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OROPOUCHE FEVER -AN EMERGING PUBLIC HEALTH CONCERN IN TROPICAL REGIONS

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Abstract

Oropouche fever is an emerging infectious disease caused by the Oropouche virus and has become an increasing concern for public health. The virus is spreading more widely across regions, influenced by environmental, social, and ecological factors such as climate change, urbanization, and vector distribution. Its symptoms-fever, headache, muscle pain, and fatigue-closely resemble those of other Arboviruses, making accurate diagnosis essential for effective management and prevention. The disease is transmitted mainly through insect vectors, particularly biting midges and mosquitoes, which play a key role in viral proliferation. Once inside the human body, the virus invades host cells and triggers immune responses that contribute to symptom development. In some cases, severe complications may arise, including neurological effects, death, and risks to unborn babies, highlighting the need for timely detection. Diagnosing Oropouche fever remains challenging due to symptom overlap with other infections. Current Diagnostic methods, including serological and molecular techniques, have limitations in accuracy, availability, and accessibility, especially in low-resource settings. As a result, misdiagnosis is common. There are no specific antiviral drugs or approved vaccines available, so Supportive care remains the primary approach to patient management. Strengthening Disease surveillance, improving diagnostic tools, and developing vaccines are crucial steps in controlling the spread of OROV and reducing its impact on affected populations.

Keywords: *Oropouche fever, Oropouche virus, Arbovirus transmission, Diagnostic methods, Supportive care, Disease surveillance.*

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Introduction

Oropouche fever is driven by factors such as climate change, urban Expansion and inadequate healthcare infrastructure is a major concern as an arboviral disease now a days. The Oropouche virus (OROV), a member of the Peribunyaviridae family with a negative-sense RNA genome, is mainly transmitted through the bites of Culicoides paraensis midges and Aedes mosquitoes. It was initially discovered in Trinidad and Tobago in1955 after a febrile sickness outbreak. Numerous cases have been reported in a number of South and Central American nations, including Brazil, Peru, and Panama. Infections had transmitted greatly to previously uninteracted regions as well as areas with a history of outbreaks by the end of 2023. Cuba reported its first case scenario of Oropouche fever on 27 may 2024. People infected with the OROV virus may develop acute fever symptoms, which includes manifestations like headache, joint pain, and muscle aches. In around 50% of cases, these symptoms may recurred after a time period of recovery, usually a week or two weeks later. usually, OROV has been identified in some patients complaining with neurological manifestations, including meningitis and encephalitis. More recently in Cuba, an association was observed between OROV infection and Guillain-Barré syndrome (GBS). Individuals who tested positive for OROV via RT-PCR subsequently developed Guillain-Barré syndrome (GBS) about 10–11 days after the onset of acute febrile symptoms [1]. The virus is transmitted by mosquitoes such as Aedes serratus

and Culex quinquefasciatus. the three distinct, varying length segments that comprise the RNA genome of Orthobunyavirus, including OROV, are referred to as s(small), m(medium) and l(large). these components aid in the formation of the nucleocapsid, two outer glycoproteins, and RNA polymerase, which are the four structural proteins. OROV belongs to simbu serogroup which identifies 22 viruses [2].

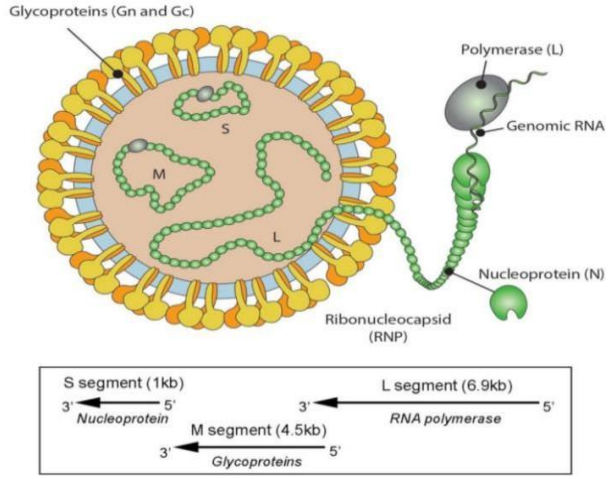


Fig 1: Structure and genome organization of an Orthobunyavirus

The Oropouche virus (OROV) has led to a significant result of Oropouche fever across the Americans, again marking the weaknesses in transmitting disease surveillance systems since October 2023. around 25,000 cases of Oropouche fever have been outreached as of the end of January 2025 [3]

