

## Emergence of West African Human T-Lymphotropic Virus 1aC Subgroup, Brazilian Amazon

Jean de Melo Silva, Emmily Myrella Vasconcelos Mourão, Enzo Miranda Santos, Luma Silva Mineiro, Paulo Henrique Rodrigues de Souza, Leonardo Calheiros de Oliveira, Jacqueline da Silva Batista, Giselle Moura Guimarães Marques, Carolina Rosadas de Oliveira, Graham P. Taylor, Antonio Carlos Rosário Vallinoto, Gemilson Soares Pontes

Author affiliations: Institute of Biological Science, Federal University of Amazonas, Manaus, Brazil (J. de Melo Silva, G.S. Pontes); Leônidas and Maria Deane Institute–ILMD/Fiocruz Amazônia, Manaus (E.M.V. Mourão); Foundation of Hematology and Hemotherapy of Amazonas, Manaus (E.M. Santos); National Institute of Amazonian Research, Manaus (L.S. Mineiro, P.H.R. de Souza, L.C. de Oliveira, J. da Silva Batista, G.M. Guimarães Marques, G.S. Pontes); Faculty of Medicine, Imperial College London, London, UK (C.R. de Oliveira, G.P. Taylor); National Centre for Human Retrovirology, St. Mary's Hospital, Imperial College Healthcare NHS Trust, London (G.P. Taylor); Federal University of Pará, Belém, Brazil (A.C.R. Vallinoto)

DOI: <https://doi.org/10.3201/eid3207.260372>

In a cross-sectional survey of 1,397 residents of Manaus, Brazil, we found a seroprevalence of 0.3% for human T-lymphotropic viruses (HTLVs) 1/2 and identified HTLV type 1aC by phylogenetic analysis. Those findings provide evidence of introduction of West African HTLV-1aC into the Brazilian Amazon and highlight regional limitations in genomic surveillance.

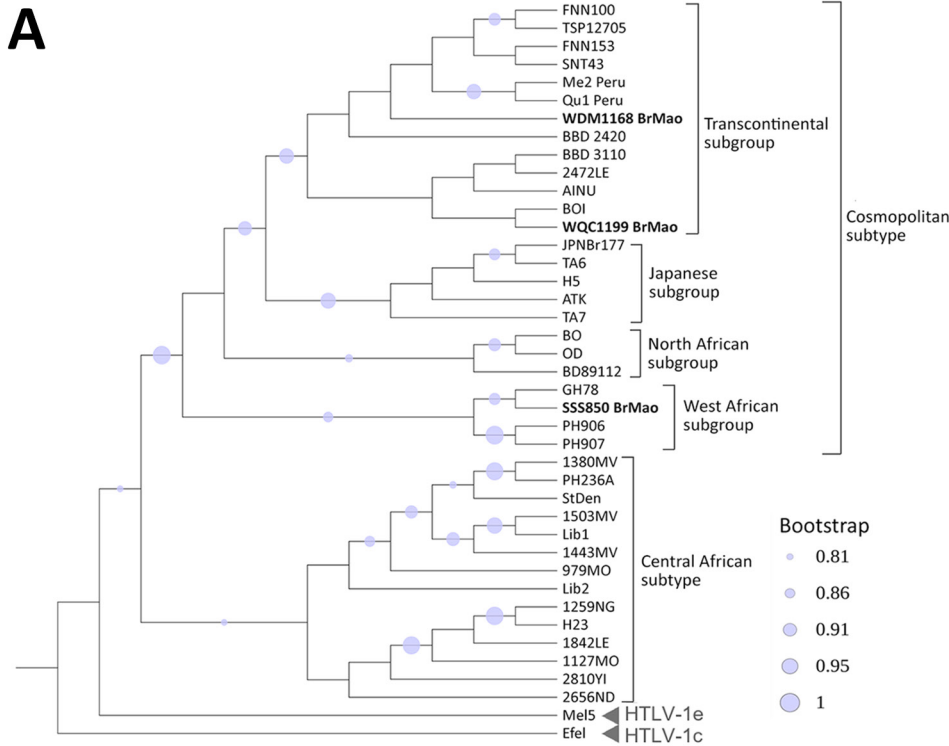
**E**pidemiologic surveillance is essential for defining the burden, geographic distribution, and transmission patterns of human T-lymphotropic viruses (HTLVs) 1 and 2 (HTLV-1/2), particularly in underserved settings such as the Brazilian Amazon. Although Brazil is estimated to harbor the largest absolute number of HTLV-1 infections worldwide, data from urban Amazonian populations remain scarce (1,2). In this context, molecular surveillance is also critical because HTLV genetic diversity is geographically structured, could have clinical relevance, and helps refine understanding of lineage distribution and viral dissemination (3). We therefore investigated HTLV-1/2 infection in the metropolitan region of Manaus in the Amazonas state of

