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Decapod Biodiversity Hotspots and Environmental Drivers: A Macroecological Approach About Bycatch Species in Brazil

Jeniffer N. Teles | Fernando L. Mantelatto

Laboratory of Bioecology and Crustacean Systematics (LBSC), Department of Biology, Faculty of Philosophy, Science and Letters at Ribeirão Preto (FFCLRP), University of São Paulo (USP), Ribeirão Preto, SP, Brazil

Correspondence: Jeniffer N. Teles (jenifferteles94@gmail.com)

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Keywords: benthic communities | biogeographic patterns | Brazilian Exclusive Economic Zone | Crustacea | marine conservation | mitogenomic markers | spatial regression models | trawling

ABSTRACT

Aim: To investigate the spatial patterns of species richness (SR), phylogenetic diversity (PD) and phylogenetic endemism (PE) in bycatch decapod crustaceans along the Brazilian Exclusive Economic Zone and to assess the influence of environmental variables and trawling effort on these diversity indices.

Location: Brazilian Exclusive Economic Zone.

Taxa: Decapoda.

Methods: We compiled *bycatch* occurrence data from peer-reviewed studies and global biodiversity repositories. Diversity indices (SR, PD, PE, ED and WE) were estimated using a phylogenetic approach incorporating mitogenomic markers. Environmental and trawling effort data were extracted from global databases, and statistical analyses, including redundancy analysis (RDA), spatial regression and random forest models, were applied to determine the drivers of diversity.

Results: Decapod diversity showed strong spatial heterogeneity across the EEZ. SR peaked in southeastern Brazil in upwelling-influenced ecotones, while PD and PE were highest in offshore and equatorial regions. PD was strongly associated with bottom temperature, primary productivity (PP) and current velocity; SR was mainly driven by salinity, light availability and PP; and PE was best explained by temperature and PP. Most hotspots of phylogenetic diversity and endemism fell outside Marine Protected Areas (MPAs), revealing significant conservation gaps in offshore and southern regions.

Main Conclusions: This study provides the first macroecological framework of decapod diversity in the Brazilian EEZ and one of the first applications of phylogenetic diversity (PD) and phylogenetic endemism (PE) metrics for decapods in the South Atlantic. We show that temperature, salinity, productivity and current dynamics differentially shape biodiversity metrics. Southeastern and offshore zones host unique evolutionary lineages but remain underrepresented in current MPA networks. By integrating

phylogenetic and environmental data, our findings offer a baseline to improve spatial biodiversity assessments and support more representative conservation planning under shifting ocean conditions.

1 | Introduction

Biodiversity assessments in marine ecosystems often rely on a combination of taxonomic and phylogenetic metrics to capture different dimensions of diversity (Guilhaumon et al. 2014; Wong et al. 2018; Mantelatto et al. 2018; Teles et al. 2024). Species Richness (SR) provides a measure of the number of species within a community, while Phylogenetic Diversity (PD) represents a range of measures that reflect the total length of all the branches connecting a set of species on their phylogeny in a given area (Magurran 1988; Faith 1992; Tucker et al. 2017). Phylogenetic Endemism (PE) is a metric that combines phylogenetic diversity with geographic range, quantifying the extent to which evolutionary history is spatially restricted (Rosauer et al. 2009). Null models are crucial for interpreting these metrics, providing a baseline to determine whether observed patterns deviate from random expectations (Gotelli and Ulrich 2012). By randomising species distributions under controlled constraints, null models help isolate the effects of species richness from other ecological and evolutionary processes, ensuring that patterns in PD and PE reflect meaningful biological or environmental drives (Gotelli and McCabe 2002). These indices are increasingly applied in marine environments to identify biodiversity hotspots and assess the impacts of environmental changes (Mardones and Scherson 2023). By extending these approaches to marine communities, researchers can gain a more comprehensive understanding of biodiversity patterns and their drivers in marine ecosystems (Tolimieri et al. 2015; Schmiing et al. 2014).

Marine ecosystems exhibit distinct patterns of diversity across their benthic, pelagic and planktonic realms, shaped by unique ecological roles and environmental factors (Costello et al. 2017). Benthic species often display high taxonomic and phylogenetic diversity due to habitat heterogeneity and substrate complexity, which support diverse adaptations and evolutionary lineages (Romoth et al. 2023). In contrast, pelagic species tend to have broader distributions but lower phylogenetic diversity, as open-water habitats impose fewer ecological constraints, favouring dominance by a few widely distributed species (Norris 2000). However, planktonic communities are taxonomically rich but characterised by rapid species turnover and reliance on fewer evolutionary clades driven by dynamic nutrient fluxes and light availability (Leibold and Norberg 2004). These differences highlight the complementary contributions of each realm to marine biodiversity (Figure 1).

Benthic communities play a crucial role in maintaining essential ecosystem functions, including nutrient cycling, habitat structuring and energy transfer across trophic levels (Griffiths et al. 2017). Despite their ecological importance, these ecosystems are increasingly threatened by anthropogenic pressures such as overfishing, pollution and habitat destruction (Costello and Chaudhary 2017). These stressors not only compromise ecosystem health but also reduce the resilience of marine environments to climate change, limiting their capacity to recover from disturbances (Chapman 2017). Furthermore, the degradation of benthic habitats can lead to declines in the abundance, body size and reproductive success of marine species that are important for human consumption, with direct implications for fisheries productivity and food security (Pauly et al. 2005; Hilborn et al. 2012, 2023). Understanding benthic diversity patterns is therefore essential for conservation strategies that aim to preserve both the evolutionary legacy of marine life and the ecosystem services that support sustainable livelihoods, objectives that align closely with global sustainability targets such as the Sustainable Development Goals (Koundouri et al. 2023; van Der Meer et al. 2023).

Marine crustaceans, particularly decapods (shrimps, crabs, lobsters and hermit crabs), are ecologically and economically significant components of benthic communities, contributing to ecosystem functions like sediment turnover and nutrient cycling while supporting valuable fisheries (Boudreau and Worm 2012). However, despite a growing interest in macroecological diversity studies for this group (Sharifian et al. 2020; Hultgren et al. 2021; Teles et al. 2024), research on their diversity patterns remains limited compared to other taxa such as fish (Araújo et al. 2018; Teichert et al. 2018). This knowledge gap is especially pronounced along the Brazilian coast, where an extensive coastline (~8000 km) encompasses diverse habitats distributed in three marine provinces (see Spalding et al. 2007), which are subject to varying levels of anthropogenic pressure. Trawl fisheries, a major threat to decapod crustaceans along the coast of Brazil, produce substantial bycatch that includes numerous non-target species with poorly understood ecological roles (Mazor et al. 2021). The physical disturbance caused by trawling alters benthic habitats and selectively removes species, leading to declines in biodiversity and ecosystem functioning (Branco et al. 2015; Beauchard et al. 2023; Dantas et al. 2025). Addressing these impacts requires robust data on decapod diversity patterns across spatial scales.

Upwelling areas in southeastern Brazil are expected to show higher diversity due to high productivity and the mixing of tropical and subtropical species in ecological transition zones (Valentin 2001; Cord et al. 2022), especially for decapods (Teles et al. 2024; Teles and Mantelatto 2024). The Cabo Frio region in southeastern Brazil is characterised by a coastal upwelling system that brings nutrient-rich cold water to the surface, enhancing primary productivity and supporting diverse marine communities (Coelho-Souza et al. 2012). This is the main upwelling system in Brazil and the one with the greatest impact on benthic biodiversity in the southeastern region, second only to the Amazon-Orinoco Plume in the north, in terms of large-scale oceanographic influence along the Brazilian coast (Coelho-Souza et al. 2012; Cord et al. 2022; Peres et al. 2022; Teles et al. 2024). These areas are essential for maintaining connectivity between marine communities and fostering ecological resilience, but they are also highly vulnerable to anthropogenic pressures (Magris et al. 2020). This highlights the need for integrating biodiversity data with environmental variables to identify conservation priorities, underscoring the critical role of transitional zones in supporting marine biodiversity amid changing environmental conditions (Benson et al. 2018; Ramírez et al. 2017). Therefore, targeted conservation strategies