Geographic spread and epidemiology

Oropouche fever is a widely knowing arboviral illness that mainly affects tropical and subtropical regions of Americas, specifically those in south and central America, because of its discovery in 1955, the virus has caused more than 30 major outbreaks, mainly in Brazil. Corresponding to recent reports, urbanization and environmental changes have caused the illness to change into highly populated in urban areas. The recent outbreaks in 2023 and 2024, which affected thousands of cases in Brazil, Peru, Panama, and other nations, revealed the virus ability to cause extensive morbidity. Urbanization and climate change are two of the primary factors of Oropouche fever's increased spread. Deforestation and rapid urbanization increase vector populations and human exposure, while warmer, wetter weather promotes midge breeding and boost transmission. Such ecological modifications has resulted in the geographical expansion of the disease beyond traditional rural and endemic zones into urban areas, enhancing the likelihood of regional and worldwide dispersion [4].

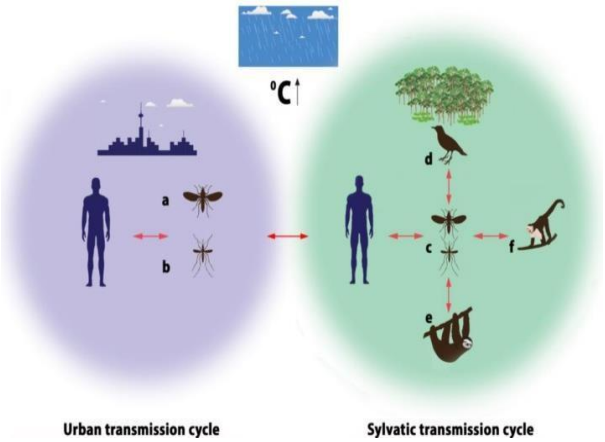
Oropouche fever is reported to have infected over 500,000 people since its discovery in 1955 with the majority of cases happening in Peru and the Brazil region especially in the amazon region [5].

Transmission Cycles and Vectors

OROV is naturally maintained through two separate cycles:

The urban cycle and the sylvatic cycle, each involving different potential vectors. In the urban cycle, Culex paraensis is the main vector, as shown by many studies. This species has occasionally caused significant outbreaks that have impacted up to 100,000 people. The notion that C. paraensis is the primary vector in urban settings is supported by both experimental and epidemiological data.. Its capacity to effectively transmit the virus, even when consuming blood with low viral concentrations, clearly indicates that it is the primary OROV vector. Although Culex quinquefasciatus is considered a minor vector for biting humans, OROV is the only Orthobunyavirus species found in this mosquito. This has been confirmed through the detection of OROV's small RNA in both human patients and the mosquitoes, using nested reverse transcription-polymerase chain reaction (RT-PCR). Research has shown that domestic animals such as cats, dogs, or chickens are not involved in the urban cycle, indicating that humans are the only vertebrate host. There is no evidence that OROV is transmitted directly from one person to another. Diagnostic tools for OROV have been developed using hemagglutinin antigens obtained from hamster brain and serum samples, which are used in epidemiological studies.

In the sylvatic cycle, various mammals, along with wild and domestic birds, serve as natural reservoir hosts for OROV. Antibodies to OROV have been detected in pale-throated three-toed sloths (Bradypus tridactylus), nonhuman primates like Capuchin monkeys (Saimiri species), black-and-gold howler monkeys (Alouatta caraya), black-tufted marmosets (Callithrix penicillata), rodents (Proechimys species), and birds from the families



Fringillidae, Taurapidae, and Columbidae, all of which are part of the transmission process of OROV [6].

