

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 (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
<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. 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> |
| ☒ | ☐ | 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 in data collection.
Data analysis	We utilized open source software for data analysis. Software used include R, fastp, SMRT Link, ccs, HICUP, Hifiiasm, ALLHiC, Juicebox, Burrows-Wheeler Aligner, BUSCO, RepeatModeler, LTR_FINDER, LTR_retriever, RepeatMasker, RepeatProteinMask, tRNAscan-SE, INFERNAL, AUGUSTUS, GlimmerHMM, Blast, Exonerate, MAKER, OrthoFinder, MAFFT, EMBOSS, CAFE, RAXML, PRANK, and HyPhy, as carefully detailed in our Materials and Methods section.

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 sequencing data generated in this study are publicly available in the NCBI SRA database under accession codes PRJNA1110373 and PRJNA1110349. GC-MS raw

data are available in Zenodo (<https://doi.org/10.5281/zenodo.19695105>). All other data are available within the paper and its Supplementary Information. No restrictions apply.

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	N/A
Reporting on race, ethnicity, or other socially relevant groupings	N/A
Population characteristics	N/A
Recruitment	N/A
Ethics oversight	N/A

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

Ecological, evolutionary & environmental sciences study design

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

Study description	We investigated the carnivory in <i>Saxifraga candelabrum</i> using field, herbarium, enzymatic, isotopic and genomic approaches, showing insect capture, digestion and nutrient uptake, thus confirming carnivory in this species and identifying genomic convergence with other carnivorous plant lineages.
Research sample	For herbarium specimen, 45 specimens spanning 1888-2016 were included for analyses. For field observation, a total of 32 individuals of <i>Saxifraga candelabrum</i> were included. For isotopic examination for nutrient uptake, more than 1500 fruit flies were used for this experiments. For genome sequencing, Fresh basal leaves of <i>Saxifraga candelabrum</i> were collected from Wufeng Mountain, Yunnan province, China. Detailed information is provided in Materials and Methods section.
Sampling strategy	Herbarium specimens spanning the full geographic and temporal range of <i>S. candelabrum</i> were examined to assess insect trapping consistency. Field individuals were sampled during peak flowering. Isotopic assays used sufficient replicates and controls, and fresh leaves were collected for genomic sequencing.
Data collection	X.J.Z., E.N.X., T.D., H.C.W., B.S. and X.H.H. carried out field investigations and sample collections. Field observations were recorded by X.J.Z. and E.N.X. using handwritten notes. Herbarium specimen data were recorded and curated by X.J.Z. in Microsoft Excel spreadsheets. X.J.Z., X.H.H., P.R.L., J.T.C., and Q.S.F. conducted the experiments on enzymatic test, and Fluorescence was documented by X.J.Z. using a Canon EOS Rebel T5 digital camera. X.J.Z., B.S. and T.D. performed the experiments on isotopic examination, with data recorded by X.J.Z. using spreadsheets. N.L. and T.D. employed the genome data analyses using standard bioinformatic pipelines.
Timing and spatial scale	Field investigations and herbarium specimen analyses were conducted in Yunnan Province, China, between 6 August 2021 and 3 October 2023. Field sampling was carried out in three discrete periods: 6 August to 6 November 2021, 14 March to 2 October 2022, and 23 April to 3 October 2023. Nutrient uptake experiments were conducted between 1 September 2021 and 1 January 2023. Genome sequencing, assembly and assessment were carried out between 1 November 2021 and 10 May 2024. Data were collected at the scale of natural populations and herbarium collections within Yunnan Province.
Data exclusions	To prevent contamination from residual isotopic substances, the stems of <i>S. candelabrum</i> , and leaves of <i>D. peltata</i> directly exposed to labeled fruit flies were excluded from isotopic analyses.
Reproducibility	All experimental procedures were independently repeated with at least three biological replicates, as described in the Methods. This includes field observations, herbarium specimen analyses, olfactory and visual cue experiments, GC-MS analyses of floral volatiles, enzymatic assays, and isotopic experiments. All attempts to reproduce the experimental findings were successful. Detailed protocols and publicly available datasets enable full reproducibility of the results.
Randomization	Randomization was not applied, as samples were grouped according to predefined biological categories (e.g. species identity and

