IDENTIFYING CONSERVATION PRIORITY AREAS USING SPATIAL PHYLOGENETIC APPROACHES IN WEST HIMALAYA

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Abstract

Human society is at a critical point in biodiversity conservation. Assessing biodiversity spatiotemporal patterns provides vital insights into the evolutionary and ecological dynamics. Using comprehensive metrics, including species richness (SR), phylogenetic diversity (PD), phylogenetic endemism (PE), weighted endemism (WE), and standardize effect size of PD (SES.PD), we explored the spatial diversity patterns and evolutionary links shaping the West Himalayan flora. Our analyses employed a species-level phylogenetic tree including 7,722 vascular plant species and 116,986 distribution records. Observed variations in SR, PD, SES.PD, PE, and WE highlight key areas: Wakhan (Afghanistan), northern regions including Azad Kashmir (Pakistan), northwestern zones like Jammu and Kashmir (India), and Nepal's western areas (e.g., Bhajang to Mustang). Our analyses of the net relatedness index (NRI) and the nearest taxon index (NTI) also emphasized these regions, revealing a sign of significant lineages with unique evolutionary histories. Ultimately, hotspot analysis identified 19 conservation priority areas, covering 78% of total hotspot regions. Amid rising anthropogenic and climate challenges, these assessments offer insights into biodiversity patterns, guiding future monitoring policies and conservation strategies.

Key words: Spatial phylogenetics, West Himalaya, Priority areas, Biodiversity conservation.

Introduction

Mountain ranges serve as crucial biodiversity reservoirs and essential resources for associated organisms (Sonne *et al*., 2022; Zu *et al*., 2019). The processes of mountain building (orogeny) have led to diverse climatic, ecological, and geographical gradients, vital for species evolution (Rahbek *et al*., 2019). Due to these topographic and environmental intricacies, mountains sustain about one-third of terrestrial biodiversity (Wambulwa *et al*., 2021). Prominent mountain systems, such as the Andes, Himalaya, and Alps, are well-known biodiversity hotspots.

The Himalayan mountains, a region of exceptional diversity and ecological importance, stand out in this regard (Basnet *et al*., 2019; Wambulwa *et al*., 2021). The Himalaya exhibits significant climatic variation across short distances, resulting in high topographic heterogeneity and diverse habitats. The Himalaya and adjacent regions have attracted extensive research interest, especially from taxonomists, geologists, evolutionary biologists, and ecologists (Anjum *et al*., 2022; Manish & Pandit, 2018a; Subedi *et al*., 2020). Climatically, the Himalaya can be categorized into Central, East, and West regions (Manish & Pandit, 2018a; Pandit *et al*., 2014; Wambulwa *et al*., 2021). Previous studies have shown that the Central and East Himalayan regions harbor high species richness because of their wet, and warm climate and monsoon precipitation, while the West Himalaya is relatively colder and drier (Manish, 2019; Rana & Rawat, 2017). However, the distribution pattern of West Himalayan flora remains largely unexplored.

The West Himalayan region showcases diverse vegetations, ranging from tropical forests to alpine meadows (Khan *et al*., 2019; Raza *et al*., 2022). Notable species include *Shorea robusta*, *Dalbergia sisso*, *Albizia lebbeck*, and *Senegalia catechu* in the tropical and sub-tropical areas, while *Cedrus deodara*, *Abies pindrow*, and species of *Quercus* and *Rhododendron* dominate the temperate zones. Sub-alpine and alpine areas feature genera such as *Anemone, Iris, Primula*, and *Potentilla* (Manish & Pandit, 2018a; Rana & Rawat, 2017).

The West Himalayan regions are rich with endemic species, such as *Aconitum violaceum* var. *weileri* (vulnerable), *Astragalus clarkeanus, Jurinea dolomiaea,* and *Tanacetum baltistanicum* (critically endangered) (Ahmed *et al*., 2020; Thakur & Chawla, 2019). Overall, the great climatic variations in West Himalaya have resulted in a remarkable array of fauna and flora, making the region a significant and ideal focal point for exploring the biodiversity patterns and evolutionary processes (Bukhari *et al*., 2022; Das & Meher, 2019).

Understanding the species distribution and underlying phylogenetic relations is significant for addressing basic ecological and evolutionary questions to improve conservation efforts (Lu *et al*., 2022; Zaman *et al*., 2022; X. X. Zhang *et al*., 2022). While traditional biodiversity assessments often rely on the distribution and species richness. Advancements in spatial phylogenetics enable the exploration of evolutionary histories in diverse global regions, revealing responses to climatic factors. Spatial phylogenetic approaches merge evolutionary and distribution data, unveiling the biodiversity patterns and associated ecological mechanisms

(Daru *et al.*, 2019). Phylogenetic information illuminates species relationships, while spatial data elucidate occurrence and richness in specific regions (Li *et al.*, 2022; Manish, 2021). Spatial phylogenetic analyses pinpoint phylogenetic hotspots with numerous indices, facilitating targeting conservation strategies for diversity hotspots and endangered species protection (Lu *et al.*, 2022; Q. Zhang *et al.*, 2022). However, spatial phylogenetic approaches rely on the availability of data, which is sometimes challenging and difficult to obtain for some areas, such as the Himalaya, due to geographic barriers and infrastructure limitations (Malik *et al.*, 2022; Manish & Pandit, 2018b; Rana & Rawat, 2017). Utilizing distribution records from published flora and databases offers a comprehensive framework to explore the interplay of evolutionary processes and spatial biodiversity distribution in the West Himalayan region (Rana & Rawat, 2017). Thus far, the West Himalayan region remains unexplored in terms of spatial distribution and evolutionary patterns.