Brazil and performed phylogenetic and phylogeographic analyses.

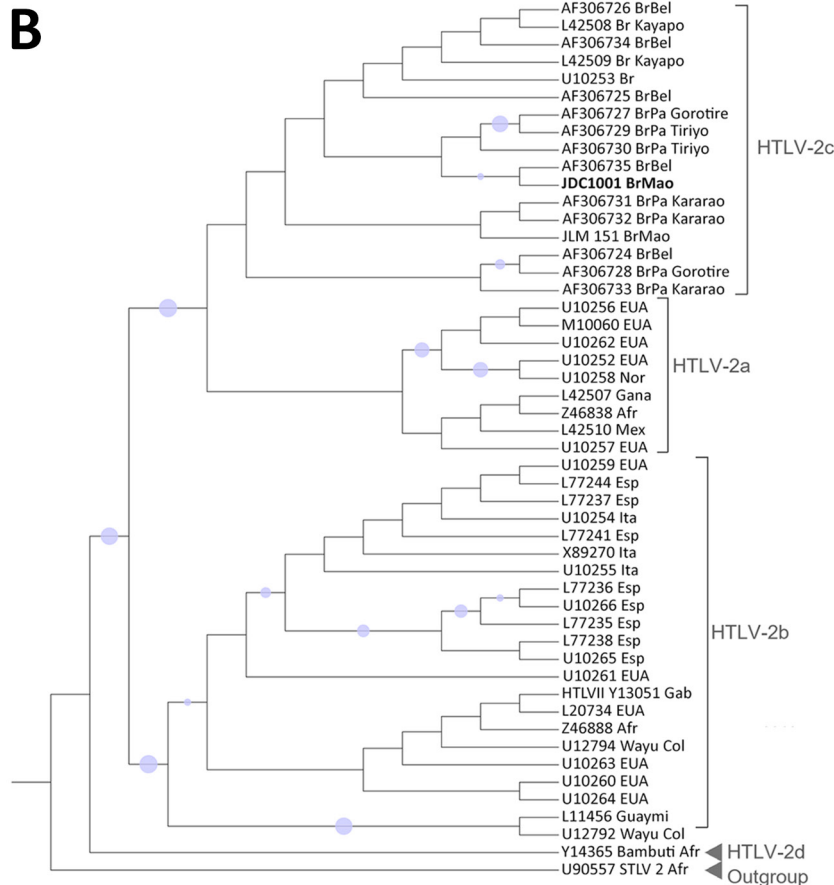
During May 2021–November 2023, we conducted a cross-sectional study of 1,397 residents of metropolitan Manaus recruited by convenience sampling across different city zones at universities, community centers, polyclinics, and primary healthcare units. Eligible participants were Manaus residents  $\geq 7$  years of age who voluntarily agreed to participate and provided written informed consent; for minors, we obtained parental or guardian consent and assent when applicable. We screened plasma samples for HTLV-1/2 antibodies by ELISA and confirmed seroreactive samples by Western blot or line immunoassay; indeterminate samples underwent molecular testing. We collected sociodemographic and behavioral data through a standardized questionnaire.

