

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 (<i>n</i>) 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 <i>Only common tests should be described solely by name; describe more complex techniques in the Methods section.</i>
☐	☒ 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. <i>F</i> , <i>t</i> , <i>r</i>) with confidence intervals, effect sizes, degrees of freedom and <i>P</i> value noted <i>Give P values as exact values whenever suitable.</i>
☐	☒ 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 <i>d</i> , Pearson's <i>r</i>), 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	Data collection included use of the UCSC Genome Browser (https://genome.ucsc.edu/) and the NCBI whole genome database (https://www.ncbi.nlm.nih.gov/genome/) to download previously published genomes, which were added to our dataset using the Basic Local Alignment Search Tool (BLAST; https://blast.ncbi.nlm.nih.gov/Blast.cgi).
Data analysis	All genetic data were analyzed using Custom R scripts available on GitHub [https://doi.org/10.5281/zenodo.15707386] and/or using the following software, programs, and packages: MAFFT v7.023b, Geneious v.2022.0.1, IQ-TREE v.2.1.3, SVDquartets v.1.0 (as implemented in PAUP* v.4.0), ASTRAL v.5.7.8, RAXML-ng v.1.0, MCMCTree v.1.0 (as implemented in PAML v.4.9), TACT v.0.5.0, MitoZ v.3.6, PhyloNet v.3.8, QulBL v.1.0 (https://github.com/miriammiyagi/QulBL), and four R packages: phytools v.1.9, hisse v.2.1, RPANDA v.2.2, and evobiR v.1.1.

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 DNA sequence data have been deposited in the NCBI SRA under BioProject ID PRJNA957840 [<https://www.ncbi.nlm.nih.gov/bioproject/PRJNA957840/>]. Sample information including origins, permits, and contact information for specimen collections are provided in Supplementary Data 1. Probes used for DNA sequencing library preparation are found in Supplementary Data 2. Previously published genomes were added to our dataset and were obtained through the NCBI; their accession numbers are provided in Supplementary Table 9. Source data for Supplementary Fig. 1 can be found in Supplementary Data 3. Source data for Supplementary Figs. 11 and 18 can be found in Supplementary Data 4. DNA sequence alignments, gene trees, and analytical input files have been deposited on FigShare [<https://doi.org/10.6084/m9.figshare.28699742>].

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	We obtained genetic data from 161 primate individuals, with particular focus on the suborder Strepsirrhini, following the Anchored Hybrid Enrichment Protocol (Lemmon et al. 2012). This protocol resulted in a targeted phylogenetic dataset comprising 334 nuclear loci with an average length of 3,339 base pairs (bp; range: 158–6,985 bp; total concatenated alignment length: 1,108,850 bp). These genetic samples were used to estimate (a) phylogenetic trees, (b) the timing of divergence among species, (c) rates of diversification, and (d) patterns of interspecific gene flow or hybridization.
Research sample	Our sampling included all strepsirrhine genera and 71% of all currently recognized species (50% of all loriforms and 79% of all lemurs). Information about individual samples and their origins can be found in Supplementary Data 1.
Sampling strategy	We obtained sequence data from n = 1-5 individuals per species for as many different species in the primate suborder Strepsirrhini as possible. This sample size is sufficient for the phylogenetic analyses we performed.
Data collection	Samples were collected from a wide variety of sources (see Supplementary Data 1 and below). For museum-sourced samples, metadata about each sample was obtained from specimen tags. For field-collected samples, metadata about each sample were recorded using pen and paper. Genetic sequences were obtained following the Anchored Hybrid Enrichment Protocol (Lemmon et al. 2012). All genetic library preparation and sequencing was performed by the Translational Lab in the College of Medicine at Florida State University. These data were supplemented with additional genetic data retrieved from previously published whole genomes available through the UCSC Genome Browser or the National Center for Biotechnology Information (NCBI; see Methods).
Timing and spatial scale	All genetic samples were obtained from individuals reflecting modern timescales (i.e., sampled within the last 30 years). The localities

Timing and spatial scale	Of these samples reflect each species' known geographic range, i.e., terrestrial regions of Madagascar (lemurs) and of Africa and Southeast Asia (lorisiforms).
Data exclusions	All genetic sequences were included in preliminary phylogenetic analyses. After evaluating the effects of missing data on our phylogenetic results (see Methods), we observed that individuals with > 50% missing data produced spurious branch lengths. As a result, 17 individuals with > 50% missing data were excluded from further analyses that relied on accurate branch length estimation (i.e., analyses of divergence time, diversification rates, and hybridization).
Reproducibility	We published all genetic data in a public repository (NCBI SRA BioProject ID PRJNA957840) and provided detailed information on samples (Supplementary Data 1) and analyses (Methods and https://github.com/keverson25/StrepsirrhineAHes) to ensure that our study can be reproduced by other scientists.
Randomization	Our study was based on phylogenetic analysis of all available samples, thus randomization was not relevant.
Blinding	Blinding was not relevant in our study, as our aim was to sequence and evaluate the evolutionary relationships among as many known species of strepsirrhines as possible.