In this study, we analyzed the spatial phylogenetic pattern of the West Himalayan flora to enhance the understanding of the region's evolutionary and ecological processes. Our goal is to highlight unexplored regions and uncover data gaps by integrating distribution and molecular data. Overall, the study will help to understand the regional biodiversity patterns in West Himalaya, revealing concealed evolutionary relationships among different taxa within the region and guiding targeted conservation efforts for its flora.

Material and Methods

Study area: West Himalaya is the part of Himalaya spanning latitudes 30°–40° N. The study region includes West of Kali Gandaki valley, areas of western Nepal, Uttarakhand, Himachal Pradesh, Jammu and Kashmir of India, northern areas of Pakistan, including Azad Kashmir and Wakhan of Afghanistan (Manish & Pandit, 2018a; Wambulwa *et al.*, 2021). The region is characterized by climatic variations with an annual rainfall average of 75–110 mm (Pandit, 2017). It comprises important mountainous ranges, such as Zanskar, Pir Panjal, parts of Siwalik, and the Great Himalaya. The highest peak, Nanga Parbat, reaches around 8,126 m, with climate transitioning from tropical at the base to perpetual ice and snow at higher elevations. This climatic diversity results in the biodiversity of various plants and animal communities in the study area. Therefore, the area is worth investigating regarding phylogenetic diversity patterns and floral diversity hotspots.

Data collection: Species distribution data were collected from regional and national floras, such as *Flora of Pakistan, Flora of Nepal, Flora of Jammu and Kashmir, Flora of Uttarakhand*, regional checklists, Global Biodiversity Information Facility (GBIF https://www.gbif.org/), and other sources provided in Table 1. Final species names were verified with Plants of the World Online (https://powo.science.kew.org/) for synonyms and unresolved names, while infraspecific taxa were combined into corresponding species. Alien species and duplicates were removed. The ultimate list was comprised of 116,986 distribution records for 7,722 species from 2,002 genera

and 224 families. The study area map was divided into 652 grid cells of 50×50 km to minimize the sample bias because of uneven sampling area. The distribution data of all collected species were assigned to the respective grid cells within the study area.

Phylogenetic tree reconstruction: The phylogenetic tree was reconstructed using four chloroplast genes (*atpB, matK, ndhF*, and *rbcL*) and one mitochondrial gene (*matR*). Sequences of the target DNA regions were extracted from the matrix of the Chinese vascular plants (Hu *et al.*, 2020). The sequences not present in the Chinese vascular plants (Hu *et al.*, 2020) were obtained from GenBank (http://www.ncbi.nlm.nih.gov/genbank/). Alignment was performed using MAFFT V.7.305 (Katoh & Standley, 2013). This study used two mosses (*Syntrichia ruralis* (Hedw.) F. Weber & D. Mohr and *Physcomitrium patens* (Hedw.) Mitt.), one hornwort (*Anthoceros angustus* Steph.), and two liverworts (*Pellia endiviifolia* (Dicks.) Dumort. and *Aneura mirabilis* (Malmb.) Wickett & Goffinet), as outgroups. Maximum likelihood (ML) was conducted for the combined dataset using RAxML 8.0.22 (Stamatakis, 2014) installed in the CIPRES science gateway (Miller *et al.*, 2011). After excluding the outgroups, we utilized the penalized likelihood method as implemented in the treePL (https://github.com/blackrim/treePL) (Smith & O'Meara, 2012) to date the divergence times based on the ML phylogram. For dating analysis, 161 calibration points were employed (Liu *et al.*, 2021). Species not present in the current tree were inserted in the dated tree using the 'V. PhyloMaker' package in R (Jin & Qian, 2019). A species-level phylogenetic tree for 7,722 species was generated for the study area.

Phylodiversity calculation: SR, PD, PE, WE, and SES.PD were analyzed to determine the diversity pattern of the West Himalayan flora. The SR was calculated to quantify the total number of plant species present within each grid cell. The PD of a grid cell was calculated by summing branch lengths connecting all its species (Faith, 1992) based on the chronogram generated by this study by using the following formula:

$$PD = \sum_{c \in C} Lc$$

where Lc is the branch length, C indicates the set of branches in the minimum spanning path joining all taxa, c represents a branch (single segment between the two nodes) in the spanning path C.

PE considered the distribution range of each branch length, where each branch's length is divided by the range of all terminal taxa descended from it using the following formula (Mishler *et al.*, 2014; Rosauer *et al.*, 2009):

$$PE = \sum_{c \in C} \frac{Lc}{Rc}$$

where L_c is the branch length, R_c represents the clade range, and c represents a branch in the spanning path C.

WE calculated the inverse of the range size of each individual taxon in the set. It is quantified to examine the conservation value of a region based on the existence of species of unique restricted range by using the following formula (Rosauer *et al*., 2009):

$$WE = \sum_{\{t \epsilon T\}} \frac{1}{Rt}$$

where t is a taxon, R_t indicates the range size of taxon t, T represents subset of the taxa.

