Title: Idiosyncrasies unveiled: examining the pace, patterns and predictors of biotic diversification in peninsular India

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Abstract:

Understanding the tempo and mode of diversification and their consequence for tropical biodiversity remains a key challenge as different clades and regions exemplify distinct patterns and processes. We examined diversification rates and their drivers across 34 well-studied endemic lineages in peninsular India, one of the oldest regions of differentiation in the Oriental Realm, using birth-death models and their variations. We show that 18 lineages supported gradual species accumulation, suggesting that the historic stability of the landscape was an important driver. Additionally, paleotemperature, Miocene aridification, monsoon intensification and existing species diversity explained time-varying diversification patterns among the other 16 lineages. Net-diversification rates influenced differences in species diversity more than clade ages of peninsular Indian clades, where speciation rates mainly drove diversification, as extinction rates were low across taxa. Our results emphasise the importance of regional biogeographic, phylogenetic and geoclimatic history on the diversification dynamics among tropical landscapes.

Keywords: speciation-extinction analyses; biogeography; climate; animals and plants; regional biota; species diversity and richness

1. Introduction:

Diversification, a balance between speciation and extinction rates, is known to shape the biodiversity patterns in a region and the tropics, the most species-rich terrestrial biome, have been central to diversification studies [1–4]. Many hypotheses, including a long time for speciation - being the oldest biome [5], greater climatic stability [4], habitat and climatic heterogeneity [6] have been invoked to explain the high diversity in the tropics. For example, a recent study from Neotropics showed that gradual expansion was the most supported scenario, irrespective of biogeographic subregions and that diversification rates differed substantially across clades [7]. On the other hand, in Australia, aridification and biogeographic barriers were important drivers of diversification [8]. In Madagascar, a continental island, wet-forest-adapted species showed accelerated diversification [9]. These studies suggest that patterns and drivers of diversification vary across the Tree of Life and depend on regional biogeographic and geoclimatic processes across tropical areas. Therefore, there is a need to identify and characterise the processes responsible for generating differential species diversity among distinct geographical regions and clades for a nuanced understanding of the processes contributing to species diversity.

In this regard, Peninsular India (PI) of South Asia remains relatively unexplored despite being one of the oldest regions for diversification in the Oriental Realm [10,11]. The geological and climatic history of PI has played an important role in generating this complex landscape [12–14], and has influenced the diversification of flora and fauna in PI [10,15–17] (Table 1). PI harbours the Western Ghats biodiversity hotspot (WG), which is an escarpment along the west coast, along

with the 66 million-year-old Deccan trap or peninsula, and the Eastern Ghats (EG), which is a broken chain of mountains along the east coast [18,19]. Historical biogeographic studies indicate that the peninsular Indian biota has distinct biogeographic and evolutionary affinities with Gondwana, Asia or Eurasia [11,20,21]. Interestingly, irrespective of biogeographic origins, many clades have undergone extensive in-situ speciation in peninsular India, making peninsular India a distinct region within the Oriental realm [11]. However, our understanding of diversification tempo and mode remains poorly studied for peninsular Indian flora and fauna.

Given this, we examine the relative roles of geoclimatic processes, biogeographic affinities, and species traits likely to have shaped the extant diversity in peninsular India in a comparative framework. We use state-of-the-art methods to examine the tempo and mode of in-situ diversification for endemic plants and animal lineages in PI [22,23]. We compiled a dataset of 28 studies relevant to a total of 34 lineages (clades) belonging to diverse taxonomic groups - arthropods, amphibians, birds, plants, and reptiles where data is available on species distribution, molecular phylogenetic relationships, and divergence time estimates [11,24]. Many of these lineages are endemic to peninsular India and have undergone in-situ diversification, making the landscape an ideal system for examining biotic diversification patterns and drivers in a comparative framework. These lineages also have distinct biogeographic and habitat affinities. We build on these systematic and phylogenetic studies to infer diversification rates, patterns, and potential drivers for peninsular Indian biota. Importantly, we outline the testable predictions for diversification dynamics of the endemic peninsular Indian biota as outlined below.