We amplified the 5' long terminal repeat (LTR) region of HTLV-1 (579 bp) and HTLV-2 (788 bp) by nested PCR and sequenced the amplicons by Sanger sequencing. We inferred phylogenetic relationships by maximum-likelihood analysis in MEGA12 (<https://www.megasoftware.net>) using the Kimura 2-parameter model with 1,000 bootstrap replicates and a geographically diverse panel of HTLV-1 and HTLV-2 reference sequences retrieved from GenBank from a previously assembled dataset. We deposited sequences generated in this study into GenBank (accession nos. PV647910 for sequence WDM1168\_BrMao, PV647909 for sequence WQC1199\_BrMao, PV647908 for sequence SSS850\_BrMao, and PV742404 for sequence JDC1001\_BrMao). To investigate the timing and geographic history of HTLV-1 lineages, we performed Bayesian time-scaled phylogenetic and discrete phylogeographic analyses in BEAST X version 10.5 (<https://beast.community>).

Overall HTLV-1/2 seroprevalence was 0.3% (95% CI 0.11%–0.73%; 4/1,397 participants), comprising 3 HTLV-1 and 1 HTLV-2 infections. All seropositive participants were  $>40$  years of age and shared a profile of socioeconomic vulnerability: 75% were female, earned no more than minimum wage, had only elementary education, lacked marital partnerships, and relied on government assistance (Appendix, <https://wwwnc.cdc.gov/EID/article/32/7/26-0372-App1.pdf>). Phylogenetic analysis classified sequence SSS850\_BrMao as HTLV-1aC, the West African subgroup, providing evidence of this lineage in the Brazilian Amazon (Figure 1, panel A). The remaining isolates were HTLV-1aA (WDM1168\_BrMao and WQC1199\_BrMao) and HTLV-2c (JDC1001\_BrMao), indicating co-circulation of distinct HTLV lineages in this population (Figure 1).