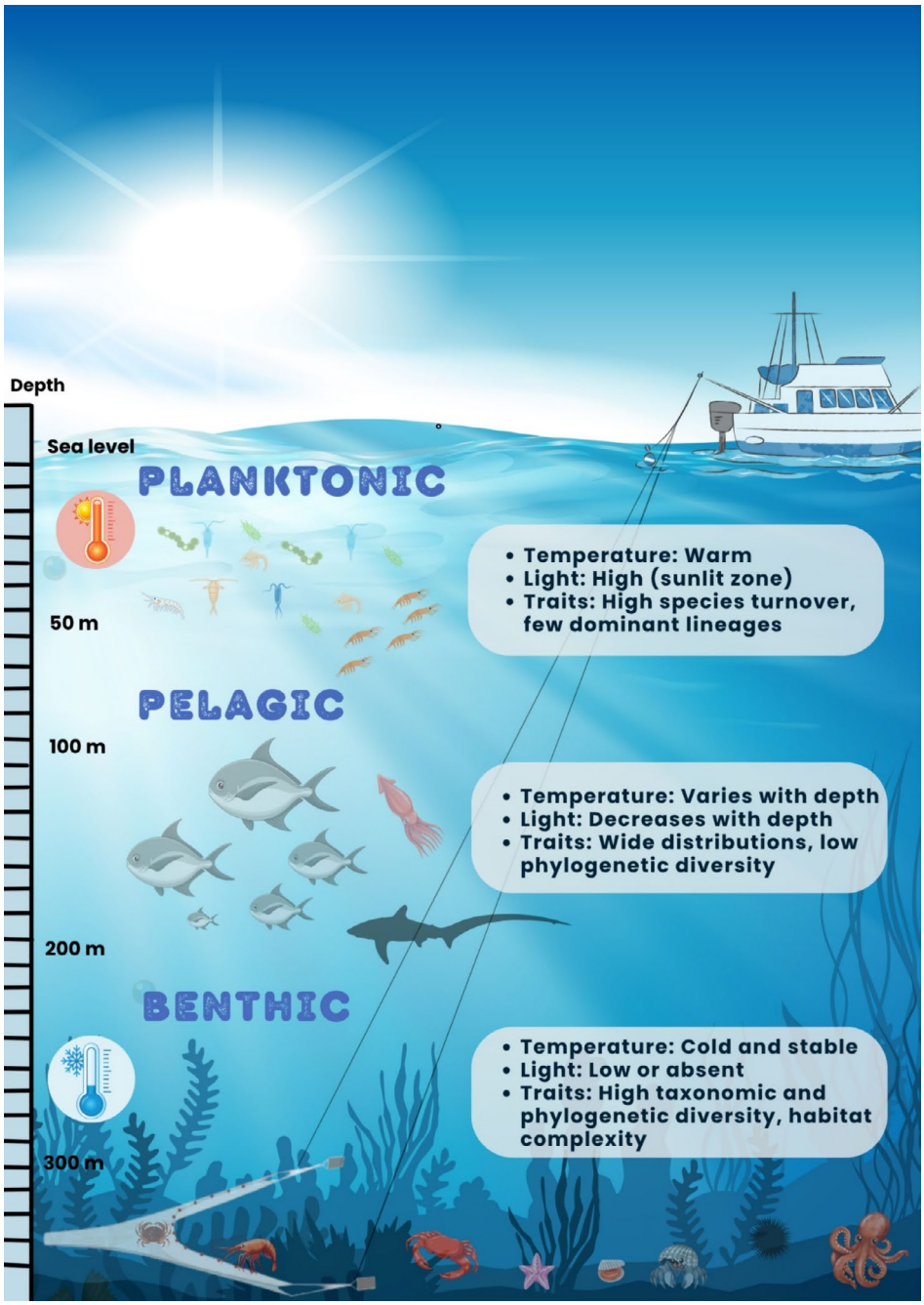

FIGURE 1 | Conceptual diagram illustrates the main ecological realms of the ocean (planktonic, pelagic and benthic) with their general characteristics. The realms differ in depth, temperature, light availability and biodiversity attributes. Planktonic communities, restricted to the sunlit zone, are characterised by high species turnover. Pelagic organisms occupy mid-water depths and tend to have broad distributions but low phylogenetic diversity. Benthic habitats, located on the seafloor, are cold and darker but host high taxonomic and phylogenetic diversity due to habitat complexity. The diagram also depicts a bottom trawling operation impacting the benthic zone, illustrating the physical disturbance and potential biodiversity loss caused by this fishing practice.

are required to address the unique dynamics of hotspot regions and other transitional habitats along the Brazilian coast.

Environmental factors play a pivotal role in shaping the distribution and composition of marine decapod communities. Temperature is a key driver of species distribution, influencing physiological processes such as metabolism and reproduction, such as gonadal maturation, timing and frequency of spawning, and embryonic development (Furlan et al. 2013; Monteiro, de Castro, et al. 2023), especially in the context of global ocean warming (Cheung et al. 2021). Ocean currents affect larval dispersal and adult movement patterns, thereby structuring population connectivity across spatial scales (Queiroga and Blanton 2005). Light plays a fundamental role in regulating circadian rhythms, foraging behaviours and vertical migration patterns of these organisms (Forward Jr and Buswell 1989; Aréchiga and Rodríguez-Sosa 1997). Primary productivity, in turn, is a key factor in food availability for marine species,

directly influencing population dynamics and community structure (Sommer et al. 2002; Kearney et al. 2013). In areas of high productivity, such as coastal upwellings or estuaries, benthic decapods often exhibit greater abundance and diversity (De Léo and Pires-Vanin 2006; Pantaleão et al. 2016). Anthropogenic activities such as bottom trawling disrupt these dynamics by altering substrate composition and reducing habitat complexity (Kumar and Deepthi 2006). Additionally, fluctuations in salinity and oxygen levels (whether natural or anthropogenic) can significantly impact species survival and distribution (Anger 2003; Monteiro, Cruz, et al. 2023). Comparisons with other taxa reveal similar environmental dependencies. For instance, coral reef fish exhibit strong associations with temperature gradients and habitat complexity (Bellwood and Hughes 2001), while seagrass-associated fauna are influenced by sediment characteristics and water quality parameters (Orth et al. 2006). These parallels underscore the importance of understanding environmental drivers across taxa to inform conservation strategies that address multiple facets of biodiversity.

In this study, we investigate the diversity indices—species richness (SR), phylogenetic diversity (PD) and phylogenetic endemism (PE)—of benthic decapod crustaceans recorded as bycatch in trawl fisheries across the Brazilian Exclusive Economic Zone. This approach provides broad spatial coverage and captures the majority of benthic species relevant to our ecological assessments, as most marine decapods are demersal and highly susceptible to bottom trawling. Specifically, we aim to identify relationships between SR, PD and PE with key environmental factors (such as bottom temperature, salinity, primary productivity, current velocity and bottom light) and trawling effort predictors. By integrating these metrics with environmental data across macroecological scales, we seek to provide insights into the factors shaping bycatch decapod diversity along Brazil's extensive coastline. The findings will contribute to broader conservation efforts by integrating insights from other taxa and regions to address multiple facets of biodiversity. We hypothesise that (i) regions closer to urban or industrial areas are expected to exhibit lower phylogenetic diversity and greater loss of phylogenetic endemism, owing to pollution and habitat degradation; (ii) in contrast, upwelling zones in southeastern Brazil are anticipated to support higher diversity (SR, PD, PE) due to enhanced productivity and the mixing of tropical and subtropical species in ecological transition zones; (iii) environmental gradients are expected to shape spatial patterns of decapod diversity in predictable ways: we expect SR, PD and PE to be positively associated with higher temperature, salinity and primary productivity, which favour physiological performance, reproductive output and resource availability in benthic environments.

2 | Material and Methods

2.1 | Taxa Selection and Occurrence Data

To identify decapod species occurring in the Brazilian Exclusive Economic Zone (EEZ), we conducted a comprehensive search using Google Search with combinations of the following keywords: Brazil, bycatch, Crustacea, trawling and Decapoda. The search included publications from all available years (until 2023). We selected all decapod crustacean species reported in peer-reviewed scientific journals indexed in the Journal Citation Reports (JCR), except for three journals (Marine & Fishery Sciences, Acta of Fisheries and Aquatic Resources, and Research, Society and Development) which are indexed in at least four other academic databases, including Latindex, and are also peer-reviewed. From these sources, we retained studies that provided species-level biodiversity lists for decapods collected by trawling methods in marine environments up to 200 m depth along the entire Brazilian EEZ.

The nomenclature followed the most recent taxonomic proposal verified at World Register of Marine Species (Ahyong et al. 2025). All species names were manually checked and, when necessary, synonymised names were corrected to their most recent valid nomenclature according to WoRMS. These species also have documented occurrence points in the Ocean Biodiversity Information System (OBIS 2024) platform accessed through the 'robis' R package (Provoost and Bosch 2022). Additional records from the Crustacean Collection of the Department of Biology (CCDB) at the Faculty of Philosophy, Sciences and Letters of Ribeirão Preto (FFCLRP) in Brazil were also included to improve spatial coverage whenever available (Tables S1 and S2). Geographic data were filtered using the clean_coordinates function from the CoordinateCleaner package (Zizka et al. 2019), with the following tests enabled: 'centroids', 'duplicates' and 'zeros'. This configuration allowed us to flag and exclude records located at country centroids, exact duplicates and coordinate zeros, all of which are known to reflect potential georeferencing errors.

We constructed a regular grid of $1° \times 1°$ resolution (latitude/longitude; ~111 km^2) using the lets.presab.points() function from the 'letsR' package (Vilela and Villalobos 2015), with spatial bounds defined from −53.35° to −25.95° longitude and −33.85° to 5.2° latitude to fully encompass the Brazilian Exclusive Economic Zone (EEZ). The grid origin was implicitly aligned to these bounds, and cells were generated in the WGS84 geographic coordinate reference system. We used the remove.cells = TRUE argument to exclude empty cells without species occurrences. The resulting grid was cropped using the official shapefile of the Brazilian EEZ via the lets.pamcrop() function to ensure that only cells fully or partially overlapping the EEZ were retained. No additional buffer or exclusion criteria were applied to coastal overlap; thus, cells partially covering land and ocean were included, provided they intersected the EEZ polygon.

