

A comprehensive dated phylogeny of China's vascular plants reveals a hidden Global Biodiversity Hotspot

Corresponding Author: Professor Li-Min Lu

This manuscript has been previously reviewed at another journal that is not operating a transparent peer review scheme. The manuscript was considered suitable for publication without further review at Nature Ecology & Evolution.

Version 0:

Decision Letter:

10th November 2025

*Please ensure you delete the link to your author homepage in this e-mail if you wish to forward it to your co-authors.

Dear Professor Lu,

Your manuscript entitled "A hidden Global Biodiversity Hotspot in Central China" has now been seen by 3 reviewers, whose comments are attached. The reviewers have raised a number of concerns which will need to be addressed before we can offer publication in Nature Ecology & Evolution. We will therefore need to see your responses to the criticisms raised and to some editorial concerns, along with a revised manuscript, before we can reach a final decision regarding publication.

In particular, Reviewer #2 feels that the discussion of drivers of diversification needs amending, while Reviewer #3 has requested some additional analysis quantifying phylogenetic uncertainty, a stronger rationale for using fixed temporal thresholds, a sensitivity analysis on ranges size estimates, and a broader discussion of the paleoclimatic and geological models.

In addition to this, we have an Editorial request to amend the title to something more informative of the broader results. For example "A comprehensive dated phylogeny of China's vascular plants reveals an hidden global biodiversity hotspot". Other suggestions are welcome. Titles should be brief, informative and not contain punctuation.

We therefore invite you to revise your manuscript taking into account all reviewer and editor comments. Please highlight all changes in the manuscript text file [OPTIONAL: in Microsoft Word format].

We are committed to providing a fair and constructive peer-review process. Do not hesitate to contact us if there are specific requests from the reviewers that you believe are technically impossible or unlikely to yield a meaningful outcome.

When revising your manuscript:

* Include a "Response to reviewers" document detailing, point-by-point, how you addressed each reviewer comment. If no action was taken to address a point, you must provide a compelling argument. This response will be sent back to the reviewers along with the revised manuscript.

* If you have not done so already please begin to revise your manuscript so that it conforms to our Article format instructions at <http://www.nature.com/natecolevol/info/final-submission>. Refer also to any guidelines provided in this letter.

* Include a revised version of any required reporting checklist. It will be available to referees (and, potentially, statisticians) to aid in their evaluation if the manuscript goes back for peer review. A revised checklist is essential for re-review of the paper.

* Extended Data Figures - please ensure that any supplementary figures and tables that are crucial to the manuscript's conclusions are converted into Extended Data figures and tables to increase visibility of these data. Extended Data figures and tables are online-only (present in the online PDF and full-text HTML versions of the paper), peer-reviewed display items that provide essential background to the article but are not included in the main article due to space constraints. A maximum of ten Extended Data display items (figures and tables) is permitted.

Please use the link below to submit your revised manuscript and related files:

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Note: This URL links to your confidential home page and associated information about manuscripts you may have submitted, or that you are reviewing for us. If you wish to forward this email to co-authors, please delete the link to your homepage.

We hope to receive your revised manuscript within four to eight weeks. If you cannot send it within this time, please let us know. We will be happy to consider your revision so long as nothing similar has been accepted for publication at Nature Ecology & Evolution or published elsewhere.

Nature Ecology & Evolution is committed to improving transparency in authorship. As part of our efforts in this direction, we are now requesting that all authors identified as 'corresponding author' on published papers create and link their Open Researcher and Contributor Identifier (ORCID) with their account on the Manuscript Tracking System (MTS), prior to acceptance. ORCID helps the scientific community achieve unambiguous attribution of all scholarly contributions. You can create and link your ORCID from the home page of the MTS by clicking on 'Modify my Springer Nature account'. For more information please visit <http://www.springernature.com/orcid>.

Please do not hesitate to contact me if you have any questions or would like to discuss these revisions further.

We look forward to seeing the revised manuscript and thank you for the opportunity to review your work.

[redacted]

Reviewer expertise:

Reviewer #1: Plant systematics, evolution, diversity

Reviewer #2: Plant ecology, evolution, diversity

Reviewer #3: Plant diversity, biogeography, phylogenetics

Reviewers' comments:

Reviewer #1 (Remarks to the Author):

Characterizing the flora of China and understanding its evolutionary history is highly important. This flora has a combination of features that is globally unique. These features include its geographic breadth, particularly the extent of its latitudinal range, its high species diversity overall, the species richness of particular biomes, and the persistence of paleoendemic lineages, to name a few. It presents so many opportunities to test classic ecological and evolutionary hypotheses such as those involving the latitudinal gradient and cradle vs museum ideas and to support studies on the interplay between speciation and global change. Due to the presence of global biodiversity hotspots and the high number of endemic species, understanding the history of its flora is also critical for conservation efforts. For these reasons, this study is very timely.

The authors have assembled a new checklist that demonstrates the high levels of endemism in the flora (about half of its total vascular plants), and have used a newly generated dated phylogeny with improved representation of the Chinese flora to characterize temporal patterns of lineage accumulation and spatial patterns of endemism and diversity. Their findings have important implications for conservation and they increase foundational knowledge for studies of ecology and evolution. Among important results for conservation is the identification by the authors of Central China as a previously overlooked Global Biodiversity Hotspot. While this is not surprising, the authors make a compelling case by drawing on their own results and data from Species 2000 China Node the (further highlighting the value of these digital databases).

MINOR COMMENTS

1. Lines 88-89. Here, just a minor grammatical suggestion to improve readability, change "Our geospatial analysis reveals molecular data gaps among ..." to "Our geospatial analysis reveals gaps in available molecular data from ..."

2. Lines 202-203. It wasn't clear to me why competing land-use contributes to fragmentation. Many forms of land use contribute to fragmentation; others do not. The fact that they might be competing need not contribute to fragmentation. Do you mean uses involving clearing for agricultural or urban development versus preservation, or something along those lines?

3. The study is very sound methodologically and the Methods section is clear and well-detailed (much appreciated). It might be worth adding a line mentioning that TreePL is an appropriate method for estimating divergence times on large phylogenies. Perhaps most but not all readers will be aware of this.

Extended Data Fig. 1. The "gray" lines indicating mountains are not consistently gray. On a green background they are gray. On backgrounds with pinker tones, they are blue.

Extended Data Fig. 2. The legend in my copy says only "Review drawing number for map: GS(2019)1823. Is something missing here?"

Signed: Sarah Mathews

Reviewer #1 (Remarks on code availability):

The data site states that "Most of the code files related to data analyses and charting are in the Scripts folder." This leaves open the question of what might be missing.

There were no README files, and the scripts did not include examples of usage.

Additionally, data files and trees that need to be read into the scripts were not found by me. So while I could install the code, not everything was available to run the code.

Reviewer #2 (Remarks to the Author):

Feng et al. provide detailed phylogenetic and geographic analyses supporting the existence of a previously unrecognized global plant diversity hotspot in Central China, supporting > 14,000 vascular plant species, of which more than 2000 are endemic to this region. The data base is, in my opinion, monumental and the analyses are state-of-the-art and extraordinary in scope. The implications for conservation in China are very important, and globally significant that, overall, China has the third largest flora in the world (after Brazil and Colombia), and the largest of any country in a temperate climate.

I have only a few suggestions for improvement:

1. If possible, the authors should include the total number of vascular plant species, and the total number of endemic species, for the new hotspot in the abstract.
2. On line 57, insert the missing "Hengduan" before "Mountains".
3. I suggest the authors should rewrite lines 57-59. The sentence seems to pin the most important driver of speciation and endemism on uplift of the Qinghai-Tibet plateau and intensification of the monsoon. I find this problematic for a few reasons. First, the Hengduan Mountains are substantially more diverse at the species level (and, I believe, the generic level too) than either the QT plateau or the Himalayas. The Hengduan Mountains were uplifted somewhat later than the Himalayas, in a related but seemingly separate orogeny. Second, while these orogenies helped strengthen the monsoon, I don't see a paper cited that makes a compelling case that such intensification actually did or should have led to greater species diversification and/or coexistence and persistence. For example, Lu et al. 2018 describe the strengthening of the monsoon but don't outline any theoretical or empirical reason connecting it to plant diversification, and especially, to diversification in China. Third, it's not clear to me what region(s) the sentence refers to – China as a whole, the four hotspots, or some subset of the hotspots. It clearly cannot apply with accuracy to China as a whole or the four hotspots, given the seeming absence of influence of the monsoon, Himalayas, or QT on, say, the mountains of northwestern China. The connection and limitation of the effects of uplift and monsoon intensification need to be clarified, and this should not be a throwaway line. Fourth, the exceptional topographic and climatic diversity of China (mentioned earlier in the paragraph) AND the great spatial extent of the country (not mentioned) should not be (seemingly, from the way the sentence in question is written) thrown under the bus while emphasizing the Himalayan uplift and monsoon intensification. Finally, the authors should acknowledge that the relatively recency per se of the orogenies of the Himalayas and Hengduan Mountains could also play a role in species diversification, given similar arguments/findings for the Andes in South America, and given that Feng et al. themselves show that the Hengduan Mountains are, quantitatively, the hottest of the four Chinese hotspots at the species level. It should be straightforward to rewrite this sentence (perhaps as two sentences) to address all of these concerns.
4. Lines 74-75: At the first mention of the new hotspot, perhaps the authors might give the readers some idea of where "Central China" is, given that it's not in the actual center of the country. What about saying, here, that it's centered on Hunan, Jiangxi, etc. in an area of moderate relief and dense human populations? Perhaps mention its area here (or later)??
5. Lines 124-125: please state the median divergence ages of endemic vs. non-endemic species here (4.8 vs. 7.1 My). I realize that those numbers are shown in Fig 2, but it's an important result and should be mentioned in the text as well.
6. Line 143: "an established method¹⁶" does not convey the substance of the method in any way. Can the authors insert a clarifying phrase here?
7. Line 144: Suggest you insert a table giving area, number of species, and number of endemic species for each of these hotspots.
8. Line 198: Suggest you draw the Hu Huanyong Line on one of the maps, so that those unacquainted with it can see where it is (and, in the caption, how it is defined).
9. Final paragraph of narrative: it would be nice to know where the new Central China hotspot sits on the ranked list of global hotspots, based on total number of vascular plant species and number of endemic species. I also wonder whether the authors might mention in the abstract that this hotspot sits in "unique East Asian subtropical evergreen broad-leaved forest ecoregion" as well as the other items mentioned under point 1 above.

