

New progress in exploring the mechanisms underlying extraordinarily high biodiversity in global hotspots and their implications for conservation

1 | INTRODUCTION

The extraordinarily high species richness makes global biodiversity hotspots the top priorities for conservation planning and management, and natural laboratories for biological studies. The term 'biodiversity hotspot' was proposed by Norman Myers, and the original 25 hotspots covered 2.1 million square kilometres, or 1.4% of the Earth's land surface (Myers, 1988; Myers et al., 2000). The updated range of global biodiversity hotspots included additional nine hotspots and increased the total range to 3.3 million square kilometres, 2.3% of the land surface (Mittermeier et al., 2004). These areas are characterized by a high level of species richness, endemism and anthropogenic pressures. In particular, they maintain 77% of all endemic plant species, 43% of vertebrates (including 60% of threatened mammals and birds), and 80% of all threatened amphibians. In addition to those terrestrial ecosystem's hotspot, Roberts et al. (2002) identified the 10 richest centers of endemism covering up to 15.8% of the world's coral reefs (0.012% of the oceans), but include between 44.8% and 54.2% of all restricted-range marine species. The natural resources of all hotspots are of great significance for developing agriculture, forestry, livestock and fisheries, as well as for scientific research and education. However, the earth is experiencing the sixth mass extinction, with current extinction rates are ~1000 times higher than natural background rates of extinction and future rates are likely to be 10,000 times higher (Ceballos et al., 2020; De Vos et al., 2015). Accelerated species loss under climate change and anthropogenic disturbance call for research on the mechanisms underlying the generation and maintenance of biodiversity in these hotspots, which can help support management and conservation decision-making (Margules & Pressey, 2000).

The extraordinary species diversity in biodiversity hotspots is often attributed to an accumulation of narrow-ranged/endemic species through elevated speciation rates, and/or preservation of species over a long time through low extinction rates. As such, biodiversity hotspots usually host ancient and young species and

serve as "museums, where older lineages persist through evolutionary time, and "cradles", where new species continue to be generated at the same time, as well as "accumulation centers", which host a high proportion of species that migrate from nearby regions (Feijó, Ge, Wen, Cheng et al., 2022). Many of them are now relic taxa or living fossils that have historically flourished tremendously (Scheyer et al., 2013; Sun et al., 2020). Moreover, speciation rates are arguably higher in tropical regions (Brown, 2014; Schluter & Pennell, 2017). Given the current era of rapid biodiversity loss, there is an urgent need to understand the mechanisms driving the biodiversity dynamics in biodiversity hotspots because these results could guide make conservation actions to protect species under threat from rapid environmental changes and extensive human impacts.

To achieve this goal, we have organized this special issue in *Diversity and Distributions* that aims to explore patterns of community-level diversity in biodiversity hotspots, and identify key factors that determine phenotypic and genetic diversity. We also seek to better understand historical or contemporary processes that shape speciation and adaptation in different taxa, and illustrate the current diversity patterns of many taxa. Utilizing combined knowledge across different taxonomic groups, diverse geographical areas and research fields, we hope to not only provide novel insights into the mechanisms generating biodiversity, but to also identify conservation gaps that require future attention in conservation planning and management. This special issue includes 35 articles that, on the one hand, improve our knowledge of the mechanisms underlying the extraordinary diversity of hotspots, and, the other hand, propose new strategies to mitigate biodiversity losses (Table 1). These articles are broadly focused on the following four aspects: (1) Community composition and diversity patterns, (2) Ecological and genomic mechanisms underlying diversification and speciation, including phylogeographic pattern of representative taxa; (3) The current status of fauna and flora hotspots; (4) Conservation gaps and implications for future planning and management.

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TABLE 1 Summary of objectives, taxa, datasets, geographical information and author information of this issue.