Randomization	control groups) rather than randomly assigned. This approach is appropriate for the comparative nature of the study and does not introduce bias due to the use of objective measurements.
Blinding	Blinding was not applied in this study, as the experiments did not involve subjective assessment or group allocation that could introduce bias. Data collection and analysis were based on objective measurements, including instrument-generated outputs (e.g. GC–MS, isotope analyses) and microscopy imaging with defined controls.
Did the study involve field work?	☒ Yes ☐ No

Field work, collection and transport

Field conditions	Fieldwork was conducted in Shangri-La, Yunnan, China, where the mean annual temperature is approximately 5.4 °C and the annual precipitation is about 620 mm. Collect samples under the natural conditions in day-time.
Location	Field work was conducted in Shangri-La, Yunnan Province, China, including Wufeng Mountain (27.820°N, 99.723°E; 3438 a.s.l.), Napahai (27.891°N, 99.640°E; 3280 m a.s.l.), and Songzanlin-Lamasery (27.860°N, 99.706°E; 3320 m a.s.l.). Samples for genome sequencing were collected from Wufeng Mountain (27.820°N, 99.723°E; 3438 m a.s.l.).
Access & import/export	Field sampling was conducted in Yunnan Province, China, in accordance with local and national regulations. The studied species is not protected, and no specific permits were required for collection. No import or export of biological materials was involved in this study.
Disturbance	Only target samples were collected from fields and no other plants or animals were removed or transported outside the fields. The disturbance to natural habitats was minimized.

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	This study did not involve laboratory animals.
Wild animals	Adult <i>Drosophila melanogaster</i> were attracted and captured in the field using fermented fruit bait. No procedures involving behavioral experiments or manipulation of wild animals in their natural habitat were conducted.
Reporting on sex	Sex was not recorded or considered in the study design, as the experiments were not sex-specific and involved pooled individuals. No sex-based analyses were performed.
Field-collected samples	Field-collected <i>Drosophila melanogaster</i> were maintained under laboratory conditions for approximately two months prior to use in experiments. <i>Drosophila melanogaster</i> were fed either a standard diet (control) or a diet supplemented with ¹⁵ N-labeled amino acids at room temperature under natural photoperiod conditions. Offspring produced under these conditions were collected as mature adults and stored at –20 °C prior to use in experiments. Freezing was used as a standard method to preserve samples for subsequent analyses. No specific ethical approval was required for the use of this species.
Ethics oversight	No ethical approval was required for this study, as it involved only invertebrates (<i>Drosophila melanogaster</i>), which are not subject to animal ethics regulations.

Note that full information on the approval of the study protocol must also be provided in the manuscript.

Dual use research of concern

Policy information about [dual use research of concern](#)

Hazards

Could the accidental, deliberate or reckless misuse of agents or technologies generated in the work, or the application of information presented in the manuscript, pose a threat to:

No	Yes
☒	☐ Public health
☒	☐ National security
☒	☐ Crops and/or livestock
☒	☐ Ecosystems
☒	☐ Any other significant area

Experiments of concern

Does the work involve any of these experiments of concern:

No	Yes
☒	☐ Demonstrate how to render a vaccine ineffective
☒	☐ Confer resistance to therapeutically useful antibiotics or antiviral agents
☒	☐ Enhance the virulence of a pathogen or render a nonpathogen virulent
☒	☐ Increase transmissibility of a pathogen
☒	☐ Alter the host range of a pathogen
☒	☐ Enable evasion of diagnostic/detection modalities
☒	☐ Enable the weaponization of a biological agent or toxin
☒	☐ Any other potentially harmful combination of experiments and agents

Plants

Seed stocks	Field-collected seeds of <i>S. candelabrum</i> were used in this study, and sampling procedures described in the Materials and Methods section. No seed stock centre or catalogue number is applicable.
Novel plant genotypes	Not applicable. This study did not involve the generation or use of novel plant genotypes.
Authentication	Not applicable.