

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](#).

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

No software was used to collect data.

Data analysis

Analyses were conducted using the program BayesTraits V3 and R version 3.4.2.

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. 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

The dataset generated and analysed during the current study is available in the Dryad Digital Repository: xxxxxxxx

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 assembled a species-level data set on female reproductive mode and male sexually selected traits in the live-bearing fish family Poeciliidae. We combined this data set with a molecular timetree of this group and performed phylogenetic comparative analyses (ancestral state reconstructions, correlated evolution analyses, and diversification analyses) to test predictions of the viviparity driven conflict hypothesis.
Research sample	We assembled a dataset containing information on female reproductive mode (internal fertilization, viviparity, placentation, superfetation, and the matrotrophy index) and male sexually selected traits (courtship, dichromatism, ornamentation, gonopodium length, and magnitude of sexual dimorphism) for 150 poeciliid species.
Sampling strategy	All poeciliid species for which we were able to find the relevant character data were included in the study.
Data collection	Over the past 30 years, data on female reproductive mode in poeciliid species was gathered in the laboratory of David Reznick (through dissection of preserved specimens). This data was supplemented with data from the literature for a limited number of additional species. Data on male sexually selected traits in poeciliid species was taken from the paper: Pollux, B.J.A., Meredith, R.W., Springer, M.S., Garland, T. and Reznick, D.N., 2014. The evolution of the placenta drives a shift in sexual selection in livebearing fish. <i>Nature</i> , 513(7517), p.233-236. This data was organized in Excel spreadsheets by Andrew Furness.
Timing and spatial scale	The dataset was assembled between January 2016 and September 2018.
Data exclusions	For ancestral state reconstructions of female reproductive mode (i.e. fertilization, viviparity, superfetation, and placenta), we excluded four outgroup taxa (Atheriniformes, Characiformes, Ophidiiformes, and Scorpaeniformes) that were polymorphic for some reproductive mode characters.
Reproducibility	All BayesTraits MCMC analyses were run in triplicate. Independent runs always produced qualitatively similar results.
Randomization	Our study was not experimental in nature and did not involve assigning individuals to different groups, so randomization is not relevant.
Blinding	Our study utilized phylogenetic comparative methods. Blinding is not relevant.
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
☒	☐ Animals and other organisms
☒	☐ Human research participants
☒	☐ Clinical data

n/a	Involved in the study
☒	☐ ChIP-seq
☒	☐ Flow cytometry
☒	☐ MRI-based neuroimaging