2.2 | Environmental Factors

Data from environmental factors were extracted from Bio-ORACLE: Marine data layers for Ecological Modelling version 2.2 (Assis et al. 2017) using the R package 'sdmpredictors' (Bosch and Fernandez 2023). Were extracted 24 present benthic layers for the following environmental factors: pH, currents velocity ($m\,s^{-1}$), bathymetry mean (m), dissolved molecular oxygen mean ($mol\,m^{-3}$), dissolved molecular oxygen range ($mol\,m^{-3}$), dissolved molecular oxygen maximum ($mol\,m^{-3}$),

chlorophyll mean (mg m^{-3}), chlorophyll range (mg m^{-3}), nitrate (mol m^{-3}), phosphate (mol m^{-3}), salinity mean (PSS), salinity range (PSS), salinity maximum (PSS), temperature mean (°C), temperature range (°C), temperature maximum (°C), iron (umol m^{-3}), primary productivity mean (g m^{-3} day^{-1}), primary productivity range (g m^{-3} day^{-1}), silicate (mol m^{-3}), bottom light (E/m^2/year), carbon phytoplankton biomass mean (micromol/m^3), carbon phytoplankton biomass range (micromol/m^3), carbon phytoplankton biomass maximum (micromol/m^3) and calcite (mol m^{-3}).

The platform Global Fishing Watch (https://globalfishingwatch.org) was used as a proxy of fishing pressure using the 'gfwr' package (Clavelle et al. 2023). Monthly fishing effort data from trawlers were downloaded from the Global Fishing Watch database for the period 2019 to 2023, and an average fishing effort raster layer was generated for the Brazilian Exclusive Economic Zone (EEZ). We selected this five-year window because data coverage and quality became substantially more consistent from 2018 onwards, due to improved AIS tracking, satellite monitoring, and platform standardisation. We excluded cells with fewer than 24 fishing hours and log transformed the total fishing hours to better visualise the results.

Multicollinearity among environmental factors and trawling pressure was assessed using Pearson's correlation and Variance Inflation Factor (VIF) value (Table S3), and variables were removed if Pearson coefficients >0.7 and VIF >7 (Figure S1). The final variables selected were current velocity (VIF = 2.50), bottom light (VIF = 2.17), trawling pressure (VIF = 1.44), mean bottom temperature (VIF = 6.23), mean surface temperature (VIF = 1.63), mean salinity (VIF = 2.92) and mean primary productivity (VIF = 4.24).

2.3 | Species Richness and Phylogenetic Diversity Index

We calculated species richness (SR) for each 1° × 1° grid cell by counting the number of unique decapod species with occurrence records within each cell.

To estimate the Phylogenetic Diversity index, the mitogenomic phylogenetic Decapod tree from Shen et al. (2013) was reconstructed, and additional sequences from species captured in bycatch were added (Figure S2 and Table S2). A total of 12 mitochondrial protein-coding genes (COI, COII, ATP8, ATP6, COX3, NAD3, NAD5, NAD4, NAD4L, NAD6, COB and NAD2), plus 12 s rRNA and 16 s rRNA of 173 species were used (Table S1). We selected one individual per species available and retrieved sequences of COX1, 16S rRNA and 12S rRNA deposited on the GenBank platform (Table S1). Species were chosen based on marker completeness and correct taxonomic identification. Since the original phylogeny lacked a broad representation of Brazilian species, this approach was essential to ensure their correct placement in the resulting topology.

Each molecular marker was aligned separately using MAFFT v.7 (Katoh et al. 2019), and poorly aligned regions and gaps were trimmed manually in Geneious Prime 2023.1 (Kearse et al. 2012). The alignments were concatenated in the same order as the gene sequences described above. We used IQ-TREE2 (Minh et al. 2020) to infer the phylogenetic tree using a single partition and the Maximum Likelihood method. The best-fit model of nucleotide substitution (GTR + F + ASC + R8) was selected using ModelFinder under the Bayesian Information Criterion (BIC). Statistical support was assessed using the ultrafast bootstrap approximation with 1000 replicates, and support values are provided on the nodes of the resulting tree (Figure S2). Non-target species not captured as bycatch along the Brazilian coast were removed using the 'ape' R package (Paradis and Schliep 2019), while branch lengths were preserved for downstream diversity analyses.

The diversity metrics calculated in this study included Faith's phylogenetic diversity (PD), phylogenetic endemism (PE), weighted endemism (WE) and evolutionary distinctiveness (ED), using the 'phyloraster' R package (Alves-Ferreira et al. 2024). PD measures the total branch length of the phylogeny connecting all species in a community (Faith 1992). PE quantifies how much of the total phylogenetic diversity is geographically restricted, highlighting areas with evolutionarily unique and spatially limited lineages (Rosauer et al. 2009). WE accounts for the range size of each species, giving greater weight to narrowly distributed taxa (Williams et al. 1994). ED reflects the evolutionary isolation of a species, based on the amount of unique evolutionary history it represents in the tree (Isaac et al. 2007).

Additionally, standardised effect sizes (SES), which are null models widely used to control for richness effects in diversity measures (Gotelli and Ulrich 2012), were computed for these metrics using the SESraster R package (Heming et al. 2023). We applied spatial and phylogenetic randomisations based on 999 iterations (Kembel et al. 2010). These randomisations were designed to maintain observed species richness per grid cell while shuffling species identities across the phylogeny or spatial space, allowing the generation of robust null distributions. After evaluating the correlation matrix, we found that the non-standardised indices were all highly correlated ($R^2>0.9$), and the standardised SES variables exhibited lower correlation values. Based on this, SR, PD.SES and PE.SES were selected for further analyses due to their sufficiently independent patterns (Figure S3).

To identify and visualise spatial biodiversity patterns, we classified each grid cell for SR, PD.SES and PE.SES according to their percentile values. Cells falling within the upper 10% (≥90th percentile) were designated as biodiversity hotspots, while those in the lower 10% (≤10th percentile) were categorised as coldspots. To contextualise these patterns in terms of conservation coverage, we overlaid the spatial distribution of Brazil's Marine Protected Areas (MPAs), encompassing both strict protection and sustainable use categories. Spatial data were obtained from the August 2025 version of the World Database on Protected Areas (WDPA), maintained by UNEP-WCMC and IUCN. This dataset includes federally, state and municipally designated MPAs and is accessible via www.protectedplanet.net (UNEP-WCMC and IUCN 2025).

2.4 | Data Analyses

All analyses and visualisations were conducted using R software (version 4.4.2; R Core Team 2024). Trawling effort and species richness (SR) data were log10-transformed to reduce data heterogeneity.

To investigate the environmental drivers influencing overall diversity indices (SR, PD.SES and PE.SES) within the Brazilian EEZ, we adopted a multi-model analytical framework designed to compare and complement different statistical approaches. This strategy aimed to evaluate the consistency and relative explanatory power of environmental and spatial predictors across models.

As a first step, we performed Redundancy Analysis (RDA) using the rda function from the 'vegan' package (Oksanen et al. 2022). However, after detecting spatial autocorrelation in model residuals through Multiscale Ordination (MSO), we applied a Partial RDA (RDAp) to account for spatial structure. Moran's Eigenvector Maps (MEMs), calculated via the scores.listw function from the 'spdep' package (Bivand 2022), were used as covariables in the conditional matrix. These MEMs were generated using Principal Coordinates of Neighbourhood Matrices (PCNM) based on Euclidean distances among grid cell centroids. The response variables included SR, PD.SES and PE.SES, and the predictors consisted of six environmental variables plus trawling effort. The significance of each predictor was tested via forward selection and Monte Carlo permutation tests (999 permutations) using anova.cca.

To complement the ordination analysis and assess the individual importance of predictors from a modelling and predictive perspective, we applied two additional approaches: Random Forest (RF) and regression-based models (Breiman 2001). We applied Random Forest regression modelling using the rf() function from the 'spatialRF' package (Wright and Ziegler 2015; Benito 2021), which allows for enhanced diagnostics and model interpretation. The model was implemented with default parameters for tree construction (e.g., number of trees, mtry) and run with 30 repetitions to increase robustness. Each tree was built using bootstrap resampling (~63% of the data), and performance was assessed using the out-of-bag (OOB) data (~37%). As spatial autocorrelation in the residuals was not significant (Moran's I, $p > 0.005$), no spatial regression adjustment was required. Variable importance was estimated by randomly permuting each predictor in the OOB dataset and calculating the average decrease in node impurity. These procedures were applied across all diversity indices (SR, PD.SES and PE.SES).

In parallel, we compared three regression-based models to predict each diversity index: Generalised Linear Models (GLM) using the glmer function from the 'lme4' package (Bates et al. 2015), Generalised Additive Models (GAM) using the gam function from the 'mgcv' package (Wood 2017), and Spatial Generalised Linear Mixed Models (spaGLMM) using the fitme function from the 'spaMM' package (Rousset and Ferdy 2014). For spaGLMM, a Matérn spatial correlation structure was incorporated based on the geographic coordinates of the grid cell centroids. The model with the lowest Akaike Information Criterion (AIC) was selected as the best-fitting model for each index.

Additional R packages were employed throughout the analyses, including 'ggplot2' (Wickham 2011), 'readxl' (Wickham and Bryan 2025), 'raster' (Hijmans 2024), 'rgdal' (Bivand et al. 2006–2023), 'dplyr' (Wickham et al. 2023), 'picante' (Kembel et al. 2010), 'writexl' (Ooms 2025), 'rnaturalearth' (Massicotte et al. 2023), 'rnaturalearthdata' (South et al. 2024), 'sf' (Pebesma and Bivand 2023), 'ggmap' (Kahle and Wickham 2013), 'gridExtra' (Auguie 2017), 'ggpubr' (Kassambara 2023) and 'cluster' (Maechler et al. 2023), 'car' (Fox and Weisberg 2019), 'ggord' (Beck 2022), 'adespatial' (Dray et al. 2023), 'ape' (Paradis and Schliep 2019), 'terra' (Hijmans 2024), 'phylobase' (Hackathon et al. 2024), 'SESraster' (Heming et al. 2023), 'plyr' (Wickham 2011), 'readr' (Wickham et al. 2024) and 'gstat' (Gräler et al. 2016).

