

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

R version 4.3.2 (all code available in the supplementary material).
QGIS version 3.30.1-'s-Hertogenbosch

Data analysis

R version 4.3.2 (all code available in the supplementary material).
QGIS version 3.30.1-'s-Hertogenbosch
Packages: ggplot2 (version 3.4.4), factoextra (version 1.0.7), circlize (version 0.4.15), glmmTMB (version 1.1.9), usdm (version 2.1.7), dplyr (version 1.1.4), tidyr (version 1.3.0), GGally (version 2.2.1), geosphere (version 1.5.18), paletteer (version 1.6.0) and patchwork (version 1.2.0)

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 used are available in the Supplementary Data 1 folder. The code to repeat the data analysis is available in the Supplementary Code 1 folder

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

Reporting on race, ethnicity, or other socially relevant groupings

Population characteristics

Recruitment

Ethics oversight

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](https://www.nature.com/documents/nr-reporting-summary-flat.pdf)

Ecological, evolutionary & environmental sciences study design

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

Study description

This study compiles and analyses records of human introduced non-native mosquito species known to be vectors for human diseases. We performed a literature search for first records of these species on a global scale and assessed their temporal patterns, introduction pathways, geographical distributions, and the factors driving their spread. The study aims to understand the patterns and drivers of non-native mosquito introductions to inform future bio-security measures.

Research sample

In our data collection we included 186 disease vector mosquito species known to transmit pathogens to humans in the wild. Our data collection of regional first introductions resulted in 698 records in new regions of which 610 records lead to the species' establishment. These records were obtained from a literature search and are included in a comprehensive database detailing the species' first year of introduction, introduced region, and modes of introduction.

Sampling strategy

Sampling was based on documented first records of non-native mosquito species, compiled from scientific publications and databases. The selection criteria included species known to be vectors for human diseases in the wild, and records were standardized across 477 regions, including countries, the regional subdivisions of the six largest countries, and significant islands.

Data collection

Data was collected through a literature review conducted between March and December 2023. Search terms included combinations of mosquito species names, country names, and keywords related to introduction and invasion. Data were compiled into a database, including species names, year of first record, mode of transportation, establishment status, and sources of information.

Timing and spatial scale

Data collection was carried out from March to December in 2023. The first introduction record was from 1495 and the latest records from 2022. The spatial scale included 477 regions across all continents.

Data exclusions

We only considered records resulting from human mediated introductions or the natural secondary spread of populations originating from them (i.e., so-called non-native species). Records for which it was unclear if the species' appearance in a region was due to natural dispersal from native populations (in literature e.g., discovery of species) were not included in our database. This is described in the manuscript.

Reproducibility

The methods for data collection, including search strategies and criteria for inclusion, are fully documented in the methods to allow replication. The database created from the literature review, and the analysis R scripts for statistical modeling and along with all aggregated driver variables are publicly available on Zenodo at <https://doi.org/10.5281/zenodo.15731142>.

Randomization

n/a

Blinding

n/a

Did the study involve field work?

☐ Yes☒ No

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

Methods

- 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

- 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