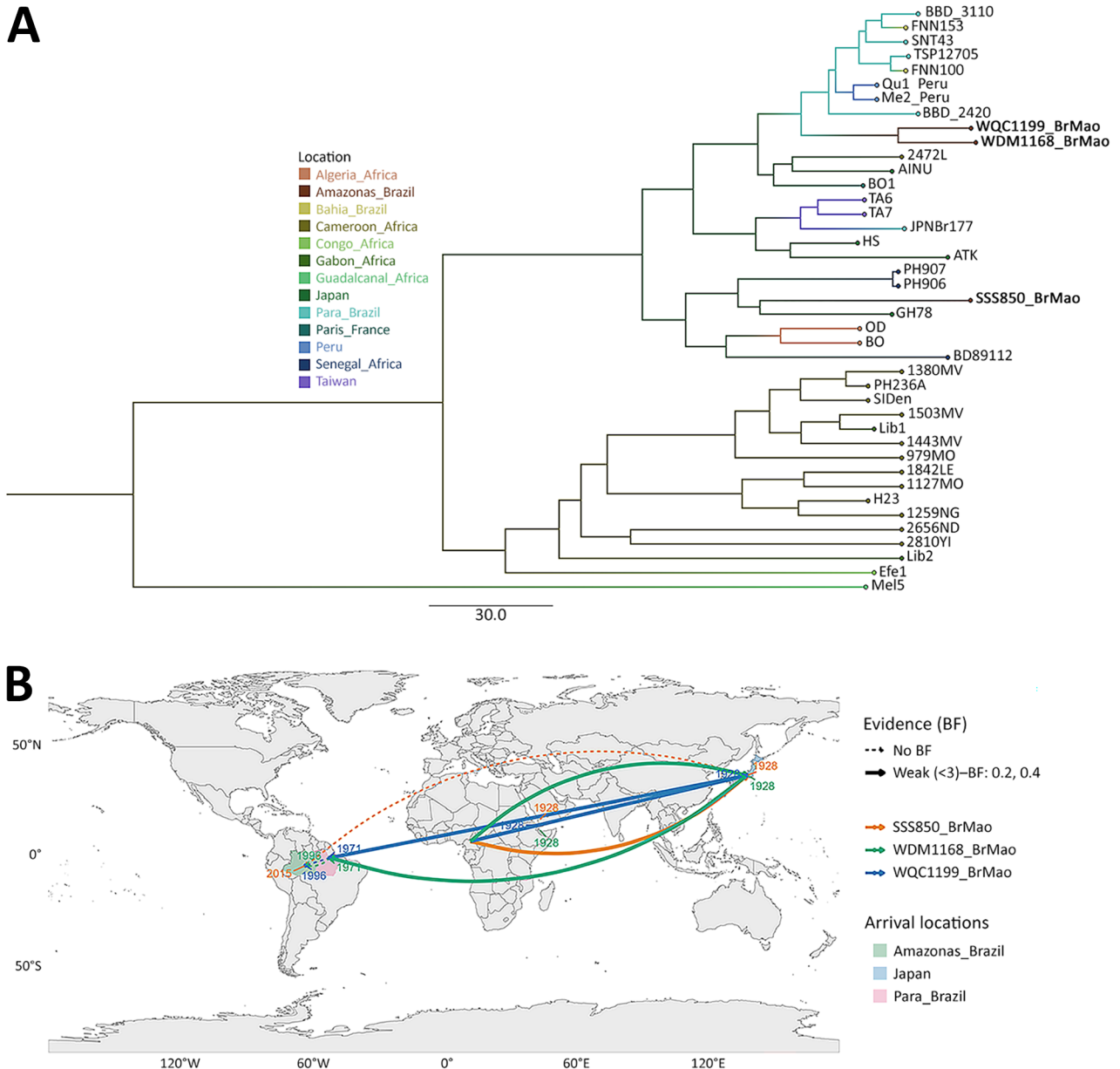


**Figure 1.** Phylogenetic tree of HTLV isolates in study of emergence of West African HTLV-1aC subgroup, Brazilian Amazon. A) HTLV-1 sequences obtained in this study (bold text) were analyzed with 38 reference sequences from GenBank. The Manaus isolates clustered within the Cosmopolitan subtype, including the Transcontinental subgroup (WDM1168\_BrMao and WQC1199\_BrMao) and the West African subgroup (SSS850\_BrMao). B) The HTLV-2 sequence identified in Manaus (JDC1001\_BrMao, bold text) was analyzed with 49 reference sequences from GenBank (accession numbers provided) and clustered within subtype HTLV-2c. Trees were inferred using the maximum-likelihood method under the Kimura 2-parameter substitution model. The best-scoring trees (log-likelihood  $-14,610.1$  for panel A and  $-2,247.45$  for panel B) were selected through heuristic searches initiated with neighbor-joining and maximum parsimony starting topologies. Branch support was assessed with 1,000 bootstrap replicates. HTLV, human T-lymphotropic virus.



After we identified the HTLV-1aC lineage, we performed Bayesian time-scaled phylogenetic and discrete phylogeographic analyses to infer its introduction and evolutionary history (Figure 2). Our results demonstrate that strain SSS850\_BrMao clusters

robustly within the HTLV-1aC clade, supporting its introduction into Amazonas around 2015 without evidence of intermediate dispersal through Pará. In contrast, 2 HTLV-1aA sequences clustered with reference sequences from Japan, indicating a separate



