Position Statement

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Oropouche virus

Background

Oropouche virus (OROV) is an arbovirus belonging to the family *Peribunyaviridae*, genus *Orthobunyavirus*, with a segmented single-stranded RNA genome. It is spread by infected biting midges and mosquitoes and maintained in sylvatic and urban cycles where the vectors exist.

OROV is a neglected arthropod-borne virus that has caused outbreaks of Oropouche fever in Central and South America since at least the 1950s. Oropouche fever has recently re-emerged in Brazil, with rapid geographical expansion to other areas of Latin America, in association with enhanced transmissibility and pathogenicity. In 2024, a total of 16,239 confirmed OROV cases, including 4 deaths, were reported across 11 countries and 1 territory in the Americas. The surge of OROV was driven by genetic reassortment, where a new viral lineage emerged by exchanging genomic segments between co-circulating strains. This process enhanced viral fitness, transmissibility and geographic expansion outside the Amazon basin. There has been sustained transmission in 2025 and 2026.

OROV disease was reported for the first time in travellers returning to England, Wales and Northern Ireland in 2025, with 3 imported cases linked to travel to Brazil.[1,2]

At this time, there have been no reported cases of OROV transmission via substances of human origin (SoHO).

Epidemiology, pathogenesis, infection dynamics and clinical characteristics relevant to SoHO safety

OROV is endemic in parts of Central and South America. A new lineage has recently emerged through reassortment of co-circulating strains, leading to increasing incidence and geographical spread in the Americas. Infection is primarily associated with presence in or travel to affected areas and exposure to insect vectors.

[1] Houston H, et al (2025). Will you do the fandango? Oropouche virus reaches the UK. J Infect, 91(5), 106630

[2] GOV.UK | UKHSA | Travel-associated infections in England, Wales and Northern Ireland: 2025 (accessed 21 October 2026)

It is estimated that roughly 60% to 80% of infections result in clinically apparent self-limiting disease, while severe disease and neuroinvasive complications (such as meningitis or encephalitis) occur in a very small fraction of cases (under 2% to 4%). The incubation period can range from 1 to 10 days. Exact population-wide incidence rates remain poorly defined due to underreporting and overlap of symptoms with other co-circulating mosquito-borne viruses. The Pan American Health Organization (PAHO) has reported 3 confirmed deaths directly attributed to OROV across the Americas during the recent outbreak cycle.

According to PAHO and the World Health Organization (WHO), while vertical transmission has been demonstrated by detection of viral RNA and antibodies in foetal and placental tissues, definitive population-level causality for specific birth defects is still under active investigation alongside other co-circulating arboviruses.

From a SoHO safety perspective, OROV RNA has been detected in asymptomatic blood donors and can persist in whole blood for longer than in plasma or serum. Viral RNA has also been identified in peripheral blood mononuclear cells, suggesting a potential cell-associated phase of viraemia. However, no cases of transfusion transmission have been reported and the link between viral RNA detection and infectivity remains unclear.

Significant knowledge gaps remain regarding pathogenesis, duration of infectivity, component-specific transmission risk and correlates of protective immunity. Nevertheless, asymptomatic infection, detectable viraemia in donors, and prolonged persistence in blood highlight a theoretical risk of transmission via SoHO that warrants ongoing surveillance and assessment.

Risk mitigation

Current UK donor selection measures are likely to mitigate much of the potential risk from OROV, as travel to endemic regions and exposure to tropical arboviral diseases are already considered within existing geographical risk assessments and donor deferral criteria. Donor selection measures relating to malaria and American trypanosomiasis (Chagas disease) provide additional risk mitigation because areas affected by OROV substantially overlap those where these measures already apply. Donors returning from affected areas who develop compatible symptoms, or receive a diagnosis of OROV infection, would also be excluded from donation.

Enveloped viruses are susceptible to pathogen reduction methods in use at this time; therefore, the current manufacturing processes for medicinal products will reduce OROV in materials.

There are no commercially available NAT or serological assays available in the UK.

There are currently no licensed vaccines or specific antivirals available. Treatment is symptomatic and supportive, depending on the manifestation of disease.

Given the high clinical benefit of certain SoHO types (e.g. haematopoietic stem cells) weighed against an as yet unquantifiable risk of transmission, a risk assessment is permitted for donor clearance and release of donations; decisions are made in conjunction with the transplant team and the prospective recipient, as per other similar situations.

Conclusion and recommendations

Existing measures for other mosquito-borne viruses offer acceptable risk mitigation at the moment, but the addition of OROV to the mosquito-borne viruses guideline entry will be informed by data acquired through formal monitoring by the Standing Advisory Committee on Transfusion Transmitted Infection (SACTTI).

OROV will continue to be monitored through horizon scanning, specifically following data on sustained transmission, further geographical expansion (primary vector presence exclusively in the Western Hemisphere), correlates of clinical outcomes (particularly congenital abnormalities) and the availability of screening and diagnostic assays. Currently, entries in the Geographical Disease Risk Index (GDRI) for regions with OROV risk overlap with risks for Dengue and Chikungunya viruses; therefore, there is a potential reduction in OROV risk due to GDRI exclusion of donors.



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