Phylogenetic Diversity and Distribution Patterns of the Asterid Clade of Angiosperms in Yunnan (Postprint)

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Abstract

Biodiversity loss driven by factors such as global climate change and human activities has drawn considerable attention to biodiversity conservation from various sectors worldwide. Traditional biodiversity conservation has primarily focused on the species composition and distribution patterns of species, endemic species, and threatened species, while neglecting the role of evolutionary history in biodiversity conservation. As a convergence zone of global biodiversity hotspots, Yunnan has long been a focal point for biodiversity conservation efforts. To better explore conservation measures for biodiversity in Yunnan, this study focuses on asterid species of angiosperms in Yunnan, using evolutionary relationships among species combined with their geographical distribution to explore the distribution patterns of species composition and phylogenetic composition of species, endemic species, and threatened species from an evolutionary history perspective, and integrates the spatial distribution of protected areas to identify key conservation areas for biodiversity. The results indicate that species density of all species, endemic species, and threatened species of asterids in Yunnan is significantly positively correlated with phylogenetic diversity; standardized phylogenetic diversity gradually decreases from south to north; southern, southeastern, and northwestern Yunnan represent key conservation areas for asterids in Yunnan, and enhancing protection in these regions will maximize the conservation of both the evolutionary history and potential of biodiversity. This demonstrates that integrating evolutionary history information into analyses of plant diversity patterns not only deepens understanding of the formation and evolution of plant diversity, but also provides valuable insights for formulating biodiversity conservation strategies.

Full Text

Phylogenetic Diversity and Its Distribution Pattern of Asterids in Yunnan Angiosperms Flora

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Abstract: Biodiversity loss driven by global climate change and anthropogenic activities has heightened worldwide concern for conservation. Traditional biodiversity conservation has primarily focused on taxonomic composition and distribution patterns of species, endemics, and threatened taxa, while largely overlooking the role of evolutionary history. Yunnan represents a convergence zone of global biodiversity hotspots, and its biodiversity conservation has long been a priority. To better inform conservation strategies, this study examines the asterid lineage of Yunnan' s angiosperm flora, integrating phylogenetic relationships with geographic distributions to analyze distribution patterns of taxonomic and phylogenetic diversity for all species, endemics, and threatened species. By overlaying these patterns with the spatial distribution of nature reserves, we identify priority areas for biodiversity conservation. Our results reveal significant positive correlations between species density and phylogenetic diversity for all species, endemics, and threatened species across Yunnan' s counties. Standardized phylogenetic diversity shows a gradual decrease from south to north. Southern, southeastern, and northwestern Yunnan emerge as priority conservation areas; strengthening protection in these regions would maximize preservation of evolutionary history and potential. These findings demonstrate that incorporating evolutionary history into plant diversity pattern analysis not only deepens understanding of diversification processes but also provides valuable insights for developing more effective biodiversity conservation strategies.

Keywords: species richness, endemic species, threatened species, evolutionary history, biodiversity conservation

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Introduction

Biodiversity represents the natural assemblage of all species within a region and is intimately linked to human wellbeing. The composition and structure of biodiversity vary dramatically across regions due to differences in geological history, ecological conditions, and economic development. For instance, mountains—covering approximately one-quarter of land area—harbor over half of global species, while tropical regions exhibit exceptionally high species diversity (Brown, 2014; Rahbek et al., 2019; Kougioumoutzis et al., 2021). Explaining such patterns constitutes a central question in ecology and biogeography and represents a critical issue for conservation biology (Gaston, 2000; Kreft & Jetz, 2007; Quintero & Jetz, 2018).

Research on biodiversity distribution patterns dates back to the German geographer Humboldt' s exploration of latitudinal and elevational gradients in plant diversity (Morueta-Holme et al., 2015). Subsequent work by Kreft & Jetz (2007) on global vascular plant distributions confirmed a general decline in species diversity from equator to poles. More recently, advances in DNA sequencing and construction of regional phylogenetic trees have provided novel approaches to examine biodiversity patterns from an evolutionary perspective (Lu et al., 2018; Qian, 2018; Mishler et al., 2020). Phylogenetic diversity (PD), defined as the sum of branch lengths on a phylogenetic tree for all species within a region (Faith, 1992), has become the most widely used metric in evolutionary biodiversity studies. Forest et al. (2007) first incorporated phylogenetic metrics in their study of South Africa' s Cape flora, while Lu et al. (2018) applied this approach to Chinese angiosperms, revealing distinct phylogenetic composition between eastern and western China, with higher phylogenetic diversity in the east.