**Figure 2.** Time-scaled phylogeny and discrete phylogeographic diffusion of HTLV-1 lineages in study of emergence of West African HTLV-1aC subgroup, Brazilian Amazon. A) Time-calibrated maximum clade credibility tree inferred in BEAST version 10.5 (<https://beast.community>) from the long terminal repeat (LTR) dataset (3 sequences from this study plus reference sequences), using sampling year as tip date, a strict molecular clock, and discrete geographic-state reconstruction under a continuous-time Markov chain model with Bayesian stochastic search variable selection. Branches and tips are colored by inferred location (see key); bold text indicates sequences generated in this study. B) Spatiotemporal diffusion reconstructed from Markov jumps. Trajectory colors correspond to each Manaus lineage: orange, SSS850\_BrMao; green, WDM1168\_BrMao; blue, WQC1199\_BrMao. Numbers indicate posterior median year of first arrival (labels shown for years  $\geq 1970$ ; Cameroon→Japan step,  $\approx 1928$ , is retained for context). Line style indicates support: dashed, no Bayers factor recovered; solid, weak support ( $<3$ ; here, 0.2–0.4). Shaded polygons indicate inferred arrival locations (Amazonas and Pará states, Brazil, and Japan). HTLV, human T-lymphotropic virus.

introduction into northern Brazil via Pará ( $\approx 1971$ ) followed by spread to Amazonas ( $\approx 1996$ ). Together, those findings reveal  $\geq 2$  subtype-stratified introductions and identify HTLV-1aC as an epidemiologically relevant lineage in the region. However, because the phylogeographic inferences were based on a  $\approx 579$ -bp 5' LTR region fragment, they should be interpreted cautiously.

We observed a HTLV-1/2 prevalence in metropolitan Manaus, lower than estimates from other regions of Brazil, including Salvador and Mato Grosso do Sul (4,5). However, comparisons should be made with caution because sampling strategies and population composition differ across studies. Beyond prevalence, the key finding was detection of HTLV-1aC. Although this subgroup has previously been reported in Brazil by restriction fragment length polymorphism analysis (6), our study provides phylogenetically supported evidence of HTLV-1aC's occurrence in the country and places it in phylogeographic context. This result broadens the known distribution of HTLV-1aC and suggests that viral diversity in northern Brazil may be greater than previously recognized, despite evidence that HTLV-1aA predominates nationwide (7,8). Phylogeographic analyses supported  $\geq 2$  subgroup-specific introductions into the region, highlighting HTLV-1aC as an epidemiologically relevant lineage. We also identified HTLV-2c in an urban resident, reinforcing evidence that this subtype is not restricted to Indigenous populations and might circulate across multiple epidemiologic settings in northern Brazil (9,10).

The first limitation of our study is that we used convenience sampling at multiple sites, rather than a population-based design. Therefore, the sample might not fully represent the city's general population. The small number of positive participants precluded robust inference on risk factors or transmission routes. Phylogeographic reconstruction was further constrained by use of a short 5' LTR fragment from a slowly evolving virus and by uneven regional sequence availability, reducing temporal and geographic resolution.

Despite those limitations, detection of HTLV-1aC in Manaus has surveillance relevance because rare lineages might remain unnoticed in settings with limited molecular monitoring. Broader epidemiologic surveillance combined with longer genomic regions and regionally representative sampling will be essential to refine lineage dispersion patterns, strengthen transmission hypotheses, and support HTLV prevention, diagnosis, and care policies tailored to the Brazilian Amazon.

### Acknowledgments

We thank the Amazonas State Research Support Foundation, the Coordination for the Improvement of Higher Education Personnel (CAPES), the National Council for Scientific and Technological Development (CNPq), the Pan American Health Organization, the World Health Organization, the Ministry of Health, and the Ministry of Science, Technology and Innovation for their support of this project. We also thank SEMSA (Municipal Health Department) and SES-AM (Amazonas State Health Department) for help with participant recruitment. In addition, we are grateful to the Federal University of Amazonas, as well as the staff of the laboratory of Virology and Immunology-INPA, for their valuable assistance, particularly with sample collection.

Ethical approval was granted by the National Commission for Ethics Research and the INPA Human Research Ethics Committee on October 21, 2020 (CAAE: 39320120.2.3000.0106).

