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
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☑️ 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 coefficients), 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 wherever possible.

☑️ □ 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 for data collection.

Data analysis

For the ecological niche modelling analyses, we employed the boosted regression trees approach implemented in the R package “dismo” (version 1.3-8), and selected the optimal number of trees for the BRT models using a spatial cross-validation procedure based on five spatially separated folds generated with the “blockCV” R package (version 2.1.4). The alignment of genomic sequences was made using the program MAFFT version 7 ([https://mafft.cbrc.jp/alignment/server/](https://mafft.cbrc.jp/alignment/server/)) and manually edited using the program Geneious ([https://www.geneious.com](https://www.geneious.com)). Continuous phylogenographic and phyloecological inferences were performed with the Bayesian methods implemented in the open-source program BEAST version 1.10.4 ([https://beast.community/program](https://beast.community/program)) and the BEAGLE library (version 3) to improve computational performance ([github.com/beagle-dev/beagle-lib](https://github.com/beagle-dev/beagle-lib)). We used the program Tracer version 1.7 ([https://beast.community/tracer](https://beast.community/tracer)) to identify the number of sampled trees to discard as burn-in as well as to inspect the convergence and mixing properties of the BEAST outputs. We used the program TreeAnnotator version 1.10.4 ([https://beast.community/program](https://beast.community/program)) to obtain the maximum clade credibility tree. Subsequent dispersal statistics estimation and landscape phylogeographic analyses were implemented and performed with R functions available in the open-source package “seraphim” version 1.0 ([https://github.com/ddell/coursera](https://github.com/ddell/coursera)). The BEAST XML files of the continuous phylogeographic and skygrid analyses, as well as the R scripts and related files needed to run all the ecological niche modelling analyses, landscape phylogeographic testing analyses, and phyloecological simulations, are available at [https://github.com/ddell/coursera/lassa_speads](https://github.com/ddell/coursera/lassa_speads).

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.
All source data used in this study are available at https://github.com/sdellicour/lassa_spreads (DOI: 10.5281/zenodo.6989624). The sources of the different raster files used in this study are provided in Table S6. We obtained occurrence data for the Muridae family from the Global Biodiversity Information Facility (http://www.gbif.org), accessed 2019-07-19, GBIF occurrence downloads https://doi.org/10.15468/dl.cs3c41). For the M. natalensis species, we obtained occurrence data from the Global Biodiversity Information Facility (http://www.gbif.org, accessed 2019-07-19, GBIF occurrence downloads https://doi.org/10.15468/dl.harjyj1), the Integrated Digitized Biocollections (http://www.idigbio.org/portal (2020), Query: {"filtered": {"filter": {"and": [{"exists": {"field": "geopoint"}}, {"term": {"scientificname": "mastomys natalensis"}}]}}, 4348 records, accessed on 2020-01-04T05:40:06.945, contributed by 19 Recordsets), the Field Museum of Natural History Zoological collections (Field Museum of Natural History (Zoology) Mammal Collection https://collections-zoology.fieldmuseum.org/list?f%5B0%5D=ss_CatCatalog%3A%22Mammals%22&_ga=2.123662347.1070684726.1508778418-143671043.1493067972, accessed 2019-12-13), and the African Mammalia database (African Mammalia, http://projects.biodiversity.be/africanmammalia/search, accessed 2019-12-14). Full citations are provided in "Citations_rodent_occurrence_data.txt" available on the GitHub repository referenced above. This data set was supplemented with the data available in the scientific literature (search for term “Mastomys natalensis”, in PubMed and Google) for each record used in this analysis, the specific record or collection ID is specified in the file "Mastomys_natalensis_RK050820.csv" or "Muridae_family_allData_RK220819.csv", both available on the GitHub repository referenced above. The sources used to retrieve sampling coordinates for Lassa virus samples are listed in Table S5. For Lassa virus, occurrence data were obtained from the scientific literature (search for term “Lassa virus”, in PubMed and Google) and the source of each record used in this analysis is specified in the file “Lassa_virus_cases_RK070920.csv” available on the GitHub repository referenced above. The sources of the different raster files used in this study are provided in Table S6. Data for the environmental factors used in the BRT analyses was obtained from the Inter-Sectoral Impact Model Intercomparison Project phase 2b (ISIMIP2b, https://data.isimip.org/). LASV sequences analysed in the present study were available on GenBank before November 20, 2019, except for the LASV sequences from cases sampled during the year 2019 in Nigeria, which are are publicly available on the website virological.org (https://virological.org/t/lassa-virus-sequencing-in-nigeria-final-field-report-75-samples/291). Accession numbers of selected genomic sequences are listed in the file "LASV_all_the_metadata.csv" available on the GitHub repository referenced above. All processed data (BRT models, BRT predictions, phylogeographic inferences, dispersal statistics estimations, and seraphim analyses) generated in this study are also available on the GitHub repository referenced above.