3 | Results

A total of 104 species were analysed to calculate SR, comprising 43,002 occurrence points, while 98 species were used for PD.SES and PE.SES metrics, distributed across 169 grid cells with 1° × 1° resolution within the Brazilian Exclusive Economic Zone. Across all grid cells, species richness (SR) ranged from 1 to 65 species per cell (mean = 8.18, SD = 10.7), PD.SES ranged from −4.28 to 2.18 (mean = −0.403, SD = 1.24) and PE.SES ranged from −1.72 to 4.11 (mean = −0.121, SD = 0.97). The largest groups used for PD and PE index calculations were the Brachyura (crabs) and Anomura (hermit crabs, squat lobster, porcelain crabs) infraorders, respectively (Figure 2).

The spatial distribution of marine decapod biodiversity within the Brazilian Exclusive Economic Zone (EEZ) exhibits distinct patterns for Species Richness (SR), Phylogenetic Diversity standardised effect sizes (PD.SES) and Phylogenetic Endemism standardised effect sizes (PE.SES). Species Richness (SR) displays two prominent hotspots: a primary peak between −20° S and −25° S in the southeastern region and a secondary peak around −15° S (Figures 3a and 4a). PD.SES reveals a heterogeneous distribution, with higher values concentrated in offshore regions of the southeastern and southern areas, particularly between −15° and below −30°, as well as in the northern region of Brazil, defined here as the equatorial zone between approximately 5° N and −2° S (including Amapá to northern Maranhão). Notably, greater diversity is observed in oceanic areas compared to coastal regions, where lower values predominate, especially along the northeastern coast, which we define as the area between −2° S and −15° S (from central Maranhão to Bahia) (Figures 3b and 4b). PE.SES exhibits a spatial pattern similar to PD.SES, with a primary peak observed in the southeastern region between −15° S and −25° S. However, areas of notable endemism are also present in the northern region of Brazil, particularly between 5° and −2° (Figures 3c and 4c). Overall, the southernmost areas (> 30° S) show consistently lower values across all indices.

The spatial analysis revealed distinct patterns of overlap between biodiversity hotspots and Marine Protected Areas (MPAs) along the Brazilian coast (Figure 4). For SR hotspots, they were primarily concentrated in the Southeastern and Southern regions, covering the coastal areas of Espírito Santo, Rio de Janeiro and São Paulo states, with additional important hotspots in Santa Catarina, Bahia and Paraíba statesgi (Figure 4a). Although most of these areas show partial overlap with MPAs, indicating

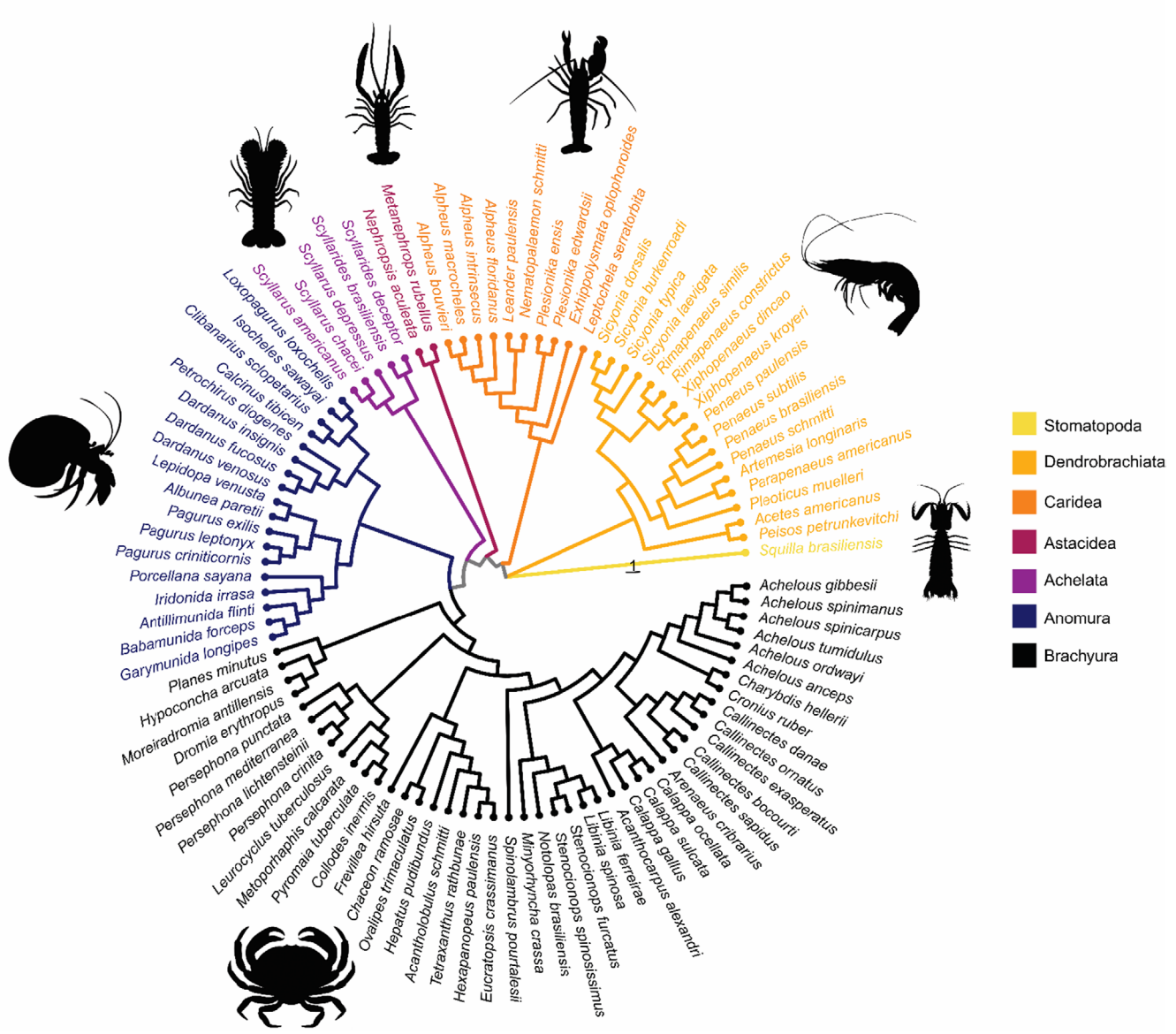

FIGURE 2 | Maximum likelihood mitogenomic phylogenetic tree of decapod crustaceans, based on the concatenated alignment of 12 mitochondrial protein-coding genes plus 12S and 16S rRNA genes. The tree was pruned to include only the species used to calculate phylogenetic diversity. Colours represent the taxonomic groups of the Decapod species.

a relatively high level of coverage, notable hotspots along the coasts of Bahia, and especially in Rio de Janeiro and Espírito Santo, remain entirely outside protected zones, highlighting critical gaps in the taxonomic representativeness of decapod species. PD.SES showed more scattered hotspots, mostly located farther from the immediate coastline, where MPAs are concentrated (Figure 4b). As a result, only a small proportion of these areas of high phylogenetic diversity are currently protected, with some level of protection occurring in Maranhão, Amapá, Ceará and Bahia states. In the case of PE.SES, hotspots were concentrated in equatorial areas (Amapá state) and in tropical and temperate regions such as Espírito Santo and Rio Grande do Sul states, respectively (Figure 4c). Similar to the pattern observed for PD.SES, most PE.SES hotspots are located beyond the nearshore zone and therefore fall outside the effective coverage of MPAs. Nevertheless, it is worth noting that the MPAs in Amapá and Espírito Santo contribute to the protection of areas with high evolutionary value. Conversely, Rio Grande do Sul hosts a major PE.SES hotspot that is completely unprotected, revealing a significant shortfall in the conservation of endemic lineages in the southern region.

The partial Redundancy Analysis (RDAp) model explained 6.65% of the variation in the diversity indices (adjusted $R^2 = 3.94\%$) after controlling for spatial effects (Figure S4). The first two canonical axes of the RDAp explained the majority of the constrained variation, with RDA1 accounting for 80.24% and RDA2 for 16.47% of the explained variance (Figure 5). Based on the permutation test, RDA1 was statistically significant ($F = 12.45$, $p = 0.012$), while RDA2 was not ($F = 2.56$, $p = 0.827$). Among the environmental predictors, bottom mean temperature was the only variable showing a significant relationship with the diversity indices ($F = 7.65$, $p = 0.001$). The ordination plot illustrates that PD.SES and SR are mainly associated with the first axis, whereas PE.SES shows a weaker relationship with both axes (Figure 5).

