

Spatial phylogenetics of the Chinese angiosperm flora provides insights into endemism and conservation

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Abstract

Background The flora of China is well known for its high endemism. Identifying centers of endemism and designating conservation priorities for the Chinese flora are essential goals for biodiversity studies. We used a phylogeny that included 2,909 Chinese angiosperm genera and 1.39 million spatial distribution records to conduct spatial phylogenetics analyses. Then, we identified centers of neo- and paleo-endemism in the Chinese angiosperm flora using spatial phylogenetic methods. Phylogenetic endemism centers were compared with taxonomic endemism centers, and their implications for conservation were examined. **Results** (1) The majority of grid cells with significant phylogenetic endemism (PE) were dominated by mixed- or super-endemism in China, but only one grid cell dominated by neo-endemism was located in the Qinghai–Tibet Plateau. (2) Ten geographic centers of grid cells with high PE were identified. Four of these found in northern China are recognized for the first time here. (3) Arid and semiarid regions were commonly linked to PE centers in both our study and other spatial phylogenetics studies worldwide. (4) Five priority conservation gaps were detected by overlaying the boundaries of China's nature reserves on these centers of endemism. **Conclusions** The spatial phylogenetics approach provides an evolutionary perspective to understanding the diversity and endemism patterns. These integrated methods are necessary for broad-scale conservation planning, especially when aiming to conserve evolutionary history.

Background

Identifying 'centers of endemism' plays a prominent role in establishing biodiversity conservation priorities [1–5]. Centers of endemism have been widely recognized as potential refugia (i.e., paleo-endemism) or as places where young species are diversifying (i.e., neo-endemism) [6, 7]. A center of paleo-endemism was described as a location with many ancient lineages, which perhaps had widespread or narrow ranges in the past that contracted into its currently observed small range [3, 8, 9]. A center of neo-endemism was considered an area that harbors many recently diverged species that have not migrated out of their area of origin [3, 8, 9]. Identifying and explaining paleo-endemism and neo-endemism can help inform historical biogeography, evolution, and biodiversity conservation [10–13]. It should be noted that until the development of the methods applied here, however, centers of paleo- and neo-endemism were difficult to clearly distinguish in practice because of poor fossil evidence and lack of a standard threshold for the geological time scale that can delineate temporal boundaries [14–16].

The absolute endemism concept, which is traditionally employed, identifies a center of endemism by the presence of taxa that are completely restricted to a particular area [17]. A more nuanced approach is to use a relative endemism concept based on range sizes of taxa [1, 18, 19], using indices of weighted endemism (WE) and corrected weighted endemism (CWE). WE and CWE scores take into account the endemism of each taxon in that area on a continuous scale. The relative endemism concept has been increasingly adopted in endemism studies, because it can provide a quantitative measure to clearly and easily identify centers of endemism for a given area [1, 18, 19]. Rosauer *et al.* [20] extended the relative endemism concept to include phylogenetic trees, thereby incorporating evolutionary history into

measures of endemism, and applied the concept of WE to all branches of a phylogenetic tree, which resulted in a phylogenetic endemism (PE) metric. The PE value is a quantitative measure that takes into account the range size of the branches connecting all organisms in a given area. Each operational taxonomic unit (OTU) on the tree has one PE value, which is equal to the branch length of the OTU divided by its range size. A given study area was divided into many equal-area grid cells. The PE value of each grid cell is the sum of the PE values for each OTU in the grid cell [20, 21]. Thus, PE adds an evolutionary perspective to understanding endemism and has drawn a lot of attention [22–25].

Recently, PE methods have been developed to identify and distinguish centers of endemism using large spatial datasets [12, 25–32]. With Australian *Acacia* as a case study, Mishler *et al.* [12] proposed spatial randomization tests of phylogenetic diversity (PD) [33], PE, and two new metrics called relative phylogenetic diversity (RPD) and relative phylogenetic endemism (RPE). The latter metric is applied in a test called categorical analysis of neo- and paleo-endemism (CANAPE); this test uses a metric called relative phylogenetic endemism (RPE) to quantitatively distinguish between centers dominated by neo-endemism (rare short branches) or paleo-endemism (rare long branches) [12]. This phylogenetic approach to endemism has been used to analyze different taxonomic groups and different regions, such as the Australian native Asteraceae [27], five taxonomic groups (plant genera, fish, tree frogs, acacias, and eucalypts) in the Murray–Darling Basin region of southeastern Australia [26], New World bats [31], and Cyperaceae in the United States and Canada [25]. Additionally, using large regional phylogenies, CANAPE has been used in endemism studies of whole floras, such as the angiosperm flora of the Australian continent and the vascular floras of California, Chile, Florida, Mexico, and New Zealand (see Additional file 1 for a complete list). All of these studies showed the feasibility and utility of using phylogenetic measures of endemism, and the importance of testing these measures in more distinct taxonomic groups and locations has become paramount.

China has one of the richest floras worldwide, with more than 30,000 native vascular plant species and a high percentage of endemic taxa (e.g., 52.1% of seed plant species are endemic) in the absolute endemism sense [34]. China has approximately 2–8 endemic families; Ginkgoaceae and Eucommiaceae are uncontroversial paleo-endemic families, but debate remains over other several endemic families due to their variable taxonomic status, such as Acanthochlamydeaceae, Bretschneideraceae, Davidiaceae, Kingdoniaceae, Rhoipteleaceae, Sargentodoxaceae, and Tapisciaceae [35–38]. Ying and Zhang [39] reported that China has 243 endemic genera of seed plants, and they identified three centers of endemism (Additional file 2: Figure S1a). Wang and Zhang [40] identified eight centers of endemism for 269 genera that are endemic to China (Additional file 2: Figure S1b). Using 12,980 seed plant species that are endemic to China [34], Huang *et al.* [41, 42] identified 19 centers of endemism for the Chinese flora (Additional file 2: Figure S1d). Lópes-Pujol *et al.* [3] identified 20 centers of endemism in central and southern China based on the distribution pattern of 555 Chinese endemic species (Additional file 2: Figure S1c). These studies all showed that mountainous areas harbored the largest number of endemism hotspots; in particular, the Hengduan Mountains and central China were two regions of critical conservation priority (Additional files 2 & 3). The previous studies are very helpful for understanding endemism and guiding biodiversity conservation in China, but they focused on taxonomic endemism or

used relatively coarse phylogenetic data (e.g., Huang *et al.* [41]). Therefore, a more comprehensive study of diversity and endemism from a phylogenetic perspective using more rigorous analytical measures should be conducted for the Chinese flora.