Objective	Title	Taxa	Data sets	Locations	First author
Section A. Community composition and diversity pattern	Seasonal elevational patterns and the underlying mechanisms of avian diversity and community structure on the eastern slope of Mt. Gongga	Birds	Occurrences	Mt. Gongga, China	He et al. (2022)
	Elevational patterns of amphibian functional and phylogenetic structures in eastern Nepal Himalaya	Amphibian	Occurrences	Eastern Nepal	Zhao et al. (2022)
	Multiple β -diversity patterns and the underlying mechanisms across amphibian communities along a subtropical elevational gradient	Amphibian	Occurrences	Mt. Emei, Sichuan, China	Wang, Zhong et al. (2022)
	Spatio-temporal turnover and drivers of benthic-demersal community and food web structure in a high-latitude marine ecosystem	Large benthic invertebrates	Occurrences and traits	Barents Sea	Pecuchet et al. (2022)
	Frugivore distributions are associated with plant dispersal syndrome diversity in the Caribbean archipelagos	Plants and vertebrate frugivores	Occurrences	Caribbean archipelagos	Kim et al. (2022)
	Elevational patterns of phylogenetic structure of angiosperms in a biodiversity hotspot in eastern Himalaya	Plants	Occurrences	Mt. Namjagbarwa, eastern edge of the Himalaya	Li et al. (2022)
Section B. Ecological and genomic mechanisms underlying speciation and diversification	Energy and physiological tolerance explain multi-trophic soil diversity in temperate mountains	Soil sample	Meta-barcoding	French Alps	Calderón-Sanou et al. (2022)
	Demographic history, local adaptation and vulnerability to climate change in a tropical mountain bird in New Guinea	Birds	Morphology and Genomics	New Guinea	Ericson et al. (2022)
	Quantifying adaptive divergence of the snowfinches in a common landscape	Birds	Genomics	Qinghai-Tibetan Plateau	She et al. (2022)
	Ancient introgression underlying the unusual mito-nuclear discordance and coat phenotypic variation in the Moupin pika	Mammals	Occurrences and genomics	Hengduan Mountain Region, China	Ge et al. (2022)
	Phylogenomics of Northeast Asian <i>Pungitius</i> sticklebacks	Fish	Genomics	Northeast Asia	Wang, Wang et al. (2022)
	Comparative phylogeography in a marine biodiversity hotspot provides novel insights into evolutionary processes across the Atlantic-Indian Ocean transition	Marine fish and invertebrate species	Occurrences and multi-locus DNA markers	South African coastline, Indian/Atlantic Oceans	Dalongeville et al. (2022)
	Reptile richness and genetic divergence patterns were shaped by current and past climate in and around the Irano-Anatolian global biodiversity hotspot: Implications for conservation	Reptile	Occurrences	Iran and Turkey	Yousefi et al. (2022)
	Large mountains make small barriers: Species composition and spatial dynamics history of the <i>Odorrana schmackeri</i> complex in the karst area of Guizhou, China	Amphibian	Occurrences and multi-locus DNA markers	Karst area of Guizhou, China	Jiang, Yan et al. (2022)

(Continues)

TABLE 1 (Continued)

Objective	Title	Taxa	Data sets	Locations	First author
	Genomic evidence for adaptive differentiation among <i>Microthyla fissipes</i> populations: Implications for conservation	Amphibian	Genomics	China	Jin et al. (2022)
	Detecting the phylogenetic signal of glacial refugia in a biodiversity hotspot outside the tropics	Bryophyta (mosses)	Barcode markers, rbcL and trnL-F, occurrences	Haida Gwaii archipelago, north-west coast of British Columbia, Canada	Wu et al. (2022)
	New insights into the formation of biodiversity hotspots of the Kenyan flora	Angiosperms	Occurrences and multi-locus DNA markers	Kenya	Zhang et al. (2022)
	Conservation prioritization based on past cascading climatic effects on genetic diversity and population size dynamics: Insights from a temperate tree species	Plants	Occurrences and genomics	Pacific Northwest	Liu et al. (2022)
Section C. The current status of fauna and flora hotspots	Marine mammal hotspots across the circumpolar Arctic	Marine mammals	Occurrences and traits	Circumpolar Arctic	Hamilton et al. (2022)
	Conservation hotspots of insular endemic mammalian diversity at risk of extinction across a multi-dimensional approach	Mammals	Occurrences	Worldwide Islands	Leclerc et al. (2022)
	A hotspot of groundwater amphipod diversity on a crossroad of evolutionary radiations	Subterranean amphipods	Nuclear and mitochondrial genes, occurrences	Europe, Western Balkans.	Borko et al. (2022)
	Identifying hotspots and priority areas for Xenarthran research and conservation	Mammals	Occurrences	Neotropics	Feijó, Ge, Wen, Xia et al. (2022)
	An analytically derived delineation of the West African Coastal Province based on bivalves	Bivalves	Occurrences	Eastern Atlantic Ocean	Caballero-Herrera et al. (2022)
	Habitat suitability of neotenic net-winged beetles (Coleoptera: Lycidae) in China using combined ecological models, with implications for biological conservation	Insects	Occurrences	China	Liu et al. (2022)
	Diversity and conservation of endemic true bugs for four family groups in China	Insects	Occurrences	China	Jiang, Dong et al. (2022)
	DNA barcoding of Chironomidae from the Lake Skadar region: Reference library and a comparative analysis of the European fauna	Insects	DNA barcoding	Lake Skadar basin and adjacent area	Gadawski et al. (2022)
	Delineating biogeographic regions in Indian Ocean deep-sea vents and implications for conservation	Deep Sea invertebrate	COI	Indian Ocean	Zhou et al. (2022)
	Linking evolutionary dynamics to species extinction for flowering plants in global biodiversity hotspots	Plants	Occurrences	Global biodiversity hotspots	Fu et al. (2022)