I hope the authors find these comments useful.

Respectfully submitted,

Thomas J. Givnish
Henry Allan Gleason Professor Emeritus
University of Wisconsin-Madison

Reviewer #3 (Remarks to the Author):

The manuscript addresses a highly significant topic—the identification of critical, yet overlooked, biodiversity hotspots using a comprehensive phylogenetic and spatial framework. The scale of the manuscript data, including the extensive phylogeny and distribution records, is impressive and represents a major step forward for the field. The proposal to designate Central China as a new Global Biodiversity Hotspot is both timely and compelling, with substantial implications for global conservation policy. However, I feel that several major points need to be addressed before the manuscript can be considered for publication.

1) While the manuscript have used 100 bootstrap trees to account for phylogenetic uncertainty in divergence time estimation, the impact of this uncertainty on the key downstream analyses (e.g., the identification of neo- and paleo-endemism centers via CANAPE and the quartile method) is not fully demonstrated. I request a more explicit analysis of how sensitive your primary conclusions are to phylogenetic uncertainty. This could involve repeating the CANAPE and endemism center identification on a subset of the bootstrap trees to show the stability of the identified hotspots.

2) The use of fixed temporal thresholds (23 Ma for genera, 5 Ma for species) in your robustness check, while following previous studies, requires a stronger biological justification within the context of your specific dataset and the regional history of China. Please provide a more detailed rationale for why these specific cut-offs are the most appropriate, or discuss the potential implications if alternative thresholds were used.

3) The manuscript appropriately acknowledge the "border effect" and conduct a separate analysis on strictly endemic taxa. However, the method for estimating species geographic ranges (based on 100 km grid cells and county-level records) could inherently overestimate the range size of narrow endemics. Please discuss this limitation and consider, if feasible, a sensitivity analysis using a more refined range estimation method (e.g., alpha hulls or expert-drawn ranges for key endemics) to confirm that the patterns for Central China hold.

4) The geographic delineation of the proposed "Central China" hotspot is critical to your argument. While you reference Takhtajan's Floristic Province and your own endemism centers, the process of drawing the final boundary in Figure 4 needs more explicit description in the main text or methods. A clearer, step-by-step explanation will strengthen the defensibility of this proposed hotspot's borders.

5) The results convincingly show peaks of diversification in the Miocene and Pleistocene. However, the discussion of the drivers remains somewhat correlative. I encourage you to more deeply integrate your findings with specific paleoclimatic and geological models for the region. For instance, can you more directly link the Pleistocene diversification peak to models of refugia in Central China, rather than primarily the Hengduan Mountains?

6) To strengthen the case for Central China's global significance, I recommend adding a comparative table or paragraph in the results/discussion. This should quantitatively compare Central China's metrics (species richness, endemism, habitat loss) with other established Global Biodiversity Hotspots, particularly other subtropical ones.

7) The discussion rightly highlights the conservation gap. However, it would be strengthened by a more realistic and nuanced discussion of the challenges and opportunities for conservation in this densely populated region. What specific strategies (beyond expanding protected areas) could be effective? How can connectivity be achieved in such a fragmented landscape? Engaging with the socio-economic literature on conservation in human-dominated landscapes would be beneficial.

8) The manuscript would benefit from a dedicated paragraph in the discussion that explicitly outlines the key limitations of the study. This should include, but not be limited to, the incomplete species sampling in the phylogeny (notably in Xinjiang and the Qinghai-Tibet Plateau), the reliance on public and herbarium records with inherent spatial biases, and the limitations of the molecular markers used for dating deep and rapid radiations.

9) The discussion could be more focused. I suggest streamlining the explanation of the differences between taxonomic and phylogenetic endemism and instead placing greater emphasis on the novel, synthetic conclusion: that combining these approaches was essential for revealing the critical importance of Central China, a region that would be missed by frameworks relying on a single metric.

*****END*****

Version 1:

Decision Letter:

14th January 2026

Dear Dr. Lu,

Thank you for submitting your revised manuscript "A comprehensive dated phylogeny of China's vascular plants reveals a hidden Global Biodiversity Hotspot" (NATECOLEVOL-25093432A). It has now been seen again by the original reviewers and their comments are below. The reviewers find that the paper has improved in revision, and therefore we'll be happy in principle to publish it in Nature Ecology & Evolution, pending minor revisions to satisfy the reviewers' final requests and to comply with

our editorial and formatting guidelines.

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Thank you again for your interest in Nature Ecology & Evolution. Please do not hesitate to contact me if you have any questions.

[redacted]

Reviewer #2 (Remarks to the Author):

The authors have addressed each of my concerns in compelling fashion. I fully support acceptance of the revised manuscript, which makes a monumental contribution to our understanding of diversification of the Chinese flora.

Thomas J. Givnish
Henry Allan Gleason Professor Emeritus of Botany
University of Wisconsin-Madison
givnish@wisc.edu

Reviewer #3 (Remarks to the Author):

The authors have made comprehensive revisions to the entire manuscript based on the reviewer's comments. It is now suitable for acceptance and publication in Nature Ecology and Evolution.

Version 2:

Decision Letter:

18th February 2026

Dear Professor Lu,

We are pleased to inform you that your Article entitled "A comprehensive dated phylogeny of China's vascular plants reveals a hidden Global Biodiversity Hotspot", has now been accepted for publication in Nature Ecology & Evolution.

Over the next few weeks, your paper will be copyedited to ensure that it conforms to Nature Ecology and Evolution style. Once your paper is typeset, you will receive an email with a link to choose the appropriate publishing options for your paper and our Author Services team will be in touch regarding any additional information that may be required

After the grant of rights is completed, you will receive a link to your electronic proof via email with a request to make any corrections within 48 hours. If, when you receive your proof, you cannot meet this deadline, please inform us at rjsproduction@springernature.com immediately.

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Manuscript No.: NATECOLEVOL-25093432-T

Title: A comprehensive dated phylogeny of China's vascular plants reveals a hidden Global Biodiversity Hotspot

Authors: Ya-Lei Feng, Hai-Hua Hu, Bing Liu, Dan-Xiao Peng, Yu-Chang Yang, Russell L. Barrett, Alexandre Antonelli, Zhi-Duan Chen*, Li-Min Lu*

Date: December 9, 2025

Reviewer #1:

Comments for the Author:

Characterizing the flora of China and understanding its evolutionary history is highly important. This flora has a combination of features that is globally unique. These features include its geographic breadth, particularly the extent of its latitudinal range, its high species diversity overall, the species richness of particular biomes, and the persistence of paleoendemic lineages, to name a few. It presents so many opportunities to test classic ecological and evolutionary hypotheses such as those involving the latitudinal gradient and cradle vs museum ideas and to support studies on the interplay between speciation and global change. Due to the presence of global biodiversity hotspots and the high number of endemic species, understanding the history of its flora is also critical for conservation efforts. For these reasons, this study is very timely.

The authors have assembled a new checklist that demonstrates the high levels of endemism in the flora (about half of its total vascular plants), and have used a newly generated dated phylogeny with improved representation of the Chinese flora to characterize temporal patterns of lineage accumulation and spatial patterns of endemism and diversity. Their findings have important implications for conservation and they increase foundational knowledge for studies of ecology and evolution. Among important results for conservation is the identification by the authors of Central China as a previously overlooked Global Biodiversity Hotspot. While this is not surprising, the authors make a compelling case by drawing on their own results and data from

Species 2000 China Node the (further highlighting the value of these digital databases).

Response: Thank you for your thoughtful and constructive comments, and for recognizing the importance of our work on the evolutionary history and conservation of China's endemic flora. We are particularly encouraged by your positive assessment of our conservation-related findings, including the identification of Central China as a previously overlooked Global Biodiversity Hotspot. We agree that this highlights the critical value of digital databases, such as Species 2000 China Node, in advancing our knowledge. In response to your comments, we have carefully addressed all of your concerns in the revised manuscript. Detailed responses to each point are provided below.

MINOR COMMENTS

1. Lines 88-89. Here, just a minor grammatical suggestion to improve readability, change "Our geospatial analysis reveals molecular data gaps among ..." to "Our geospatial analysis reveals gaps in available molecular data from ..."

Response: Thank you for your helpful suggestion. We have revised the sentence from "Our geospatial analysis reveals molecular data gaps among ..." to "Our geospatial analysis reveals gaps in available molecular data from ..." accordingly (**Lines 99–100**).

2. Lines 202-203. It wasn't clear to me why competing land-use contributes to fragmentation. Many forms of land use contribute to fragmentation; others do not. The fact that they might be competing need not contribute to fragmentation. Do you mean uses involving clearing for agricultural or urban development versus preservation, or something along those lines?