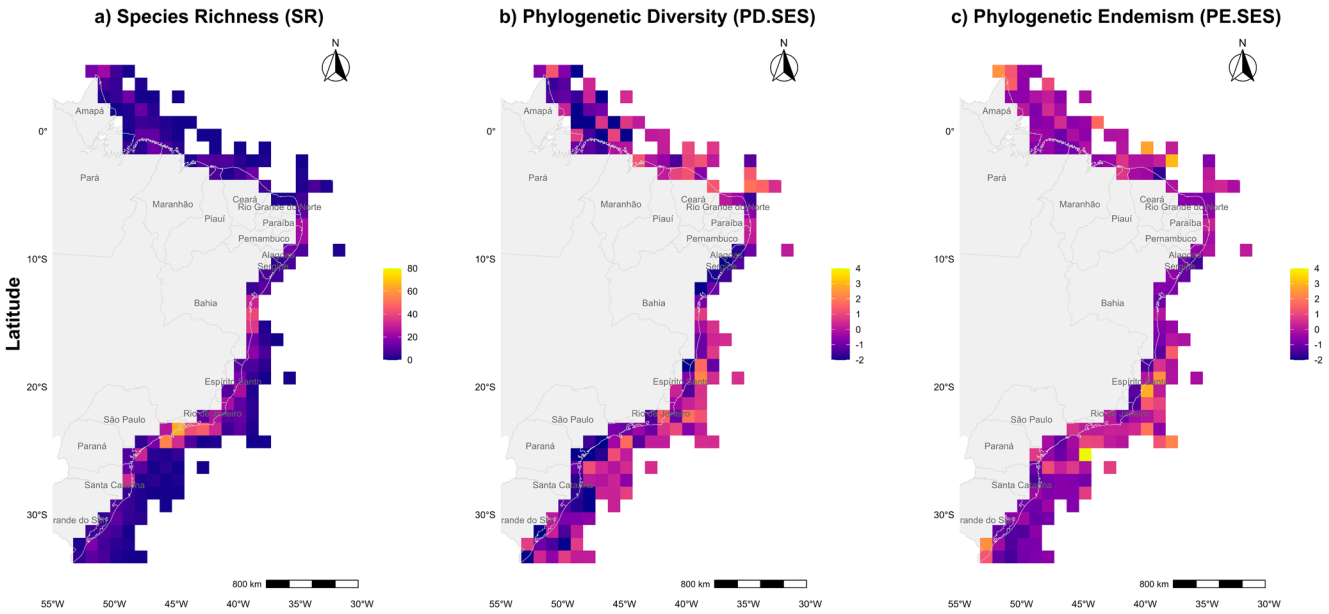

FIGURE 3 | Mapping of species richness (SR), standardised effect sizes of phylogenetic diversity (PD.SES) and phylogenetic endemism (PE.SES) in the Brazilian Exclusive Economic Zone. The scale bars on the left are aligned with the numbers of their respective indices. Cell grid of 1° edge length (latitude/longitude, approx. 111 km).

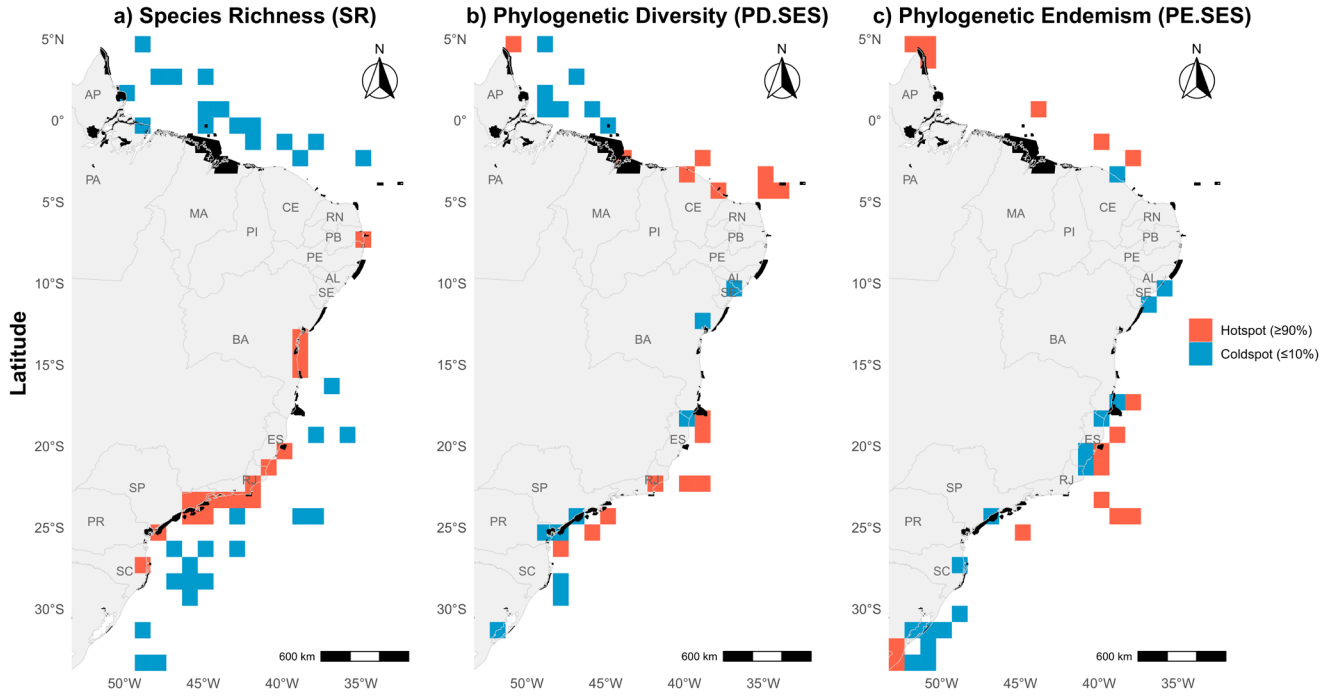

FIGURE 4 | Spatial distribution of biodiversity hotspots (red) and coldspots (blue) for species richness (SR), standardised phylogenetic diversity (PD.SES) and phylogenetic endemism (PE.SES) of decapod crustaceans in the Brazilian Exclusive Economic Zone. Grid cells were classified based on the 90th (hotspots) and 10th (coldspots) percentiles of each diversity metric. Overlaid black polygons indicate Marine Protected Areas (MPAs), based on official spatial data of UNEP-WCMC and IUCN (2025). These abbreviations correspond to the following Brazilian states: AP = Amapá, PA = Pará, MA = Maranhão, PI = Piauí, CE = Ceará, RN = Rio Grande do Norte, PB = Paraíba, PE = Pernambuco, AL = Alagoas, SE = Sergipe, BA = Bahia, ES = Espírito Santo, RJ = Rio de Janeiro, SP = São Paulo, PR = Paraná, SC = Santa Catarina, RS = Rio Grande do Sul.

The spatial regression models revealed distinct patterns for SR, PD.SES and PE.SES in relation to environmental predictors and trawling effort. For SR, bottom temperature emerged as the most influential factor, displaying a significant positive relationship (0.312 ± 0.083, $t = 3.762$) (Table 1). The PD.SES model identified current velocity as a significant predictor with a positive relationship (0.327 ± 0.156, $t = 2.096$). In contrast, the PE.SES model did not reveal any significant relationships with the predictors. Random effects, incorporated to account for spatial autocorrelation, showed varying strengths of spatial dependence (λ)

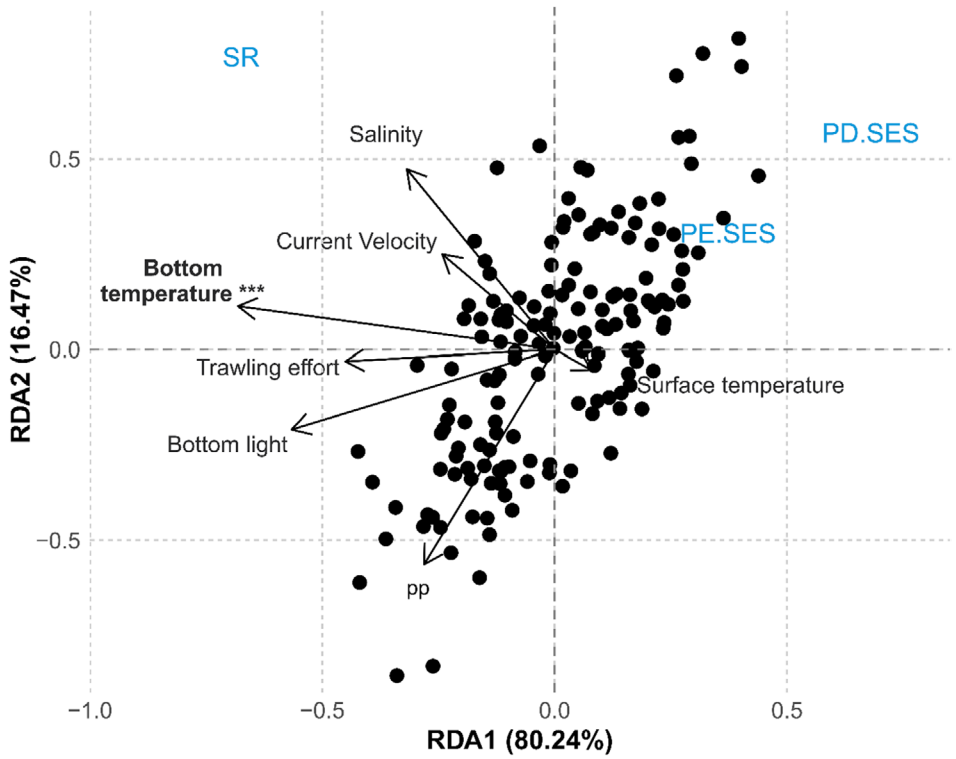

FIGURE 5 | Biplots from partial redundancy analysis showing the relationships between predictors and diversity index. Species richness (SR), standardised effect sizes of phylogenetic diversity (PD.SES) and phylogenetic endemism (PE.SES). *** indicate predictors statistically significant ($p < 0.002$).

across the models: SR ($\lambda = 0.085$), PD.SES ($\lambda = 0.145$) and PE.SES ($\lambda = 0.113$).