Endemic species—those restricted to specific geographic areas—directly reflect spatial variation in species composition and play a crucial role in revealing biodiversity distribution patterns and evolutionary processes (Crisp et al., 2001; Huang et al., 2013). Mishler et al. (2014) identified centers of neo- and paleo-endemism for Australian *Acacia* based on endemic species distributions, inferring different evolutionary histories across regions. Endemics are also widely used in identifying biodiversity hotspots and priority conservation areas due to their typicality and representativeness (Brooks et al., 2006; Huang et al., 2016). For example, Conservation International identified 36 global biodiversity hotspots based on endemic species analyses. Furthermore, biodiversity faces severe threats from climate change and human activities (Thomas et al., 2004; Brandt et al., 2019). The IUCN Red List categories provide comprehensive assessments of species threat status (Miller et al., 2007), and analyzing threatened species distributions offers critical support for understanding climate change responses and implementing conservation measures (Pimm et al., 2014). Zhang & Ma (2008) identified 12 priority conservation areas in China through gap analysis of threatened plants.

While accumulating data and open sharing enable multi-angle exploration of biodiversity patterns, Orme et al. (2005) found that distribution patterns of species richness, endemism, and threat status do not always coincide in global bird studies. Therefore, comprehensive investigation across different taxonomic groups and perspectives is necessary to fully understand biodiversity patterns and inform more precise conservation strategies.

Yunnan harbors China' s richest flora in terms of species, endemics, and threatened taxa (Wu et al., 1994-2012; Li, 1985, 1994; Huang et al., 2016) and lies at the intersection of three global biodiversity hotspots: the Himalayas, Indo-

Burma, and the Mountains of Southwest China (Myers et al., 2000). Yunnan’ s angiosperm flora exhibits diverse phylogenetic composition, including magnoliids, monocots, asterids, and rosids (APG IV, 2016). The asterid lineage is particularly species-rich and widespread, comprising 13 orders including Lamiales, Ericales, Asterales, and Gentianales, and accounting for approximately 25% of Yunnan’ s angiosperm diversity (Wu, 1977-2006). Major families include Asteraceae, Lamiaceae, and Ericaceae, while prominent genera include *Rhododendron*, *Pedicularis*, and *Primula*. Asterids encompass diverse life forms—trees, shrubs, herbs, vines, parasites, and saprophytes—and many are dominant community components, such as *Schima* and *Camellia* (Theaceae), *Rhododendron* (Ericaceae), and *Ilex* (Aquifoliaceae) (Li, 1985; Zhu, 2021).

This study focuses on Yunnan’ s asterid flora, integrating phylogenetic relationships and geographic distributions to examine distribution patterns from an evolutionary perspective. We address two key questions: (1) Do species, endemic, and threatened species diversity show congruent patterns between taxonomic richness and phylogenetic diversity? (2) What factors shape these diversity patterns in Yunnan’ s asterid flora?

1. Materials and Methods

1.1 Study Area Yunnan Province is located in southwestern China between 97°31 39 -106°11 47 E and 21°8 32 -29°15 8 N. Since the Late Tertiary and Early Quaternary, large-scale mountain uplift and plateau dissection have created deeply incised valleys and towering topography, with a general northwest-to-southeast slope (Yang, 1990). Influenced by the Indian Ocean southwest monsoon and Pacific southeast monsoon, the climate features distinct wet and dry seasons, abundant precipitation, small annual temperature variation, and large diurnal temperature variation (Wang, 2006). This complex topography combined with abundant water and heat has fostered Yunnan’ s remarkably diverse flora (Wu et al., 1987).