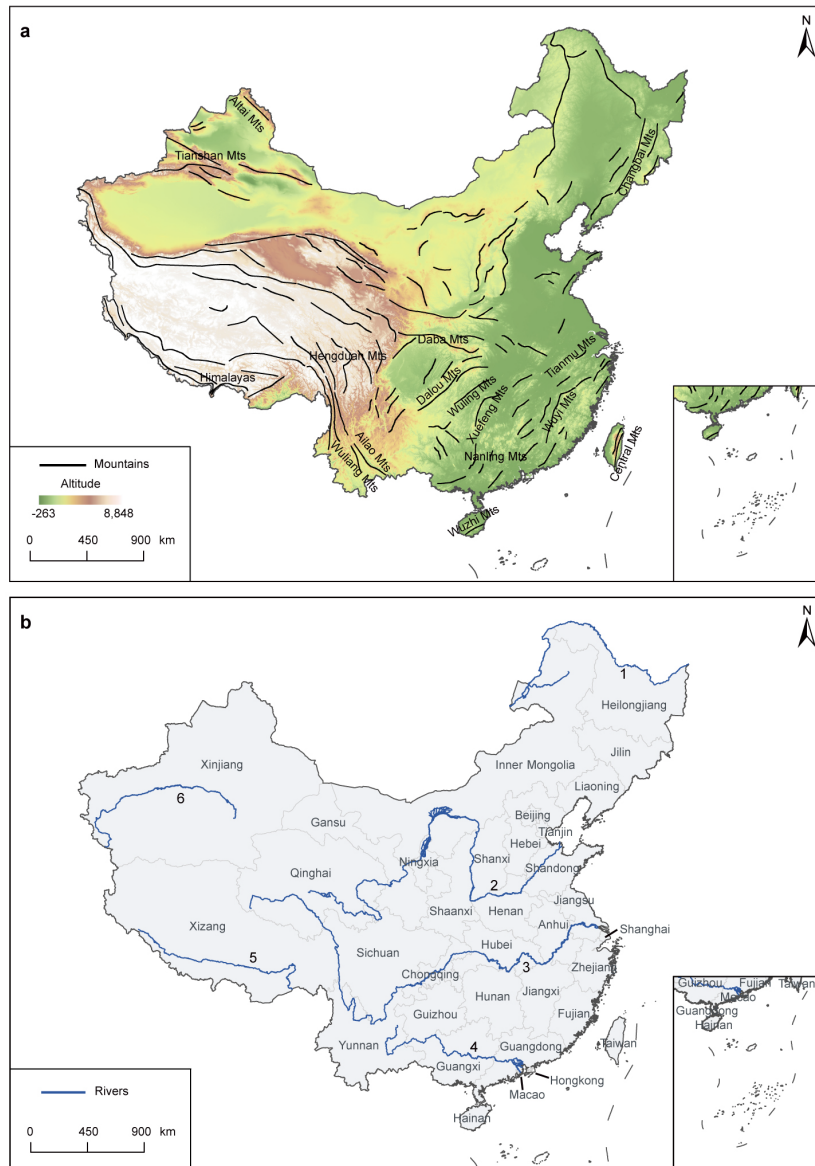
Response: Thank you for your insightful comment. We agree that not all forms of competing land use contribute to fragmentation. Our intent was to refer specifically to land-use types that involve the clearing and conversion of natural habitats, which directly drive habitat loss and fragmentation. To clarify this, we have revised the text by replacing "urbanization and competing land-use" with "land-use conversion for urban, agricultural, and infrastructural development" to more accurately describe the processes responsible for fragmentation (**Lines 238–239**).

3. The study is very sound methodologically and the Methods section is clear and well-detailed (much appreciated). It might be worth adding a line mentioning that TreePL is an appropriate method for estimating divergence times on large phylogenies. Perhaps most but not all readers will be aware of this.

Response: We appreciate the reviewer's positive assessment of our methodological approach. We have added the phrase "a computationally efficient and widely adopted method for dating large phylogenies" after "Divergence times were estimated using the penalized likelihood (PL) approach implemented in treePL" to clarify the suitability of the treePL method for large-scale phylogenetic analyses (**Lines 372–373**).

Extended Data Fig. 1. The "gray" lines indicating mountains are not consistently gray. On a green background they are gray. On backgrounds with pinker tones, they are blue.

Response: Thank you for pointing this out. We apologize for the inconsistent color rendering of the mountain lines. To eliminate ambiguity and ensure visual consistency across backgrounds, we have replaced the original gray lines with standard black (RGB: 0,0,0) to represent the mountain ranges (see the revised Extended Data Fig. 1 below).

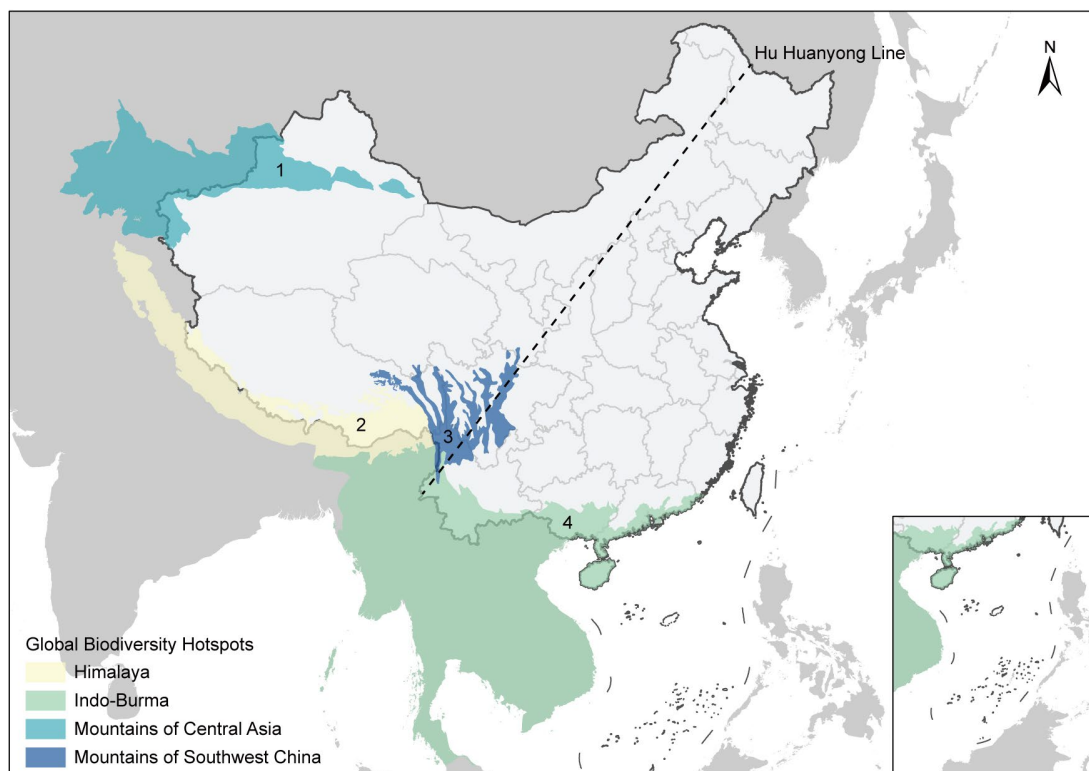


Extended Data Fig. 1 | China's physical geography and administrative divisions. a, Topography and major mountain ranges in China. Black lines depict major mountain ranges in China, with labeled ranges (in black text) indicating mountains within or adjacent to endemism centers identified in this study. Geographic data of mountains were obtained from the digital mountain map of China (National Tibetan Plateau Data Center)¹²³. **b, China's administrative divisions.** Blue lines show major rivers: (1) Amur River; (2) Yellow River; (3) Yangtze River; (4) Pearl River; (5) Yarlung Tsangpo River; (6) Tarim River. The river's geospatial data were downloaded from the Resource and Environmental Science Data Platform (<https://www.resdc.cn/>, accessed May 2025). Review drawing number for map: GS(2019)1823. Mts: Mountains.

Extended Data Fig. 2. The legend in my copy says only "Review drawing number for map: GS(2019)1823. Is something missing here?

Response: Thank you for pointing out this omission. Our previous legend was indeed

overly concise. To improve clarity, we have now added numerical labels in the figure to indicate the four recognized Global Biodiversity Hotspots that intersect China and have explained these labels in the legend. In addition, as suggested by Reviewer #2, we have incorporated the Hu Huanyong Line, the well-known demographic boundary dividing eastern and western China, to highlight the underrepresentation of Global Biodiversity Hotspots in eastern China (see the revised Extended Data Fig. 2 and legend below).



Extended Data Fig. 2 | Geographic extent of the four recognized Global Biodiversity Hotspots overlapping China. The map shows the spatial distribution of four recognized Global Biodiversity Hotspots intersecting China: (1) Mountains of Central Asia, (2) Himalaya, (3) Mountains of Southwest China, and (4) Indo-Burma. The black dashed line represents the Hu Huanyong Line, which delineates China's east-west population divide, extending from Heihe City (Heilongjiang Province) to Tengchong City (Yunnan Province). Review drawing number for map: GS(2019)1823.

Remarks on code availability:

The data site states that "Most of the code files related to data analyses and charting are in the Scripts folder." This leaves open the question of what might be missing.

Response: Thank you for your helpful comments on our Code Availability section. Our

intention was to convey that the complete set of analysis and scripts is provided; however, we agree that the phrase “Most of” could imply that some files are missing. To eliminate any confusion, we have thoroughly reviewed the dataset and code repository, confirmed that all relevant scripts are included, and revised the wording from “Most of” to “All” for greater clarity and accuracy. The updated materials are available at: <https://www.scidb.cn/s/vqYjAv>.

There were no README files, and the scripts did not include examples of usage.

Response: Thank you for your constructive comment. In response, we have updated the repository to include detailed README files and example scripts that demonstrate the usage of the code. We hope these updates will help clarify the analytical workflow and improve readers’ understanding of the methods employed in this study.

Additionally, data files and trees that need to be read into the scripts were not found by me. So while I could install the code, not everything was available to run the code.

Response: We sincerely apologize for the confusion. It seems that the file organization in the previous version of our data repository may have caused some inconvenience in running the scripts. Large datasets, such as tree files and distribution data, were stored in separate folders rather than alongside the scripts, which likely led to the issue.

To address this, we have reorganized the repository and updated the relevant code. The README file now includes explicit instructions on the directory structure and relative paths to access these large datasets. In addition, we have placed all small input tables required for specific scripts in the same directory as the scripts to ensure easier access. As long as the original directory structure is preserved when downloading the data, the scripts should now be able to access all required files without issue. We hope these updates will help and appreciate your understanding.

Reviewer #2:

Feng et al. provide detailed phylogenetic and geographic analyses supporting the existence of a previously unrecognized global plant diversity hotspot in Central China, supporting > 14,000 vascular plant species, of which more than 2000 are endemic to this region. The data base is, in my opinion, monumental and the analyses are state-of-the-art and extraordinary in scope. The implications for conservation in China are very important, and globally significant that, overall, China has the third largest flora in the world (after Brazil and Colombia), and the largest of any country in a temperate climate.