TABLE 1 (Continued)

Objective	Title	Taxa	Data sets	Locations	First author
Section D. Conservation gaps and implications for future planning and management	Climate change is expected to restructure forest frugivorous bird communities in a biodiversity hot-point within the Atlantic Forest	Forest frugivorous bird communities	Occurrences	Central Corridor of the Atlantic Forest (CCAF), Brazil	Mota et al. (2022)
	Land-use changes conservation network of an endangered primate (<i>Rhinopithecus bieti</i>) in the past 30 years in China	Mammals	Occurrences	Three Parallel Rivers Region on the Qinghai-Tibetan, China	Su et al. (2022)
	Conservation hotspots of insular endemic mammalian diversity at risk of extinction across a multidimensional approach	Mammals	Occurrences	Worldwide	Leclerc et al. (2022)
	Anthropogenic pressures coincide with Neotropical biodiversity hotspots in a flagship butterfly group	Insects	Occurrences	Neotropics	Doré et al. (2022)
	Effects of land use and climate change on functional and phylogenetic diversity of terrestrial vertebrates in a Himalayan biodiversity hotspot	Terrestrial vertebrates	Occurrences	Eastern Himalayan, Bhutan	Penjor et al. (2022)
	Protected areas have remarkable spillover effects on forest conservation in the Qinghai-Tibet Plateau	No taxon	Range data	Protected areas on the Qinghai-Tibet Plateau	Shen et al. (2022)
	Forest regeneration may reduce the negative impacts of climate change on the biodiversity of a tropical hotspot	Birds and arboreal mammals	Occurrences	Brazilian Atlantic Forest (BAF)	Tonetti et al. (2022)

2 | THIS ISSUE

2.1 | Community composition and diversity pattern

Community diversity is an important measure of ecosystem stability. Indeed, communities with high diversity tend to form more complex relationships among species, and food chains and webs tend to be more stable to environmental variations. There are many ways of measuring community diversity, but among the most common are taxonomic diversity (TD), phylogenetic diversity (PD) and functional diversity (FD). Taxonomic diversity directly reflects the richness and abundance distribution of species, while the latter two account for functional and phylogenetic proximities between species and have often been used to investigate the processes of community assemblies, including the strength of environmental filtering, interspecific competition, as well as evolutionary history (Münkemüller et al., 2020). Interestingly, community-level patterns and associated processes can be decomposed through α , β and γ diversity. The first one describes a single community diversity, the second one describes the species, trait or phylogenetic turnover between communities or ecosystems, while the last one represents the overall diversity of the region of interest (Whittaker, 1960). Seven articles included in our special issue focused on the different facets and scales to unveil (meta-) community structure in biodiversity hotspots.

In previous studies, much attention had been paid to the elevational gradient of species richness, but little attention had been paid to seasonal differences and species ranges. In mountainous regions, hump-shaped patterns of species richness were common both in angiosperms in Mt. Namjagbarwa, a biodiversity hotspot in eastern Himalaya (Li et al., 2022) and birds in Mt. Gongga, the highest mountain in Hengduan Mountains (He et al., 2022). Li et al. (2022) utilized a comprehensive dataset of angiosperms of Mt. Namjagbarwa and integrated phylogenetic diversity, mean family age and phylogenetic relatedness, for all elevation belts to study the elevational patterns of the phylogenetic structure of Mt. Namjagbarwa and to explore potential causes for the patterns. The results show a zig-zag pattern of phylogenetic metrics. Neither tropical niche conservatism (TNC) nor out-of-the-tropics (OTT) can fully explain the pattern of floristic assembly of the elevational gradient of Mt. Namjagbarwa. The OTT is a better explanation at low elevations, indicating that niche convergence has played a significant role in species assembly at low elevations. In contrast, the TNC explains the pattern best at middle elevations, indicating that niche conservatism has played a significant role in species assembly at middle elevations of the mountain region. Interestingly, He et al. (2022) identified seasonal differences in diversity patterns. For small-ranged species, it was found that multi-faceted diversity patterns (TD, PD and FD) were strongly related to climatic and vegetation factors during the breeding season. Instead, large range species and resulting diversity patterns seemed to be rather constrained by space (mid-domain effect).

