported vectors and distribution, as well as its current implications.

On March 26, the MoH of Venezuela reported the diagnosis of five cases of OROV infection, apparently originating from the states of Miranda (3 cases, in Petare [La Dolorita], Los Teques and Barlovento), Barinas (1 case), and Portuguesa (1 case) (Fig. 1). Petare is part of the Great Caracas Metropolitan Area. These cases were confirmed at the National Institute of Hygiene, Caracas. In Miranda state, previous reports [2] indicated the presence of *Culicoides paraensis* (Fig. 1). In Barinas state, other species of *Culicoides* have been historically reported, including *C. guttatus*, *C. insignis*, and *C. pusillus*; however, these have not been implicated as vectors of OROV in Venezuela to date (Fig. 1) [3]. Recently, OROV has been detected in *Culicoides insignis* in Peru (https://www.medrxiv.org/content/10.1101/2024.12.06.24318268v1). In Portuguesa state, no species of *Culicoides* have been reported in the national or international literature (Fig. 1) [3]. In addition to those states, reports

of *Culicoides paraensis* have been documented in Amazonas, Aragua, the Capital District, Falcon, Miranda, Vargas and Yaracuy (Fig. 1). Beyond Miranda, which now has OROV circulation in humans, there are at least four additional states in Venezuela with OROV's primary vector (Fig. 1). Notably, the states and localities where OROV has been reported overlap with the virus potential distribution as modelled using ecological niche modeling approaches [4] (Fig. 1).

The confirmation of OROV cases in Venezuela marks a significant development in the regional epidemiology of this emerging arbovirus [1]. With five cases originating from Miranda, Barinas, and Portuguesa states, and the identification of the primary vector, *Culicoides paraensis*, in various regions—including Miranda, Aragua, and Yaracuy—Venezuela is now clearly part of the expanding OROV transmission map in the Americas [2]. This reemergence has critical implications for national public health planning and international disease surveillance [1].

Nationally, the detection of OROV highlights the need to maintain arboviral surveillance and enhance diagnostic capacities (Table 1). While *C. paraensis* has been documented in a state with OROV circulation (Miranda), other *Culicoides* species not previously implicated as vectors are present in affected areas such as Barinas [2]. This gap in entomological data needs further research into vector competence and distribution to determine accurate and targeted vector control measures. The absence of reported *Culicoides* species in Portuguesa suggests either an underreporting issue or the involvement of alternate vectors or transmission dynamics, warranting comprehensive field studies [2].

Moreover, the historical isolation of the MDDV in a monkey in Anzoátegui in 2010 reveals the longstanding but underappreciated sylvatic transmission cycles of OROV in Venezuela [4]. These sylvatic reservoirs could serve as sources for future spillover events, particularly in rural or ecotonal areas where human-wildlife contact is increasing. This further strengthens the case for implementing a One Health approach that integrates human, animal, and environmental health perspectives into surveillance and response strategies (Table 1).

Internationally, the implications are profound. Venezuela has experienced significant outward migration in recent years, with over seven million people relocating to neighboring countries and beyond [5].

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Fig. 1. Oropouche in Venezuela: cases and vectors. **A.** Cases confirmed up to March 26, 2025, by the Ministry of Health of Venezuela, with historical distribution of vectors. **B.** Phylogenetic analysis of the L segment of OROV, which is the most informative taxonomically (74 sequences). **C.** OROVs potential distribution in Venezuela developed via ecological niche modelling approaches [4].

Many of these migrants have transited through the Darien Gap between Colombia and Panama—a region that has recently reported hundreds of OROV cases. In 2024, Panama reported 14 cases of OROV and 214 cases in 2025 (including one fatal case), up to epidemiological week 12. The cases were distributed as follows: 207 in Darien, 13 in East Panama, and 1 in Metro Panama. Despite the recent decrease in the number of migrants crossing in Darien Gap, given the newly confirmed circulation of OROV in Venezuela, Colombia and Ecuador, and the previous magnitude of population movement across the Darien Gap, it is plausible to hypothesise a potential epidemiological link [5]. Genomic surveillance studies are urgently needed to determine whether OROV strains detected in Panama are phylogenetically related to those circulating in Venezuela (Fig. 1) [4]. Such findings would highlight the role of human mobility in arboviral spread and emphasise the need for regional coordination in surveillance and response strategies (Table 1) [1].