Response: We sincerely appreciate your generous and encouraging comments on our manuscript. We are grateful for your recognition of the significance of our work, particularly in highlighting the previously unrecognized global plant diversity hotspot in Central China. Your appreciation of the scale and quality of our analyses is truly inspiring. We have carefully addressed all your comments in the revised manuscript. Detailed responses to each of your points are provided below.

1. If possible, the authors should include the total number of vascular plant species, and the total number of endemic species, for the new hotspot in the abstract.

Response: Thank you for your valuable suggestion. We have now included the total numbers of vascular species and endemic species for the proposed hotspot in the abstract. Specifically, we added the sentence noting that Central China “harbors 14,431 vascular plant species, including 2,024 endemics, but has experienced severe loss of its original natural vegetation” (**Lines 35–36**), to provide readers with a clear and immediate understanding of the region’s biodiversity significance.

2. On line 57, insert the missing "Hengduan" before "Mountains".

Response: The term “Mountains of Southwest China” is the formal designation for this biodiversity hotspot, as defined in “*Hotspots Revisited: Earth’s Biologically Richest and Most Endangered Terrestrial Ecoregions*” (Mittermeier et al., 2004). Because this terminology has been widely adopted in subsequent studies, we prefer to retain it to maintain consistency with existing literature and avoid any potential ambiguity.

Reference:

Mittermeier, R. et al. Hotspots Revisited. Earth's Biologically Richest and Most Endangered Terrestrial Ecoregions. Conserv. Int. vol. 392 (CEMEX, Mexico City, Mexico, 2004).

3. I suggest the authors should rewrite lines 57-59. The sentence seems to pin the most important driver of speciation and endemism on uplift of the Quinghai-Tibet plateau and intensification of the monsoon. I find this problematic for a few reasons. First, the Hengduan Mountains are substantially more diverse at the species level (and, I believe, the generic level too) than either the QT plateau or the Himalayas. The Hengduan Mountains were uplifted somewhat later than the Himalayas, in a related but seemingly separate orogeny. Second, while these orogenies helped strengthen the monsoon, I don't see a paper cited that makes a compelling case that such intensification actually did or should have led to greater species diversification and/or coexistence and persistence. For example, Lu et al. 2018 describe the strengthening of the monsoon but don't outline any theoretical or empirical reason connecting it to plant diversification, and especially, to diversification in China. Third, it's not clear to me what region(s) the sentence refers to – China as a whole, the four hotspots, or some subset of the hotspots. It clearly cannot apply with accuracy to China as a whole or the four hotspots, given the seeming absence of influence of the monsoon, Himalayas, or QT on, say, the mountains of northwestern China. The connection and limitation of the effects of uplift and monsoon intensification need to be clarified, and this should not be a throwaway line. Fourth, the exceptional topographic and climatic diversity of China (mentioned earlier in the paragraph) AND the great spatial extent of the country (not mentioned) should not be (seemingly, from the way the sentence in question is written) thrown under the bus while emphasizing the Himalayan uplift and monsoon intensification. Finally, the authors should acknowledge that the relatively recency per se of the orogenies of the Himalayas and Hengduan Mountains could also play a role in species diversification, given similar arguments/findings for the Andes in South America, and given that Feng et al. themselves show that the Hengduan Mountains are, quantitatively, the hottest of the four Chinese hotspots at the species level. It should be straightforward to rewrite this sentence (perhaps as two sentences) to address all of these concerns.

Response: Thank you for these detailed and insightful comment. We agree that the original wording of lines 57–59 created an unintended impression that uplift of the Qinghai-Tibet Plateau and monsoon intensification were the primary drivers of diversification and endemism across China. As you correctly point out, this oversimplifies the complex geological and climatic history of the region, does not adequately reflect the distinct uplift histories of the Hengduan Mountains versus the Himalayas and the main plateau, and fails to account for the substantial spatial heterogeneity in how these processes influenced different parts of China.

In response, we have substantially revised the relevant sentences to ensure greater clarity and accuracy. The updated text now reads: “The country spans four currently recognized Global Biodiversity Hotspots: the Himalaya, Indo-Burma, Mountains of Central Asia, and Mountains of Southwest China²¹ (Extended Data Fig. 2). Among these, the Mountains of Southwest China hotspot exhibits the highest levels of species richness and endemism, a pattern attributed to the combined influences of tectonic uplift and the intensification of the Asian monsoon^{22–24}. These geological and climatic processes also...” (**Lines 61–68**).

These revisions clarify the spatial scale of the process discussed, incorporate updated references (Xing et al., 2017; Ding et al., 2020; Cao et al., 2025), avoid overly broad generalization, and improve the conceptual link to the emergence of evergreen broad-leaved forests.

References:

- Xing, Y. W. & Ree, R. H. Uplift-driven diversification in the Hengduan Mountains, a temperate biodiversity hotspot. *Proc. Natl. Acad. Sci. U.S.A.* 114, E3444–E3451 (2017).
- Ding, W. N., Ree, R. H., Spicer, R. A. & Xing, Y. W. Ancient orogenic and monsoon-driven assembly of the world’s richest temperate alpine flora. *Science* 369, 578–581 (2020).
- Cao, G. L. et al. Cenozoic geoclimatic changes drove the evolutionary dynamics of floristic endemism on the Qinghai–Tibet Plateau. *Proc. Natl. Acad. Sci.* 122, e2426017122 (2025).

4. Lines 74-75: At the first mention of the new hotspot, perhaps the authors might give

the readers some idea of where "Central China" is, given that it's not in the actual center of the country. What about saying, here, that it's centered on Hunan, Jiangxi, etc. in an area of moderate relief and dense human populations? Perhaps mention its area here (or later)??

Response: We sincerely appreciate this helpful suggestion. In the revised manuscript, we now provide additional contextual details at the first mention of the newly identified Central China hotspot (**Lines 84–86**). The text revised as follows: “... Our analysis uncovers a critically overlooked biodiversity hotspot in Central China, a 1.54-million-km² region characterized by moderate topographic relief and centered on Hubei, Hunan, and Jiangxi provinces. With its dense human populations, this region demands urgent conservation attention to safeguard its ...”

5. Lines 124-125: please state the median divergence ages of endemic vs. non-endemic species here (4.8 vs. 7.1 My). I realize that those numbers are shown in Fig 2, but it's an important result and should be mentioned in the text as well.

Response: Thank you for your valuable suggestion. We agree that highlighting key information from the figures directly in the text will enhance clarity for readers. Accordingly, we have included the median divergence ages for endemic and non-endemic species (4.8 Ma vs. 7.2 Ma) in the revised manuscript (**Line 144**).

6. Line 143: "an established method¹⁶" does not convey the substance of the method in any way. Can the authors insert a clarifying phrase here?

Response: Thank you for this helpful comment. We agree that the original phrasing lacked sufficient clarity. In the revised manuscript, we removed the vague expression “an established method” and replaced it with a more informative explanation: “We identify taxonomic centers of neo- and paleo-endemism as the top 5% richest grid cells within the oldest and youngest quartiles of taxa (Extended Data Fig. 7), **following a threshold widely applied in large-scale biodiversity studies**” (**Lines 163–164**), supported by representative references (López -Pujol et al., 2011; Lu et al., 2018 and Xu et al., 2024).

References:

López-Pujol, J., Zhang, F. M., Sun, H. Q., Ying, T. S. & Ge, S. Centres of plant endemism in China: places for survival or for speciation? *J. Biogeogr.* 38, 1267–1280 (2011).

Lu, L. M. et al. Evolutionary history of the angiosperm flora of China. *Nature* 554, 234–238 (2018).

Xu, W. et al. Hidden hotspots of amphibian biodiversity in China. *Proc. Natl. Acad. Sci.* 121, e2320674121 (2024).

7. Line 144: Suggest you insert a table giving area, number of species, and number of endemic species for each of these hotspots.

Response: Thank you for this valuable suggestion. We have added a new table summarizing the area, species richness, and number of endemic species of each hotspot (now included as **Supplementary Table 5**) and have incorporated the phrase “see **Supplementary Table 5 for area, richness, and endemism data**” into the revised manuscript (**Line 167**). The newly added table is provided below.

Supplementary Table 5. Taxon diversity and endemism in three taxonomic endemism centers of China. The area and richness of each endemism center was calculated from the total area of grid cells identified by the top 5% criterion (see Fig. 3a, b). Endemic genera and species listed refer specifically to taxa endemic to China.

Taxonomic endemism center	Genus-level center			Species-level center		
	Area (km ²)	No. of genera	No. of endemic genera	Area (km ²)	No. of species	No. of endemic species
Hengduan Mountains	269,257	1,772	74	383,351	13,511	7,281
Central China	170,000	1,597	59	90,000	6,319	3,013
Yunnan-Guizhou-Guangxi boundary region	30,000	1,461	36	20,000	6,182	2,090

8. Line 198: Suggest you draw the Hu Huanyong Line on one of the maps, so that those unacquainted with it can see where it is (and, in the caption, how it is defined).

Response: Thank you for your valuable suggestion. In the **revised Figure 4**, we have added a clear label for the Hu Huanyong Line and included a brief explanation of its geographic significance and definition in the figure caption. Additionally, to better

illustrate the spatial contrast of recognized Global Biodiversity Hotspots between eastern and western China, we have incorporated the Hu Huanyong Line and its description into **revised Extended Data Fig. 2**. The updated figures and legends are provided below.