Considering that Faith's PD has shown to be affected by species richness (Webb *et al*., 2002), we calculated the SES.PD using the "picante" package in R with the following formula:

$$SES.PD = (PD_{obs} - PD_{random}) / s.d. (PD_{random})$$

where PD_{obs} shows the observed PD of the actual community, PD_{random} indicates the mean PD of randomized communities, and s.d. PD_{random} is the standard deviation of PD of the randomized communities. Positive values of SES.PD represent the aggregation of lineages with long branch whereas negative values indicate the dominance of lineages with short branch.

All analyses were conducted using the spatial analysis tool deposited in Biodiverse V.4.3 (Laffan *et al*., 2010). The obtained values of all indices were joined with the map of the study area using ArcGIS software V.10.8.

Phylogenetic clustering: The phylogenetic structure of the West Himalayan flora was examined by calculating the net relatedness index (NRI) and nearest taxon index (NTI) to measure phylogenetic clustering or over-dispersion (Webb *et al*., 2002). Positive values in both measures indicate phylogenetic clustering in a grid, whereas negative values represent over-dispersion. NTI is based on the mean nearest taxon distance (MNTD), an estimate of the mean phylogenetic relatedness of the closest relative for each taxon within a grid cell, while NRI is based on the mean phylogenetic distance (MPD), an estimate of the average phylogenetic relatedness between all possible pairs of taxa within a grid cell. The NTI calculations can be performed using the following formula:

$$NTI = [-(MNTD_{obs} - MNTD_{random}) / s.d. (MNTD_{random})]$$

where $MNTD_{obs}$ indicates the observed MNTD, $MNTD_{random}$ represents the expected MNTD of randomized communities, and s.d. $MNTD_{random}$ indicates the standard deviation of the MNTD for the randomized groups (Qian & Sandel, 2017). The NRI can be analyzed by applying the following formula:

$$NRI = [-(MPD_{obs} - MPD_{random}) / s.d. (MPD_{random})]$$

where MPD_{obs} represents the observed MPD; MPD_{random} indicates the expected MPD of the randomized communities, and s.d. MPD_{random} is the standard deviation of the MPD for the randomized groups.

Both indices (NTI and NRI) were calculated using the full species tree and species-level distribution data with the R package 'picante' (Kembel *et al*., 2010). The resulting values were then transformed into NRI and NTI by multiplying them with -1.

Identifying diversity hotspots: Grid cells with the highest values covering 10% of the land area of the West Himalaya were identified as hotspot regions (Lu *et al*., 2022). The 10% criterion for each index's hotspot determined the conservation efficiency of each diversity region. Proportions of each index were calculated by dividing the number of species within each hotspot by the total study species count. The PD proportion was measured by dividing the sum of the branch lengths among all analyzed species. Additionally, Venn diagrams were used to assess spatial mismatch and overlap among SR, PD, and PE hotspots. Overlapping areas in all three indices were designated as priority conservation areas. These methods improve biodiversity understanding and emphasize conservation priorities for the West Himalayan flora.

Table 1. List of sources for distribution data collection

S. No.	Title	Reference
1.	Flora of Pakistan	(Nasir & Ali, 1984)
2.	Flora of Jammu and Plants of Neighborhood	(Sharma & Kachroo, 1981)
3.	Flora of Jammu and Kashmir	(N. Singh *et al*., 2002)
4.	Handbook of the Indian Flora	(Drury, 1869)
5.	Materials for the Flora of Arunachal Pradesh	(Hajra *et al*., 1996)
6.	The Flora of British India	(Hooker, 1872)
7.	Fauna and Flora of Nepal Himalaya	(Kihara, 1955)
8.	Alpine Flora of Kashmir Himalaya	(Dhar & Kachroo, 1983)
9.	Flora of Afghanistan	(Kitamura, 1960)
10.	Vascular Plants of Afghanistan–An Augmented Checklist	(Albach *et al*., 2013)
11.	Flora of Cold Deserts of Western Himalaya	(Murti, 2001)
12.	Flora of the Upper Gangetic Plain and of the Adjacent Siwalik and Sub-Himalayan Tracts	(Duthie, 1903)
13.	Catalogue of the Plants of Kumaon and of the Adjacent Portions of Garhwal and Tibet	(Strachey & Duthie, 1906)
14.	An enumeration of the Flowering Plants of Nepal; A Joint Project of the British Museum (Natural History) and the Univ. of Tokyo: (Angiospermae (Dicotyledones))	(Hara *et al*., 1979)
15.	Flora of Himachal Pradesh	(Chowdhery & Wadhwa, 1984)
16.	Flora of Chamoli	(Naithani, 1984)
17.	Flora of Upper Lidder Valley of Kashmir Himalaya	(Sharma & Jamwal, 1988)
18.	Forest Flora of Pir Panjal Range (Northwestern Himalaya)	(J. B. Singh & Kachroo, 1994)
19.	Flora of Great Himalayan National Park Himachal Pradesh	(S. K. Singh & Rawat, 2000)
20.	Flowering Plants of Uttarakhand	(Uniyal, 2007)