Still in Asia, Zhao et al. (2022) showed that both elevation and environmental variations (e.g. air temperature, the number of tree stumps, the number of trees showing looping, the number of trees

and water pH) drive the spatial distribution of amphibian functional and phylogenetic diversity patterns in eastern Nepal Himalaya. Also focusing on amphibians, Wang, Zhong et al. (2022) investigated the relationship between spatial distance and community similarity on Mount Emei (i.e., distance-decay). While they found a significant distance-decay for amphibian multifaceted β -diversity, they highlighted contrasted environmental drivers with temperature seasonality, annual precipitation, and elevational distance being the most important. Comparing observed patterns with null-model expectations, they suggested that both environmental filtering and competitive exclusion are important processes shaping elevational patterns of amphibian β -diversity.

Moving up from single taxa to multi-trophic assemblages, Calderón-Sanou et al. (2022) tested the role of energy, physiological tolerance, habitat heterogeneity and resource heterogeneity on the spatial variation of soil multi-trophic diversity across the French Alps. Using an environmentally stratified sampling design together with soil environmental DNA and a machine learning algorithm, the authors found the strongest support for the energy and physiological tolerance hypotheses across the 36 analysed soil trophic groups, while the other two hypotheses were important only for some specific ones.

Pecuchet et al. (2022) found that benthic-demersal fauna community and food web metrics in the Barents Sea could be partitioned to give four sub-regions where different pressures act on them, such as sea ice loss and fisheries. Community metrics (e.g., mean body length and trophic level) varied along an environmental gradient of annual mean sea bottom temperature, trawling intensity and ice cover, whereas food web metrics (e.g. nestedness and connectance) varied along an environmental gradient of depth and sediment composition. Communities had higher biomass-weighted variability in body size and omnivory values in areas where the Atlantic and Arctic water masses mix.

In the local communities, different taxa interact with each other. In Caribbean archipelagos, Kim et al. (2022) found biotic characteristics of frugivore communities are important predictors of plant diversity. In addition, this may also be influenced by climate and colonization history. Given the importance of biotic metrics in explaining plant diversity, they suggested that fruit-frugivore interactions are important components of island biogeography and that frugivorous communities should be accounted for plant biodiversity predictions and forecast models.

These studies deepened our understanding of the dynamics of community composition and diversity patterns. Information from environmental impact factors and the diversity of target groups have become increasingly sophisticated. Long-term tracking of community changes is critical in habitat conservation and recovery planning.

2.2 | Ecological and genomic mechanisms underlying diversification and speciation

With the increasing amounts of information and a variety of approaches established by technique and discipline integration in

the era of big data, we are able to better disentangle the ecological and genetic processes underlying population diversification and speciation. The former is largely based on the integration of ecology and geographic information system (GIS) by quantifying environmental variables at macro and micro scales. The latter is largely based on the rapid development of sequencing technologies and the emergence of new bioinformatics methods, with advances in these fields offering opportunities to reveal the complex mechanisms that generate and maintain biodiversity in global hotspots. This section includes studies on a larger number of taxa with a wider geographical range. Morphology, occurrence and genomic data were extensively obtained to uncover underlying mechanisms that drive diversification and speciation. These studies shed light on genomic mechanisms underlying phenotypic diversification and regional geographical and climatic history in influencing the evolutionary trajectories of both animals and plants.

In New Guinea, Ericson et al. (2022) found MacGregor's bow-erbird, *Amblyornis macgregoriae* consists of six allopatric mountain populations that occupy sky-islands with limited gene flow between them. The authors showed that these populations fall into three distinct genetic clusters. Through genotype-environment modelling, they identified annual precipitation and seasonal and day-to-night temperature fluctuations as the environmental factors that explain most of the observed genetic variation in *A. macgregoriae*. By comparing the current and predicted future (RCP 8.5 greenhouse gas scenario for the year 2070) genomic variation, they found that the populations close to the Strickland Gorge region in Central Range are those most heavily affected by the predicted climate conditions.

On the Qinghai-Tibetan Plateau, She et al. (2022) used ecological, phenotypic and genomic data for three sympatric species of snowfinches to investigate the different adaptations of these species, which is important for the understanding ecologically moderated biodiversity. They found that body and beak sizes differ significantly among the three snowfinches and that the extent of phenotypic divergence between snowfinch pairs is more strongly correlated with the magnitude of divergence in developmental genes compared to in the whole genome. The study provides novel insights into the mechanisms underlying evolutionary versatility and ecological success among sympatric species. Still in China, but moved to Hengduan Mountains, Ge et al. (2022) revealed an unusual mitochondrial lineage of *Ochotona thibetana* (Moupin pika) from the western Sichuan Basin, which was named *O. qionglaiensis* in previous studies, but verified as a product of ancient mitochondrial introgression. Extensive gene flow was detected among genetic lineages of *O. thibetana*, which has distinct phenotypic variation in hair thickness and colouration, as well as notable morphological differentiation in external and craniodental measurements. Multiple members of the keratin gene family were identified as introgressed loci from some ancient species to *O. thibetana*, which likely play important roles in phenotypic and genomic diversification.