1. How do diversification rates vary through time and across lineages? - We examined four relevant scenarios for speciation and extinction rates to determine the pattern of diversification within each lineage [7,25]. These included gradual accumulation (SC1),

saturated accumulation (SC2), waxing and waning (SC3) and recent rise (SC4) (SI Fig. 1). The gradual accumulation scenario predicts species accumulate gradually through time and have constant speciation and extinction rates, leading to constant diversification rates through time [7,26]. Prolonged environmental stability can potentially explain the gradual accumulation of lineages [27–29] (SI Fig.1 SC1). Within PI, southern parts of the WG and the mountaintops of the EG have remained stable through evolutionary time and could have served as refugia [12,30–32]. Alternatively, lineages can show time-varying diversification with an early increase in diversification followed by saturation in diversity [26,33,34]. This mode of diversification is attributed to ecological limits/ diversity-dependence [35–37] or drastic geoclimatic perturbations that decelerate species accumulation or due to damped increases [36] (SI Fig 1. SC2). Additionally, species diversity can decline following bouts of increase, ultimately leading to a loss in diversity. Such waxing and waning diversification patterns (SI Fig. 1. SC3) can be attributed to the inability of lineages to cope with a changing environment and associated decrease in available niches [26,33]. It is generally characterised by negative net-diversification rates (i.e. extinction rates exceeding speciation rates) in a certain period(s) across a lineage [7,26,33]. PI has undergone drastic climate changes through the Cenozoic, which might be relevant for many lineages. Lastly, lineages can exhibit an exponential increase of diversity towards the present (SI Fig 1. SC4) and is primarily attributed to geoclimatic perturbations and suitable environmental conditions promoting adaptive radiations. The most important geoclimatic events, like the Mid-Miocene aridification, monsoon intensification and expansion of C4-plants in peninsular India, could explain this pattern [15,38].

Furthermore, the lineages may also experience episodic shifts in diversification rates, which these four scenarios may not be able to capture [39–41]. Diversification rate shifts can also be attributed to geological episodes where certain geoclimatic events can cause rapid increase and/or decrease in diversification rates [39,41]. Species diversity within a lineage is expected to show fluctuations from general trends, as seen for SC1-4 at episodes relevant to rate shifts. Hence, we also examined episodic rate shifts in diversification scenarios. We investigated the diversification scenarios using birth-death models and their variations to explicitly examine the tempo diversification, which is lacking for PI biota.

2. What are the abiotic and biotic drivers of diversification rates and patterns for PI biota? - Among abiotic factors, we assessed the role of environmental variables, given the complex geological past of the peninsular Indian landmass over the last 100 million years [13,14]. Additionally, across different regions and taxa, environmental variables have been shown to influence the diversification rates [7,23,26]. We specifically examined the temperature in the Cenozoic (67 Mya to present) [42], pedogenic C-content [43,44], a proxy for vegetation cover/habitat, and the Himalayan orogeny [45] as a proxy for seasonality on the speciation and extinction rates (Fig. 1b), which are thought to be important events for peninsular Indian biota. For the biotic drivers, we assessed the diversity-dependent or ecological limit hypothesis, which suggests that the diversity within a lineage limits the species diversity. These different drivers were assessed by fitting birth-death models described in SI Fig. 1 and Table 1 in the likelihood framework. The biogeographic and habitat affinity could also influence the diversification pattern and rates within a clade [7,9,46]. Hence, we also assessed the role of biogeographic origin (Asian or Gondwanan)

and habitat affinity (wet and dry) on diversification rates in each lineage, given the complex geological past and landscape in PI.

