

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 |
|--------------------------|--|
| <input type="checkbox"/> | <input checked="" type="checkbox"/> The exact sample size (n) for each experimental group/condition, given as a discrete number and unit of measurement |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> 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> |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> A description of all covariates tested |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> 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) |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> For null hypothesis testing, the test statistic (e.g. F , t , r) with confidence intervals, effect sizes, degrees of freedom and P value noted
<i>Give P values as exact values whenever suitable.</i> |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> 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	<p>DNA barcodes obtained using Sanger sequencing at SourceBioscience. High-throughput data obtained using Illumina HiSeq-3000 at the Center for Genome Research and Biocomputing, Oregon State University. All software used for phylogenetic analysis is available online and includes:</p> <ul style="list-style-type: none"> - DNA barcodes (assembly): Mega v.5.0, Mega v.6.0, Geneious v.9.1.2 - DNA barcodes (alignment and phylogenetic inference): MAFFT v.7.2.1, jModelTest 2, RAxML v.8, FastTree 2, MrBayes v.3.2. - High-throughput data (assembly): YASRA, PRICE, SSPACE, BLASTN, MUSCLE, PHYLIP, SPades. - High-throughput data (alignment and phylogenetic inference): MAFFT, PRANK, GBlocks, jModelTest 2, RAxML, FastTree 2, Astral-II, MrBayes v.3.2. - Time-calibrated phylogenies: MAFFT, Gblocks, RevBayes v.1.0.4, Tracer v.1.6.0, treePL, BAMM (including set_priors.R script), BAMMtools

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

Passport data of all herbarium specimens included in the molecular studies presented in this paper is available as supplementary file. Additional records and

information of the collections included in this study and of specimens added subsequently are available through the website of the project (<https://herbaria.plants.ox.ac.uk/bol/ipomoea>). All data used for phylogenetic analysis is available in public repositories: DNA barcode sequences are available through GenBank and genome assemblies are available through the Oxford Repository Archive. Illumina raw reads are available through the Sequence Read Archive.

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

Ecological, evolutionary & environmental sciences study design

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

Study description	Monographic study of the genus <i>Ipomoea</i> (morning glories) integrating the morphological study of herbarium specimens with the use of high-throughput DNA sequencing (Hyb-Seq) and DNA barcodes for phylogenetic analysis.
Research sample	All <i>Ipomoea</i> specimens from 47 herbaria worldwide used for morphological study. 385 samples representing c. 210 species sequenced to obtain their whole chloroplast genome and 605 putative single copy nuclear coding DNA regions using Hyb-Seq. 1,560 specimens sequenced for at least one DNA barcode using Sanger sequencing.
Sampling strategy	Sampling strategy aimed at obtaining, when possible, multiple specimens from each putative species studied. When available, material collected in the last 50 years was preferred as this is more suitable to produce good sequencing results.
Data collection	Samples for DNA analysis collected from herbarium material by P.M.R., J.R.I.W., B.R.M.W. and A.S. Morphological study of the specimens conducted by J.R.I.W.
Timing and spatial scale	Project developed between 2012 and 2019 with continuous sampling of herbarium material.
Data exclusions	No data was excluded from the study.
Reproducibility	Methodology is extensively described and all data files, including raw sequence data, are made available through publicly accessible repositories.
Randomization	Does not apply in a study of this type.
Blinding	Does not apply in a study of this type.
Did the study involve field work?	<input type="checkbox"/> Yes <input checked="" type="checkbox"/> 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

n/a	Involved in the study
<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
<input checked="" type="checkbox"/>	<input type="checkbox"/> Clinical data

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