### 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
- [x] Ecological, evolutionary & environmental sciences

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

In our study we performed ecological niche modelling and phylogeographic analyses to model how the endemic range of Lassa virus (LASV) may evolve in the next five decades in response to climate change, human population growth, and land use changes. Specifically, (i) we performed ecological niche modelling analyses for Lassa virus and its reservoir host, Mastomys natalensis to identify the determinants of ecological suitability for LASV, (ii) we projected the future ecological suitability for LASV across Africa, (iii) we estimated the human population living in areas suitable for LASV based on human population projections, (iv) we used a continuous phylogeographic approach to reconstruct the dispersal history of LASV in West Africa and estimate the virus mean lineage dispersal velocity, (v) we used a first landscape phylogeographic approach to test the impact of main waterways on the dispersal history of LASV lineages, (vi) we used a second landscape phylogeographic approach to test the impact of environmental factors on the dispersal velocity of LASV lineages, and (vii) we used phylogeographic simulations to illustrate how a slow lineage dispersal velocity may limit the spatial extent of LASV spread following a potential introduction event.

#### Research sample

The rodent data sets used in the BRT analyses consist in 2,504 Mastomys natalensis spatial occurrence records and in 10,806 Muridae occurrence records. The M. natalensis dataset is meant to represent the locations where this rodent species is present. The Muridae dataset is meant to serve for sampling pseudo-absences and represents locations where the Muridae family is present. We obtained occurrence data for the Muridae family from the Global Biodiversity Information Facility (http://www.gbif.org, accessed 2019-07-19, GBIF occurrence downloads https://doi.org/10.15468/dl.cs3c41). We obtained occurrence data for the M. natalensis species from the Global Biodiversity Information Facility (http://www.gbif.org, accessed 2019-07-19, GBIF occurrence downloads https://doi.org/10.15468/dl.harjyj1), the Integrated Digitized Biocollections (http://www.idigbio.org/portal (2020), Query: {"filtered": {"filter": {"and": [{"exists": {"field": "geopoint"}}, {"term": {"scientificname": "mastomys natalensis"}}]}]}, 4348 records, accessed on 2020-01-04T05:40:06.945, contributed by 19 Recordsets), the Field Museum of Natural History Zoological collections (Field Museum of Natural History (Zoology) Mammal Collection https://collections-zoology.fieldmuseum.org/list?f%5B0%5D=ss_CatCatalog%3A%22Mammals%22&_ga=2.123662347.1070684726.1508778418-143671043.1493067972, accessed 2019-12-13), and the African Mammalia database (African Mammalia, http://projects.biodiversity.be/africanmammalia/search, accessed 2019-12-14). The BRT analyses were based on several environmental factors: harmonised present-day and future climate, land cover and population data available through the Inter-Sectoral Impact Model Intercomparison Project phase 2b (ISIMIP2b, https://data.isimip.org/). They are meant to represent the mean values observed over a spatial grid at a 0.5 decimal degrees resolution throughout Africa for the environmental factors stated above at present-time (1986-2005) and projected over the next decades.
### Data collection

We obtained data for the environmental factors used in the BRT analyses from the Inter-Sectoral Impact Model Intercomparison Project phase 2b (ISIMIP2b, [https://data.isimip.org/](https://data.isimip.org/)). We collected Mastomys natalensis species occurrence data from publicly available databases and museum collections: from the Global Biodiversity Information Facility ([http://www.gbif.org](http://www.gbif.org), accessed 2019-07-19), GBIF Occurrence Download: [https://doi.org/10.15468/dl.hrjyj1](https://doi.org/10.15468/dl.hrjyj1), the Integrated Digitized Biocollections ([http://www.idigbio.org](http://www.idigbio.org), available online from the public GBIF database ([http://www.gbif.org](http://www.gbif.org), accessed 2019-07-19, GBIF Occurrence Download: [https://doi.org/10.15468/dl.cs3c41](https://doi.org/10.15468/dl.cs3c41)).

We collected all LASV sequences available online on Nov 20, 2019 on the NCBI Nucleotide database (keywords: “lassa NOT mopeia NOT natalensis”; n = 729 L and 1202 S sequences; database accessed on October 31, 2019) and combining it with sequence data collected during 2019 in Nigeria ([https://virological.org/t/2019-lassa-virus-sequencing-in-nigeria-final-field-report-75-samples/291](https://virological.org/t/2019-lassa-virus-sequencing-in-nigeria-final-field-report-75-samples/291)).

### Timing and spatial scale

We used environmental data for the African continent and the following analysis windows: analysis window (1986-2005, 2021-2040, 2041-2060, and 2061-2080). The choice of the different time windows was arbitrary but they were defined to cover distinct periods of time. Mastomys natalensis and Muridae occurrence data were collected in Africa up to 2019 and are meant to represent all known spatial records of M. natalensis and Muridae available at the time of the analysis. Genomic sequences for LASV were collected in West Africa between 1969 and 2019 and are meant to represent all Lassa virus genomes publicly available at the time of the analysis that (1) have been identified in natural settings (in rodents or humans), and (2), for which the collection time is known.

### Data exclusions

There was no data exclusion.

### Reproducibility

(No experiment was performed)

### Randomization

There was no group allocation performed in our study.

### Blinding

This study is not a clinical research study and does not involve human subjects thus blinding was not necessary.

### Did the study involve field work?

No

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### 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 |
| ✔   | Human research participants |
| ✔   | Clinical data |
| ✔   | Dual use research of concern |

### Methods

| n/a | Involved in the study |
|-----|------------------------|
| ✔   | ChIP-seq              |
| ✔   | Flow cytometry        |
| ✔   | MRI-based neuroimaging |