FIG 2: An illustration of a vector-borne disease's urban and sylvatic transmission cycles

OROV relies on insect carriers to spread. Numerous vector types have been detected in both cycles of OROV

transmission, including mosquitoes like Aedes serratus, Culex quinquefasciatus, and Coquillettidia Venezuelans, as well as midges from the genus Culicoides, which may also play a key role in the spread of OROV. Culicoides paraensis is thought to be the main OROV vector among the Culicoides species. Because of its extensive range and high populations in Amazonian locations, C. paraensis is essential to maintaining the OROV transmission cycle. In addition, other Culicoides species and Culex mosquitoes, especially Culex quinquefasciatus, could serve as possible transmitters in urban settings [7].

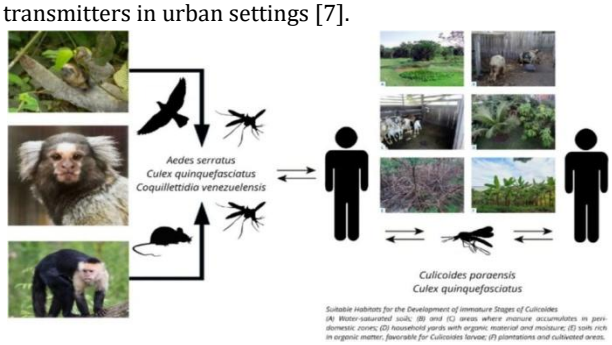


FIG -3: Diagram describing how a vector-borne disease spreads through mosquitoes (Aedes, Culex, and Coquillettidia), animal reservoirs, environmental conditions, and human infection pathways.

OROV infection cycle [4, 8]

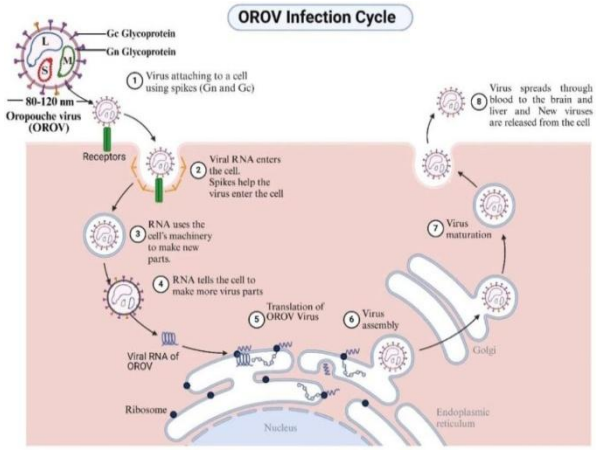


FIG-4: Diagram illustrating the Oropouche virus (OROV) infection cycle

Clinical manifestations

General symptoms

A variety of general symptoms were displayed by the patients, including fever, headache, chills, joint and muscular pain, disorientation, weariness or weakness, and neck or back pain.

Digestive tract symptoms

Digestive tract symptoms such as jaundice, nausea, vomiting, diarrhea, abdominal pain, loss of appetite, and difficulty swallowing can be caused by OROV infections. Apart from diarrhea and jaundice, other symptoms of digestive tract vary significantly from patient to patient.

Other digestive tract symptoms, with the exception of jaundice and diarrhea, varied considerably across patients.

Ocular Symptoms

Retro-orbital pain, light sensitivity, and eye redness were among the ocular problems. the most common of these was retro-orbital pain, which was followed by light sensitivity.

Respiratory symptoms

Four primary respiratory symptoms, including coughing, sore throats, and nasal congestion, were commonly observed in OROV-infected patients.

Breathing problems and shortness of breath, on the other hand, were less commonly reported symptoms.

Dermatological symptoms

OROV infection also led to skin-related symptoms, including rash, itching, and pallor. The most commonly reported skin symptom was pallor, followed by itching and rash [9].

Neurological symptoms are commonly seen in OROV infections, with headache, muscle pain, and eye discomfort being the most often reported [10].

Severe forms of the disease are indicated by significant menstrual bleeding, dark tarry stools, and gum bleeding. Additionally, it can result in neurological conditions including Guillain-Barre syndrome and meningitis, which is an inflammation of the membranes that protect the brain; birth defects are among the adverse effects of pregnancy. This illustrates how, during pregnancy, the disease can spread from mother to child.

According to reports, infections in mothers during pregnancy have been linked to birth defects, and laboratory tests found evidence of OROV infection in babies [11].