Here, we used a spatial phylogenetics approach to study diversity and endemism in the Chinese angiosperm flora. Our goals were to: (1) explore PD and PE patterns in the Chinese flora; (2) use CANAPE to identify centers of neo- and paleo-endemism; (3) examine similarities and differences among centers of endemism identified in previous studies and this study; and (4) identify priority conservation gaps from a PE perspective.

Results

Observed diversity and endemism

The orientation and the name of the significant area in this study are illustrated in Fig. 1. Richness and PD had similar observed patterns. Hengduan Mountains, Yunnan–Guizhou Plateau, Guangdong–Guangxi mountainous areas, Hainan Island, Taiwan Island, and east Sichuan–west Hubei had the highest generic richness (GR) and phylogenetic diversity (PD) (Fig. 2 a, c). Weighted endemism and PE also had similar observed patterns. Southern China, especially the Yunnan–Guizhou Plateau, Guangdong–Guangxi mountainous areas, Hainan, Taiwan, Hengduan Mountains, and east Sichuan–west Hubei, had the highest WE and PE values (Fig. 2 b, d). Other areas in southern China showed moderate levels of WE and PE. A moderate level of endemism was also identified in a small number of cells in the Tianshan–Altai Mountains and Changbai Mountains. There were low levels of endemism in the hinterland of the Qinghai–Tibet Plateau (QTP), the Tarim Basin, the Inner Mongolian Plateau, North China, and Northeast China.

Spatial randomization results

The significance test for PD (Fig. 3a) showed that virtually all cells in western China, and scattered cells in eastern China, are significantly low in PD, while significantly high PD cells were only found on Taiwan Island (Fig. 3a). In contrast, the significance test for RPD (Fig. 3b) showed widespread areas with significantly high RPD (i.e., areas that contain longer phylogenetic tree branches than expected) including the Daxing’anling and Changbai Mountains in Northeast China, the Tianshan–Altai Mountains and northeast Qinghai–central Gansu in Northwest China, Guangdong Province, Taiwan, and Hainan Island. Areas with significantly low RPD (i.e., areas that contain shorter branches than expected; Fig. 3b) were scattered in central China, central Tibet in the QTP, and the Kashi area in the arid regions of the Tarim Basin.

A total of 118 grid cells with significantly high PE values were identified by CANAPE (Fig. 4). Ten geographic centers of endemism can be recognized, numbered here as they are labeled in Fig 4: (1) the largest center of endemism was located south of the Tropic of Cancer in the mainland; other centers included (2) Hainan Island, (3) Taiwan Island, (4) the Lhoka Prefecture area, (5) the Shigatse area (on the

periphery of Qomolangma), (6) the Dabie Mountains, (7) the Karakoram Mountains, (8) the Kashi area, (9) the Tianshan–Altai Mountains, and (10) the Changbai Mountains. The majority of grid cells with significant PE showed mixed- or super-endemism (purple and darker purple cells in Fig. 4). Of all centers of endemism, areas 1 and 9 contained the most extensive amount of mixed- and super-endemism cells. Only one grid cell showed significant concentrations of neo-endemism; it was located in the Shigatse area on the periphery of Qomolangma in the QTP (red cells in Fig. 4). Ten grid cells dominated by paleo-endemism were scattered in the Changbai Mountains, Zayu from the Lhoka Prefecture area, Boluokenu Mountain, the Yunkai Mountains, and Hainan Island (blue cells in Fig. 4).

Phylogenetic turnover among CANAPE cells

The range-weighted turnover analysis grouped the CANAPE grid cells into two major clusters: northern and southern (Fig. 5). The northern cluster contained three sub-clusters: the Tianshan–Altai–Karakoram Mountains, Kashi area, and Changbai Mountains. Cells from Hainan Island and the Dabie Mountains were dissimilar to those of all other sub-clusters in southern China. The cells located in Tibet and two cells from Yunnan Province clustered together. Taiwan Island cells clustered deeply with the southern China cluster.

Conservation gaps

Of the 118 significant grid cells discovered in CANAPE, 26 cells across six regions had no overlap with current nature reserves in China (Fig. 6). Most of the conservation gap cells were located in the Tianshan–Altai Mountains (Fig. 6F), which are along the southwest edge of Junggar Basin in Northwest China. The other four regions were scattered in the Shigatse area (Fig. 6D) and Lhoka Prefecture area (Fig. 6C) in the QTP, the Dabie Mountains (Fig. 6A) in central China, the Kashi area (Fig. 6E) in Northwest China, and the Ailao–Jinzhong–Shibalian Mountains (Fig. 6B) in Southwest China.

Discussion

Patterns of phylogenetic diversity

Significantly low PD, called "phylogenetic clustering", is likely indicative of habitat filtering. Closely related organisms often share an evolutionarily conservative habitat preference, thus the organisms living together in a particular habitat will tend to be more closely related than expected by chance. Past studies [21, 28, 29, 32] have shown this is especially prevalent in dry habitats, a pattern which is confirmed here. Significantly high PD, called "phylogenetic overdispersion", may be indicative of another ecological process, competitive exclusion. This was only observed here on Taiwan Island, which may be because our study encompasses a very broad area covering several biomes. Future studies focused at a finer scale within a biotic region are more likely to uncover instances of phylogenetic overdispersion.

The discovery of several areas of significantly high RPD in northern, central, and southeastern China (blue areas in fig. 3b) indicates that the flora of those areas contains unusually long branches, i.e.

those with relatively few close relatives within China. This could indicate that the flora is relatively old, containing many relictual lineages. In some cases, particularly close to the Chinese borders, it could also indicate the presence of a few lineages of larger clades that mostly occur outside the country, e.g., the extreme southeastern tropical area of the country. The area of significantly low RPD in the middle of the QTP indicates that the flora there contains unusually short branches, potentially indicative of an evolutionary radiation there. All these regions would be worth further studies of processes responsible for the lineages present.

Centers of phylogenetic endemism in northern China

The Tianshan–Altai Mountains, Karakoram Mountains, and Changbai Mountains are boreal mountains located in northern China; these areas and the Kashi area were identified as centers of phylogenetic endemism for the first time in this study. This result adds a crucial complement to the previous non-phylogenetic studies of centers of endemism in China (Additional file 2).