3. What are the relative roles of clade- age and diversification rates on species richness in PI? - Historical biogeographic studies in peninsular India highlighted that taxa with Gondwanan origins are generally of older clade age than the Asian origins [11,47]. This has implications for the clade age hypothesis, which predicts that there could be a disparity in species richness among lineages attributed to clade age, i.e., clades with older ages would be more species-rich [5,48,49]. Alternatively, differences in species diversity may also result from differences in net-diversification rates between clades, irrespective of clade age, explaining high species richness [5,50,51]. The rate disparity could also arise due to key innovations, habitat shifts, and diversity dependence. These hypotheses have received support from multiple global, regional and taxon-specific studies [5,50–52].

2. Methods:

2.1. Data compilation - endemic lineages from peninsular India

We sifted through the published molecular phylogenetic studies on peninsular Indian taxa and identified well-sampled dated phylogenetic trees for the PI lineages where at least 65% of species were endemic. We found 42 time-calibrated phylogenetic trees, of which 34 trees had at least four species. We collected data on the biogeographic origin, distribution, crown age and species richness of these 34 peninsular Indian endemic lineages of animals (including arthropods, amphibians, reptiles, and birds) and plants representing 669 species, of which 633 species are endemic to PI. We requested and obtained time-calibrated tree files (maximum clade credibility trees) for 23 lineages from respective authors (see acknowledgements and SI Table 1),

and for the remaining lineages (n = 10) *newick* species trees were manually written based on median node ages, from published time trees.

These lineages do not necessarily pertain to one specific taxonomic rank (ranges from species groups to family level). This was done to compare lineages based on their ages and not of specific taxonomic ranks (like genus), as time (clade age) is thought to be one of the major drivers of diversification [5], taxa of different taxonomic ranks can have similar ages and taxonomic ranks are arbitrary [50].

2.2 Assessing the tempo and mode of species accumulation within each of the lineages

<u>The tempo of diversification</u> - The net diversification rates were calculated to assess the relative pace of diversification for each lineage. The rates were calculated by fitting the constant-rate birth-death model (CBD) using the package *RPANDA* [42]. The Wilcoxon test was performed using the *stat_compare_means()* function from the *ggplot2* package [53] in R to check if the tempo of diversification for each lineage type is significantly different from the other and the overall mean.

<u>Assessing mode of diversification</u> - The constant-rate and time-varying models were fitted to all 34 lineages. Constant-rate models included constant-rate pure birth (CB - only a constant speciation rate, no extinction) and constant-rate birth and death models (CBD - constant and finite speciation and extinction rates). Time-varying models included combinations of linearly ($\square(t) = \square_0 + \square \cdot t$, $\square(t) = \square_o + \square \cdot t$) or exponentially ($\square = \square_0 \cdot e^{\square \cdot t}$, $\square = \square_o \cdot e^{\square \cdot t}$) varying (with time - t) birth ($\square$) and death ($\square$) rates ($\square_0$ and $\square_o$ are the expected speciation and extinction rates at t=0, $\square$ and $\square$ are the coefficients of gain or decay in the functions and time, here, is interpreted as time from the present) [26]. These combinations also included constant-rate models for scenarios

where one rate (birth or death) varies with time, and the other remains constant. In the models above, the absolute values of speciation and extinction rates are considered even when the models infer negative values. The negative values for speciation and extinction rates are not biologically informative but are feasible mathematically. Therefore, we followed the approach described by Morlon et al, (2020) [54] to include a set of models with the same mathematical formulations but instead take a value of 0 in cases where rates become negative. We refer to these models as the "non-negative models" hereafter. These functions capture the broad trends in diversification mode within a lineage.