Diagnostic Challenges

Because of its mild symptoms, OROV fever is frequently misdiagnosed, or because of its comparable clinical features, it is confused with other illnesses as dengue, zika, chikungunya, malaria, leptospirosis, and yellow fever. Because symptoms like leucopenia and high alanine transaminase levels are not specific to OROV fever, blood testing like as hematology and full blood counts are not accurate in detecting the illness. Findings including pleocytosis, low glucose, and elevated total cerebrospinal fluid (CSF) proteins are not unique to OROV in situations where the illness affects the neurological system, rather, they are frequently observed with other viral infections.

ELISA detection of certain IgM and IgG antibodies during the acute stage of the infection is usually the first step in the diagnosis of OROV. Cross- reactivity with other arboviruses, however, can make it difficult to interpret the data. Within the first week following the onset of symptoms, OROV-specific plaque reduction neutralization tests and IgM-based serological tests are typically positive in people with a healthy immune system [12].

Table 1: Comparison of different diagnostic criteria for OROV fever

Diagnostic Method	Description	Advantages	Limitations
Molecular diagnosis (RT-PCR, qRT-PCR, met genomic sequencing)	Early infection detection of OROV RNA in serum, plasma, cerebrospinal fluid (CSF), saliva, and urine.	Fast detection, high sensitivity and specificity, helpful for early diagnosis.	Costly; requires skilled workers and specialized equipment.
Serological tests (IgM, IgG detection, ELISA, neutralization assays)	Identifies OROV antibodies in serum, plasma, and CSF, indicating recent or past infection.	Important for epidemiological research as it can verify prior exposure.	Delay in antibody response during early infection; cross-reactivity with other Simbu serogroup viruses.
Virus isolation	The virus is grown in cell cultures using patient samples.	Gold standard for detecting viral activity.	Time-consuming, requires biosafety level-3 facilities, not practical for routine diagnostics.
Histopathology & immunohistochemistry	Examines tissue samples for viral presence and immune response markers.	Provides insights into disease pathogenesis.	Limited to research use; not a primary diagnostic tool.

Treatment and vaccine research

Symptomatic treatment

There are currently no authorized antiviral medications specifically designed to treat OROV disease. Supportive care is therefore the main method of sickness management. Getting adequate sleep, drinking fluids to stay hydrated and utilizing painkillers and fever reducing drugs to reduce discomfort and elevated temperatures are all examples of common supportive care.

Hospitalization is advised for patients with severe symptoms so they can get ongoing monitoring and, if necessary, more sophisticated supportive care.

There are currently no antiviral drugs that have been proven to be successful in treating OROV infection.

Several medications, including interferon alpha (IFN-alpha), mycophenolic acid (MPA), and ribavirin(RBV), have investigated for their ability to prevent OROV. Although ribavirin proved effective against two related viruses, the guama virus (GMAV) and the tacaiuma virus(TCMV), it was found to have no antiviral impact against OROV in laboratory tests [14].

Paracetamol and other antipyretic drugs are used as the main treatment for the disease in order to reduce fever and muscle aches.

Pain killers or Non-steroidal anti-inflammatory medicines are not prescribed because; they tend to be causes increase the risk of blood loss. It is difficult to keep subjects well-hydrated, especially those with chronic symptoms. To treat less pain related to joints and muscles, gentle pain relievers are prescribed, and the rest is suggested. Subjects, especially with chronic clinical manifestations, should be monitored closely for any complications, such as neurological issues, though these are not common.

Health care service is not required provided until there are complications like chronic dehydration or any other infections that may cause later. However, Oropouche fever is often not well-known to both the public and healthcare workers in regions where it is routine. A lack of awareness about this disease can result in incorrect diagnoses and ineffective management, making it harder to effectively manage and treat the illness [15]. Modification of Climatic changes has been spread of virus and, consequently, the development of pathogens [16].

Prevention is still the most important way to control diseases caused by arboviruses. At the moment, there are no vaccines that have been approved for use, and any potential vaccines are not yet ready for implementation. They are still in the early research phase and have not entered human testing. The ongoing appearance and return of OROV highlight the complex difficulties associated with arboviral diseases in the 21st century [17].