The Random Forest model for SR demonstrated the best performance (R^2-oob = 0.574 ± 0.0041; RMSE-oob = 0.317 ± 0.0015), followed by PE.SES (R^2-oob = 0.156 ± 0.0073; RMSE-oob = 0.897 ± 0.0039) and PD.SES (R^2-oob = 0.111 ± 0.0114; RMSE-oob = 1.177 ± 0.0076). All models showed no spatial autocorrelation (Moran's I, $p > 0.05$) and exhibited normality except for PE.SES (Figure S5). Also, distinct response patterns are revealed across different biodiversity metrics. The key predictors across the three models were: primary productivity, bottom light and salinity for SR; bottom temperature, current velocity and primary productivity for PD.SES; and surface temperature, bottom temperature and primary productivity for PE.SES (Figure S6).

The response curves of the Random Forest models (Figure 6) revealed distinct non-linear patterns for each diversity index. For SR, values sharply declined in areas where primary productivity was below 0.025 and continued to decrease more gradually up to 0.075. SR also increased rapidly with bottom light up to approximately 10 units, after which it plateaued around 1.0. In response to salinity, SR remained stable up to 35 PSU, showed a sharp increase near 36 PSU, and then slightly declined beyond 37 PSU. PD.SES values showed a complex relationship with bottom temperature, decreasing steeply below 10°C and then oscillating between −0.5 and −0.75. PD.SES declined with increasing current velocity, showing multiple fluctuations as velocity increased. It also decreased rapidly when primary productivity exceeded 0.025 and remained consistently low (~1.25) at higher values. For PE.SES, a unimodal response was observed with surface temperature: values were lowest (~0.75) at 20°C, peaked (0.25) above 27.5°C. PE.SES also showed a generally negative response to bottom temperature, fluctuating between −0.1 and −0.2. With increasing primary productivity, PE.SES decreased until ~0.025 and then stabilised around 0.2 with minor variation.

4 | Discussion

4.1 | Diversity Indices

The observed patterns of decapod biodiversity in the Brazilian Exclusive Economic Zone (EEZ), as measured by Species Richness (SR), standardised effect sizes of Phylogenetic Diversity (PD.SES) and Phylogenetic Endemism (PE.SES), are largely driven by environmental factors. These patterns align with broader biogeographic trends observed in other taxa, as well as with the unique environmental characteristics of the Brazilian coast (Araújo et al. 2018; Magris et al. 2020; Cord et al. 2022).

The southeastern region (−20° S to −25° S) emerges as a biodiversity hotspot for SR, likely due to its status as an ecotone where tropical and subtropical species overlap. This region is influenced by the Brazil Current and upwelling systems near Cabo Frio (Peterson and Stramma 1991), which are known to enhance nutrient availability and primary productivity, fostering diverse habitats (Cord et al. 2022; Martins et al. 2022). Similar patterns have been documented in nearshore fish communities, where transitional zones between tropical and temperate

TABLE 1 | Spatial regression models (spaGLMM) for species richness (SR), phylogenetic diversity (PD.SES), phylogenetic endemism (PE.SES) and environmental and trawling effort predictors. Estimated coefficients, standard errors, and t-values are shown. Statistical significance was assessed based on the t-values, with asterisks indicating predictors with $p < 0.05$.

Diversity metrics	Predictors	Coefficient estimate ± SE	*t*-value	Random effects (Latitude + Longitude)	Pseudo-R^2
SR	**Intercept**	**0.621 ± 0.061***	**10.171**	λ = 0.085	0.522
	Current velocity	−0.087 ± 0.059	−1.464		
	Bottom temperature	**0.312 ± 0.083***	**3.762**		
	Salinity	0.082 ± 0.049	1.669		
	Surface temperature	−0.009 ± 0.066	−0.140		
	Light at bottom	−0.043 ± 0.050	−0.864		
	Primary productivity	−0.102 ± 0.062	−1.640		
	Trawling effort	0.052 ± 0.043	1.211		
PD.SES	**Intercept**	**−0.421 ± 0.175***	**−2.406**	λ = 0.145	0.213
	Current velocity	**0.327 ± 0.156***	**2.096**		
	Bottom temperature	−0.427 ± 0.230	−1.857		
	Salinity	−0.232 ± 0.157	−1.478		
	Surface temperature	−0.094 ± 0.175	−0.537		
	Bottom light	−0.006 ± 0.142	−0.042		
	Primary productivity	−0.153 ± 0.180	−0.850		
	Trawling effort	−0.188 ± 0.118	−1.593		
PE.SES	Intercept	−0.113 ± 0.120	−0.942	λ = 0.113	0.138
	Current velocity	0.001 ± 0.142	0.007		
	Bottom temperature	−0.135 ± 0.206	−0.655		
	Salinity	−0.114 ± 0.131	−0.870		
	Surface temperature	0.077 ± 0.137	0.562		
	Bottom light	−0.044 ± 0.123	−0.358		
	Primary productivity	−0.046 ± 0.161	−0.286		
	Trawling effort	−0.044 ± 0.124	−0.355		

Note: Predictors in bold were significant values in the models.

regions exhibit high richness due to overlapping species distributions and habitat heterogeneity (Araújo et al. 2018). The relatively lower SR in southernmost areas (> 30° S) reflects harsher environmental conditions and reduced habitat diversity typical of temperate zones, a trend also observed in other marine taxa (Cord et al. 2022).

The high PD.SES values offshore in southeastern and southern Brazil (–15° to below –30°) suggest the presence of older lineages that have persisted in stable deep-sea environments. This includes species such as *Squilla brasiliensis* (Stomatopoda), *Pleoticus muelleri, Parapenaeus americanus* (Dendrobranchiata) and anomuran species like *Babamunida forceps* and *Iridonida irrasa*, which are typically found in deeper offshore habitats and represent evolutionarily distinct lineages. Offshore habitats often act as refugia for phylogenetically diverse species due to their relative isolation from human impacts such as trawling (Teles and Mantelatto 2024). The northern region (–5° to 0°) also shows elevated PD.SES, potentially due to historical isolation mechanisms such as the Amazon River plume, which acts as a biogeographic barrier limiting gene flow and promoting genetic differentiation (Martins et al. 2022; Peres et al. 2022). Coastal regions with lower PD.SES values, particularly along northeastern Brazil, may reflect anthropogenic pressures like overfishing and habitat degradation, which reduce both genetic diversity and population connectivity (Cord et al. 2022; Teles and Mantelatto 2024).

PE.SES hotspots in southeastern Brazil (–15° S to –25° S) highlight areas with unique evolutionary lineages shaped by habitat diversity and oceanographic features like upwelling zones (Coelho-Souza et al. 2012; Martins et al. 2022). Notable endemism in northern Brazil (5° to –2°) may be attributed to historical isolation caused by riverine barriers and limited larval dispersal across freshwater plumes (Martins et al. 2022). These