The arid Northwest China biome was influenced by significant climatic oscillations and environmental changes in the Quaternary [43]. There are multiple separate glacial refugia for plants located in the Tianshan–Altai Mountains, such as those for *Hippophae* [44], *Gymnocarpos przewalskii* [45], and *Reaumuria soonarica* [46]. Our results confirmed the above conclusions. The flora of this region was derived from Tethys coastal xerophytes or immigrated from East Asia, and the flora is xeromorphic and ancient [43, 47]. This region's aridification began in the early Miocene, and drastically increased by desert expansion during the Pleistocene [48, 49]. The lower elevation valleys or mountainous edges of the Tianshan–Altai Mountains likely served as refugia in the Quaternary [43]. During the interglacial periods, refugial lineages may have been able to expand their ranges. Meanwhile, this region's aridification also stimulated plant diversification [50–53]. These paleobotanical interpretations are supported by our CANAPE results, which showed that relict endemics (rare long branches) and young endemics (rare short branches) are concentrated in the region. In particular, paleo-endemism is concentrated in the Tianshan Mountains, which contains long-branch genera that survived extinction events. The area from Junggar Basin to the Altai Mountains has mainly mixed-endemism. These results indicated co-occurrence in these areas of some relict genera with rare long-branches and young genera with range-restricted short branches. These young genera are concentrated from the Tianshan Mountains to the Altai Mountains and show significantly low PD, especially at the edge regions between mountains and desert. The aridity of this center of endemism might be driving rapid diversification in its core areas of the Gurbantunggut Desert in Junggar Basin [50–53].

The center of phylogenetic endemism discovered in the Changbai Mountains is dominated by paleo-endemism. Our results indicate that these mountains have served as refugia for multiple lineages. Some genera present here, such as *Anemarrhena*, *Mukdenia*, and *Schisandra*, are long isolated branches in the phylogenetic tree, likely because of extinction of close relatives. The preservation of some Tertiary relict plants in the Changbai Mountains refugia was confirmed by previous studies on Asian butternuts (*Juglans* section *Cardiocaryon*) [54, 55]. Fossil evidence indicated that the Asian butternuts' ancestors

were widespread in higher latitudes in the northern hemisphere during the early Miocene and then migrated southward because of the late Neogene cooling climates [55]. Extant Asian butternuts are distributed in two large independent refugia, and one of them is in Northeast China with several small-scale refugia scattered across the Changbai Mountains [54].

The linkage of centers of endemism with arid regions seen in this study supports similar findings in other studies. For example, the Sonoran Desert and Chihuahuan Desert were also inferred to have concentrations of paleo-, neo-, super-, and mixed-endemism based on spatial phylogenetic studies of vascular plants in California [21] and Mexico [32]. Likewise, the relatively younger biome of arid areas in northern Chile and the interior of Australia showed mixed- and neo-endemism [28, 29]. Arid and semiarid centers of endemism generally receive less attention and conservation globally because of their lower observed richness at all taxonomic levels, yet the CANAPE approach provides a new view of the unique evolutionary history contributed by xeromorphic lineages.

Centers of phylogenetic endemism in southern China

The Hainan Island center of endemism was relatively distinct in the clustering analysis from the other four centers in southern China (Fig. 5b). The Shigatse and Lhoka Prefecture centers were located in the middle and eastern segments of the Himalaya Mountains, respectively. The two Himalayan centers displayed a close similarity to each other, and clustered at a deeper level with the large center south of the Tropic of Cancer and the Taiwan Island center. The close relationship between these centers indicated that there is close floristic affinity between Taiwan and mainland China, especially southern and southwestern China.

The QTP is the largest, highest, and youngest plateau in the world, and has experienced several uplift events from the early Miocene to the Quaternary [56]. In the QTP, the Himalayan and Hengduan Mountains were previously recognized as areas of high biodiversity and endemism, with many young endemic species [41, 57]. The Shigatse and Lhoka Prefecture centers in Himalaya identified in our CANAPE results are consistent with those recognized by Huang *et al.* [41] and Zhang *et al.* [57]. Several previous studies indicated that most endemic genera of the QTP originated *in situ* or in adjacent regions [58-61], although we detected only one cell significantly dominated by neo-endemism. The significant centers of endemism found here did not include the middle section of the Hengduan Mountains, which has been identified as a center of endemism by previous studies based on traditional taxon-based measures [3, 39-41]. This difference is mainly because we used genera as OTUs in the present study. Several lineages on the QTP have been reported to have undergone extensive radiations in the last million years at the species level [56]; for example, *Rhododendron* is a species-rich genus of Ericaceae, and many of these species (ca. 159) have restricted distributions in the QTP [62]. Molecular data indicated that the rapid radiation of the *Rhododendron* subgenus *Hymenanthes* was driven by hybridization among lineages in the Himalayan region [63-65]. As our study was limited to the genus level, it does not address evolution at the species level. Thus, unlike paleo-endemism, neo-endemism is underrepresented in this study (as discussed in a similar genus-level analysis of the Australian flora by Thornhill *et al.* [28]). In the

future, as more molecular data at species level become available, patterns of neo-endemism can be better estimated.

Southern China is mountainous with a warm and humid subtropical/tropical climate. In our CANAPE analyses, the southern Chinese mountainous areas and Taiwan and Hainan Islands are supported as refugia; these findings were consistent with several other lines of evidence [3, 6, 41].

Conservation concerns

CANAPE can be used to identify areas with significant concentrations of range-restricted long or short branches [26], thus areas harboring relict or new lineages. In our study, nearly all centers of phylogenetic endemism corresponded to mountain ranges. The topographic heterogeneity and relatively stable microclimate of mountains are often cited as being conducive to endemism [1, 6, 7, 66]. Comparing our results with existing nature reserves showed that the majority of the conservation gaps occur in Northwest China (Fig. 6, locations E, F). These conservation gaps of the extensive arid areas include more xeromorphic plant lineages than other areas of China. Additionally, we found that gaps in the Ailao–Jinzhong–Shibalian Mountains should receive conservation attention in the near future (Fig. 6, location B). These conservation gaps are located in the junction of the three mountains and can provide migratory corridors for plants to maintain natural gene flow. Similarly, a conservation gap was found in the Dabie Mountains of central China (Fig. 6, location A), which are considered transition zones for plant exchange [67–69]. Several conservation gaps were also identified in the Shigatse area and Lhoka Prefecture range (Fig. 6, location C and D). Consequently, it is vital to provide more protection to the conservation gaps described above by reducing human disturbance in these areas. Range-restricted taxa require long-term, stable habitats to prosper and persist. Spatial phylogenetic methods allow us to develop approaches for conserving the diversity of rare lineages from an evolutionary standpoint.