In the southeast of China, Jin et al. (2022) utilized 20,572 SNP loci, and explored genome-wide genetic variability and

differentiation within and among *Microhyla fissipes* populations covering a large geographic area in southeast China. Numerous SNPs were found to be in strong association with variation in average annual temperature and/or precipitation across the sampled locations, suggesting that ecological factors play an important role in driving genetic differentiation among local *M. fissipes* populations. Jiang, Dong et al. (2022) found Miaoling Mountains were not a geographical barrier to the dispersal of Schmacker's frog, *Odorrana kweichowensis* and *O. huanggangensis*, and the Dalou Mountains, Foding-Wuling-Leigong-Yueliang Mountains were geographical distribution boundaries in the formation of the current distribution of the three species in Guizhou Province. No population expansion was detected within *O. hejiangensis*. Population expansion in the late Pleistocene for *O. kweichowensis* and *O. huanggangensis* was less affected by the glacial period, and was related to the presence of refugia.

In reptiles, Yousefi et al. (2022) found that the Zagros Mountains, Central Iranian Plateau and the northern Persian Gulf have the highest lizard richness. The Zagros Mountains, Central Iranian Plateau, the northern Persian Gulf and the regions around the Lut Desert and Jazmourian Plain have the highest total genetic divergence in Iran. Alborz and Kopet Dag mountains and southwestern parts of Turkey have the highest average genetic divergence. The annual temperature was the most important predictor of lizard richness, and temperature change velocity was the most influential determinant of the genetic divergence pattern. Noteworthy, species diversity and most areas with high genetic divergence are located outside of Irano-Anatolian biodiversity hotspots.

Different from the complex geographical system in the terrestrial ecosystem, salinity and temperature are the most important environmental barriers in the aquatic ecosystem (Costa et al., 2017). Wang, Wang et al. (2022) took comprehensive genomic data to investigate the phylogenetic relationships and geographical distribution patterns in a group of popular model organisms in evolutionary biology—*Pungitius* sticklebacks in Northeast Asia. The study led to the discovery of two new recorded species (*P. kaibarae* and *P. bussei*) and previously unknown divergent *P. sinensis* lineages in China and raised conservation concerns associated with unintentional translocations and possible admixture, which is highly relevant for biodiversity conservation and management of *Pungitius* sticklebacks. Dalongville et al. (2022) found that temperature is a prominent source of intraspecific genetic variation in marine fish and invertebrate species that inhabit a strong biogeographical gradient across the Atlantic and Indian ocean transition. Patterns of genetic diversity differ between species and bioregions, but do not display higher levels within the core of each species' range; thus there is no clear support of the 'central-margin' hypothesis. The South-West bioregion of the South African coast was highlighted as a conservation priority area that represented both high genetic diversity and differentiation across taxa.

By studying the population divergence of Black Cottonwood (*Populus trichocarpa*) using assembled genome data, and climatic and species occurrences, Liu (2022) showed that the British

Columbia (BC)-North and BC-South populations are ancestral and subject to more recent bottlenecks than the Oregon population. Consistently, ecological niche modelling illustrates that compared to the Last Glacial Maximum (~21 Ka), the present niche suitability of the BC-North and -South populations is overall marginally inferior to that of the Oregon population. However, genomic analysis demonstrates that the Oregon harbours the lowest genetic diversity, possibly due to an extended bottleneck experienced by the population.

Wu et al. (2022) reconstructed the regional phylogeny of the mosses of Haida Gwaii, a putative glacial refugium and 'hotspot' of moss diversity, and used phylogenetic comparative methods to examine the macroecological imprint of glacial refugia on the geographic range structure and phylogenetic attributes of present-day moss assemblages. The islands of Haida Gwaii represent an extratropical hotspot of bryophyte diversity. They illustrated how the present-day phylogenetic structure of mosses on Haida Gwaii might have been shaped by glacial history and highlighted the importance of glacial refugia in maintaining extratropical moss diversity.