Venezuela should prioritise strengthening laboratory capacities at national and regional levels to ensure prompt identification of OROV cases and other circulating *Orthobunyavirus oropoucheense*. Sentinel surveillance should be extended to include areas with known vectors and high human mobility, which can also benefit from the potential distribution of OROV in Venezuela [4] (Fig. 1). Educational outreach is also crucial in enhancing public awareness about OROV symptoms and vector avoidance measures (Table 1). International support, through organisations such as PAHO and neighboring countries, can bolster these efforts, especially given the virus's potential to spread into an epidemic.

In 2025, Venezuela stands at a pivotal point. With decisive action and regional cooperation, the country can contain the current spread, enhance its understanding of OROV ecology, and make meaningful contributions to global efforts against emerging arboviral threats.

CRediT authorship contribution statement

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Formal analysis, Investigation, Methodology, Resources, Software, Supervision, Validation, Visualization, Writing - original draft, Writing review & editing. Juan-Carlos Navarro: Conceptualization, Data curation, Formal analysis, Investigation, Methodology, Resources, Software, Supervision, Validation, Visualization, Writing - original draft, Writing - review & editing. Alberto Paniz-Mondolfi: Conceptualization, Data curation, Formal analysis, Funding acquisition, Investigation, Methodology, Resources, Supervision, Validation, Visualization, Writing - original draft, Writing - review & editing. David A. Forero-Peña: Conceptualization, Data curation, Formal analysis, Investigation, Methodology, Project administration, Resources, Software, Supervision, Validation, Visualization, Writing - original draft, Writing - review & editing. Daniel Romero-Alvarez: Conceptualization, Data curation, Formal analysis, Investigation, Methodology, Project administration, Resources, Software, Supervision, Validation, Visualization, Writing original draft, Writing - review & editing. Laura Naranjo-Lara: Conceptualization, Data curation, Formal analysis, Investigation, Methodology, Project administration, Resources, Software, Supervision, Validation, Visualization, Writing - original draft, Writing - review & editing. Jose A. Suárez: Conceptualization, Data curation, Formal analysis, Investigation, Methodology, Project administration, Resources, Software, Supervision, Validation, Visualization, Writing - original draft, Writing - review & editing.

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.

Table 1

Recommended actions for the diagnosis, surveillance, prevention, and control of OROV in Venezuela.

Category	Recommended Actions
Diagnosis	 Expand molecular diagnostic capabilities (RT-PCR) at regional laboratories beyond the National Institute of Hygiene. Implement syndromic surveillance protocols to detect dengue-like illnesses with atypical features, especially in states with presence of <i>Culicoides paraensis</i> (Fig. 1). Ensure the training of health workers in the clinical recognition of OROV infection, including neurological and congenital presentations.
Surveillance	 Promote the development and deployment of serological tests (ELISA, IgM, and IgG) and antigen detection tools. Establish sentinel surveillance sites in high-risk states (e.g., Miranda, Aragua, Yaracuy). Conduct entomological surveillance, focusing on <i>Culicoides paraensis</i> and potential alternative vectors, especially in areas such as Miranda, Barinas and Portuguesa. Integrate One Health approaches by including sylvatic and peri-
	 domestic animal surveillance. Develop and maintain a national OROV genomic surveillance program to track viral evolution and detect reassortants. Coordinate surveillance with neighboring countries, especially Colombia and Panama, to track migrant-linked transmission.
Prevention	 Launch nationwide vector control programs targeting <i>Culicoides</i> breeding habitats, such as organic matter-rich stagnant water. Educate the public on personal protection measures (e.g., repellents, window screens, reducing outdoor activity at dusk and dawn). Implement school and workplace-based educational campaigns, particularly in rural and peri-urban areas. Promote community participation in reducing midge breeding sites. Include OROV in arbovirus prevention materials and campaigns traditionally focused on dengue. Zika, and chikungunya
Control	 Develop and disseminate clinical management guidelines for OROV cases. Strengthen emergency response protocols for outbreaks in coordination with PAHO and regional health entities. Assess need for temporary mobility restrictions in outbreak zones. Explore the feasibility of integrated vector management (IVM) strategies that combine chemical, biological, and environmental control. Encourage academic and institutional research collaborations on OROV pathogenesis, ecology, and control methods, among other presented.

Data availability

Data is available upon reasonable request.

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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.

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