Possible limitations due to border effects

Most centers of endemism detected here are near the borders between China and its neighboring countries (Fig. 4). Unlike studies done on biogeographic islands (e.g., Australia [28], Chile [29], and the New Zealand archipelago [70]), our results might be influenced by a political border cutting off a broader floristic region containing lineages with restricted ranges in China that are more broadly distributed across the border. WE and PE are relative only to a given study region, as is indeed true of all biodiversity metrics. Until the data exist to do a world-wide spatial phylogenetic study, this will remain a cause of potential problems with interpretation. Nonetheless, even if some of the relative endemism seen here is only local, it is still significant for biogeographic understanding of the region. Furthermore, it is quite significant for conservation as well, given that countries and other management areas often target organisms that are rare with their boundaries even if present elsewhere.

Conclusions

Our investigation used an evolutionary framework to discover new and different patterns, compared with traditional non-phylogenetic approaches to biodiversity assessment. These findings help us better understand endemism patterns and their causes. We identified 10 significant centers of phylogenetic endemism in China, four of them not previously described, which can be used for comparison with previous taxonomic centers of endemism. We were able to divide the 10 centers into distinct northern and southern sections using range-weighted phyloturnover. Furthermore, we detected six conservation gaps among these centers. The arid and semiarid regions require additional conservation attention in the future, because these regions have been ignored in the past. Our results provide useful information that should be used for conservation planning that is increasingly urgent in the face of rapid land use and climate changes.

Methods

Phylogenetic reconstruction and spatial data

All phylogenetic analyses in this study were based on a phylogeny of the Chinese vascular plant genera reconstructed by Chen *et al.* [73], which sampled 6,098 species from 3,114 genera of vascular plants in China. In this study, we focused on angiosperm genera. Their phylogram was thus trimmed to include only angiosperms using the 'ape' package's 'drop.tip' function [74] in R v3.4.4 [75]. Monophyletic OTUs in the phylogeny are the finest scale for analysis and understanding of the evolutionary relationships and phylogenetic patterns. One species was selected to represent each genus, all genera were assumed to be monophyletic, and one genus was recognized as one OTU. In total, 2,909 angiosperm genera were included in the phylogeny, which represented approximately 93.4% of Chinese vascular plant genera. The phylogeny is archived in the DarwinTree website (<http://www.darwintree.cn>).

The spatial distribution dataset is the same as that used in Lu *et al.* [76], which was normalized at the county level. A total of 1,397,452 records were contained in the dataset representing 26,973 native angiosperm species and 2,591 native angiosperm genera. We followed their methods to divide the map of China into 100 × 100 km grid cells, and used the standard map of China (<http://www.sbsm.gov.cn>; review drawing number: GS (2016)1576). The dataset is available from http://www.darwintree.cn/resource/spatial_data

Spatial phylogenetic analysis

We used Biodiverse V2.0 [77] to calculate six metrics: GR, WE, PE, RPE, PD, and RPD [12]. Then, a total of 999 iterations of a randomization test were run using the "rand_structured" model for PE, RPE, PD, and RPD. CANAPE was carried out as described in Mishler *et al.* [12] and Thornhill *et al.* [28].

Comparisons among significant CANAPE cells

A phylogenetic turnover analysis was used to identify regions that share similar range-restricted branches of the phylogeny. All significant CANAPE cells were compared by spatial clustering analyses using the

unweighted pair group method and the range-weighted phylogenetic metric (PHYLO_RW_TURNOVER) in Biodiverse V2.0 [12, 21, 28, 77]. Phylogenetic turnover metrics operate on the branches of the phylogenetic tree; the range-weighted turnover metric assigns higher weights to narrow ranged branches [13]. This makes these turnover measures more comparable with the CANAPE results.

Priority conservation gap identification

To identify conservation gaps for the centers of CANAPE, the significant CANAPE cells were overlaid with the distribution of protected areas in China (i.e., nature reserve boundaries). The nature reserves of mainland China were digitized by Zhang *et al.* [78]. The protected areas of Taiwan were downloaded from the Database of Protected Areas (<https://www.protectedplanet.net/>; accessed August 2017). If no nature reserves occurred within a grid cell, then that cell was designated a “conservation gap.” The conservation gaps were then grouped for discussion by closely adjacent geographical positions.

Abbreviations

CANAPE, Categorical Analysis of Neo- and Paleo-Endemism; OTU, Operational Taxonomic Unit; GR, Generic Richness; PD, Phylogenetic Diversity; PE, Phylogenetic Endemism; RPD, Relative Phylogenetic Diversity; RPE, Relative Phylogenetic Endemism; WE, Weighted Endemism; QTP, Qinghai–Tibet Plateau

Declarations

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Availability of data and materials

All data were generated and analyzed during this study are included in this published article and the distribution data are deposited in the DarwinTree website (http://www.darwintree.cn/resource/spatial_data).

Authors' contributions

ZDC and JTM conceived the project. XXZ conducted the phylogenetic analyses. SWL checked the phylogenetic results. XXZ, JFY, SWL, BDM, and AHT analyzed the results. XXZ and JFY wrote the draft manuscript. All authors wrote, edited and approved the manuscript.

Ethics approval and consent to participate

Not applicable.

Consent for publication

Not applicable.

Competing interests

The authors declare that they have no competing interests.