Results

Database of the West Himalayan flora: Given the study area's cross-border coverage, it's essential to assess species ratios and records from each country to explore the West Himalayan regional diversity. The dataset comprises 7,722 species across 2,002 genera and 225 families, with 116,986 distribution records. Afghanistan contributed 1,336 species (1,496 records), India (including Jammu and Kashmir) contributed 5,713 species (59,749 records), Nepal contributed 2,516 species (30,573 records), and Pakistan (including Azad Kashmir) contributed 4,242 species (25,168 records). In terms of phylum, the dataset includes 7,556 angiosperm species (116,570 records), 21 gymnosperm species (212 records), four lycopod species (four records), and 141 pteridophyte species (200 records). Prominent families were Asteraceae (784 species and 12,094 records), Poaceae (681 species and 9,912 records), Fabaceae (641 species and 7,505 records), Lamiaceae (300 species and 5,464 records), Cyperaceae (272 species and 4,284 records), and Ranunculaceae (215 species and 4,050 records). Conversely, certain families like Styracaceae, Stylidiaceae, Petiveriaceae, and more were represented by only one species. These findings address data gaps in the West Himalayan regions, guiding future studies, particularly the *Flora of Pan-Himalaya* project (Table 1).

Spatial distribution patterns of diversity measures: The West Himalayan region's distribution pattern was assessed using SR, PD, PE, WE, and SES.PD. In this study, SR and PD showed similar spatial patterns (Fig. 1a and 1b), with highest values in northern parts of Pakistan (including Abbottabad, Mansehra, Battagram, Dir, Kohistan, Neelum,

Bagh, Sudhnoti, and Poonch from Azad Kashmir), areas of Jammu and Kashmir (India), districts of Uttarakhand and Uttar Pradesh (India), and Nepal's regions such as Bhajang, Bajura, Jumla, and Mustang. Conversely, areas like Gilgit Baltistan, Ladakh, Kargil, Spiti, Nichar, and Bhajang in western Nepal showed lower PD and SR (Fig. 1a and 1b). Both SR and PD offer crucial insights into current biodiversity within the West Himalayan regions.

The West Himalayan region's unique evolutionary history and plant distribution were examined. PE and WE indices, when calculated, exhibited similar patterns (Fig. 1c and 1d), indicating the presence of both endemic species and distinct branches on the phylogenetic tree. Particularly, the highest values of PE and WE were observed in Chamoli (northwest India), Bhajang and Mustang (western Nepal), areas of Jammu and Kashmir, Chitral and Dir (northern Pakistan), Bagh and Muzaffarabad (Azad Kashmir), and Wakhan (Afghanistan). Conversely, regions like Anantnag, Pahalgam, Rajouri (Jammu and Kashmir), Keylang, Spiti, Kangra, Dharamshala (northwest India), and Baijnath, Jumla, and Humla (western Nepal) showed lower values of PE and WE.

Calculated SES.PD values ranged from -16.496 to 2.943 for the entire region (Fig. 1e). The highest SES.PD values in northern Pakistan, Azad Kashmir, Jammu and Kashmir, Uttarakhand, and areas of western Nepal indicate higher-than-expected phylogenetic diversity, signifying a tendency toward phylogenetic over-dispersion. Conversely, negative values suggest the presence of closely related species or phylogenetic clustering (Fig. 1e). These findings highlight diverse ecological processes in species assembly within the West Himalaya (Fig. 1e).
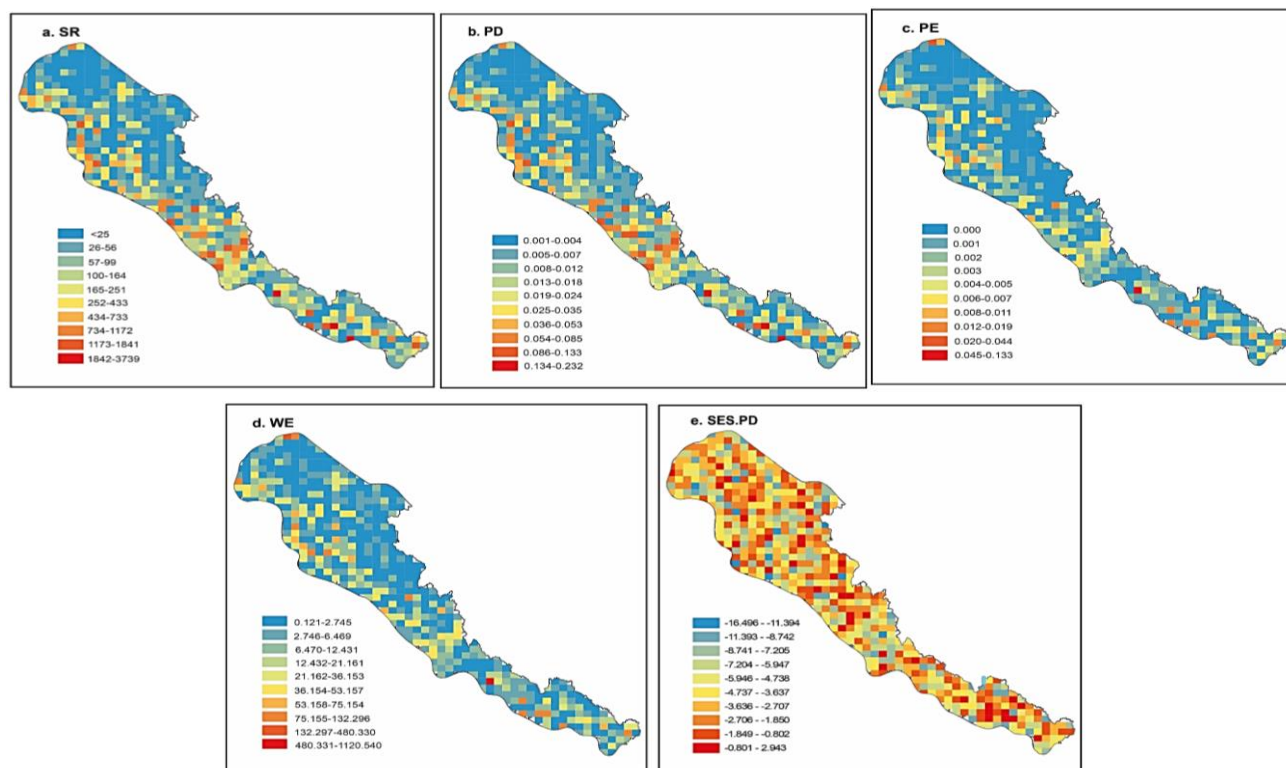