1.2 Data Sources We compiled a comprehensive database of wild asterid species in Yunnan based on *Flora Yunnanica* and the *Yunnan Species Catalogue (2016 Edition)*. Following the APG IV classification system (APG IV, 2016), we revised species names and confirmed county-level distributions using Flora of China, The Plant List, Plants of the World, CVH, and NSII databases, excluding exotic and cultivated species. Species endemic to Yunnan were defined as those occurring only within the province, while stenotopic endemics were restricted to a single county.

Threatened species were identified based on the *Red List of China’ s Higher Plants* (Qin et al., 2017), including critically endangered (CR), endangered (EN), and vulnerable (VU) species.

1.3 Phylogenetic Tree Construction We used the GBOTB phylogenetic tree, which combines GenBank DNA data with the Open Tree of Life (Smith & Brown, 2018), as a backbone. Using V.PhyloMaker package (Jin & Qian, 2019) in R 3.6.2, we generated a phylogeny for all asterid species in our database. For genera or species not covered in GBOTB, we added them to their respective families or genera using V.PhyloMaker' s Scenario 3 method (Jin & Qian, 2019).

1.4 Biodiversity Measurement We quantified taxonomic and phylogenetic composition using species richness and phylogenetic diversity for all species, endemics/stenotopic endemics, and threatened species across Yunnan's counties.

Species richness (SR) represents absolute species counts per county. To account for area effects, we used species density (SD) as a standardized metric (Li et al., 2015):

[Equation reference: SD calculation formula]

Phylogenetic diversity (PD) is the sum of branch lengths for all species in a county on a rooted phylogenetic tree (Faith, 1992). Because SR and PD are often highly correlated (Morlon et al., 2011; Fritz & Rahbek, 2012), we used the standardized effect size of phylogenetic diversity (ses.PD) to control for SR effects (Cai et al., 2021):

[Equation reference: ses.PD calculation formula]

Where PDobserved is observed PD, PDrandomized is PD from null models, and sdPDrandomized is the standard deviation. Negative ses.PD values indicate phylogenetic clustering (lower diversity), while positive values indicate overdispersion (higher diversity) (Webb, 2000). Analyses were conducted using the picante package in R 3.6.2 (Kembel et al., 2010).

1.5 Regional Threatened Status Assessment We measured threat levels using proportion index (PI) and weighted index (WI):

[Equation references: PI and WI calculation formulas]

Where SRt is threatened species richness (CR+EN+VU), SR is total species richness, and GE represents threat-level scores (CR=3, EN=2, VU=1).

1.6 Priority Conservation Area Identification Pearson correlation analysis tested relationships between species density and phylogenetic diversity. Using ArcGIS 10 (ESRI, 2011), we overlaid patterns of species density, phylogenetic diversity, and threatened status with nature reserve distributions to identify priority conservation areas for Yunnan' s asterid flora.

2. Results

2.1 Diversity Patterns of Yunnan Asterids The asterid flora of Yunnan comprises 62 families, 711 genera, and 4,462 species and varieties, including 1,080 Yunnan endemics, 474 stenotopic endemics, and 315 threatened species (40 CR, 91 EN, 184 VU).

Species density and phylogenetic diversity were significantly positively correlated for all species, endemics/stenotopic endemics, and threatened species (Fig. 1). Southern and northwestern Yunnan exhibited the highest species densities and phylogenetic diversity values (Fig. 2). After controlling for species richness effects, standardized phylogenetic diversity decreased gradually from south to north (Fig. 3).

2.2 Regional Threatened Status Pearson correlation analysis revealed a significant positive relationship between PI and WI ($r = 0.91$, $P < 0.001$). Both indices identified the most threatened regions in northwestern and western Yunnan (Diqing Tibetan Autonomous Prefecture, Nujiang Lisu Autonomous Prefecture, Dali Bai Autonomous Prefecture, Lijiang City, Baoshan City) and southeastern/southern Yunnan (Honghe Hani and Yi Autonomous Prefecture, Wenshan Zhuang and Miao Autonomous Prefecture, Xishuangbanna Dai Autonomous Prefecture) (Fig. 4).