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Figures

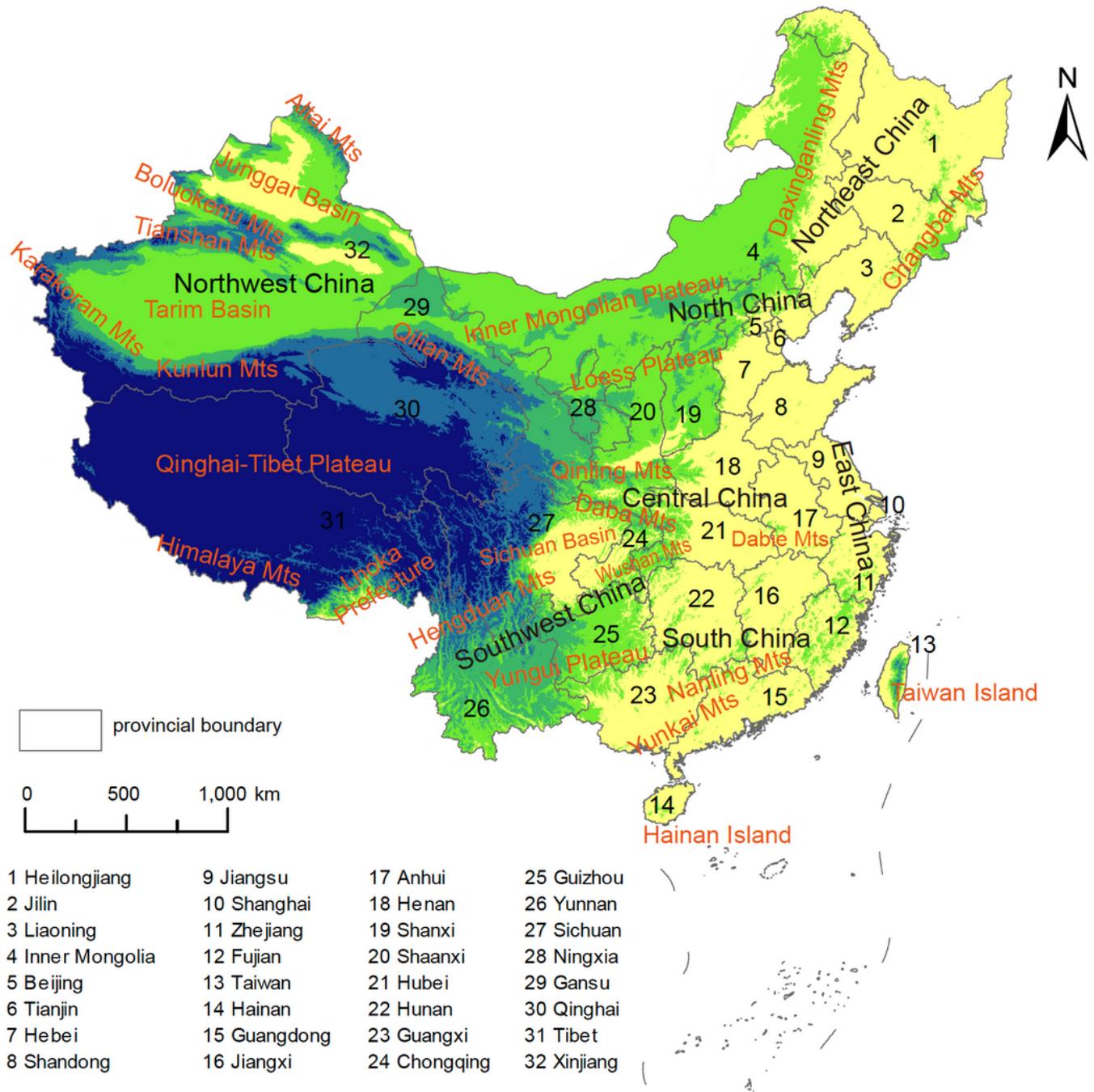
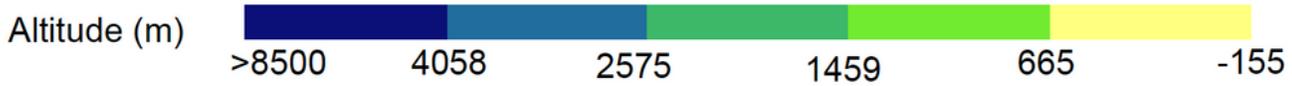


Figure 1

Topographic map of China showing locations mentioned in this study. Mts, Mountains. The designations employed and the presentation of the material on this map do not imply the expression of any opinion whatsoever on the part of Research Square concerning the legal status of any country, territory, city or area or of its authorities, or concerning the delimitation of its frontiers or boundaries. This map has been provided by the authors.