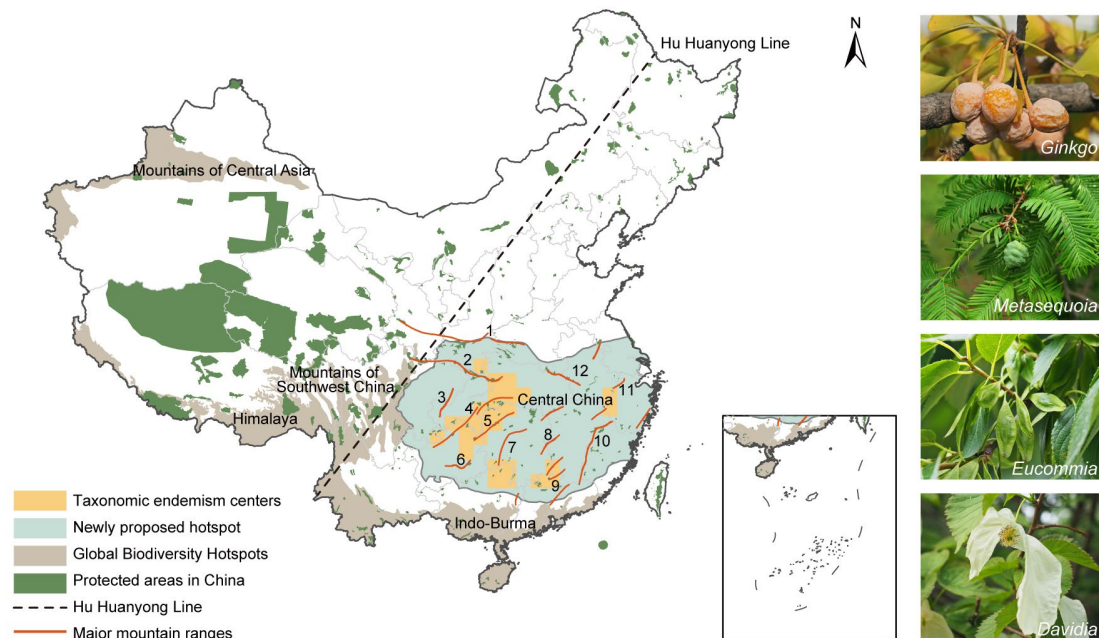
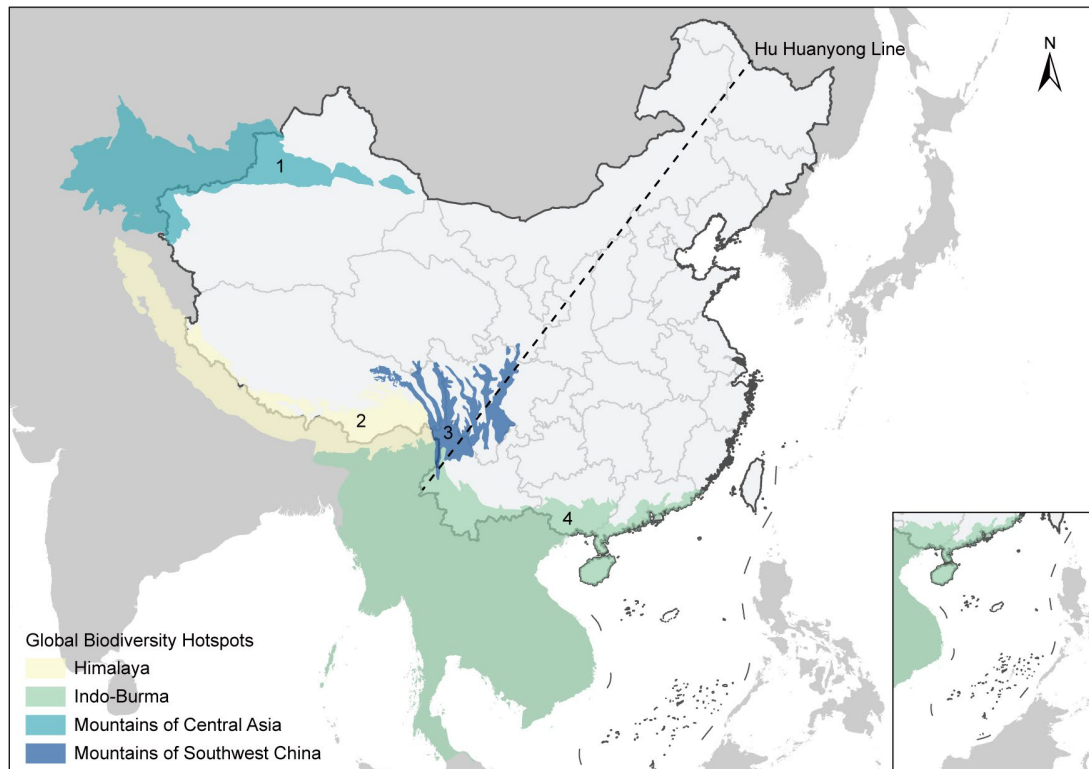


Fig. 4 | Geographic range and protection status of the newly proposed Central China Global Biodiversity Hotspot. The newly proposed Central China hotspot (light green) encompasses taxonomic endemism centers (yellow grid cells) at genus and species levels using quartile and temporal threshold (23 Ma/5 Ma) criteria. Brown shading shows partial overlap with four recognized Global Biodiversity Hotspots in China and dark green indicates current national nature reserves. The Hu Huanyong Line (black dashed) demarcates China's east-west population divide, extending from Heihe City (Heilongjiang Province) to Tengchong City (Yunnan Province). Orange curves indicate major mountain ranges in Central China: 1. Qinling, 2. Daba, 3. Huaying, 4. Dalou, 5. Wuling, 6. Miaoling, 7. Xuefeng, 8. Luoxiao, 9. Nanling, 10. Wuyi, 11. Tianmu, and 12. Dabie. Representative vascular plant genera endemic to Central China are illustrated on the right. Review drawing number for map: GS(2019)1823.



Extended Data Fig. 2 | Geographic extent of the four recognized Global Biodiversity Hotspots overlapping China. The map shows the spatial distribution of four recognized Global Biodiversity Hotspots intersecting China: (1) Mountains of Central Asia, (2) Himalaya, (3) Mountains of Southwest China, and (4) Indo-Burma. The black dashed line represents the Hu Huanyong Line, which delineates China's east-west population divide, extending from Heihe City (Heilongjiang Province) to Tengchong City (Yunnan Province). Review drawing number for map: GS(2019)1823.

9. Final paragraph of narrative: it would be nice to know where the new Central China hotspot sits on the ranked list of global hotspots, based on total number of vascular plant species and number of endemic species. I also wonder whether the authors might mention in the abstract that this hotspot sits in "unique East Asian subtropical evergreen broad-leaved forest ecoregion" as well as the other items mentioned under point 1 above.

Response: Thank you for this thoughtful suggestion. We agree that the global ranking of Central China is an important detail that will interest many readers. Based on a review of key sources on biodiversity hotspots (e.g., Mittermeier et al., 2004; Williams et al., 2011, and Noss et al., 2015), we found that the newly proposed Central China hotspot ranks 6th in total vascular plant species and 27th in endemic vascular plant species among all global biodiversity hotspots. We have incorporated this information

into the revised manuscript as follows: “**While the exact figures require further validation, current data place Central China 6th in total vascular plant species richness and 27th in endemics among the 36 recognized Global Biodiversity Hotspots^{21,61,62}**” (Lines 265–267).

Regarding your suggestion to include the key vegetation type of the Central China hotspot (East Asian subtropical evergreen broad-leaved forest) in the abstract, we agree this is an important addition. We have updated the abstract to include this vegetation feature, along with the total number of vascular plant species and endemic species for Central China, as suggested in point 1 (Lines 33–34). We believe these revisions significantly enhance the clarity and completeness of both the abstract and the main text.

References:

- Mittermeier, R. et al. Hotspots Revisited. Earth’s Biologically Richest and Most Endangered Terrestrial Ecoregions. Conserv. Int. vol. 392 (CEMEX, Mexico City, Mexico, 2004).
- Williams, K. J. et al. Forests of East Australia: the 35th biodiversity hotspot. In: Zachos, F. E., Habel J. C. (eds) Biodiversity hotspots: distribution and protection of conservation priority areas. (Springer, Heidelberg, 2011).
- Noss, R. F. et al. How global biodiversity hotspots may go unrecognized: lessons from the North American Coastal Plain. Divers. Distrib. 21, 236–244 (2015).

Reviewer #3:

The manuscript addresses a highly significant topic—the identification of critical, yet overlooked, biodiversity hotspots using a comprehensive phylogenetic and spatial framework. The scale of the manuscript data, including the extensive phylogeny and distribution records, is impressive and represents a major step forward for the field. The proposal to designate Central China as a new Global Biodiversity Hotspot is both timely and compelling, with substantial implications for global conservation policy. However, I feel that several major points need to be addressed before the manuscript can be considered for publication.

Response: We sincerely appreciate your constructive suggestions and the recognition of the significance of our work for global conservation policy. We have carefully considered your suggestions and incorporated the analyses you recommended and revised the manuscript accordingly. All of the concerns you raised have been addressed in the revised version. A detailed point-by-point response is provided below.

1. While the manuscript have used 100 bootstrap trees to account for phylogenetic uncertainty in divergence time estimation, the impact of this uncertainty on the key downstream analyses (e.g., the identification of neo- and paleo-endemism centers via CANAPE and the quartile method) is not fully demonstrated. I request a more explicit analysis of how sensitive your primary conclusions are to phylogenetic uncertainty. This could involve repeating the CANAPE and endemism center identification on a subset of the bootstrap trees to show the stability of the identified hotspots.