Fig. 1. Spatial patterns of (a) species richness (SR) (b) phylogenetic diversity (PD) (c) phylogenetic endemism (PE) (d) weighted endemism (WE) and (e) standardized effect size of phylogenetic diversity (SES.PD) across West Himalaya. The color spectrum indicating varying levels of all metrics denoting from blue (low values) to dark red (high values).
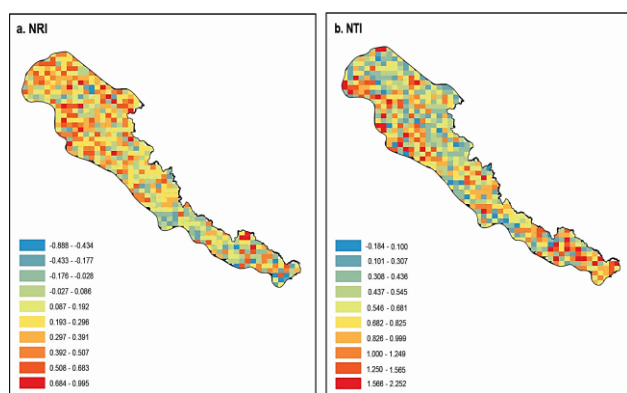
Fig. 2. Spatial patterns of phylogenetic structure including (a) NRI and (b) NTI. The color spectrum indicating varying levels of all metrics denoting from blue (low values) to dark red (high values).
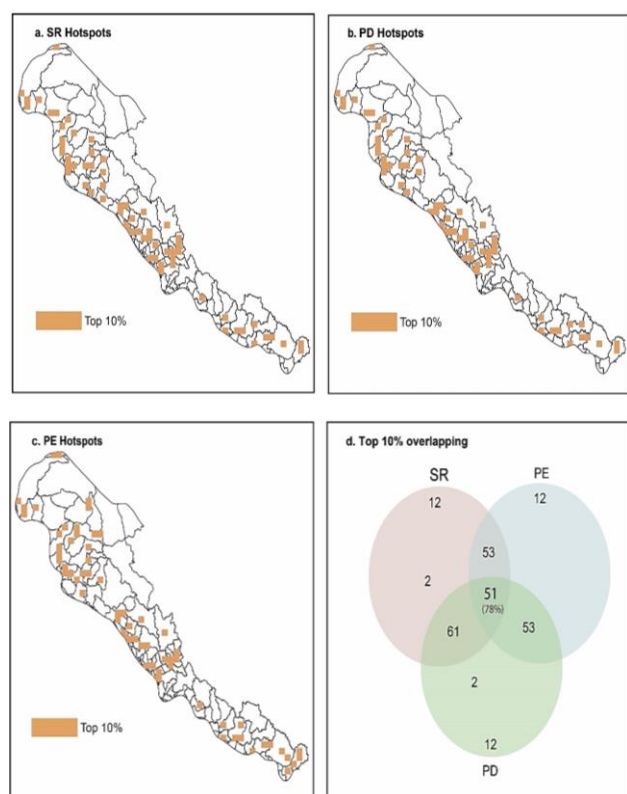

Fig. 3. Spatial patterns of biodiversity hotspot analysis by combining (a) SR (b) PD (c) PE and (d) Venn diagram showing overlapping and unique grid cells.

Phylogenetic structure patterns: Phylogenetic structure was assessed via NRI and NTI, offering insights into species assembly across the West Himalayan region. Index values were calculated for each grid cell and compared with null models to assess significant deviations from randomness.

NRI and NTI spatial patterns showed distinct differences (Fig. 2a and 2b). Positive NRI values were observed in areas like Wakhan (Afghanistan), northern parts of Pakistan including Chitral to Neelum valley, Jammu and Kashmir, Chamoli and Spiti, Kullu and Mandi in northwest India, and Dolpa, Myagdi, Humla, Bhatwari, Kalpa in western Nepal, indicating a tendency toward phylogenetic over-dispersion. Conversely, negative NRI

values were found in Gilgit, Ladakh, Himachal Pradesh, Uttar Pradesh, Bhajang, Darchula, Jumla, and Humla, suggesting a tendency toward phylogenetic clustering (Fig. 2a). Regarding NTI, high positive values were noted in certain northern areas of Pakistan (Dir, Swat, Abbottabad, Mansehra), Azad Kashmir (Bagh, Neelum), Jammu and Kashmir (Samba, Jammu), and regions like Mustang, Dolpa, and Darchula in western Nepal. Grids with negative NTI values were distributed in Gilgit, Kohistan, Ladakh, Lahul, Spiti, Keylang, Srinagar, Baramulla, Anantnag, Humla, and Mugu (Fig. 2b).