The data that support the findings of this study are available from the corresponding author upon reasonable request.

This work was supported by the Amazonas State Research Support Foundation, the Coordination for the Improvement of Higher Education Personnel Brazil (grant nos. 88881.933595/2024-01 and PROCAD AMAZONIA 88881.200581/201801), and the National Council for Scientific and Technological Development (grant nos. 401569/2023-3 and 302935/2021-5).

J.M.S. conceived and designed the study, collected blood samples, performed laboratory assays, curated and analyzed data, and prepared the original draft. G.S.P. conceived and designed the study, supervised all activities, secured funding, managed the project, interpreted data, and contributed to writing and critical revision of the manuscript. A.C.R.V. secured funding, supported study oversight and data interpretation, and contributed to writing and revision of the manuscript. C.R.O. and G.P.T. contributed to the study design and data interpretation and also participated in writing and critical revision of the manuscript. J.S.B. and G.M.G.M. performed sample purification and HTLV-1/2 LTR amplicon sequencing, curated sequencing data, and supported laboratory quality control. E.M.S., E.M.V.M., L.S.M., P.H.R.S., and L.C.O. collected blood samples and field data and assisted with data curation. All authors reviewed and approved the final version of the manuscript.

### About the Author

Dr. de Melo Silva is a biomedical scientist with the Institute of Biological Science, Federal University of

Amazonas, Manaus, Brazil. His research interest is the epidemiology of viral infections, particularly emerging viruses, in the Brazilian Amazon.

## References

1. Brazil Ministry of Health. Clinical management guide for HTLV infection. 2021 [in Portuguese] [cited 2026 Feb 24]. <https://www.gov.br/aids/pt-br/central-de-conteudo/publicacoes/2021/guia-de-manejo-clinico-da-infeccao-pelo-htlv>
2. Rosadas C, Espinosa Miranda A, Gonçalves DU, Caterino-de-Araujo A, Assone T, Ishak R. Prevalence of HTLV-1/2 infection in Brazil [in Portuguese]. *Bol Epidemiol (Porto Alegre)*. 2020;51:25–33.
3. Furukawa Y, Yamashita M, Usuku K, Izumo S, Nakagawa M, Osame M. Phylogenetic subgroups of human T cell lymphotropic virus (HTLV) type I in the tax gene and their association with different risks for HTLV-I-associated myelopathy/tropical spastic paraparesis. *J Infect Dis*. 2000;182:1343–9. <https://doi.org/10.1086/315897>
4. Dourado I, Alcantara CJ, Barreto ML, Da M, Teixeira G, Galvão-Castro B. HTLV-I in the general population of Salvador, Brazil: a city with African ethnic and sociodemographic characteristics. *J Acquir Immune Defic Syndr*. 2003;34:527–31. <https://doi.org/10.1097/00126334-200312150-00013>
5. Amianti C, Bandeira LM, Cardoso WM, da Silva ASP, de Jesus MDS, Ibañez R, et al. HTLV infection in urban population from Mato Grosso do Sul, Central Brazil. *Retrovirology*. 2024;21:18. <https://doi.org/10.1186/s12977-024-00650-1>
6. Segurado AA, Biasutti C, Zeigler R, et al. Identification of human T-lymphotropic virus type I (HTLV-I) subtypes using restricted fragment length polymorphism in a cohort of asymptomatic carriers and patients with HTLV-I-associated myelopathy/tropical spastic paraparesis from São Paulo, Brazil. *Mem Inst Oswaldo Cruz*. 2002;97:329–33. <https://doi.org/10.1590/s0074-02762002000300009>
7. Afonso PV, Cassar O, Gessain A. Molecular epidemiology, genetic variability and evolution of HTLV-1 with special emphasis on African genotypes. *Retrovirology*. 2019;16:39. <https://doi.org/10.1186/s12977-019-0504-z>
8. Amoussa AER, Wilkinson E, Giovanetti M, de Almeida Rego FF, Araujo TH, de Souza Gonçalves M, et al. HTLV-1aA introduction into Brazil and its association with the trans-Atlantic slave trade. *Infect Genet Evol*. 2017;48:95–101. <https://doi.org/10.1016/j.meegid.2016.12.005>
9. Pontes GS, Ribeiro HHH, Toro DM, Moura Neto JP, Souza V, Almeida MEM, et al. HTLV-2 infection in Manaus, Brazil: first description of HTLV-2c subtype in an urban area of the Western Amazon region. *Rev Soc Bras Med Trop*. 2020;54:e20200066. <https://doi.org/10.1590/0037-8682-0066-2020>
10. Vallinoto ACR, Ishak MOG, Azevedo VN, Vicente AC, Otsuki K, Hall WW, et al. Molecular epidemiology of human T-lymphotropic virus type II infection in Amerindian and urban populations of the Amazon region of Brazil. *Hum Biol*. 2002;74:633–44. <https://doi.org/10.1353/hub.2002.0059>

