

## Reporting Summary

Nature Research 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 Research policies, see [Authors & Referees](#) and the [Editorial Policy Checklist](#).

### Statistical parameters

When statistical analyses are reported, confirm that the following items are present in the relevant location (e.g. 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
- ☐ ☒ An indication of 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 statistics 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
- ☐ ☒ Clearly defined error bars  
*State explicitly what error bars represent (e.g. SD, SE, CI)*

Our web collection on [statistics for biologists](#) may be useful.

### Software and code

Policy information about [availability of computer code](#)

Data collection

Custom scripts written in the R programming language were used to extract and process data; all scripts are provided in the Dryad data package that accompanies our article.

Data analysis

Analysis: we used numerous statistical routines developed for the R programming language (many specific packages: ape, spdep, BAMMtools, and others), including many custom approaches for this study. Many standard phylogenetics software programs including RAxML, treePL, BAMM, PHLAWD, and PartitionFinder.

All computer code and associated workflows are archived in the Dryad data repository (see Data and Code Availability statement).

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/reviewers upon request. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Research [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 list of figures that have associated raw data
- A description of any restrictions on data availability

All data, scripts, and code necessary to repeat the analyses described here have been made available through the Dryad digital data repository (doi:10.5061/dryad.fc71cp4). Phylogenetic tree distributions are also available through <http://fishtreeoflife.org>. There are no restrictions on data availability.

## Field-specific reporting

Please select 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/authors/policies/ReportingSummary-flat.pdf](https://www.nature.com/authors/policies/ReportingSummary-flat.pdf)

## Ecological, evolutionary & environmental sciences study design

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

|                                   |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
|-----------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| Study description                 | We tested the relationship between assemblage-wide rates of speciation and latitude, and between species-specific rates of speciation and latitude. The study focused on marine fishes.                                                                                                                                                                                                                                                                                                                           |
| Research sample                   | The research sample included all species of marine fishes for which we could obtain DNA sequence data such that they could be included in a comprehensive phylogenetic tree of marine fishes. The sample was global in scope, and there were no data exclusions.                                                                                                                                                                                                                                                  |
| Sampling strategy                 | Sample size was determined by availability of genetic and geographic data for marine fishes. We used all available data in our study. The sample size used in our study exceeds the vast majority of published trait-dependent diversification studies. Moreover, the extent of speciation rate heterogeneity across fishes as inferred using BAMM is sufficiently great as to enable us to detect effects (see Rabosky and Huang, 2016, DOI:10.1093/sysbio/syv066 for relevant discussion of statistical power). |
| Data collection                   | DNA sequence data were extracted from public DNA sequence databases (GenBank) or sequenced de novo for this study. Spatial data were extracted from the AquaMaps spatial data repository. Ecological data for fishes (e.g., depth classification) were extracted from the publicly available FishBase database.                                                                                                                                                                                                   |
| Timing and spatial scale          | Spatial scale (scope) of the study is global. However, this question is generally not applicable to our study.                                                                                                                                                                                                                                                                                                                                                                                                    |
| Data exclusions                   | No data were excluded.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |
| Reproducibility                   | Our data are not experimental and experiments were thus not replicated. However, we used multiple distinct statistical tests (e.g., FISSE, STRAPP, generalized linear models) and all approaches yielded concordant results. We also tested extensively for artifacts that might explain the pattern (see Extended Data 10).                                                                                                                                                                                      |
| Randomization                     | We did not perform an experiment and there was thus no group allocation. We used all species of marine fishes for which (1) DNA sequence data were available, and (2) spatial data were available. There was no further group partitioning of data beyond the natural groupings associated with geography and clade membership.                                                                                                                                                                                   |
| Blinding                          | Blinding was not relevant to our study, because all available data were used (our study did not perform an experiment).                                                                                                                                                                                                                                                                                                                                                                                           |
| Did the study involve field work? | <input type="checkbox"/> Yes <input checked="" type="checkbox"/> No                                                                                                                                                                                                                                                                                                                                                                                                                                               |

## Reporting for specific materials, systems and methods

Materials & experimental systems

| n/a                                 | Involved in the study                                |
|-------------------------------------|------------------------------------------------------|
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Unique biological materials |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Antibodies                  |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Eukaryotic cell lines       |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Palaeontology               |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Animals and other organisms |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Human research participants |

Methods

| n/a                                 | Involved in the study                           |
|-------------------------------------|-------------------------------------------------|
| <input checked="" type="checkbox"/> | <input type="checkbox"/> ChIP-seq               |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Flow cytometry         |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> MRI-based neuroimaging |