nature portfolio

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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<br>*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<br>*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 | Clinical, epidemiological, environmental and laboratory data were collected through REDCap databases, field investigation forms, and laboratory information systems. Viral genome sequencing data were generated using established laboratory workflows described in the Methods section. |
| Data analysis | Data analyses were conducted using Stata and R software. |

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 data supporting the findings of this study are available within the manuscript and Supplementary Information. All data generated and analysed during this study

will be made publicly available prior to publication. Relevant datasets, including viral genome sequences and associated metadata, will be deposited in appropriate public repositories, and accession numbers will be provided in the final published article.

## 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 | Participants of both sexes were included in the study. Sex was recorded as part of routine epidemiological surveillance and was incorporated into descriptive analyses where appropriate. No gender-based intervention or stratification was performed because the primary objectives focused on outbreak investigation, transmission dynamics, phylogeography, and environmental determinants of OROV transmission. |
| Reporting on race, ethnicity, or other socially relevant groupings | The study was conducted in Darién Province, Panama, a region composed of diverse populations including mestizo, Afro-descendant, Indigenous communities, and migrant populations. These social characteristics were considered important for describing the study population and understanding transmission dynamics. Classification was based on demographic information collected during surveillance activities and participant interviews. |
| Population characteristics | The study included 1,040 individuals recruited through integrated clinical and community-based surveillance activities conducted during the Oropouche virus outbreak investigation in Darién Province, Panama. Participants included symptomatic individuals seeking medical care, community contacts, household members, and participants enrolled through active surveillance activities. |
| Recruitment | Participants were recruited through passive surveillance at healthcare facilities, active community surveillance, household investigations, and enhanced outbreak response activities. The study design sought to capture the full spectrum of OROV infection, including symptomatic and asymptomatic individuals. |
| Ethics oversight | The study was approved by the Comité de Bioética de la Investigación del Instituto Conmemorativo Gorgas de Estudios de la Salud (ICGES), Panama, under the protocols cited in the manuscript. Written informed consent was obtained from all participants or their legal guardians before enrollment. |

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 | The study included 1,040 individuals tested for OROV infection as part of outbreak surveillance and investigation activities. Sample size was determined by outbreak occurrence and surveillance coverage rather than by prospective power calculations. |
| Data exclusions | No participants were excluded after enrollment except where laboratory results or metadata were incomplete and unsuitable for specific analyses. Exclusion criteria were predefined in the study protocol. |
| Replication | Multiple independent epidemiological, laboratory, genomic and environmental datasets were integrated to evaluate the outbreak. Findings were reproducible across analytical approaches. |
| Randomization | This was an observational surveillance and outbreak investigation study. Participants were not randomized. |
| Blinding | Blinding was not applicable because this was an observational epidemiological investigation. |

# 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 |

# Antibodies

Antibodies used: We used a comercial kit to detect IgM and IgG antibodies.

Validation: Validation of the comercial ELISA was assesed by Plaque reduction neutralization test as described in the supplementary material.

# Plants

Seed stocks: *Report on the source of all seed stocks or other plant material used. If applicable, state the seed stock centre and catalogue number. If plant specimens were collected from the field, describe the collection location, date and sampling procedures.*

Novel plant genotypes: *Describe the methods by which all novel plant genotypes were produced. This includes those generated by transgenic approaches, gene editing, chemical/radiation-based mutagenesis and hybridization. For transgenic lines, describe the transformation method, the number of independent lines analyzed and the generation upon which experiments were performed. For gene-edited lines, describe the editor used, the endogenous sequence targeted for editing, the targeting guide RNA sequence (if applicable) and how the editor was applied.*

Authentication: *Describe any authentication procedures for each seed stock used or novel genotype generated. Describe any experiments used to assess the effect of a mutation and, where applicable, how potential secondary effects (e.g. second site T-DNA insertions, mosiacism, off-target gene editing) were examined.*