Diversity hotspots: Using spatial analysis, the 10% criterion hotspots were pinpointed across the West Himalaya. These regions display notable patterns of high SR, PD, and PE compared to adjacent areas. Notably, significant SR and PD hotspots emerged in northwestern India and western Nepal, with considerably more plant species than neighboring regions (Fig. 3a and 3b). For PE, hotspots included Wakhan (Afghanistan), Chitral (Pakistan), and border areas of northwestern India and western Nepal (Fig. 3c). The 10% criterion hotspots of richness and phylogenetic-based indices shared 51 grid cells (78% of cumulative hotspot grid cells), resulting in identification of 19 priority areas for conservation (Fig. 4 and Table 2). SR and PD consistently overlapped in 63 grid cells (96% of cumulative hotspot grid cells) (Fig. 3d). Additionally, PE overlapped in 53 grid cells with both SR and PD (81% of cumulative hotspot grid cells) (Fig. 3d). These overlaps revealed unique grid cells scattered across the study region (Fig. 3d). Based on these findings, 19 priority areas were identified, most of them lacking conservation or protection areas (indicated by asterisks in Table. 2). Detailed information is in Table 2. These results underscore that hotspot regions host diverse taxa assemblages and unique lineages, advocating targeted conservation strategies for West Himalaya's evolutionary uniqueness (Fig. 3, Fig. 4, and Table 2).
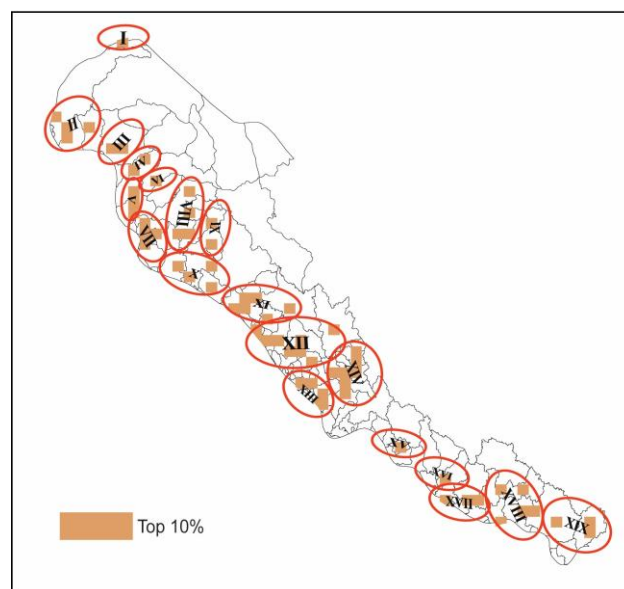

Fig. 4. Conservation priority areas identified by 10% criterion hotspots based on SR, PD, and PE. Numbers of the encircled areas correspond to serial numbers in Table 2.

Table 2. Names, characteristics, and justifications for 19 identified priority areas for conservation in West Himalaya.

S. No.	Region	Country	Ecosystems	Mountain range	Conservation status	Threats
I	Wakhan	Afghanistan	Alpine grasslands	Hindukush and Pamirs	Wakhan National Park	Wars, forest smuggling, lack of scientific research and political instability
II	Chitral, Dir*, Swat*	Pakistan	Coniferous, alpine and sub-alpine forest, and dwarf scrub vegetation	Hindukush	Chitral Gol National Park	Forest smuggling, lack of scientific research and political instability
III	Kohistan*	Pakistan	Tropical or temperate forest, alpine and sub-alpine forest	Hindukush	No national park	Anthropogenic activities, forest smuggling and lack of scientific research
IV	Battagram*, Mansehra	Pakistan	Mountain sub-tropical scrub vegetation, mountain dry temperate coniferous forest, and Northern dry scrub vegetation	Himalaya, and Hindu Kush	Kamal Ban National Park	Anthropogenic activities, forest smuggling and lack of scientific research
V	Abbottabad, Muzaffarabad	Pakistan	Mountain sub-tropical scrub vegetation, mountain dry temperate coniferous forest, sub-alpine forest, and Northern dry scrub vegetation	Himalaya	Ayubia National Park, Machiara National Park	Anthropogenic activities, forest smuggling and lack of scientific research
VI	Neelum	Pakistan	Sub-tropical forest, temperate coniferous forest, and alpine forest	Himalaya	Gumot, Musk Deer National Park	Anthropogenic activities, forest smuggling and lack of scientific research
VII	Bagh, Kotli*, Poonch, Sudhnoti*	Pakistan	Sub-tropical forest, temperate coniferous forest, and alpine forest	Himalaya	Panjal Mastan National Park, Tolipir National Park	Anthropogenic activities, forest smuggling and lack of scientific research
VIII	Srinagar, Budgam*, Pulwama*, Baramula*, Ganderbal*	India	Sub-tropical forest, temperate coniferous forest, and alpine forest	Himalaya	Dachigam National Park	Anthropogenic activities, forest smuggling and lack of scientific research
IX	Anantnag, Ramban*	India	Tropical dry deciduous forest, sub-tropical pine forest, sub-tropical dry evergreen forest, Himalayan moist temperate forest, moist alpine scrub vegetation, and dry alpine scrub vegetation	Himalaya	Kishtwar National Park	Anthropogenic activities, forest smuggling and lack of scientific research
X	Jammu, Samba*, Rajouri*, Reasi*, Kathua*	India	Sub-tropical forest, temperate coniferous forest, and alpine forest	Himalaya	Dachigam National Park	Anthropogenic activities, forest smuggling and lack of scientific research