2.3 Priority Conservation Areas Overlay analysis integrating species density, phylogenetic diversity, threatened status, and nature reserve distributions identified priority conservation areas in southern Xishuangbanna, southeastern Honghe and Wenshan prefectures, and northwestern Diqing, Nujiang, Dali, and Lijiang prefectures. Key counties include Jinghong, Menghai, Mengla in the south; Pingbian, Xichou in the southeast; and Dali, Lijiang, Zhongdian, and Gongshan in the northwest (Fig. 5).

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3. Discussion

3.1 Evolutionary History of Yunnan Asterid Diversity The significant positive correlation between species density and phylogenetic diversity aligns with previous studies (Tang et al., 2014; Li & Yue, 2020). However, null model analyses revealed that areas with high species density or phylogenetic diversity do not necessarily harbor diverse evolutionary lineages. Standardized phylogenetic diversity decreases from south to north, indicating higher lineage diversity in southern Yunnan and lower diversity in the north (especially northwest). This pattern reflects geological history and diversification processes.

Northwestern Yunnan, located on the eastern edge of the Himalayas, has experienced complex habitat diversification since the Tertiary due to Indian-Eurasian plate collision and river incision (Li & Fang, 1999; An et al., 2001). This region served as a cradle for many recently evolved groups such as *Soroseris* and

Saussurea (Zhang et al., 2011, 2021), most originating from single lineages (e.g., Asteraceae), resulting in high species richness but low phylogenetic diversity. In contrast, southern Yunnan' s low-elevation mountains have maintained long-term connections with tropical Southeast Asia and stable geological and climatic conditions, escaping major Quaternary glaciation impacts (Harrison et al., 2001; Zhu, 2013). This stability provided refugia for Tertiary relict plants like *Davidia* and *Nouelia* (Manchester et al., 2009) and facilitated diversification of lineages such as *Ilex*, *Schefflera*, and *Oreocharis* (Chen et al., 2014; Li & Wen, 2014; Yao et al., 2021) from diverse evolutionary origins (Aquifoliaceae, Araliaceae, Gesneriaceae). Consequently, southern Yunnan exhibits high diversity in both species composition and phylogenetic structure.

3.2 Conservation Implications for Yunnan Asterids Combined PI and WI analyses reveal the highest numbers and severity of threatened species in southern, southeastern, and western Yunnan. Previous studies indicate that anthropogenic activities—including habitat loss from large-scale development and overexploitation of wild resources—are primary threat drivers (Forester & Machlist, 1996; Brandt et al., 2019). For example, research on *Manglietia ovoidea* (Han et al., 2020) and *Firmiana major* (Li et al., 2020) documented small, fragmented populations persisting in highly disturbed roadside and agricultural habitats. Intrinsic biological factors such as reproductive barriers, inbreeding depression, and low germination rates also contribute to threat status (Sun et al., 2021). *Manglietia ventii* faces population decline due to limited pollen production (Wang et al., 2017), while hybridization-induced inbreeding depression threatens *Rhododendron pubicostatum* (Zhang et al., 2020).

Spatial analysis integrating diversity metrics with nature reserve distributions confirms southern, southeastern, and northwestern Yunnan as priority areas. These regions not only harbor high species richness and phylogenetic diversity but also contain elevated numbers of threatened species and threat levels. Strengthening conservation in these areas is crucial for addressing extinction risks from global change and human activities.

Southern and southeastern Yunnan exhibit the highest lineage diversity and most diverse evolutionary composition (Zhu, 2016, 2017). Protecting these areas would maximize preservation of evolutionary history. Conversely, northwestern Yunnan, despite low lineage diversity, concentrates numerous recently evolved groups that represent future evolutionary potential (Xing & Ree, 2017; Ding et al., 2020). Conservation efforts here would safeguard both current diversity and evolutionary capacity. However, existing nature reserves do not fully cover these priority areas. We recommend expanding reserve coverage and optimizing spatial planning to achieve comprehensive plant diversity conservation that protects both evolutionary history and potential.

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References: [References section preserved exactly as provided]

Note: Figure translations are in progress. See original paper for figures.

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