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Reporting Summary

Nature Portfolio wishes to improve the reproducibility of the work that we publish. This form provides structure for consistency and transparency in reporting. For further information on Nature Portfolio policies, see our Editorial Policies and the Editorial Policy Checklist.

Statistics

For all statistical analyses, confirm that the following items are present in the figure legend, table legend, main text, or Methods section.

n/a	Confirmed	
☐	☒	The exact sample size (*n*) for each experimental group/condition, given as a discrete number and unit of measurement
☒	☐	A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
☐	☒	The statistical test(s) used AND whether they are one- or two-sided *Only common tests should be described solely by name; describe more complex techniques in the Methods section.*
☐	☒	A description of all covariates tested
☐	☒	A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons
☒	☐	A full description of the statistical parameters including central tendency (e.g. means) or other basic estimates (e.g. regression coefficient) AND variation (e.g. standard deviation) or associated estimates of uncertainty (e.g. confidence intervals)
☒	☐	For null hypothesis testing, the test statistic (e.g. *F*, *t*, *r*) with confidence intervals, effect sizes, degrees of freedom and *P* value noted *Give P values as exact values whenever suitable.*
☐	☒	For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
☒	☐	For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
☐	☒	Estimates of effect sizes (e.g. Cohen's *d*, Pearson's *r*), indicating how they were calculated

Our web collection on statistics for biologists contains articles on many of the points above.

Software and code

Policy information about availability of computer code

Data collection	no software was used
Data analysis	Geneious Prime v2024.0.7: Naveca, F.G., et al. Human outbreaks of a novel reassortant Oropouche virus in the Brazilian Amazon region. Nature medicine (2024). MAFFT v7: Katoh, K., Misawa, K., Kuma, K. & Miyata, T. MAFFT: a novel method for rapid multiple sequence alignment based on fast Fourier transform. Nucleic acids research 30, 3059-3066 (2002). IQ-TREE v2.1.1: Minh, B.Q., et al. IQ-TREE 2: New Models and Efficient Methods for Phylogenetic Inference in the Genomic Era. Molecular biology and evolution 37, 1530-1534 (2020). ModelFinder: Kalyaanamoorthy, S., Minh, B.Q., Wong, T.K.F., von Haeseler, A. & Jermiin, L.S. ModelFinder: fast model selection for accurate phylogenetic estimates. Nature methods 14, 587-589 (2017). FigTree v1.4.4 (https://github.com/rambaut/figtree/releases). TempEst v.1.5.3: Rambaut, A., Lam, T.T., Max Carvalho, L. & Pybus, O.G. Exploring the temporal structure of heterochronous sequences using TempEst (formerly Path-O-Gen). Virus evolution 2, vew007 (2016). BEAST 1.10 with BEAGLE library v.4: Suchard, M.A. & Rambaut, A. Many-core algorithms for statistical phylogenetics. Bioinformatics 25, 1370-1376 (2009). SPREAD v.1.0.7 software: Bielejec, F., Rambaut, A., Suchard, M.A. & Lemey, P. SPREAD: spatial phylogenetic reconstruction of evolutionary dynamics. Bioinformatics 27, 2910-2912 (2011). ggplot2, and naturalearth R packages: Wickham, H. ggplot2. Elegant Graphics for Data Analysis, (2016), GitHub. rnaturalearth. (2024) https://github.com/ropensci/rnaturalearth TRACER v1.7: Rambaut, A., Drummond, A.J., Xie, D., Baele, G. & Suchard, M.A. Posterior Summarization in Bayesian Phylogenetics Using Tracer 1.7. Systematic biology 67, 901-904 (2018).

TreeAnnotator v1.10: Yu, G., Smith, D., Zhu, H., Guan, Y. & Lam, T. ggtree : an R package for visualization and annotation of phylogenetic trees with their covariates and other associated data. Methods in Ecology and Evolution 8(2016).
GISAID: https://gisaid.org/

For manuscripts utilizing custom algorithms or software that are central to the research but not yet described in published literature, software must be made available to editors and reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Portfolio guidelines for submitting code & software for further information.

Data

Policy information about availability of data

All manuscripts must include a data availability statement. This statement should provide the following information, where applicable:

- Accession codes, unique identifiers, or web links for publicly available datasets
- A description of any restrictions on data availability
- For clinical datasets or third party data, please ensure that the statement adheres to our policy

All the OROV genomes generated in this study were deposited at GISAID under accession numbers EPI_ISL_19611792 - EPI_ISL_19611830 (https://doi.org/10.55876/gis8.241214tm).

Research involving human participants, their data, or biological material

Policy information about studies with human participants or human data. See also policy information about sex, gender (identity/presentation), and sexual orientation and race, ethnicity and racism.

Reporting on sex and gender	Biological atributtes
Reporting on race, ethnicity, or other socially relevant groupings	N/A
Population characteristics	Age
Recruitment	The samples processed were obtained anonymously from material exceeding the routine arbovirus diagnosis, according the case definition established by the Cuban Ministry of Health as part of the national clinical-epidemiological and laboratory surveillance to identify OROV transmission.
Ethics oversight	The study was reviewed and approved by Ethical committee of the Institute of Tropical Medicine, Pedro Kouri (CEI-IPK 54-24).

Note that full information on the approval of the study protocol must also be provided in the manuscript.

Field-specific reporting

Please select the one below that is the best fit for your research. If you are not sure, read the appropriate sections before making your selection.

☒ Life sciences ☐ Behavioural & social sciences ☐ Ecological, evolutionary & environmental sciences

For a reference copy of the document with all sections, see nature.com/documents/nr-reporting-summary-flat.pdf

Life sciences study design

All studies must disclose on these points even when the disclosure is negative.

Sample size	Real-time RT-PCR confirmed 147 Oropouche cases; 39 (26.5%) were selected for genomic characterization based on the Ct value (≤ 28.5), geographical location representativeness, and the sample collections was selected chronologically by epidemiologic week.
Data exclusions	Ct value > 28.5
Replication	N/A
Randomization	It is not relevant
Blinding	N/A

Reporting for specific materials, systems and methods

We require information from authors about some types of materials, experimental systems and methods used in many studies. Here, indicate whether each material, system or method listed is relevant to your study. If you are not sure if a list item applies to your research, read the appropriate section before selecting a response.

Materials & experimental systems

n/a	Involved in the study
☒	☐ Antibodies
☒	☐ Eukaryotic cell lines
☒	☐ Palaeontology and archaeology
☒	☐ Animals and other organisms
☒	☐ Clinical data
☒	☐ Dual use research of concern
☒	☐ Plants

Methods

n/a	Involved in the study
☒	☐ ChIP-seq
☒	☐ Flow cytometry
☒	☐ MRI-based neuroimaging

Plants

Seed stocks	N/A
Novel plant genotypes	N/A
Authentication	N/A