Address for correspondence: Gemilson Soares Pontes, Laboratory of Virology and Immunology, National Institute of Amazonian Research (INPA), Av. André Araújo, 2.936–Petrópolis, Manaus, Amazonas, Brazil; email: pontesbm1@gmail.com or gemilson.pontes@inpa.gov.br

# Neurologic Alveolar Echinococcosis in Postpartum Zoo-Housed Gorilla, the Netherlands, 2024

Laura A.N. Derks, Marieke Opsteegh, Denise Hoek-van Deursen, Jorrit J. Hofstra, Christine Kaandorp-Huber, Jooske IJzer, Erik A.W.S. Weerts, Volker H. Hackert, Anna R. Tellegen, Vanessa X.N. Visser, Joke W.B. van der Giessen

Author affiliations: Centre for Infectious Disease Control, National Institute for Public Health and the Environment, Bilthoven, the Netherlands (L.A.N. Derks, M. Opsteegh, D. Hoek-van Deursen, J.J. Hofstra, J.W.B. van der Giessen); GaiaZOO, Kerkrade, the Netherlands (C. Kaandorp-Huber); Veterinary Pathology Diagnostic Centre, Utrecht University, Utrecht, the Netherlands (J. IJzer, E.A.W.S. Weerts); Public Health Service South Limburg, Heerlen, the Netherlands (V.H. Hackert); Faculty of Veterinary Medicine, Utrecht University, Utrecht, (A.R. Tellegen); Dutch Food and Consumer Product Safety Authority, Utrecht (V.X.N. Visser)

DOI: <http://doi.org/10.3201/eid3207.260136>

We report a case of postpartum alveolar echinococcosis in a zoo-housed gorilla in the Netherlands in 2024, with cerebral involvement causing neurologic symptoms. Infection was likely acquired via contaminated feed. This case highlights diagnostic challenges, public health risks, and the need for preventive feed hygiene and surveillance in endemic regions.

*Echinococcus multilocularis*, a zoonotic tapeworm with foxes as the main definitive host and rodents as intermediate hosts, was first detected in foxes in the Netherlands in 1996 (1) and is considered an emerging parasitic pathogen (2). Humans and other primates can be infected via contaminated food or fomites, risking potentially fatal alveolar echinococcosis (AE). We describe a case of neurologic AE in a postpartum, zoo-housed gorilla in the Netherlands, complicated by pregnancy and neonatal care.

In April 2024, a 25-year-old female western lowland gorilla (*Gorilla gorilla gorilla*), born in England and transferred to GaiaZOO (Kerkrade, the Netherlands) in 2013, gave birth to her second young. The gorilla had no prior health issues. After parturition, lethargy and intermittent anorexia developed, followed by intermittent neurologic symptoms in 1 arm (hemiplegia) and both legs (paraplegia).