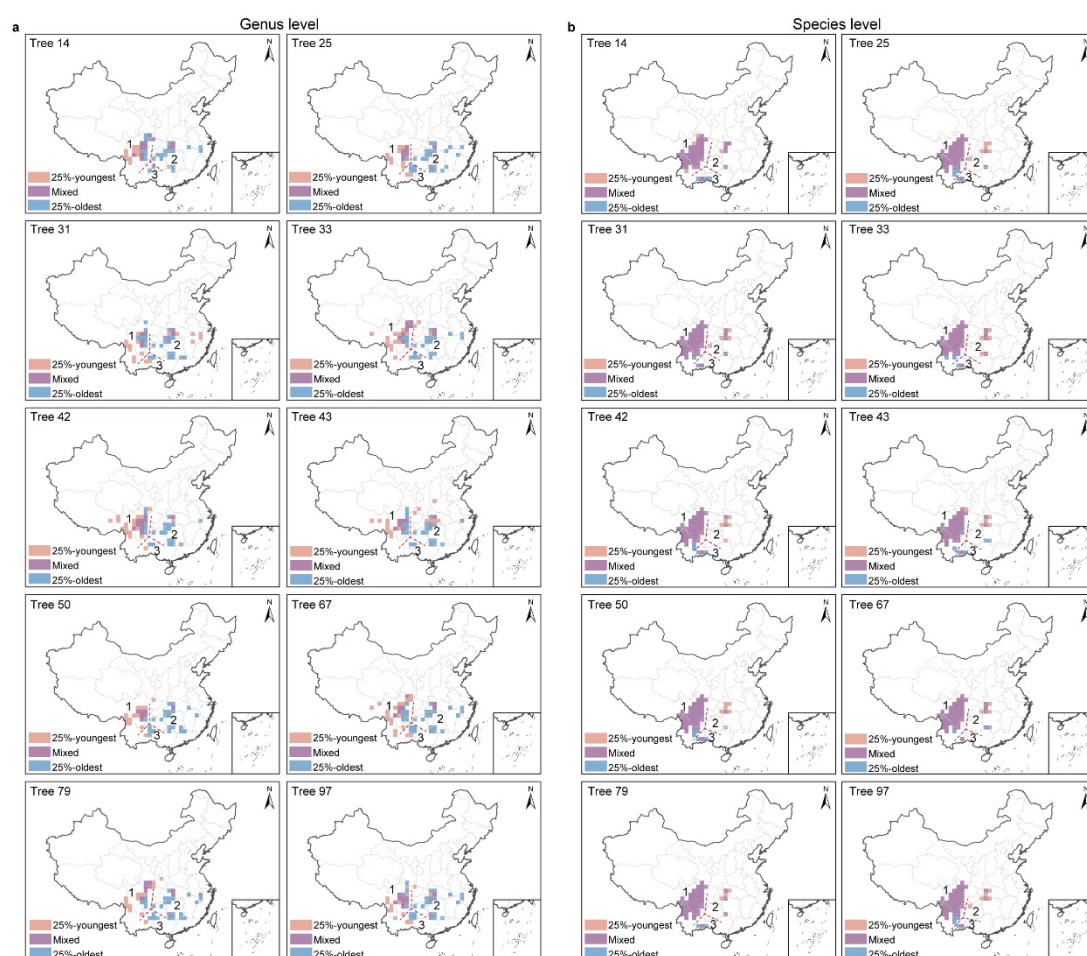
Response: Thank you for raising this important issue. We fully agree that phylogenetic uncertainty must be rigorously evaluated before drawing conclusions from downstream biodiversity analyses. To address this, we performed additional parallel analyses and present the results in two newly added Supplementary Figures (**Supplementary Fig. 5 and Supplementary Fig. 6**).

Specifically, we randomly selected 10 trees from the original set of 100 bootstrap trees and applied the same analytical methods described in the main text (i.e., CANAPE and the quartile method) to identify neo- and paleo-endemism centers. We then summarized and mapped the resulting taxonomic and phylogenetic endemism patterns for comparison.

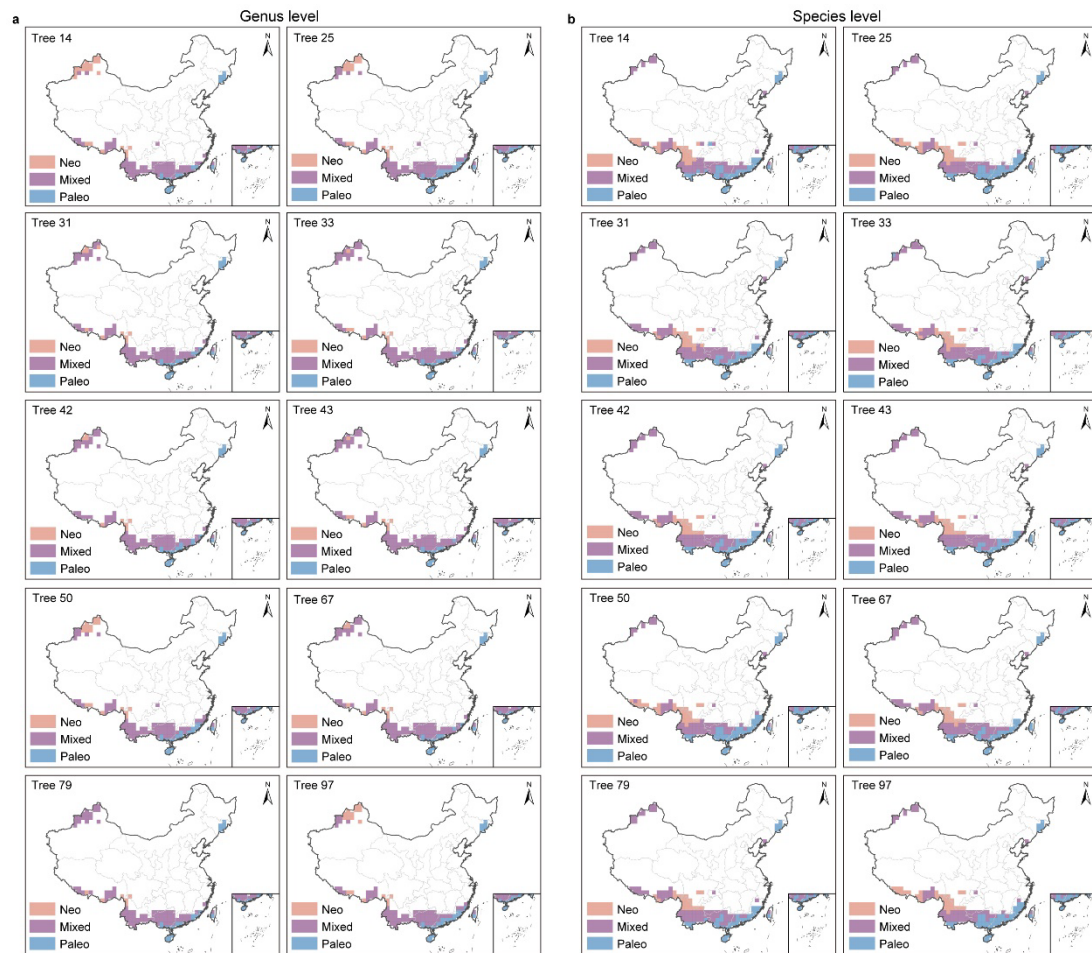
For taxonomic endemism, the three primary endemism centers remained consistent across both genus- and species-level analyses based on the 10 randomly selected trees (**Supplementary Fig. 5**). Likewise, the phylogenetic endemism analyses showed high stability: both genus- and species-level results strongly resembled those obtained from the optimal tree, consistently revealing a contiguous phylogenetic endemism center

across southern China, as well as centers in Xinjiang and northeastern China. At the species level, all subsampled trees also consistently recovered the prominent neo-endemism center in the Hengduan Mountains (**Supplementary Fig. 6**).

Overall, these additional analyses indicate that phylogenetic uncertainty introduces only minor variation and does not alter our key results or conclusions, thereby reinforcing the robustness of our findings. We have updated the corresponding sections of the main text (**Lines 224–229**) and Methods (**Lines 497–499; Lines 549–551**).



Supplementary Figure 5. Geographic distribution of taxonomic endemism centers for vascular plants in China based on 10 randomly selected bootstrap trees. Taxonomic endemism centers based on the top 5% criterion at the genus (a) and species (b) levels: (1) the Hengduan Mountains, (2) Central China, and (3) Yunnan-Guizhou-Guangxi boundary region. Grid cells in pink represent hotspots of the youngest quartile, blue the oldest quartile, and purple mixed hotspots of the two types. The index of the specific bootstrap replicate (selected from 100 trees) is shown in the upper-left corner of each map. Review drawing number for maps: GS(2019)1823.



Supplementary Figure 6. Geographic distribution of phylogenetic endemism centers for vascular plants in China based on 10 randomly selected bootstrap trees. Phylogenetic endemism centers identified by the CANAPE analysis at the genus (a) and species (b) levels. Grid cells in pink represent centers of neo-endemism, blue centers of paleo-endemism, and purple centers of mixed-endemism. The index of the specific bootstrap replicate (selected from 100 trees) is shown in the upper-left corner of each map. Review drawing number for maps: GS(2019)1823.

2. The use of fixed temporal thresholds (23 Ma for genera, 5 Ma for species) in your robustness check, while following previous studies, requires a stronger biological justification within the context of your specific dataset and the regional history of China. Please provide a more detailed rationale for why these specific cut-offs are the most appropriate, or discuss the potential implications if alternative thresholds were used.

Response: Thank you for your thoughtful comment. We appreciate the opportunity to clarify the rationale behind the fixed temporal thresholds used in our robustness analyses. We acknowledge that our earlier description was too brief, and we now

provide a more detailed justification for the cut-offs applied at the genus and species levels.

No universal temporal threshold exists for distinguishing paleo- from neo-endemism, as the appropriate boundary depends on the unique evolutionary and geological history of the focal region. For endemic genera in China, early work integrating geological, fossil, morphological, and molecular evidence indicates that many classic paleo-endemic genera, such as *Ginkgo*, *Metasequoia*, *Davidia*, and *Eucommia*, originated in the Late Cretaceous to Paleogene and once had broad Northern Hemisphere distributions before contracting into China during Neogene climatic cooling (Wu et al., 2007). In contrast, recent large-scale phylogenetic studies consistently show that most neo-endemic genera diversified during the Neogene, with the Miocene emerging as the primary diversification epoch for China's plant genera (Lu et al., 2018; Chen et al., 2018; Hu et al., 2022). This pattern is also reflected in our dataset (Figure 2a) and supports using the Paleogene–Neogene boundary at 23 Ma as a biologically justified threshold for distinguishing paleo- from neo-endemic genera in China.