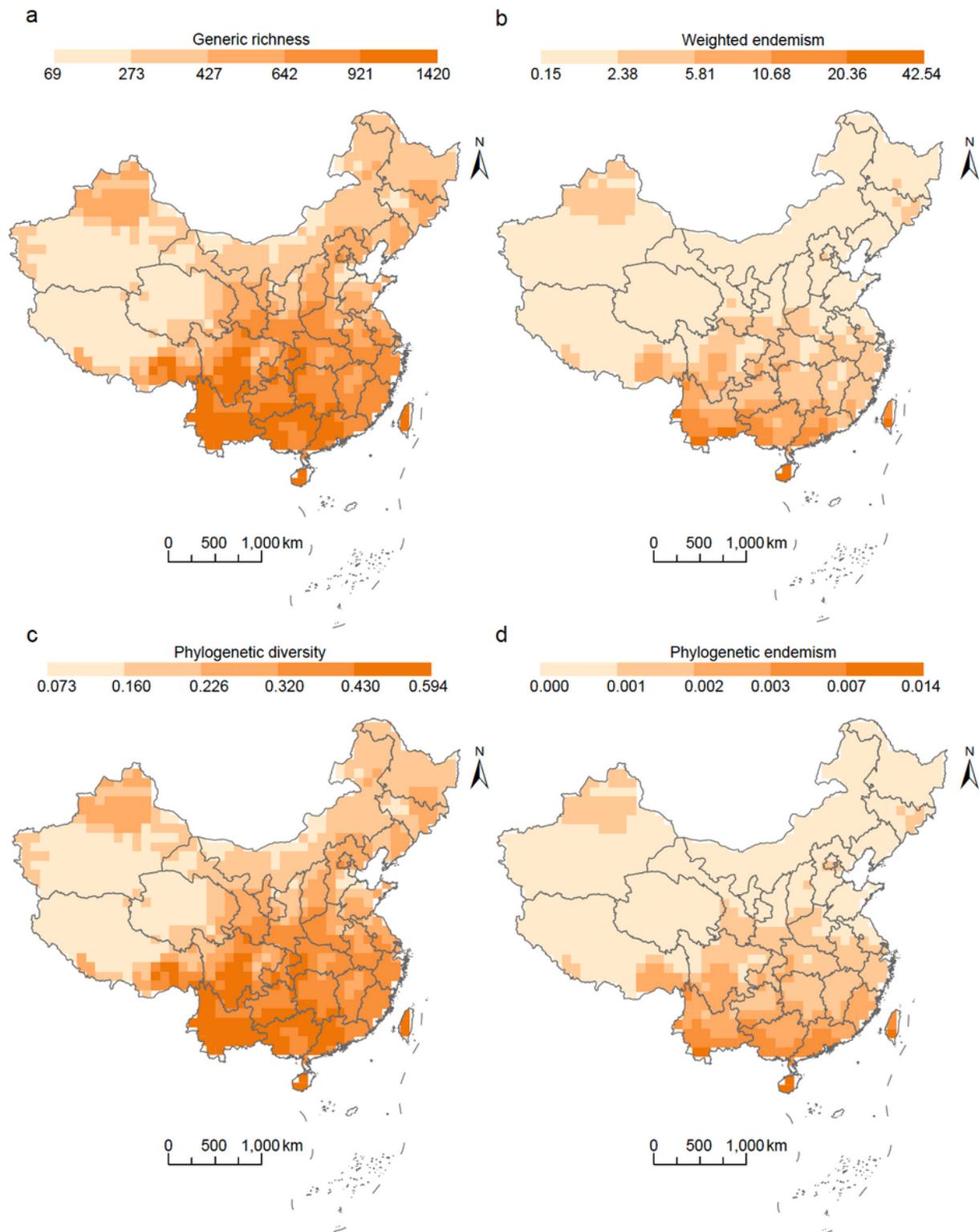


Figure 2

Observed endemism of Chinese angiosperm genera. a Generic richness, b weighted endemism, c phylogenetic diversity, and d phylogenetic endemism. The designations employed and the presentation of the material on this map do not imply the expression of any opinion whatsoever on the part of Research Square concerning the legal status of any country, territory, city or area or of its authorities, or concerning the delimitation of its frontiers or boundaries. This map has been provided by the authors.

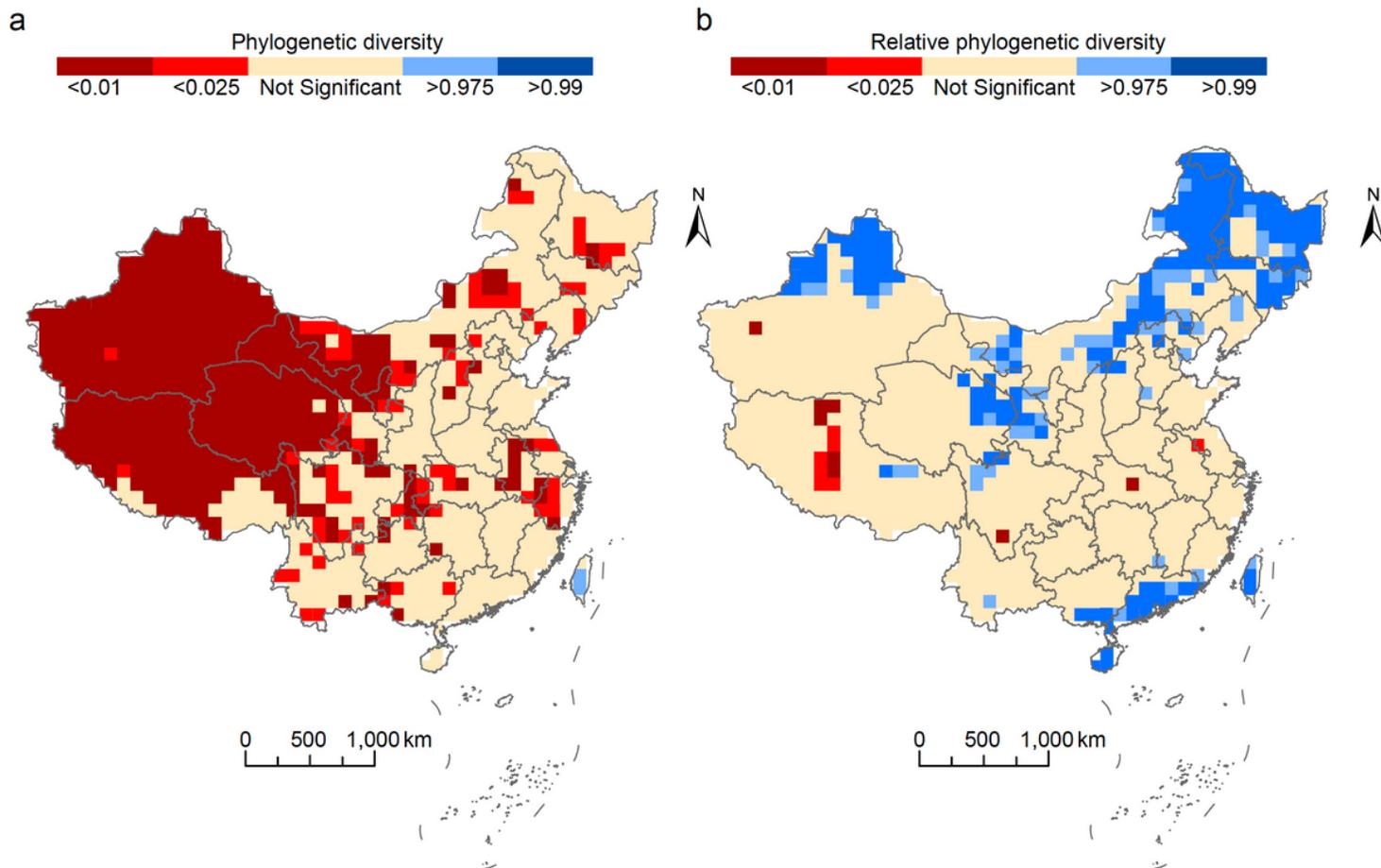


Figure 3

Significance results from randomization test. a Randomized phylogenetic diversity and b randomized relative phylogenetic diversity. The designations employed and the presentation of the material on this map do not imply the expression of any opinion whatsoever on the part of Research Square concerning the legal status of any country, territory, city or area or of its authorities, or concerning the delimitation of its frontiers or boundaries. This map has been provided by the authors.