Zhang et al. (2022) investigated the distribution patterns of plant diversity in Kenya, how climatic fluctuations and orogeny shaped them, and the formation of its β -diversity using a well-resolved phylogenetic tree and extensive distribution records from public databases and other published sources. The phylogenetic turnover of the Kenyan flora, intersecting with the biodiversity hotspots Eastern Afromontane, Coastal Forests of Eastern Africa, and Horn of Africa, shows a non-monotonic pattern along a latitudinal gradient that is strongly structured into volcanic and coastal areas. The other areas are mainly dominated by phylogenetic nestedness, even in the eastern part of the equatorial region parallel to the volcanic area. Variations in turnover gradient and coexistence are highly dependent on the regional biogeographical history resulting from climatic fluctuations and long-lasting orogeny, which jointly shaped the biodiversity patterns of the Kenyan flora.

2.3 | Current status of fauna and flora hotspots

Different organisms have their own preference for habitats, and this makes their geographical pattern varies largely. Conservation requires the development of prioritization schemes due to limited funds and resources. In order to build ecological corridors and biodiversity protection networks so as to improve the quality and stability of ecosystems, it is essential to understand the current status of different organisms in the terrestrial and aquatic ecosystems. The present Section C contains 10 papers related to the current status of fauna and flora hotspots. Moreover, robust reference databases for poorly studied taxa are essential for a comprehensive understanding of the diversity pattern; for example, the study conducted by Gadawski et al. (2022) filled a gap in barcoding data of the European Chironomidae of the Balkan region lake flies. Research regions are diversified and representative, including the circumpolar Arctic, Neotropics, Worldwide Islands,

Western Balkans, Indian Ocean ridges and China. Furthermore, taxa contain mammals, reptiles, deep Sea invertebrate, insects and plants. These papers identified the current distribution patterns of species diversity in different taxa and provided insight for future conservation activities.

By analyses of marine mammal hotspots across the circumpolar Arctic, Hamilton et al. (2022) identified hotspots and areas with high species richness that occurred within the Arctic continental-shelf seas and within the marginal ice zone, particularly in the "Arctic gateways" of the North Atlantic and Pacific oceans. Summer hotspots were generally found further north than winter hotspots, but there were exceptions to this pattern, including bowhead whales in the Greenland-Barents Seas and species with coastal distributions in Svalbard, Norway and East Greenland. Areas with high species richness generally overlapped high-density hotspots.

By combining species richness, past collection efforts, and degree of habitat loss accessibility, Feijó, Ge, Wen, Xia et al. (2022) identified major Xenarthran diversity hotspots including the Amazonian lowlands of Bolivia and the dry Chaco of Paraguay and Argentina. Amazon holds a high diversity that remains poorly explored. Central Argentina and eastern Brazil are priority areas for research and conservation given the low sampling efforts, high diversity and endemic species, high levels of habitat loss and a dense road network.

Insular regions represent 5% of the Earth's surface and host more than 20% of all known plants and vertebrates. By analysing occurrence data of mammals from 1799 islands across 19 insular regions at a global scale, Leclerc et al. (2022) identified four hotspots for endemic mammalian conservation through the three diversity facets: Indo-Burma, Madagascar and the Indian Ocean Islands, Mesoamerica and Galápagos Islands, and Wallacea. Except for Mesoamerica and Galápagos Islands, the protected areas coverage is low (<8%) within the hotspots.

Borko et al. (2022) analysed biodiversity patterns of *Niphargus* using two biodiversity metrics, species richness and phylogenetic diversity, on a grid-based approach in Western Balkans. They found that species richness does not predictably correlate with phylogenetic diversity. This difference suggests that different processes have led to the formation of species-rich areas in the Western Balkans: through a combination of dispersal and speciation in the northwest, and local radiation in the southeast, respectively.

Neotenic net-winged beetles with limited dispersal ability generally occur in restricted ranges but rarely occur in China, which makes them ideal models for biogeographical studies to define biodiversity hotspots. Liu et al. (2022) modelled to simulate the habitat suitability for neotenic Lycidae occurring in China under different climate scenarios by using all available distribution information in Southeast Asia. The results indicated that potentially suitable habitats for neotenic Lycidae were mostly located in the montane areas and mountainous islands in southern China, including the eastern Himalayas, Gaoligong Mountains, Ailao Mountains, Hengduan Mountains, Wumeng Mountains, Miaoling Mountains, Daba Mountains, Wu

Mountains, Yunkai Mountains, Wuzhi Mountains and Central Mountains. Therefore, more attention and biological conservation efforts should be used in these areas.