Determining a species-level threshold is more challenging (López -Pujol et al., 2011). However, given that the majority of China's endemic species are concentrated in the Hengduan Mountains, an area generally considered to have experienced rapid and relatively recent uplift during the late Miocene to late Pliocene (Clark et al., 2005; Wang et al., 2012). These geological transitions likely promoted elevated rates of in situ diversification (Xing et al., 2017). Recent work on the Sino-Himalayan flora further demonstrates that the past ~5 Ma were characterized by rapid radiations driven by orogeny and monsoon intensification, which facilitated the emergence of many narrowly distributed young species, particularly within *Rhododendron*, *Pedicularis*, and *Corydalis* (Liu et al., 2023). Collectively, these studies indicate that ~5 Ma represents a key turning point in the assembly of the regional flora, thus providing a well-supported basis for our species-level threshold.

Although these thresholds are supported by the regional geological and evolutionary literature, any fixed temporal boundary remains an approximation. For this reason, our main analyses rely on the quartile-based approach, which identifies the oldest and youngest 25% of endemic lineages. This method avoids dependence on potentially arbitrary cut-offs and enhances the contrast between paleo- and neo-endemism by excluding intermediate-age lineages. We have revised the Methods section accordingly to clarify the rationale and implementation of fixed threshold strategy (**Lines 506–517**).

References:

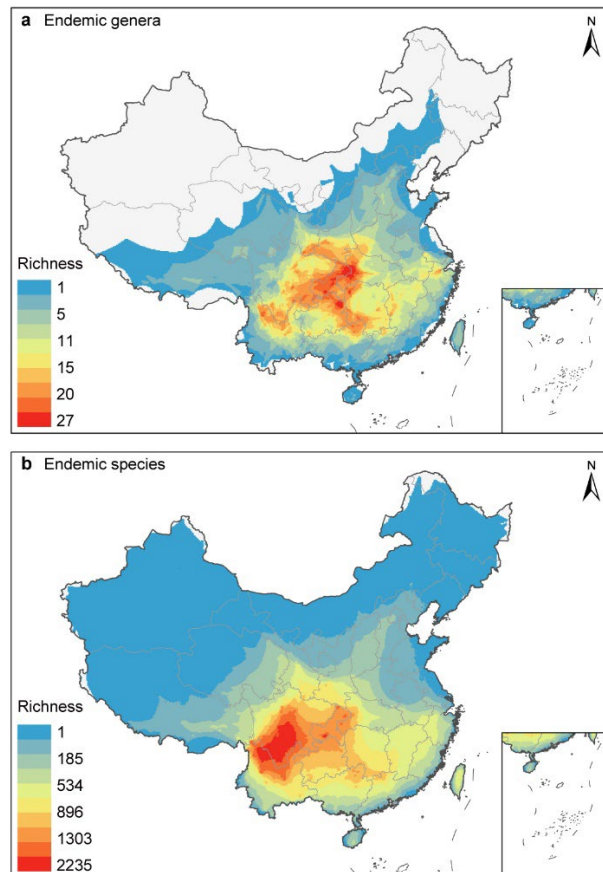
- Wu, Z., Sun, H., Zhou, Z., Peng, H. & Li, D. Origin and differentiation of endemism in the flora of China. *Front. Biol. China* 2, 125–143 (2007).
- Lu, L.M. et al. Evolutionary history of the angiosperm flora of China. *Nature* 554, 234–238 (2018).
- Chen, Y. S., Deng, T., Zhou, Z. & Sun, H. Is the East Asian flora ancient or not? *Natl. Sci. Rev.* 5, 920–932 (2018).
- Hu, H.H. et al. Temporal and spatial comparisons of angiosperm diversity between eastern Asia and North America. *Natl. Sci. Rev.* 9, nwab199 (2022).
- López-Pujol, J., Zhang, F. M., Sun, H. Q., Ying, T. S. & Ge, S. Centres of plant endemism in China: places for survival or for speciation? *J. Biogeogr.* 38, 1267–1280 (2011).
- Wang, E. et al. Two-phase growth of high topography in eastern Tibet during the Cenozoic. *Nat. Geosci.* 5, 640–645 (2012).
- Clark, M. K. et al. Late Cenozoic uplift of southeastern Tibet. *Geology* 33, 525 (2005).
- Xing, Y. & Ree, R. H. Uplift-driven diversification in the Hengduan Mountains, a temperate biodiversity hotspot. *Proc. Natl. Acad. Sci. U.S.A.* 114, E3444–E3451 (2017).
- Liu, Y. et al. The Sino-Himalayan flora evolved from lowland biomes dominated by tropical floristic elements. *BMC Biol.* 21, 239 (2023).

3. The manuscript appropriately acknowledge the "border effect" and conduct a separate analysis on strictly endemic taxa. However, the method for estimating species geographic ranges (based on 100 km grid cells and county-level records) could inherently overestimate the range size of narrow endemics. Please discuss this limitation and consider, if feasible, a sensitivity analysis using a more refined range estimation method (e.g., alpha hulls or expert-drawn ranges for key endemics) to confirm that the patterns for Central China hold.

Response: Thank you for raising this important consideration. In response to your suggestion, we downloaded all available occurrence records of Chinese vascular plants

from the Global Biodiversity Information Facility (GBIF, <https://www.gbif.org/>, accessed November 16, 2025). We then applied a rigorous data-processing protocol, including taxonomic name standardization, coordinate cleaning, and removal of non-native records. This procedure yielded 432,834 cleaned occurrence records for 12,973 Chinese endemic species. We then constructed species range estimates using the alpha-hull approach (with convex hulls or buffered points applied for species with limited records). Overlaying these modelled ranges revealed endemism patterns broadly consistent with those derived from our county-level distribution data (**Figure 3a, b**), as presented in the newly added **Supplementary Fig. 8**.

Regarding the number of endemic species in Central China, our GBIF-based assessment strongly supports the validity of this newly proposed hotspot. Specifically, we identified 1,675 species with ranges restricted to Central China based on records available in GBIF. When we incorporated additional endemics identified via the *Catalogue of Life China* to address any GBIF omissions, the total number of species endemic to this region increased to **2,158**. This number is largely consistent with the estimate (2,024) based on our county-level distribution data, reinforcing that Central China meets the strict criterion of over 1,500 endemics for hotspot designation. We have now included a detailed description of the sensitivity analysis in the Methods section (**Lines 638–671**) and explicitly discussed the findings in the main text (**Lines 264–266**). These additions further strengthen the recognition of the newly proposed Central China hotspot.



Supplementary Figure 8. Spatial distribution of richness for Chinese endemic vascular plant genera and species based on coordinate data. (a) Richness of endemic genera (b) Richness of endemic species. Light gray cells indicate the absence of endemic genera or species. Review drawing number for maps: GS(2019)1823.

Reference:

GBIF Occurrence download <https://doi.org/10.15468/dl.vmupyc> (GBIF.org, 2025).

4. The geographic delineation of the proposed "Central China" hotspot is critical to your argument. While you reference Takhtajan's Floristic Province and your own endemism centers, the process of drawing the final boundary in Figure 4 needs more explicit description in the main text or methods. A clearer, step-by-step explanation will strengthen the defensibility of this proposed hotspot's borders.

Response: We greatly appreciate this valuable suggestion. We fully agree that a more detailed explanation of how the boundaries of the proposed Central China hotspot were delineated will strengthen the credibility of this newly recognized region. Accordingly, we have added a comprehensive description in the Methods section (**Lines 585–615**)

outlining how the southern, western, and northern boundaries were defined (with the eastern boundary corresponding to the coastline) and detailing the climatic, vegetational, and floristic criteria used to inform these delineations. We also clarify that these combined lines of evidence consistently support the recognition of Central China as a distinct and biogeographically important region clearly differentiated from surrounding floristic units. Additionally, a brief cross-reference has been added in the main text (**Lines 257–258**) to guide interested readers to the expanded methodological description.

5. The results convincingly show peaks of diversification in the Miocene and Pleistocene. However, the discussion of the drivers remains somewhat correlative. I encourage you to more deeply integrate your findings with specific paleoclimatic and geological models for the region. For instance, can you more directly link the Pleistocene diversification peak to models of refugia in Central China, rather than primarily the Hengduan Mountains?

Response: Thank you for your thoughtful review and insightful suggestion. In response, we have expanded the discussion of the diversification history and potential driving factors of endemic taxa by incorporating a thorough examination of the region's geological and climatic history. The newly added content is organized into two levels: genera (**Lines 118–125**) and species (**Lines 132–141**).

Our findings indicate that endemic genera, which originated in the Eocene and Miocene coinciding with the peak in lineage accumulation rate (LAR; Fig. 2a), reach their highest diversity in the Hengduan Mountains (revised **Supplementary Fig. 2a, c**, where the map now highlights mountain ranges in areas of high diversity). As a result, the discussion focuses on these genera centered around the Hengduan Mountains, where orogeny and monsoon intensification are likely major driving forces (Ding et al., 2020; Cao et al., 2025).