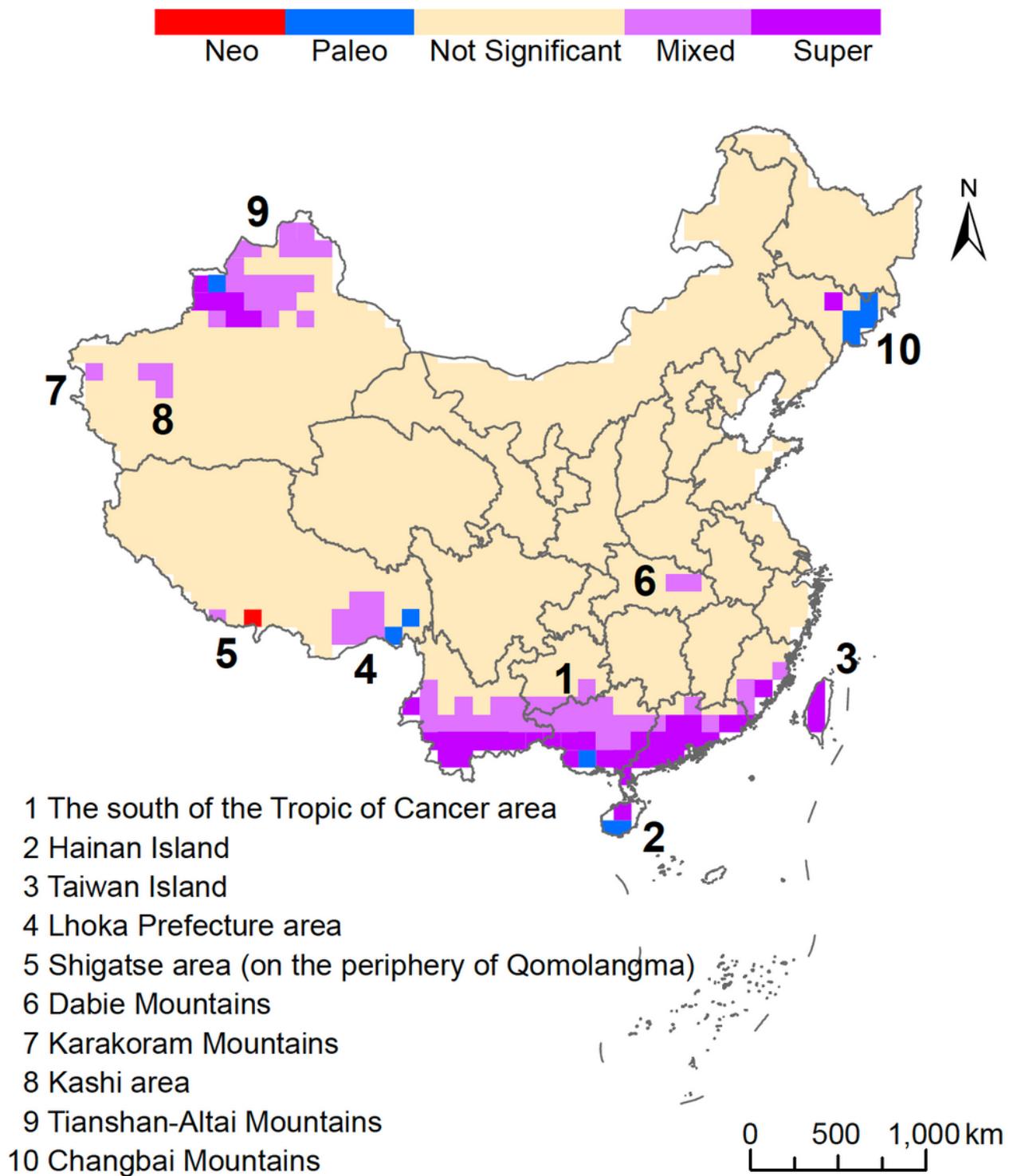


Figure 4

Centers of phylogenetic endemism discovered by CANAPE analysis. Beige cells are not significant. Red cells indicate a predominance of neo-endemism. Blue cells indicate a predominance of paleo-endemism. Purple cells represent a mixture of neo- and paleo-endemism; darker purple cells show super-endemism (i.e., highly significant PE). The code numbers (1–10) refer to centers of endemism discussed in text. The designations employed and the presentation of the material on this map do not imply the expression of

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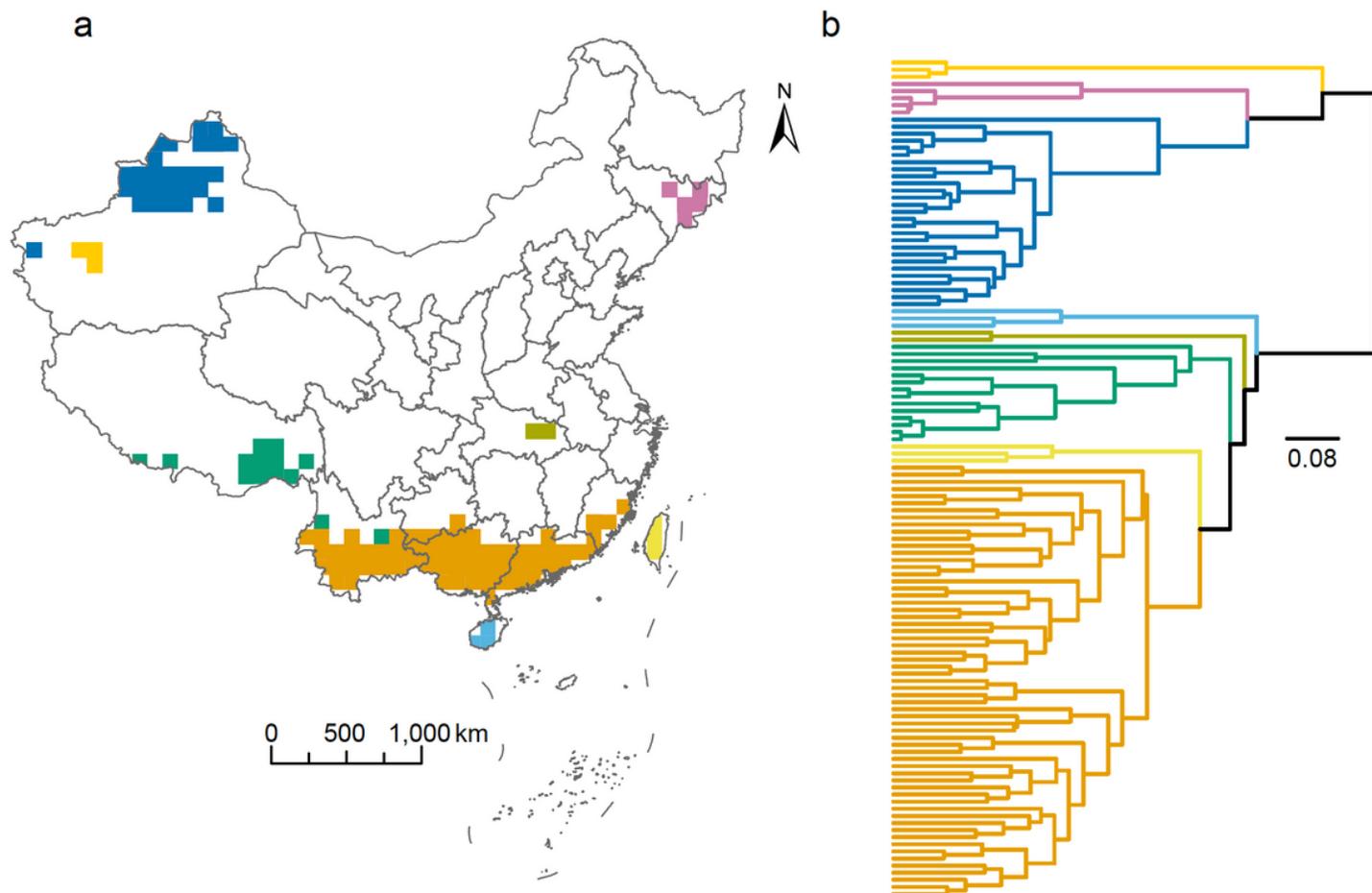