In addition, to model the possibility of symmetrical local peaks and dips (sharp increase followed by a decrease in diversification rates or *vice versa*) in diversification rate in time, we developed a continuous time-varying mathematical function "witch of agnesi" curve, to model symmetrical local peaks in diversification, diverging from a baseline constant rate: $\square(t) = \square_0 + \frac{\alpha\square}{\square} \cdot \left(\frac{\square}{(\square - \square)^2 + \square}\right)$, where $\square_0$ represents a baseline rate of speciation, $\square$ represents the intensity of the peak (or dip), $\square$ represents the spread of the peak or dip, and *p* represents the position of the peak (or dip) in Ma [55]. Similar rate shifts in extinction were also modelled using the same formulation where $\square_o$, $\square$ and $\square$ and represented the baseline rate, intensity and spread of the peak or dip in extinction rate, respectively. This was done to check the prevalence of symmetrical local peaks (or dips) in diversification, which might be best fitted by the constant-rate models otherwise, among other models. Additionally, using this function, we intended to qualitatively assess the role of specific geoclimatic events (Table 2) on the diversification of lineages corresponding to the time of occurrence of a peak (or dip). We refer to this model as the "local episodic shift"/"symmetrical episodic shift" model henceforth, and it was implemented in the *RPANDA* model-fitting framework. Model fitting using constant-rate and time-varying birth-

death models was executed in *RPANDA* using the *fit_bd()* function to determine the diversification pattern of each lineage.

Best-fitting models were selected based on AICc scores to account for over-fitting. □AICc scores were calculated as absolute differences in the AICc scores between each model and the model with the lowest AICc score. The models with □AICc scores lesser than two were chosen for each lineage. If multiple models showed □AICc below two, i.e., all models were equally likely, then the model with the least parameter complexity was chosen as the best-fitting model. If there were multiple models of similar AICc and the same complexity, the model with the least AICc was chosen as the best-fitting model. However, if CB or CBD were found along with other models to be equally likely, the corresponding constant-rate model was considered the best-fitting model for a lineage, as the simplest model could not be rejected. We used the parameter values (□$_0$, □, □$_o$ and □) of the selected diversification models to evaluate the scenarios mentioned in Table 1 and SI Fig. 1.

In addition, we performed the CoMET (CPP on Mass-Extinction Times) analysis using the R package *TESS* [22,39] to detect significant rate shifts in a lineage's history and generate rates-through-time (RTT) plots. The CoMET analysis involves binning the history of a clade into 100 time points at equal intervals. For each lineage, we extracted the Bayes Factor (BF) supports for rate shifts at these 100 time points and chose the ones where 2 * ln(BF) scores were substantially higher than constant rates (≥4.6 [40,56]).

□-statistic - In addition to birth-death models, we used the □-statistic to assess the branching patterns within a lineage, as some clades had fewer tips [57]. □-statistic is a metric designed to assess the nature of species accumulation within a clade by checking the relative positions of internal nodes from the root and tips of a dated phylogenetic tree. For a phylogenetic tree under a pure-Birth model or a Yule process (no extinction), □ = 0, i.e. each internal node is equally distant from the tips and the root. If □ < 0, the internal nodes are closer to the root (i.e. early rise in diversification). If □ > 0, then the internal nodes are closer to the tips than in comparison to a tree under a pure-birth model (i.e. recent rise in diversification). However, very few lineages would show an exact value of □ = 0 in empirical datasets. Therefore, we used the *gammatest()* function in R to calculate the metric for every lineage and to compute the *p*-value to check the probability of a null hypothesis of constant rate birth-death, which can explain the branching pattern within a clade [58]. Additionally, for each lineage, a distribution of □-statistic was generated from 1000 simulated trees under the constant rate pure birth model using the *mccr()* function from the *phytools* package [58]. The position of the empirical value was checked against the mean of the distribution using a two-tailed t-test.

To summarise, diversification scenarios were inferred from the results of these three analyses - □-statistic, *RPANDA* models, and CoMET.

2.3. Determining drivers of diversification rates and diversity

Assessing drivers of diversification patterns: We assessed the role of important environmental variables on the diversification patterns of biota from PI, mainly temperature, changes in seasonality patterns and Miocene aridification on the diversification patterns. We obtained paleoclimate data for temperature [42], reconstructed Himalayan elevations [45] (as a proxy for the

