Letter to the Editor / Carta al editor

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# Emerging Threat of Orthobunyavirus oropouchense in Paraguay: The importance of Genomic Surveillance and Innovative Diagnostic Tools

## Amenaza emergente del ortobunyavirus Oropouche en Paraguay: La importancia de la vigilancia genómica y de herramientas diagnósticas innovadoras

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Dear Editor,

The *Orthobunyavirus oropoucheense* (formerly known as Oropouche virus, OROV) is emerging as a significant public health concern in South America. This arbovirus has shown a remarkable ability to evolve and adapt. OROV has been increasingly reported throughout numerous countries within South America, including Brazil, Peru, Bolivia, Colombia, Venezuela, Panama, and Ecuador[(1)]. Following a recent outbreak in Brazil during 2022 and 2023, a new viral lineage emerged due to intraspecies reassortment. This new lineage has been linked to an array of severe clinical manifestations, such as neurological complications, vertical (mother-to-child) transmission as a potential mode of transmission, and even fatalities. The typical clinical symptoms of OROV are similar to those of other arboviruses, such as Dengue, Chikungunya, and Zika virus. The emergence of new clinical manifestations highlights the critical need for effective virological surveillance. As such, OROV poses a serious threat to public health in Paraguay, thus underscoring a critical need to prepare through genomic surveillance and innovative diagnostic strategies[(2-4)].

Furthermore, the ecological and climate conditions in Paraguay heavily favour increased activity of the primary vector, *Culicoides paraensis*, thereby further exacerbating the dissemination of OROV. The existence of non-human reservoirs, such as sloths and primates, further elevates this risk, as these animals can facilitate spillover events. In addition, Paraguay shares open borders with Brazil and Bolivia, where OROV is currently endemic. This geographic proximity increases the likelihood of viral introduction via human travel or vector migration[(5,6)]. It is worth noting that, to date, there are no published reports confirming the presence or distribution of *Culicoides paraensis* in Paraguay, according to the *Servicio Nacional de Erradicación del Paludismo* (SENEPA), the national authority responsible for

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vector control and surveillance[7]. Given the species' role as the primary vector of OROV, this absence of entomological data highlights an important knowledge gap. Addressing this gap should be considered a priority within broader surveillance efforts, as understanding local vector dynamics is essential for accurately assessing the country's risk profile. Additionally, recent evidence indicates that *Culex spp.* mosquitoes, which are widespread in regions such as Paraguay, may exhibit potential competence as secondary vectors of OROV[8]. While *Culicoides paraensis* remains the principal vector, the involvement of *Culex* species in the transmission cycle warrants further laboratory and field investigation[9].

Genomic surveillance is essential for tracking viral evolution and detecting the emergence of novel, potentially more virulent strains. These data are crucial for informing public health responses and highlight the need for innovations in diagnostics, vaccine development, and targeted therapeutics[4,10,11].

Although reverse transcription polymerase chain reaction (RT-PCR) remains the diagnostic gold standard, its use is often limited in low-resource settings. Therefore, alternative rapid and field-deployable methods are gaining traction. Techniques such as reverse transcription loop-mediated isothermal amplification (RT-LAMP) and recombinase polymerase amplification (RT-RPA) provide efficient and sensitive diagnostics, making them valuable tools for early detection of OROV and similar viruses in remote or underserved areas[12,13]. However, these techniques should be thoroughly evaluated for sensitivity and specificity before being implemented in diagnostic settings to ensure their reliability and accuracy.

Although OROV has been detected in saliva, and this sample type shows great potential as a diagnostic tool[14,15] its use has not yet been systematically evaluated for clinical application. Further research is needed to validate its effectiveness. Saliva could serve as an alternative specimen when serum samples are unavailable, as illustrated in Figure 1.

The World Health Organization's Global Arbovirus Initiative emphasizes the importance of international collaboration in fighting emerging arboviral threats. Regional coordination, through shared genomic data, standardized surveillance strategies, and public education, is crucial for controlling the spread of viruses. Equally important is community engagement to promote awareness of OROV symptoms, transmission routes, and preventive measures[16].

In conclusion, the emergence of a novel, more virulent OROV lineage underscores the urgent need for robust entomological vector and genomic surveillance, rapid diagnostic innovations, and coordinated public health responses in Paraguay and across the region.

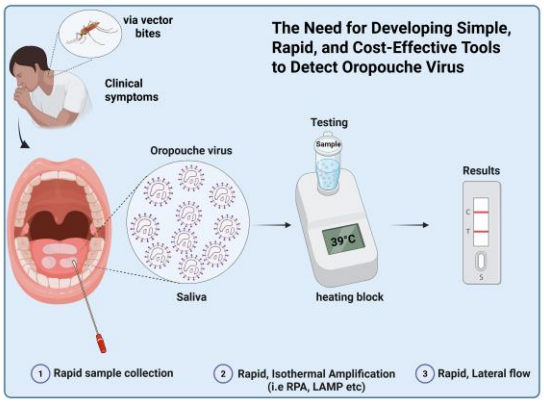


**Figure 1. Schematic Illustration of Point-of-Care Rapid Genomic Diagnostics**

This figure shows a proposed diagnostic process for detecting OROV using non-invasive saliva samples. Infected individuals may develop clinical symptoms after being bitten by a vector. Saliva is collected from symptomatic individuals using an oral swab (Step 1), then tested with isothermal amplification, such as Recombinase Polymerase Amplification (RPA) or Loop-Mediated Isothermal Amplification (LAMP), conducted at 39 °C with a simple heating device (Step 2). The amplified product is identified using a lateral flow strip (Step 3), where a positive result displays both control (C) and test (T) lines. This process helps create portable, affordable tools for early OROV detection in resource-limited areas. Illustration made with BioRender.com.

**PEER REVIEW:**

This article was evaluated through a double-blind peer review process, in accordance with the journal's editorial transparency policy. Of the reviewers who participated in the process, one authorized the publication of their name and review comments, while the other preferred to remain anonymous. The observations and suggestions from both reviewers were considered by the authors, who made the necessary modifications to arrive at the final published version. The full comments of the reviewer who authorized their disclosure can be accessed at the following link: Reviews

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