Jiang, Yan et al. (2022) mapped the spatial distributions of 1028 endemic true bugs in China and investigated the distribution and diversity of endemic true bugs for four family groups (i.e., Miridae, Lygaeoidea, Pentatomidae, and Reduviidae), the environmental factors shaping these diversity patterns, and the effectiveness of China's Protected areas (PAs) in safeguarding their diversity. They found that most (84.9%) diversity hotspots for total species were located in mountainous areas of southern China. Additionally, the diversity patterns are shaped by the combined effects of different environmental factors and PAs in China could not provide sufficient protection for this diversity and protecting these endemic true bugs diversity should be valued more in mountainous areas of southern China.

Zhou et al. (2022) characterized fauna from three new vent fields on the Carlsberg Ridge (CR) for the first time and revealed species turnover along the Indian Ocean ridges by identifying biogeographic regions based on beta diversity measurement β_{sim} . Faunal assemblages at three new vents on the CR hosted a total of 34 species. Species turnover along the ridges supported the separation of Indian Ocean vents into three discrete biogeographic units, boundaries between which largely corresponded to genetic breaks for shared species with lower dispersal capabilities. The results clearly show that the conservation of Indian Ocean vents must target three provinces, simultaneously.

Caballero-Herrera et al. (2022) identified three strong biotic boundaries that delimits four biotic regions in Eastern Atlantic Ocean based on studies of Bivalvia (1) European Atlantic and Mediterranean; (2) West African, from western Sahara to southern Angola; (3) Baia dos Tigres/Namibia; and (4) Saint Helena/Ascension. They found with 429 species present in West Africa, 261 (60.7%) are endemic, and 19 genera (7.2%) are endemic. Sixteen chorotypes were identified; the European BR is correlated with chorotypes C5 (149 species mostly European and Mediterranean) and C3 (38 species mostly in northern Europe), whereas the West African BR is mainly characterized by chorotype C6 (221 species). This study highlighted the underestimated biodiversity in aquatic system.

Fu et al. (2022) explored whether extinction can be predicted from the evolutionary measures using angiosperm diversity from 27 regions covering all 36 worldwide hotspots. Family species richness, family age and family diversification rate appeared as good predictors of extinction risk as inferred from species status according to IUCN. However, the role of these predictors is spatially specific. Specifically, when all the 27 regions were considered as a whole, families with higher species richness, older age and/or faster diversification rates have a higher risk of species extinction. By contrast, in temperate regions, high extinction risk experienced families with low species richness and low diversification rates.

2.4 | Conservation gaps and implications for future management

In the terrestrial ecosystem, the joint effects of land use, habitat degradation and climate change are accelerating the global decline of biodiversity. In the aquatic environment, inappropriate management of freshwater resources, anthropogenic climate change pollution and overfishing are irreversibly changing aquatic habitats and the global water cycle that led to massive translocation of biotas and accelerated extinctions (Dudgeon et al., 2006). Increased homogenization of faunas facilitated the demographic increase of habitats generalist, often invasive, but wiped out many endemic native species (Poff et al., 2007). Commercial fish stocks are pushed beyond their capacity to renew themselves. This kind of biodiversity loss is not only presented in vertebrates but mainly in invertebrates. The implications of these changes are of great concern for human health and ecosystem sustainability.

In this issue, Su et al. (2022) showed that the area of priority protection habitats of the Yunnan snub-nosed monkey (*Rhinopithecus bieti*) dramatically decreased from 212.1 km² in 1990 to 101.6 km² in 2020. The average length of connectivity corridors among potential core habitat patches and priority protection habitats decreased from 75.9 km in 1990 to 56.8 km in 2020. They suggest that the protection of this species requires a conservation network of five protection areas.

In Eastern Himalayas, Buthan, anthropogenic land use and climate change accelerate biodiversity decline. Penjor et al. (2022) analysed the response of functional and phylogenetic diversity of mammal and bird communities to the land use and climate variables and showed filtering effects of anthropogenic pressure and climate change on all biodiversity facies in both groups. Association with land use suggests the potential for ecosystem services, particularly by birds. Alarmingly, the loss of species at the edge of functional space is nonrandom and could result in the loss of irreplaceable traits impacting long-term ecological and evolutionary processes.

Leclerc et al. (2022) analysed three biodiversity facies (taxonomic, functional, phylogenetic) of threatened endemic insular mammals worldwide. They identified four global hotspots and showed that the coverage of protected areas in two of them is low (<8%) within the hotspots, and that most of the mammal species occurring in the hotspots were prone to either direct threats that affect their mortality or indirect threats that only alter their habitat. Mixed threats such as biological invasions or climate change were less represented in those regions.