Did the study involve field work? ☒ Yes ☐ No

Field work, collection and transport

Field conditions	Of the 161 genetic samples that we analyzed in this study, 12 were collected in the field. These samples were collected between the years 2000 and 2018 in a variety of seasons and field conditions. Specific field conditions (e.g., temperature and rainfall) were not relevant to the objectives of this study and were not recorded. Additional information about these samples can be found in Supplementary Data 1.
Location	The 12 field samples were collected from the following localities in Madagascar: Montagne d'Ambre, Anjiamangirana, Sahafina, Lokobe, Mariarano, Ankaramibe, Mantadia, Antsaonjo, Ankarafa, Mangabe, and Andrafiarena.
Access & import/export	For the 12 samples that were collected from wild animals in the field, approvals were granted by Madagascar National Parks, the Ministère de l'Environnement et du Développement Durable de Madagascar and the Committee for Environmental Research (permit numbers 004-MEF/SG/DGEF/DADF/SCB, 072-MINENV.EF/SG/DGEF/DADF/SCB, 100-MINENV.EF/SG/DGEF/DPB/SCBLF, 124/09/MEFT/SG/DGEF/DSAP/SLRSE, 130/16/MEEF/SG/DGF/DAPT/SCBT.Re, 137/13/MEF/SG/DGF/DCB.SAP/SCB, 186/11/MEF/SG/DGF/DCB.SAP/SCB, 78/17/MEEF/SG/DGF/DSAP/SCB.Re, 79/17/MEEF/SG/DGF/DSAP/SCB.Re, 82/18/MEEF/SG/DGF/DSAP/SCB.Re). Samples were exported under CITES permit 19US36412D/9 and imported to the U.S. under U.S. Fish and Wildlife Service permit numbers 2019NW2505894-905. Capture and handling procedures followed routine protocols approved by the Institute of Zoology, University of Veterinary Medicine Hannover Foundation.
Disturbance	All 12 collected individuals were promptly released after tissue sample collection, and local and international guidelines were followed to minimize environmental disturbance (including guidelines from Madagascar National Parks, the Ministère de l'Environnement et du Développement Durable de Madagascar and the Committee for Environmental Research, the International Primatological Society, and the International Union for the Conservation of Nature).

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

Animals and other research organisms

Policy information about [studies involving animals](#); [ARRIVE guidelines](#) recommended for reporting animal research, and [Sex and Gender in Research](#)

Laboratory animals	We obtained genetic sequence data from 15 individuals that were raised in captivity at the Duke Lemur Center (Duke University, Durham, North Carolina). Information about these individuals can be found in Supplementary Data 1.
Wild animals	The majority of our genetic samples (149 out of 161) were obtained from museum collections, the Duke Lemur Center, or previously published datasets. However, 12 individuals were collected from the wild through field sampling. All 12 collected individuals were promptly released after tissue sample collection, and were captured and handled in full accordance with the legal guidelines of Madagascar (including Madagascar National Parks, the Ministère de l'Environnement et du Développement Durable de Madagascar and the Committee for Environmental Research) and the ethical guides of the International Primatological Society and the International Union for the Conservation of Nature. Further information on all genetic samples, including the years, localities, collectors, and permit numbers associated with field samples, can be found in Supplementary Data 1.
Reporting on sex	Sex information was not relevant in our study. All of our analyses were based on genetic sequence data, and none of the genetic loci we evaluated were sex-specific.
Field-collected samples	No wild animals collected from the field were held in captivity for laboratory work. Samples were taken in the field and individuals were immediately released.
Ethics oversight	[Repeated from the fieldwork access and import/export section above:] For the 12 samples that were collected from wild animals in the field, approvals were granted by Madagascar National Parks, the Ministère de l'Environnement et du Développement Durable de Madagascar and the Committee for Environmental Research (permit numbers 004-MEF/SG/DGEF/DADF/SCB, 072-MINENV.EF/SG/DGEF/DADF/SCB, 100-MINENV.EF/SG/DGEF/DPB/SCBLF, 124/09/MEFT/SG/DGEF/DSAP/SLRSE, 130/16/MEEF/SG/DGF/DAPT/SCBT.Re, 137/13/MEF/SG/DGF/DCB.SAP/SCB, 186/11/MEF/SG/DGF/DCB.SAP/SCB, 78/17/MEEF/SG/DGF/DSAP/SCB.Re, 79/17/MEEF/SG/DGF/DSAP/SCB.Re, 82/18/MEEF/SG/DGF/DSAP/SCB.Re). Samples were exported under CITES permit 19US36412D/9 and imported to the U.S. under U.S. Fish and Wildlife Service permit numbers 2019NW2505894-905. Capture and handling procedures followed routine protocols approved by the Institute of Zoology, University of Veterinary Medicine Hannover Foundation.

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