Table 2. (Cont'd).

S. No.	Region	Country	Ecosystems	Mountain range	Conservation status	Threats
XI	Chaurah*, Saluni*, Chamba*, Dalhousie*, Baijnath*, Kyelang	India	Sub-tropical forest, temperate coniferous forest, and alpine forest	Himalaya	The Great Himalayan National Park,	Anthropogenic activities, forest smuggling and lack of scientific research
XII	Kullu, Spiti, Dharamshala, Jogindarnagar*, Palampur*, Mandi*, Brahmaur*	India	Sub-tropical to alpine range forest and dry scrub vegetation	Pir Panjal, Lower Himalayan and Great Himalayan Ranges	Dhauladhar National Park, The Great Himalayan National Park, Pin Valley National Park	Anthropogenic activities, forest smuggling and lack of scientific research
XIII	Rampur*, Rohru*, Nermand*, Banjar*, Karsog*	India	Tropical dry deciduous forest, sub-tropical pine forest, Himalayan moist temperate forest, sub-alpine forest, moist alpine scrub vegetation	Himalaya	No national park	Anthropogenic activities, forest smuggling and lack of scientific research
XIV	Purola, Kalpa*, Morang*, Puh*, Nichar*, Sangla*	India	Dry scrub forests at lower altitudes to alpine pastures	Himalayan mountains, Greater Himalaya	Govind Wildlife Sanctuary	Anthropogenic activities, forest smuggling and lack of scientific research
XV	Chamoli, Joshimath*	India	Tropical dry deciduous forest, sub-tropical pine forest, Himalayan moist temperate forest, sub-alpine forest, moist alpine scrub vegetation, and dry alpine scrub vegetation	Himalaya	Valley of Flowers National Park, Nanda Devi National Park	Anthropogenic activities, forest smuggling and lack of scientific research
XVI	Darchula	India	Sub-tropical forest to alpine grasslands	Himalayan mountains	No National Park	Anthropogenic activities, forest smuggling and lack of scientific research
XVII	Baitadi, Bajhang	Nepal	Sub-tropical forest to alpine grasslands	Himalayan mountains	Baitadi Wildlife Sanctuaries & National Park, Khaptad National Park	Anthropogenic activities, forest smuggling and lack of scientific research
XVIII	Mugu, Jumla, Humla, Kalikot*	Nepal	Sub-tropical forest to alpine grasslands, and dry deciduous forest	Himalayan mountains	Rara National Park,	Anthropogenic activities, forest smuggling and lack of scientific research
XIX	Dolpa, Mustang,	Nepal	Sub-tropical forest to alpine grasslands	Himalayan mountains	Shey Phoksundo National Park, Chitwan National Park	Anthropogenic activities, forest smuggling and lack of scientific research

*The priority areas were identified by 10% criterion overlapping hotspots of the SR, PD, and PE. [Justification for priority areas based on PD (antiquity), SR (richness) and PE (uniqueness)]

Discussion

Data collection and data gaps: Collecting data is vital for understanding species composition, abundance, and distribution, particularly in specific regions like West Himalaya. This study stands as the first to report the highest species collection for this area. Prior studies either focused on smaller regions with limited species or highlighted specific taxa in small areas (Dar & Sundarapandian, 2016; Manish *et al.*, 2022). An earlier study noted around 10,000 species in the broader Himalayan region, though West Himalaya was mostly unexplored (Rana & Rawat, 2017). In contrast, this study identified approximately 7,722 species from 2,002 genera and 225 families, with 116,986 distribution records — the most extensive dataset for the region. These results align with previous findings that identified specific taxa like *Shorea robusta, Dalbergia sisso, Albizia lebbeck, Quercus* spp., *Rhododendron* spp. *Cedrus deodara* and *Abies pindrow* (Manish & Pandit, 2018a; Wambulwa *et al.*, 2021). However, despite this progress, many areas still lack sufficient data for comprehensive exploration, and this is compounded by disputed territories and geopolitical constraints among Himalayan countries, which hinder scientific research in certain zones. Furthermore, challenging geophysical conditions, including high altitudes, stringent environments, inadequate infrastructure, and transportation limitations, contribute to data gaps. It's also worth noting that incomplete sampling or missing taxa can impact phylogeny-based indices (Jantzen *et al.*, 2019; Roure *et al.*, 2013; Scherson *et al.*, 2012). To summarize, data collection is not just a scientific step but an essential prerequisite for conserving and sustainably developing biodiversity hotspots. Thus, further comprehensive studies are necessary to deeply explore the West Himalayan diversity, starting from field exploration and creating regional repositories. This endeavor will significantly enrich the species occurrence database.

