

3. Forshey BM, Guevara C, Laguna-Torres VA, Cespedes M, Vargas J, Gianella A, et al. Arboviral etiologies of acute febrile illnesses in Western South America, 2000–2007. *PLoS Negl Trop Dis*. 2010;10:4:e787. PubMed
4. Manock SR, Jacobsen KH, de Bravo NB, Russell KL, Negrete M, Olson JG, et al. Etiology of acute undifferentiated febrile illness in the Amazon basin of Ecuador. *Am J Trop Med Hyg*. 2009;81:146–51.
5. Wood DE, Salzberg SL. Kraken: ultrafast metagenomic sequence classification using exact alignments. *Genome Biol*. 2014;15:R46. <http://dx.doi.org/10.1186/gb-2014-15-3-r46>
6. Weidmann M, Rudaz V, Nunes MRT, Vasconcelos PFC, Hufert FT. Rapid detection of human pathogenic orthobunyaviruses. *J Clin Microbiol*. 2003;41:3299–305. <http://dx.doi.org/10.1128/JCM.41.7.3299-3305.2003>
7. Farajollahi A, Fonseca DM, Kramer LD, Marm Kilpatrick A. “Bird biting” mosquitoes and human disease: a review of the role of *Culex pipiens* complex mosquitoes in epidemiology. *Infect Genet Evol*. 2011;11:1577–85. <http://dx.doi.org/10.1016/j.meegid.2011.08.013>
8. Márquez S, Carrera J, Pullan ST, Lewandowski K, Paz V, Loman N, et al. First complete genome sequences of Zika virus isolated from febrile patient sera in Ecuador. *Genome Announc*. 2017;5:e01673–16. <http://dx.doi.org/10.1128/genomeA.01673-16>
9. Zambrano H, Waggoner JJ, Almeida C, Rivera L, Benjamin JQ, Pinsky BA. Zika virus and Chikungunya virus coInfections: a series of three cases from a single center in Ecuador. *Am J Trop Med Hyg*. 2016;95:894–6. <http://dx.doi.org/10.4269/ajtmh.16-0323>
10. Robinson ML, Manabe YC. Reducing uncertainty for acute febrile illness in resource-limited settings: the current diagnostic landscape. *Am J Trop Med Hyg*. 2017;96:1285–95. <http://dx.doi.org/10.4269/ajtmh.16-0667>

Address for correspondence: Emma L. Wise, Public Health England Porton–NIS, PHE Porton Down Manor Farm Road, Salisbury, Wiltshire SP4 0JG, UK; email: emma.wise@phe.gov.uk

etymologia

Oropouche [o'ro-poo"che] Virus

Ronnie Henry and Frederck A. Murphy

In September 1955, a virus was isolated from a 24-year-old forest worker from the community of Vega de Oropouche, near the town of Sangre Grande, on the island of Trinidad (country: Trinidad and Tobago), who presented with fever, backache, and cough, which resolved spontaneously after 3 days. The virus was isolated from the patient’s blood by intracranial inoculation of suckling mice at the Trinidad Regional Virus Laboratory. Five years later, the virus was isolated from *Coquillettidia venezuelensis* (Theobald) mosquitoes collected ~30 miles away in the Bush Bush Forest. The urban vector was later identified as the midge *Culicoides paraensis*, but the sylvatic vector remains unknown. Virus has been isolated from the three-toed sloth, which is believed to be involved in the sylvatic transmission cycle.

The virus was shown to be unique but antigenically related to Simbu virus, which had recently been described from South Africa. It therefore became a member of the large family of bunyaviruses.¹

The virus, Oropouche virus, named in keeping with the tradition of designating arboviruses by using local geographic names, stems from the name of the village, a nearby swamp (wetland), and river. It derives from an Amerindian word, but the ancient meaning of the word is not clear.

Oropouche virus has since proven to be one of the most common arthropodborne viruses infecting humans in the tropics of the Western Hemisphere. Clinical signs of infection include headache, myalgia, arthralgia, and chills; no deaths have been reported. It has been estimated to have infected more than half a million persons in Brazil alone, and there have also been large outbreaks in Panama and Peru. In keeping with the recent emergence of other arboviruses such as West Nile, chikungunya, and Zika viruses, Oropouche virus is a candidate for possible further urban spread and therefore warrants increased surveillance and diagnostics.

¹In 2017, the International Committee on Taxonomy of Viruses (ICTV) reclassified the family *Bunyaviridae*, elevating the family to an order. The formal taxonomic placement of Oropouche virus is order *Bunyavirales*; family *Peribunyaviridae*; genus *Orthobunyavirus*; species; *Oropouche orthobunyavirus*.

Sources

1. Anderson CR, Spence L, Downs WG, Aitken TH. Oropouche virus: a new human disease agent from Trinidad, West Indies. *Am J Trop Med Hyg*. 1961;10:574–8. <http://dx.doi.org/10.4269/ajtmh.1961.10.574>
2. Travassos da Rosa JF, de Souza WM, Pinheiro FP, Figueiredo ML, Cardoso JF, Acrani GO, et al. Oropouche virus: clinical, epidemiological, and molecular aspects of a neglected orthobunyavirus. *Am J Trop Med Hyg*. 2017;96:1019–30.
3. Virus Taxonomy. V. The Classification and Nomenclature of Viruses. The Online (10th) Report of the International Committee on Taxonomy of Viruses (ICTV) [cited 2018 Mar 12]. <https://talk.ictvonline.org/taxonomy/>

Address for correspondence: Ronnie Henry, Centers for Disease Control and Prevention, 1600 Clifton Rd NE, Mailstop E03, Atlanta, GA 30329-4027, USA; email: boq3@cdc.gov

DOI: <https://doi.org/10.3201/eid2405.ET2405>