onset of seasonality patterns) and pedogenic carbon content [43,44] (as a proxy for aridification and expansion of C4 plants - majorly grasses) from the Potwar plateau. The curves for all the paleo-climatic data were smoothened through spline interpolation using the *ss()* function from the *npreg* package [59] in R. Subsequently, we used the same combinations for rate-dependencies (birth and death) as on time (except the local shift model), on temperature, paleo-elevation of the Himalayas and the pedogenic Carbon content and fitted these models using the *fit_env()* function from *RPANDA* package in R. Additionally, we included the functions ($\square(T) = \square_0 \cdot e^{-\square/T}$, $\square(T) = \square_o \cdot e^{-\square/T}$) inspired by the metabolic theory of biodiversity as provided in Condamine et al., (2019) for temperature-dependence (TD) [26,60]. Among biotic drivers of diversification, we checked for diversity-dependence (DDD) on speciation and extinction rates, incorporating both linear and exponential dependent functions [26,61]. The code for calculating AICc for all DDD models referred to relevant sections of source codes for *fit_bd()* and *fit_env()* functions from *RPANDA* [42].

Factor analysis of mixed data (FAMD) was performed to assess the correlations among different ecological and evolutionary drivers explaining the patterns of species diversity (or richness) and diversification across lineages [62]. Both quantitative and qualitative (categorical) variables were used in this analysis. Quantitative variables included species richness, clade ages and net diversification rates. Categorical variables included taxonomic groups, biogeographic origins, habitat types, presence of habitat structuring within a lineage (i.e. presence of geographically structured sub-clades, indicating potential adaptations within a lineage), diversification scenarios, and whether the lineages show temperature-dependence (TD), diversity-dependence (DD), Himalayan-orogeny-dependence and C4-plant-expansion-dependence on diversification rates. First, correlations among variables were assessed, and then clustering patterns of lineages based

on categories relevant to each qualitative variable were assessed by estimating convex hulls around the centroids in the multidimensional space for each category. We also performed the permutational multivariate analysis of variance (PERMANOVA), utilising the dissimilarities (Gower's distance) between lineages calculated from FAMD coordinates of each lineage to assess the statistical significance of clustering [63]. Lastly, concordance between clusters within each qualitative variable and that of diversification scenarios was checked visually. All the analyses were performed using functions from the R packages - *FactoMineR* [64,65] and *factoextra* [65].

<u>Clade age vs diversification rate:</u> The relationship between species richness with clade age and diversification rates was examined using Phylogenetic Generalised Least Squares regression (PGLS) [58,66]. It also accounts for the influence of phylogenetic relationships on the association among studied taxa. We performed pairwise PGLS for clade age and species richness, then net-diversification rate and species richness, and lastly, between diversification rate and clade age for all the lineages. The phylogenetic tree used in PGLS was time-calibrated and constructed in timetree.org [67] and using respective taxa-specific phylogenies. Further, associations between species richness, clade age and diversification rates were also examined for biogeographic origins and habitat types. The PGLS was performed in R using the packages - *nlme* [68], *ape* [69] and *rr2* [70], and relevant plots were made using *ggplot2* [53]. The strength and statistical significance of regression was assessed using the R^2 and *p*-value (significance level - 0.05), and the phylogenetic signal for the relationships was assessed by estimating Pagel's λ. Log-transformed (natural log) values were used for species-richness and clade-ages to improve linearity in regression. For cases where PGLS could not reach convergence, ordinary least squares linear regression was performed.

The credibility of parameter estimates: 1000 phylogenetic trees were simulated using each combination of parameter estimates for the best-fitting constant-rate or time-varying birth-death models per lineage. Furthermore, the distributions of the differences in the □-statistic and number of tips between the simulated and respective empirical trees were plotted as violin plots. Simulations using accurate estimates are expected to show the distribution mean and median within two standard deviations from zero.