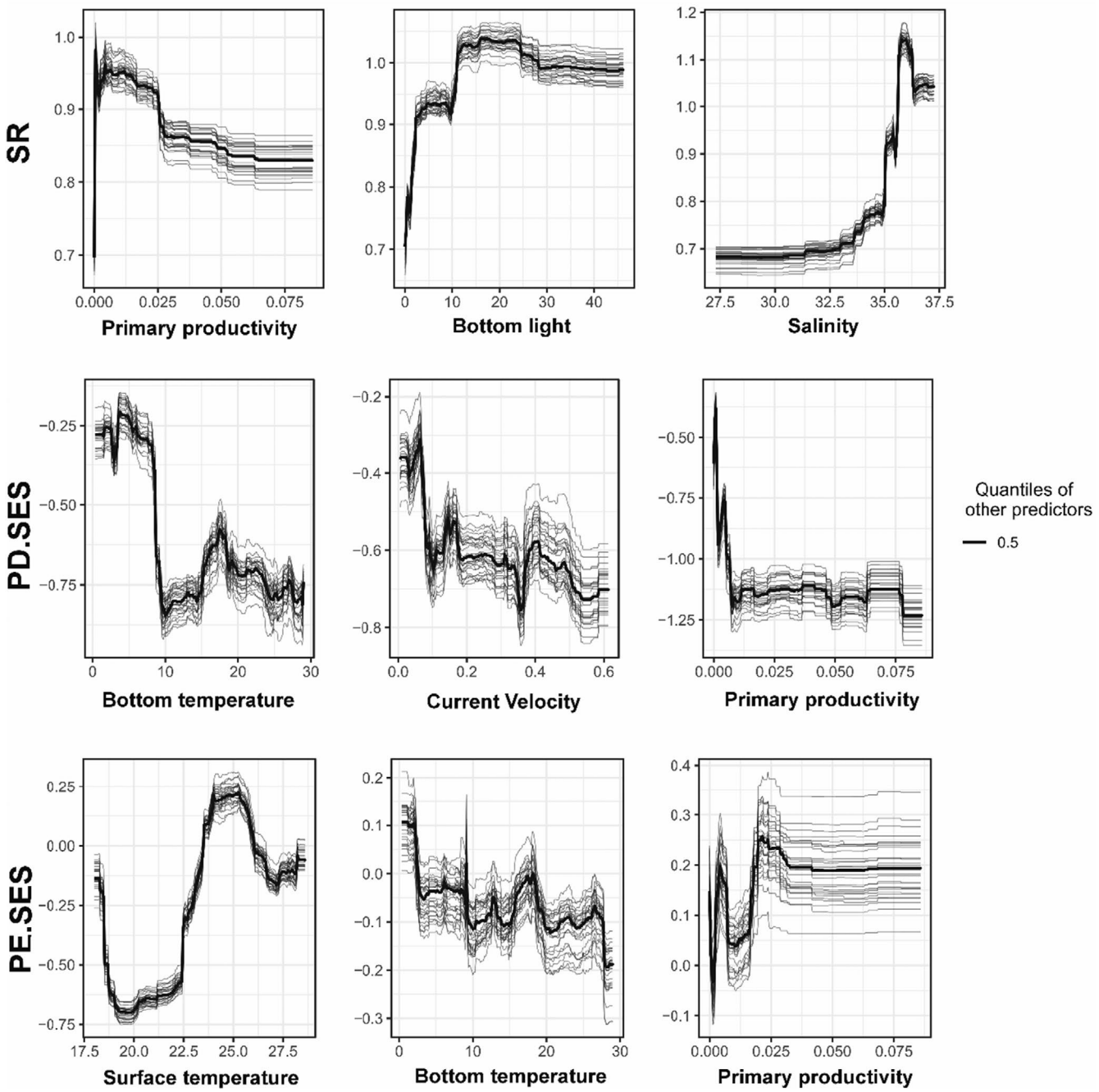

FIGURE 6 | Response curves from the random forest model showing the relationships between predictor variables and the indices of species richness (SR), phylogenetic diversity (PD.SES) and phylogenetic endemism (PE.SES). The graphs show the response of metrics as a function of changes in environmental variables: Primary productivity, bottom light, salinity, bottom temperature, current velocity and surface temperature. The bold black line indicates the median response (0.5 quantile), while the thin grey lines show the variation in response after 30 repetitions.

emphasising the importance of conserving regions with high endemism due to their contribution to global phylogenetic diversity (González-Orozco et al. 2015).

4.2 | Influence of Environmental Factors and Trawling Effort

The redundancy analysis highlighted the importance of bottom temperature as a significant predictor of diversity patterns across the indices studied. The response of diversity metrics to temperature revealed distinct patterns. For PE.SES, a unimodal relationship with surface temperature peaked between 25°C and 27.5°C, suggesting an optimal thermal condition for phylogenetic endemism. PD.SES exhibited a non-linear pattern, with two distinct peaks: one at colder bottom temperatures (< 10°C) and another around ~18°C, indicating that different phylogenetic lineages may thrive under both cold and moderately warm benthic conditions. SR, in contrast, showed a positive association with bottom temperature in the spaGLMM model, suggesting that warmer benthic environments may support greater species richness. Within this window, benthic

adults benefit from favourable bottom temperatures aligned with their habitat preferences, while pelagic larvae depend on surface temperatures for survival and dispersal (Pallas et al. 2006; Boudreau and Worm 2012; Morgan 2020). This dual thermal influence across life stages highlights the interconnected relationship between temperature and biodiversity. These findings are consistent with previous studies that have identified temperature as a key factor influencing the diversity and abundance of various decapod groups, further reinforcing its fundamental role in structuring marine ecosystems (Abele 1974; Furlan et al. 2013; Monteiro et al. 2024).

Temperature was the only environmental variable that consistently influenced all diversity indices in our study, highlighting its fundamental role in structuring marine decapod communities. Although our analyses do not model climate change projections directly, the temperature dependence observed suggests that ocean warming could affect community structure over time, especially by altering thermal conditions beyond optimal ranges. Such changes may not only reduce the evolutionary legacy of marine communities but also affect their resilience and ecological functioning (Faith and Richards 2012). Extreme temperatures act as ecological filters, limiting survival, reproduction and dispersal processes that are vital for sustaining diversity (Monteiro, de Castro, et al. 2023). Additionally, warming-driven environmental filtering may promote biotic homogenisation, a process in which phylogenetically and functionally unique species are replaced by widespread generalists, increasing the similarity among communities across space (Magurran et al. 2015; Brustolin et al. 2019). This erosion of regional distinctiveness threatens the adaptive potential of ecosystems and reduces the evolutionary and ecological complexity necessary for long-term stability. These dynamics reinforce the need for conservation strategies that protect thermally stable and heterogeneous habitats, as well as for policies that anticipate and mitigate anthropogenic stressors associated with climate change.

The relationship between primary productivity and diversity indices in marine decapod crustaceans reveals distinct patterns that highlight the ecological importance of productivity gradients. For SR, the response to primary productivity showed a sharp peak at very low productivity levels, followed by a consistent decline as productivity increased, with stabilisation at higher values. This indicates that areas of low productivity support higher species richness, while highly productive environments may be less favourable, possibly due to environmental stress or competitive exclusion. This is particularly relevant for decapods, which rely on phytoplankton and detritus as foundational food sources in their ecosystems (Boudreau and Worm 2012; Antonio and Richoux 2014). The decline in SR at higher productivity levels suggests that an excess of available resources may reduce species coexistence or favour dominance by a few generalist taxa.

Higher primary productivity was associated with lower PD.SES values, suggesting that communities in highly productive areas tend to be composed of more closely related species. This pattern may reflect environmental filtering, where certain traits favoured in nutrient-rich environments are phylogenetically conserved and shared among closely related taxa (Raeisbahrami and Naderloo 2023). In the case of decapods, this could imply that species well adapted to exploit abundant food resources become dominant in such habitats, ultimately reducing phylogenetic diversity. In contrast, PE.SES exhibited a slight positive trend with increasing productivity, indicating that highly productive regions may also support lineages with restricted evolutionary histories. In southeastern Brazil, for instance, upwelling systems like Cabo Frio enhance primary productivity and may foster both elevated local endemism and unique phylogenetic assemblages (Valentin 2001; De Léo and Pires-Vanin 2006). These areas are particularly relevant for conservation, as they simultaneously harbour high biodiversity and evolutionary distinctiveness. Together, these patterns highlight the complex role of primary productivity in shaping both the taxonomic and phylogenetic structure of marine crustacean communities. Although primary productivity is not directly manageable, the identification and protection of naturally productive zones that support diverse and unique assemblages can help buffer sensitive communities from anthropogenic nutrient inputs and eutrophication. These findings are consistent with broader ecological theories linking productivity to biodiversity and underscore the need to incorporate multiple facets of diversity into effective marine conservation strategies (Cardinale et al. 2009; Tilman et al. 2014).

Salinity is another key environmental factor influencing the distribution and diversity of marine organisms, particularly decapod crustaceans, due to its impact on physiological and ecological processes (Anger 2003; Smyth and Elliott 2016). The observed relationship between salinity and SR in this study reveals a positive correlation, with SR increasing sharply at intermediate salinity levels and stabilising at higher salinities. This pattern suggests that decapod communities are better adapted to typical marine salinity conditions, where osmotic gradients remain within tolerable limits, reducing the energetic cost of osmoregulation and supporting optimal physiological performance (Torres et al. 2011; Jaffer et al. 2024). In contrast, environments with fluctuating or low salinity can impose higher osmotic stress, particularly for stenohaline marine species. Salinity plays a crucial role in shaping decapod community structure by affecting reproductive success, larval development, molting frequency and growth rates (Anger 2003; Nagaraju 2011). For example, in the south and southeastern coast of Brazil, higher salinity levels have a positive relationship with the abundance of many decapod species captured as bycatch, such as *Libinia spinosa* (Gonçalves et al. 2020), *Hepatus pudibundus* (Teles et al. 2020) and *Achelous spinicarpus* (Sousa et al. 2021). These findings align with previous studies indicating that regions with higher salinity support greater SR, highlighting the ecological importance of salinity in maintaining diverse and resilient decapod communities (De Léo and Pires-Vanin 2006; Castilho et al. 2007).

The results for current velocity reveal a complex relationship with phylogenetic diversity (PD.SES), underscoring the critical role of ocean currents in shaping the diversity of marine decapod crustaceans. In our models, PD.SES reached its highest values at current velocities around 0.05–0.10 m/s and began to decline sharply above ~0.12 m/s, followed by a more gradual decrease at higher velocities. This threshold suggests that low-to-moderate current velocities (up to ~0.12 m/s) are more favourable for sustaining phylogenetic diversity, possibly by facilitating larval retention, local recruitment and the maintenance of evolutionarily distinct lineages. On one hand, currents enhance larval dispersal and connectivity between populations, supporting gene flow

and community structure over broad spatial scales (Álvarez-Noriega et al. 2020; Sanvicente-Añorve et al. 2018). On the other hand, increasing current velocity beyond certain thresholds may act as a stressor, disrupting larval settlement or transporting larvae away from suitable habitats, thereby limiting local diversity (Anger 2006; Hameed et al. 2018). Additionally, currents influence the delivery of food resources, such as phytoplankton and detritus, which are essential for both larval and adult feeding behaviour (Hallegraeff 2010; Pineda and Reyns 2018).