Healthcare system impact

OROV has the potential to become a major public health issue because it can infect a wide variety of hosts and vectors, survives in different environmental conditions, can lead to serious illnesses, and has strains that can infect humans, which may vary in serotype. OROV is a typical example of a neglected tropical disease that requires urgent attention to assess and minimize its potential impact on health [18].

Surveillance and Public Health Strategies

1. Surveillance and data sharing: Strengthening early detection systems through integrated community-based surveillance and digital health tools enhances response efficiency. Leveraging artificial intelligence and machine

learning can predict outbreak hotspots and facilitate timely interventions.

2. Vector management: Targeted control of vectors such as Culicoides midges and mosquitoes using environmentally sustainable methods-habitat modification, biological control, and judicious use of insecticides-are critical for reducing transmission.

3. Public education and community participation: Educating communities about transmission routes, preventive behaviors (e.g., use of bed nets, protective clothing, repellents), and involving local populations in control efforts promote behavioral changes that reduce disease spread.

4. Vaccination Development: Prioritized research and development of effective and accessible vaccines are essential. Once available, equitable distribution in high-risk areas can greatly diminish infection rates.

5.Environmental and ecological interventions: Ecological strategies, such as habitat management to reduce breeding sites and fostering natural predators, provide sustainable vector control without excessive reliance on chemicals.

6. Healthcare infrastructure and research: Strengthening healthcare systems, training health workers, and advancing diagnostics are vital for timely diagnosis and management of cases.

7. International and Cross-Border Collaboration: Sharing data, resources, and best practices at global and regional levels enhances preparedness, especially as climate change may expand vector habitats, increasing exposure risk across previously unaffected regions.

Future Directions

1. Diagnostic and Surveillance

Improve diagnostic tools to rapidly differentiate OROV from dengue, chikungunya, zika, etc. Strengthen surveillance endemic and at-high risk regions (latin america, caribbean). Implement integrated one health surveillance combining human, animal, and vector monitoring.

2. Vector Biology and Transmission

Determine primary and secondary vector species. Confirm the role of culicoides paraensis vs. Mosquitoes (eg. Culex quinquefasciatus, aedes serratus, coquillettidia venezuelensis). Conduct vector competence studies under field and lab settings. Assess contribution of urban vs. Sylvatic transmission cycles including role of culex in densely populated settings. Investigate host reservoirs (sloths, primates, birds) and their interface with human outbreaks.

3. Clinical and Epidemiological Research

Determine risk factors for severe disease (age, comorbidities, prior immunity to related viruses). Conduct longitudinal cohort studies in affected regions to track inicidence and immunity over time.

4. Genomic And Pathogenesis Studies

Potential for vertical transmission, congenital effects, and neurological disease. Maintain genomic surveillance of circulating strains to detect future re-assortment events early.

5. Preventive and therapeutic intervention

Accelerate vaccine research.

Explore antiviral testing for treatment of severe cases.

Enhance vector control strategies targeting culicoides midges and mosquitoes, tailored to local ecology. Promote community engagement for outbreak prevention (use of protective clothing, repellents, and housing improvements.

6. Modelling and Preparedness

Use models to guide resource allocation and outbreak response plans. Ensure sustained research and policy attention beyond epidemic peaks to avoid repeating boom and bust cycles seen with other arboviruses [19].

Conclusion

Oropouche fever represents an increasingly significant public health concern in tropical regions due to its expanding geographic distribution, epidemic potential, and capacity to cause severe neurological complications. The lack of specific antiviral treatments and vaccines, combined with under-diagnosis and limited healthcare infrastructure in affected areas, exacerbates its impact on vulnerable populations.

Effective management requires integrated surveillance, vector control, community engagement, and strengthened healthcare systems. Continued research and investment into diagnostic tools, therapeutics, and vaccine development are critical to mitigating future outbreaks. Heightened awareness and preparedness at local, regional, and global levels are essential to address the growing threat posed by Oropouche virus in tropical environments. Addressing these gaps through sustained research and resource allocation will be crucial to prevent Oropouche fever from evolving into a wider epidemic with severe health and socioeconomic consequences.

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Conflicts of Interest

The authors declare no conflicts of interest.

Author Contribution

All are contributed equally

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Ethical Considerations and Inform Consent

Not Applicable.

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