Figure 5

Results of clustering analyses. a Range-weighted turnover among cells with significant PE, as shown by CANAPE analysis. b Dendrogram showing similarities among these cells, and the branch colors match colors in a. The designations employed and the presentation of the material on this map do not imply the expression of any opinion whatsoever on the part of Research Square concerning the legal status of any country, territory, city or area or of its authorities, or concerning the delimitation of its frontiers or boundaries. This map has been provided by the authors.

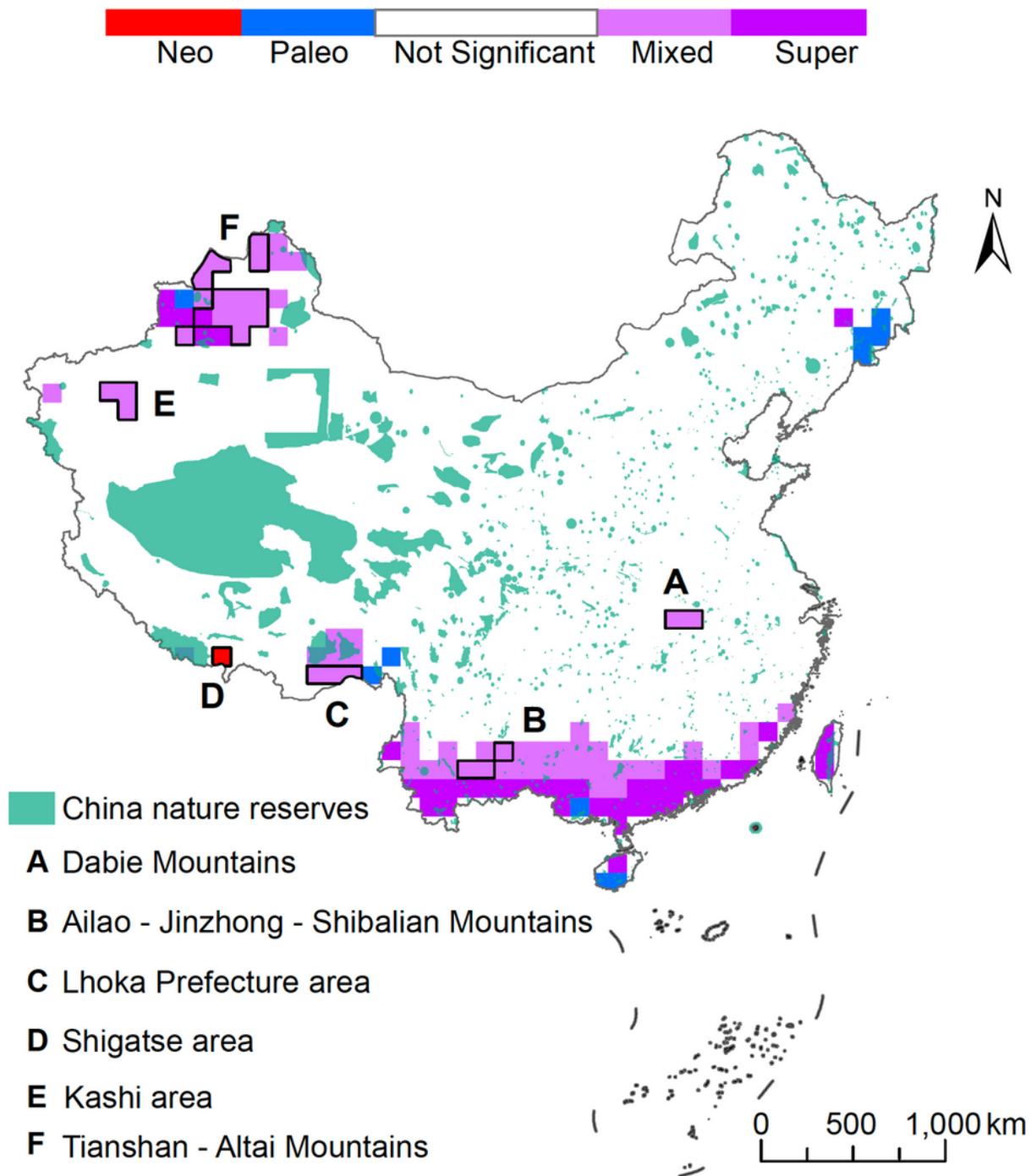


Figure 6

Overlap between CANAPE endemism grid cells and nature reserves of China. The code numbers (A–F) refer to conservation gaps discussed in the text. The designations employed and the presentation of the material on this map do not imply the expression of any opinion whatsoever on the part of Research Square concerning the legal status of any country, territory, city or area or of its authorities, or concerning the delimitation of its frontiers or boundaries. This map has been provided by the authors.

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