Mota et al. (2022) studied the impact of climate changes on alpha and beta diversity of forest frugivorous birds in Central Corridor of Atlantic Forest (CCAF), Brazil. Using ecological niche modelling most bird species were projected to lose suitable area by 2070 as a consequence of climate change, resulting in a decline of alpha diversity and an increase of temporal beta diversity, which is dominated by the nestedness component. Regardless climate scenario, species richness and differentiation of bird communities are expected to decrease and increase from the east to the west portion of the CCAF, respectively.

Clearwing butterflies (tribe Ithomiini) have been proposed as biological indicators for habitat quality in Neotropical forests, which contain the world's richest biological communities. Doré et al. (2022) quantified and mapped the overlap of diversity hotspots with areas threatened by or providing refuge from current anthropogenic pressures and supported the role of this group of animals as a suitable flagship indicator for Neotropical butterfly diversity and reinforced the position of the tropical Andes as a flagship region for biodiversity conservation in general, and insect and butterfly conservation in particular.

Shen et al. (2022) studied how the areas for forest protection in the Qinghai-Tibet Plateau influence the environment inside the areas themselves, as well as in the surrounding buffer zones. The spillover effects (i.e., the influence of the protected areas on surrounding areas) can be positive or negative. To study this, they compared deforestation rates inside the protected areas and in 20 km buffer zones around them with matched control areas. They identified that 75.9% of the nature reserves of the Qinghai-Tibet Plateau and nearby regions were effective in preventing deforestation within their boundaries. They also showed that the spillover effects were heterogeneous around the nature reserves. One hundred and twenty-two buffer zones had positive spatial spillover effects (blockages), ranging from 0.1% to 5.3%, while 119 buffer zones had negative spillover effects (leakages), ranging from -8.84% to -0.1%. Blockages slightly outnumbered leakages at different distances, while leakages became more frequent when they treated buffer zones as a whole spillover area.

For future conservation planning, Tonetti et al. (2022) explored how large-scale forest regeneration may reduce the negative impacts of climate change on the biodiversity of a tropical hotspot, Brazilian Atlantic Forest (BAF). They built a forest regeneration scenario via seed dispersal based on the potential dispersal of frugivorous fauna. Without considering the effects of climate change, the potential distribution area for each species increases on average by 72.5% (SD = 8%) in the scenario of potential regeneration, while climate change decreases the area of the potential occurrence of 252 species, which may suffer a mean reduction of 74.4% (SD = 9.3%) in their current potential distribution areas. BAF regions with the largest amounts of the forest had the greatest potential richness of species. In future climate scenarios, 3.4% of species may become extinct, but they show that large-scale regeneration may prevent these extinctions.

Both, past evidence and future predictions unambiguously showed how fragile biodiversity is (Mota et al., 2022; Penjor et al., 2022; Su et al., 2022). There is evidence that current protection networks are insufficient to protect the hotspots (Leclerc et al., 2022). On a more positive note, this paper collection showed also that we have tools allowing detection of regions and refugia where much of biodiversity could be preserved (Doré et al., 2022; Liu et al., 2022). The available data and modern analytic tools have predictive power to plan efficient nature conservation (Doré et al., 2022; Shen et al., 2022; Su et al., 2022; Tonetti et al., 2022) and even the strategies how for mitigating biodiversity decline (Tonetti et al., 2022).

3 | CONCLUSION AND PROSPECT

This special issue provided a unique opportunity to focus on biodiversity hotspots from many different perspectives, regional and taxonomic groups and ranging from mechanisms and process to conservation and management. There was a wide scope of papers and we were particularly pleased with contributions from across Africa and Asia, although we are aware of the areas where data are still lacking, particularly in several biodiversity hotspots in Southeast Asia, Africa and South America. In addition, more attention on underground biota and aquatic resources is warranted.

Extensive international cooperation is key to promote the effectiveness of research and protection since the distribution of wildlife is not confined by country borders. New technologies boosted many initiatives for data collection, for example, the Barcode of life, the European Reference Genome Atlas (ERGA), Centre for Biodiversity Genomics (Bioscan); all these aims to reveal biodiversity on the Earth. Recently, Chinese scientists have proposed the idea of "Digital Noah's Ark" and call for international scientists to build a consortium to coordinate sampling, sequencing, assembly, and annotation of complete Telomere-to-Telomere (T2T) genome for endangered species on the planet (Wei et al., 2022). The popularization and application of new technologies and methods to explore these data will help to solve more deep-level scientific problems. In addition, frequent communication between the government and researchers is conducive to the protection of the conservation gaps. Scientific research needs to be combined with practice so that the conservation gap discovered by the scientific community can be filled by practical action.

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CONFLICT OF INTEREST



None declared.

DATA AVAILABILITY STATEMENT





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PEER REVIEW

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