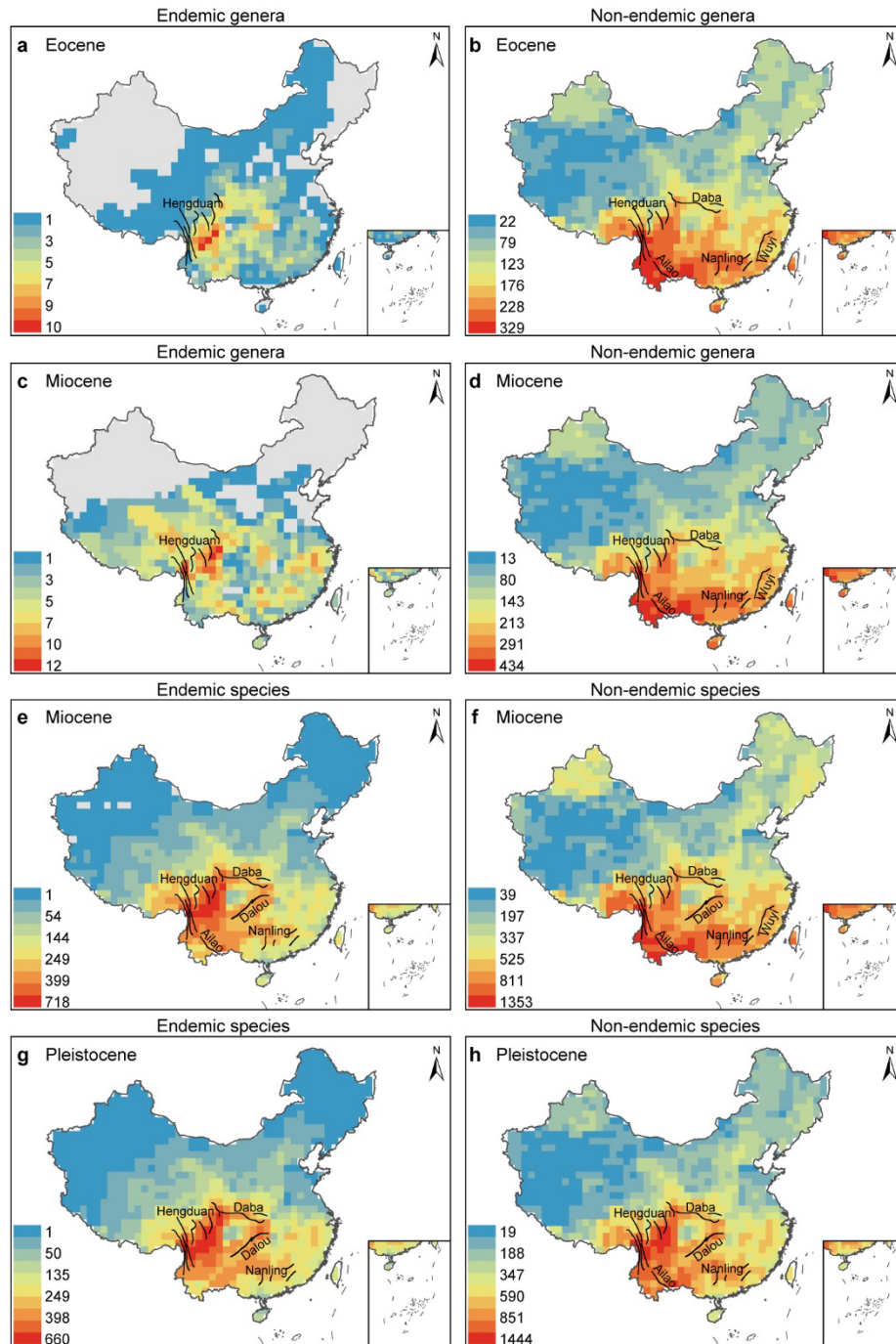
At the species level, taxa originated during the diversification peak of Pleistocene span

broader regions, including both the high-altitude Hengduan Mountain in the southwest and the continuous mid- to low-altitude mountains in the southeast (revised **Supplementary Fig. 2g**). The high species-level endemism of the Hengduan Mountains is primarily attributed to continuous high rate of *in situ* diversification since the mid Miocene (Ding et al., 2020). In addition, the southeastern mountains served as refugia during Quaternary glaciations, preserving relict species and promoting the diversification of young endemic lineages. This process was facilitated through isolation, secondary contact, and hybridization, linked to population contractions and expansions during glacial–interglacial cycles (Stewart et al., 2010; Kadereit et al., 2021).

We hope that these expanded discussions provide a clearer understanding of the temporal dynamics of endemic flora in China.

References:

- Ding, W. N., Ree, R. H., Spicer, R. A. & Xing, Y.-W. Ancient orogenic and monsoon-driven assembly of the world's richest temperate alpine flora. *Science* 369, 578–581 (2020).
- Cao, G. L. et al. Cenozoic geoclimatic changes drove the evolutionary dynamics of floristic endemism on the Qinghai–Tibet Plateau. *Proc. Natl. Acad. Sci.* 122, e2426017122 (2025).
- Stewart, J. R., Lister, A. M., Barnes, I. & Dalén, L. Refugia revisited: individualistic responses of species in space and time. *Proc. R. Soc. B: Biol. Sci.* 277, 661–671 (2010).
- Kadereit, J. W. & Abbott, R. J. Plant speciation in the Quaternary. *Plant Ecol. Divers.* 14, 105–142 (2021).



Supplementary Figure 2. Spatial richness of endemic and non-endemic genera and species originated during key geological periods in China. a-d, Richness of genera originated during the Eocene and Miocene, e-h, species originated during the Miocene and Pleistocene. Gray cells indicate the absence of China's endemic genera or species. Black lines depict major mountain ranges in areas of high richness. Review drawing number for maps: GS(2019)1823.

6. To strengthen the case for Central China's global significance, I recommend adding a comparative table or paragraph in the results/discussion. This should quantitatively compare Central China's metrics (species richness, endemism, habitat loss) with other

established Global Biodiversity Hotspots, particularly other subtropical ones.

Response: Thank you for this valuable suggestion. We agree that adding a comparative table substantially strengthens the presentation of global importance of Central China. Our previous version already included a similar table in the Supplementary Information (previous Supplementary Table 7); however, as you recommend, presenting it in the main text allows readers to more directly understand the diversity and conservation value of the newly proposed hotspot. In response, we have expanded and updated the original table and moved it into the main text as **Table 1 (Lines 260–262)**. This table provides a comprehensive quantitative comparison between Central China and four recognized subtropical hotspots at similar latitudes, including metrics such as total area, vascular plant richness, number and proportion of endemic species, and the percentage of remaining natural vegetation.

Table 1. Comparison of area, vascular plant diversity, endemism and vegetation loss between Central China and four subtropical Global Biodiversity Hotspots. Source data for the four recognized hotspots are from ref.^{21,59,60}.

Hotspot	Area (km ²)	Species	Endemic species	Percentage of endemism	Percentage of remaining natural vegetation
Central China	1,541,960	14,431	2,024	14%	7%
North American Coastal Plain	1,130,000	6,200	1,816	29%	15%
Forests of East Australia	253,200	8,257	2,144	26%	23%
Mediterranean Basin	2,085,292	22,500	11,700	52%	5%
Maputaland- Pondoland-Albany	274,136	8,100	1,900	23%	25%

7. The discussion rightly highlights the conservation gap. However, it would be strengthened by a more realistic and nuanced discussion of the challenges and opportunities for conservation in this densely populated region. What specific strategies (beyond expanding protected areas) could be effective? How can connectivity be

achieved in such a fragmented landscape? Engaging with the socio-economic literature on conservation in human-dominated landscapes would be beneficial.

Response: Thank you for this valuable suggestion. In response, we have expanded the discussion to provide a more realistic and nuanced assessment of conservation challenges and opportunities in this densely populated, highly fragmented region. Beyond expanding protected areas, we now outline a set of context-appropriate strategies informed by both ecological evidence and socio-economic considerations:

1. **Integrating remaining intact patches of native vegetation** (see the revised **Extended Data Fig. 10** attached below for priority national park pilots) into the national park system to ensure strict land-use regulation and cross-jurisdictional coordination.
2. **Implementing fine-scale conservation interventions** in human-dominated landscapes, including plant micro-reserves (Fos et al., 2017), stepping-stone habitats (Saura et al., 2014), and Other Effective Area-Based Conservation Measures (OECMs), to maintain functional connectivity (Brodie et al., 2025; Ren et al., 2025).
3. **Applying socio-economic mechanisms**, such as ecological compensation (Payment for Ecosystem Services), community co-management, and livelihood diversification to reduce conservation–development conflicts and support long-term stewardship (Pan et al., 2017).
4. **Recognizing Central China as a Global Biodiversity Hotspot** to elevate its international conservation priority and provide a broad-scale framework to guide targeted, context-appropriate planning, advancing conservation action and supporting China’s sustainability ambitions.

Together, these strategies provide a practical, evidence-based, and socio-economically informed pathway for conserving biodiversity and endemism in one of China’s most human-dominated landscapes. Additional details can be found in the revised main text (**Lines 287–308**).



Extended Data Fig. 10 | The remaining native vegetation in Central China. The black line outlines the proposed new biodiversity hotspot (Central China) in this study, while green area highlights the distribution of remaining native vegetation. Yellow dots represent established national parks, while blue dots indicate national park pilots. National parks (or pilots) in Central China: 1. Giant Panda National Park; 2. Shennongjia National Park (pilot); 3. Nanshan National Park (pilot); 4. Nanling National Park (pilot); 5. Wuyi Mountains National Park; 6. Qianjiangyuan National Park (pilot). Review drawing number for maps: GS(2019)1823.

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8. The manuscript would benefit from a dedicated paragraph in the discussion that explicitly outlines the key limitations of the study. This should include, but not be limited to, the incomplete species sampling in the phylogeny (notably in Xinjiang and

the Qinghai-Tibet Plateau), the reliance on public and herbarium records with inherent spatial biases, and the limitations of the molecular markers used for dating deep and rapid radiations.

Response: Thank you for highlighting this important point. We have now added a dedicated paragraph in the revised manuscript (**Lines 215–224**) to explicitly discuss the key limitations of our study. These include the incomplete species sampling in the phylogeny, particularly in Xinjiang and the Qinghai-Tibet Plateau, the reliance on public and herbarium records that may introduce spatial biases, and the constraints of the molecular markers used for dating deep and rapid radiations. We also outline directions for future work, including improving phylogenetic resolution and refining geographical distribution data.

9. The discussion could be more focused. I suggest streamlining the explanation of the differences between taxonomic and phylogenetic endemism and instead placing greater emphasis on the novel, synthetic conclusion: that combining these approaches was essential for revealing the critical importance of Central China, a region that would be missed by frameworks relying on a single metric.

Response: Thank you for this insightful suggestion. We have streamlined the explanation of the differences between taxonomic and phylogenetic endemism, shifting the focus to our novel, synthetic conclusion. By emphasizing the critical role of integrating both approaches, we highlight how this method revealed the importance of Central China—a region that could be overlooked in frameworks relying on a single metric. Detailed changes can be found in the revised main text (**Lines 210–214**).