The relationship between bottom light and SR in decapods reveals a positive trend, with SR increasing sharply at low light levels and stabilising at higher intensities. This pattern suggests that light availability is a critical factor influencing the diversity of decapod communities, particularly in benthic habitats where primary producers like algae and seagrasses depend on sufficient light for photosynthesis. Enhanced bottom light likely supports richer benthic ecosystems, providing decapods with abundant food resources and habitat complexity (Hallegraeff 2010; Scyphers and Powers 2013). When considered alongside other environmental predictors, such as salinity and primary productivity, the interplay between these factors becomes evident. For example, areas with high salinity and moderate to high primary productivity often coincide with optimal light conditions, creating favourable environments for diverse decapod assemblages (De Léo and Pires-Vanin 2006; Castilho et al. 2007). Furthermore, regions with stable hydrodynamic conditions that allow for consistent light penetration, such as areas with lower turbidity, may enhance larval settlement and adult foraging efficiency (Connell 2005; Maldonado-Sánchez et al. 2019). However, excessive nutrient input in coastal waters can trigger harmful algal blooms, which reduce water clarity and significantly decrease bottom light availability (Rabalais et al. 2009). These events may suppress benthic primary production and disrupt the trophic interactions for benthic invertebrate fauna (Lyons et al. 2014). Consequently, eutrophication and bloom-driven light attenuation should be considered in conservation and management plans. These combined factors underline the importance of environmental gradients in shaping the spatial distribution and richness of decapod species.

4.3 | Implications for Conservation

The findings of this study underscore the need to adopt multidimensional conservation strategies that account for the complex ecological and evolutionary factors shaping marine biodiversity. While previous discussions emphasised patterns and threats, our spatial analysis provides evidence of mismatches between decapod diversity hotspots and the current Marine Protected Areas (MPAs), reinforcing the urgency of refining conservation planning in Brazil.

A key implication is the importance of integrating multiple dimensions of biodiversity (taxonomic, phylogenetic and functional) into spatial prioritisation frameworks. MPAs are often designed based on species richness, potentially neglecting regions with unique evolutionary histories or high endemism. Our analysis showed partial overlap of species richness (SR) hotspots with MPAs in southeastern and southern Brazil, particularly in Paraíba (PB), Espírito Santo (ES), Rio de Janeiro (RJ) and São Paulo (SP). However, critical hotspots in Bahia (BA), ES, RJ and PB remain unprotected, revealing persistent gaps in taxonomic coverage. More critically, most PD.SES and PE.SES hotspots were located offshore or in poorly protected areas such as Rio Grande do Sul (RS) and parts of Ceará (CE), ES and RJ, areas of high evolutionary value that are often excluded from conservation boundaries. This is especially concerning in southeastern and southern states, which host the country's highest trawling activity.

This spatial incongruence mirrors broader global patterns. In the Mediterranean Sea, for instance, MPAs often fail to protect phylogenetically and functionally distinct species that are essential for long-term ecosystem stability (Guilhaumon et al. 2014). Likewise, global assessments suggest that protecting just 22% of marine areas could safeguard most marine biodiversity, including its evolutionary and genetic components (Fan et al. 2023). Therefore, incorporating metrics like PD and PE into marine conservation agendas is essential to enhance representativeness and ecosystem resilience.

Temperature emerged as a key driver shaping decapod diversity, a pattern consistent with other coastal taxa such as mangrove crabs and estuarine fish (Teichert et al. 2018; Teles et al. 2024). This environmental factor affects different life stages differently: surface temperatures may disproportionately impact larvae due to their planktonic and dispersive nature, whereas bottom temperatures regulate metabolism, growth and reproduction in post-larval and adult stages (Anger 2006; Lindley 1998). These findings highlight the need to implement conservation measures that include thermally stable areas, which could serve as climate refugia for vulnerable species. Moreover, expanding conservation networks in underrepresented regions such as CE, RJ, ES and RS will require data-informed spatial planning and may benefit from regional cooperation strategies already successful in places like the Mediterranean (Mazor et al. 2013). Applying similar frameworks in regions like the Brazilian Exclusive Economic Zone could enhance the protection of migratory species and interconnected habitats.

5 | Conclusion

This study provides the first integrative macroecological assessment of decapod crustacean diversity across the Brazilian Exclusive Economic Zone (EEZ), combining species richness, phylogenetic diversity and endemism with a comprehensive suite of environmental predictors. Our findings reveal that temperature, salinity, primary productivity and hydrodynamics play pivotal but distinct roles in shaping different dimensions of biodiversity, with strong spatial mismatches between current Marine Protected Areas (MPAs) and regions of high evolutionary value. Southeastern and offshore zones emerged as critical reservoirs of phylogenetic diversity and endemism, likely reflecting historical isolation, habitat stability and ecotonal dynamics driven by oceanographic features such as upwelling.

The consistent influence of temperature across life stages and diversity metrics underscores its central role in structuring

marine communities, while highlighting the vulnerability of thermal specialists to ongoing ocean warming. Furthermore, patterns of phylogenetic clustering in highly productive or hydrodynamically stressful environments suggest that environmental filtering may erode evolutionary distinctiveness, leading to biotic homogenisation.

By identifying conservation gaps and revealing the ecological and evolutionary processes that underpin decapod diversity, this work advances biogeographical theory and offers actionable insights for marine spatial planning. We advocate for the inclusion of evolutionary metrics in conservation prioritisation to ensure that protected areas safeguard not only species numbers but also deep evolutionary lineages essential for long-term ecosystem resilience. In an era of accelerating climate change and anthropogenic pressure, protecting thermally stable and ecologically heterogeneous habitats (especially offshore and transitional zones) will be key to maintaining the functional and evolutionary integrity of marine ecosystems.

Author Contributions

Jeniffer N. Teles: conceptualization, data curation, analysis and modeling, writing – original draft, review, and editing. **Fernando L. Mantelatto:** conceptualization, funding acquisition, review, and editing.

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Conflicts of Interest

The authors declare no conflicts of interest.

Data Availability Statement

Original R codes and raw datasets that support the findings of this study are openly available in Dryad at https://doi.org/10.5061/dryad.0zpc8678d.

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Supporting Information

Additional supporting information can be found online in the Supporting Information section. **Table S1:** List of species collected during bycatch activities and used to map species richness (SR), Phylogenetic Diversity (PD) and Phylogenetic Endemism (PE). Species highlighted in red were used only for the calculation of SR due to the lack of available genetic sequences. Species highlighted in green were used for the calculation of PD and PE. Species highlighted in yellow were included in the tree but discarded from the analyses due to possible accidental capture in trawl fishing environments and different habitat occurrences. Species without colour were used only to construct the cladogram. GenBank code. Species with fewer than two available genes were excluded from the phylogenetic diversity analyses. ACS = Amazon Continental Shelf; AL = Alagoas; ES = Espírito Santo; RJ = Rio de Janeiro; RS = Rio Grande do Sul; SC = Santa Catarina; SE = Sergipe; SP = São Paulo. **Table S2:** Summary of species included in the study according to data availability and usage. Categories indicate whether species were excluded (e.g., bycatch accidental), used only for species richness (SR), included in all diversity metrics (SR, phylogenetic diversity [PD] and phylogenetic endemism [PE]), or incorporated only into the phylogenetic tree due to limited molecular data (fewer than two genes). These classifications match the colour scheme used in Table S1. **Table S3:** Variance Inflation Factor (VIF) values for the predictors used in the models. **Figure S1:** Final Pearson's correlation matrix between selected predictors after multicollinearity analysis. The correlation values shown in the upper triangle represent the final dataset used in the models, where variables with $R^2 > 0.70$ were eliminated to avoid multicollinearity effects. The diagonal panels display the distribution (histograms with kernel density overlays) of each predictor, while the lower triangle panels show scatterplots with smoothed fit lines for each pairwise comparison. **Figure S2:** Mitogenomic maximum likelihood phylogenetic tree of bycatch crustaceans. Bootstrap values are indicated on nodes. The colours represent the taxonomic group of the crustacean species. **Figure S3:** Species Richness (SR), Phylogenetic Diversity (PD), Phylogenetic Endemism (PE), Weighted Endemism (WE), Evolutionary Distinctiveness (ED) and their standardised effect sizes (SES). The diagonal shows density distributions, the lower triangle displays scatter plots and the upper triangle presents correlation coefficients. Indices with correlation $R^2 > 0.70$ were removed from the analyses. **Figure S4:** Multiscale ordination (MSO) showing the spatial structure variation

of diversity indices across distance classes. The plot shows explained variance (red circles), residual variance (squares), explained plus residual variance (crosses) and confidence interval for total variance (solid line). Black squares indicate significant spatial autocorrelation. The vertical dashed line represents the truncation point. Numbers below indicate the number of point pairs in each distance class. **Figure S5:** Diagnostic plots for model residuals across three Ranfom Forest models: SR (Species Richness), PD.SES (Phylogenetic Diversity Standardised Effect Size) and PE.SES (Phylogenetic Endemism Standardised Effect Size). Each column represents a different model, with rows showing (from top to bottom): (1) Q-Q plots and histograms for normality assessment, (2) residuals vs. predicted values and (3) Multiscale Moran's I correlograms. The SR and PD.SES models exhibit normally distributed residuals (Shapiro–Wilk test p-values > 0.05), while PE.SES residuals deviate from normality. The Moran's I correlograms demonstrate no significant spatial autocorrelation across all distance thresholds for the three models, as indicated by the p-values > 0.05, eliminating the need for spatial regression models in the analysis. **Figure S6:** Variable importance plots and response curves from Random Forest models analysing biodiversity patterns. Variable importance plots showing the increase in error when permuted for three biodiversity metrics: Species Richness (SR), Phylogenetic Diversity (PD.SES) and Phylogenetic Endemism (PE.SES). Variables are ranked from most to least important (top to bottom) based on their contribution to model accuracy.