Biodiversity dimensions: This study assessed SR, PD, PE, WE and SES.PD to understand West Himalaya's spatial distribution. SR pattern aligns with regional floras (Bose *et al.*, 2019; Nanda & Reshi, 2023), but lacks full coverage. Southern regions have the highest SR due to temperate climate and diverse vegetation. This pattern reflects environmental heterogeneity's role in co-existing species (Scherson *et al.*, 2012; Zhou *et al.*, 2018). Strong positive SR-biodiversity correlation echoes in high PD areas, seen in diverse ecosystems (Morelli *et al.*, 2018). PD and PE reveal evolutionary signatures. High PD regions align with PE and WE, hosting ancient lineages (Thornhill *et al.*, 2016; Vasconcelos *et al.*, 2019). Spatial congruence between PD and PE seen in other montane ecosystems suggests general evolutionary distinctness (Thornhill *et al.*, 2016; Vasconcelos *et al.*, 2019). High PE areas - Chamoli, Bhajang, Mustang, Jammu, Azad Kashmir, Wakhan-correlate with high WE, serving as refugia for long-isolated species (Joshi & Karanth, 2013; Weber *et al.*, 2014). High WE areas signify unique evolutionary history and geographical restrictions (López‑Pujol *et al.*, 2011). SES.PD reveals regions deviating from random PD expectations, positively correlating with SR and PE zones, indicating distinct taxa

co-existence (Lin *et al.*, 2023). Positive SES.PD values, high SR, and endemism underscore conservation needs (Jarzyna *et al.*, 2021; Rahbek *et al.*, 2019). West Himalaya's phylogenetic structure enhances understanding of evolution, community dynamics, aligning with global conservation priorities (Huang *et al.*, 2016; Veron *et al.*, 2021).

Phylogenetic signal and species assembly: NRI and NTI metrics unveil species assemblage in the West Himalayan ecosystems. NRI values show phylogenetic clustering and over-dispersion trends, reflecting species relatedness variations. Some studies reported clustering (Yakimov *et al.*, 2020), others mixed patterns (Jarzyna *et al.*, 2021; Zhang *et al.*, 2022), likely due to diverse species pools, barriers, and environments (Brunbjerg *et al.*, 2014; He *et al.*, 2022). Our findings align with Alps and Andes studies showing phylogenetic clustering due to environmental filtering (Griffiths *et al.*, 2021; Smyčka *et al.*, 2017). NTI values reveal mixed evolutionary patterns, indicating phylogenetic clustering and over-dispersion. Competitive exclusion and niche partitioning contribute, shaping co-occurring species (Starko *et al.*, 2020). Consistent with recent studies, interspecific interactions impact phylogenetic patterns (Manish & Pandit, 2018b; Vasconcelos *et al.*, 2019; Zhou *et al.*, 2018).

Illuminating biodiversity hotspots: Analyzing biodiversity hotspots with SR, PD, and PE reveals key patterns and ecological significance in West Himalaya. This approach aids understanding of phylogenetic and taxonomic dimensions, guiding conservation for Himalayan flora. SR hotspot identification underscores taxonomic diversity in ecologically significant zones. Earlier research in West Himalaya noted similar SR hotspots, related to diverse habitats and altitudinal gradients (Bose *et al.*, 2019), resembling findings in East Himalaya and Andes emphasizing elevational gradients (Manish & Pandit, 2018b; Scherson *et al.*, 2012; Shrestha *et al.*, 2021). High congruence (78% overlap) among indices emphasizes conservation importance. These findings align with studies, such as in the western Ghats, where PE hotspots coincide with ancient speciation and isolation areas (Bose *et al.*, 2019; Shrestha *et al.*, 2021). Spatial overlaps were explored due to diversity concentration differences. Previous global or country-level studies show greater overlap in phylogeny-based indices than richness-based measures (Smyčka *et al.*, 2017; Weber *et al.*, 2014). Our phylogenetic pattern suggests species numbers and distribution records impact spatial distribution, alongside regional species composition and ecological factors. Overall, this study observes consistent diversity hotspots, urging protection against increasing anthropogenic activities and climate instability.

Conclusion

This study examines the West Himalayan flora's spatial distribution patterns using distribution data and phylogenetic information. By integrating diverse biodiversity metrics, it reveals intricate plant diversity patterns in this ecologically diverse zone. SR and PD observations uncover spatial

variations, enhancing understanding of evolutionary distinctions influenced by regional climatic variations, altitudinal gradients, and habitat diversity. PE and WE results illuminate unique evolutionary lineages and regions of high phylogenetic and geographic significance. Phylogenetic patterns from NRI, NTI, and SES.PD provide insights into species assembly and evolutionary processes. Hotspot analysis identifies 19 priority conservation areas (78% of cumulative hotspots) consisting of 61 districts, out of which 36 districts still lacking protection. Our results indicate that these areas are of evolutionary and ecological importance, and need urgent efforts for the protection of their flora. Our study serves as an evidence-based reference for future studies, conservation strategies, and management policies in West Himalaya. Integrating evolutionary, climatic, and geographical variables, monitoring, and predictive models can ensure sustainable conservation, addressing emerging threats to mountainous region biodiversity.

Acknowledgments

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