3. Results:

3.1. Endemic Peninsular Indian biota: Diversity, Age and Biogeographic Affinities - The dataset consists of well-sampled dated phylogenetic trees of 34 lineages encompassing 669 species, of which 94% (633 species) are endemic to peninsular India (Fig. 1a). These 34 lineages comprised five predatory soil arthropods (50 species - centipedes and scorpions), three freshwater molluscs (22 species - mussels), eight amphibians (153 species - frogs and caecilians), 12 reptiles (304 species - turtles, geckos, agamids, skinks, lacertids and snakes), one bird (4 species), and five plants (136 species - angiosperms). These lineages are distributed in both terrestrial (30 lineages) and freshwater habitats (four lineages). Among terrestrial lineages, 18 lineages are restricted to the wet zones of the Western Ghats, Eastern Ghats, and Sri-Lankan Forests, and 12 are distributed across both wet and dry zones in Peninsular India and/or Sri Lanka (Fig. 1a). These lineages also have varied biogeographic origins, where 21 of the lineages are of Asian origin and 13 are of Gondwanan origin (Fig. 1a).

3.2. Mode and tempo of species accumulation within each lineage

Speciation, extinction, and net diversification rates were calculated fitting the constant birth-death (CBD) model across all 34 lineages. Among the different taxonomic groups examined in

our dataset, arthropods showed significantly low diversification rates, and plants had significantly higher diversification rates than other taxonomic groups ($p<0.01$, Fig. 2 a.i, c.i). Within different habitat types, lineages distributed in the freshwater habitats (n=4) showed a slower pace of diversification than lineages in terrestrial habitats (n=30) ($p<0.05$ - Fig. 2 a.ii, c.ii). We also found no difference in diversification rates with respect to habitat type (i.e. terrestrial: wet and wet+dry habitats). The diversification rates were lower among the Gondwanan than in Asian lineages ($p<0.05$, Fig. 2 a.iii, c.iii). Nevertheless, the credible intervals for diversification rates overlapped for habitat types and biogeographic origins. Differences in speciation rates mainly contributed to disparities in net-diversification rates because extinction rates across groups are very low (~0), except for four lineages (*Ophisops* and Fan-throated lizards, *Montecincla* birds and *Parreysia* mussels) out of 34 lineages (Fig. 2 d, e, f).

<u>Diversification patterns based on □-statistic and diversification models</u> - Of the 34 lineages, the null hypothesis that "□=0" could not be rejected for 29 taxa, suggesting support for the gradual accumulation of lineages depicted in scenario 1 (SC1). The remaining five lineages showed a slowdown in accordance with diversification scenarios 2 and 3 (□ < 0, *gammatest* and *MCCR test* - $p < 0.05$, SI Table 2). Further, the constant-rate (CB and CBD) and time-varying models were fitted to all lineages. We found that 19 lineages supported the constant-rate birth (CB) model with gradual expansion (SC1), and 15 supported time-varying birth-death models with both slowdowns (SC2) and Waxing and Waning (SC3) (Table 3; SI Table 1, SI Fig. 2). These 19 lineages were spread across taxonomic groups, biogeographic origins and habitat types (SI Fig. 2). Among 15 lineages with time-varying birth-death models, 13 also showed episodic shifts in the diversification rates and two lineages (*Hemidactylus* lizards and *Pseudophilautus* frogs) showed saturated accumulation (SC2) without any episodic rate shifts. Among the 13 lineages

with episodic rate shifts, one lineage showed slowdown (SC2), four lineages with waxed and waned (SC3) and eight lineages showed episodic rate shifts. In lineages with rate shifts, the CoMET inferred in nine lineages, RPANDA in eight, and three in both CoMET and RPANDA. Parameter estimates of □-statistic, birth-death model-fitting (RPANDA) and CoMET analysis are provided in SI Table 2.

3. 3. Drivers of diversification and species diversity

There was no association between the diversification scenarios and taxonomic groups, habitat types or biogeographic origins (Fig. 4; SI Fig. 2), except in molluscs, where all three lineages supported the gradual accumulation scenario (SC1). The time-varying diversification rates were largely associated with paleo-temperature and existing diversity through time (Table 3; SI Table 1 and 3; Fig. 4). Of 15 lineages that supported time-varying models and/or shifts over constant rates, 10 showed temperature dependence (TD). Among these 10 TD lineages, three lineages equally supported (□AICc ≤ 2) diversity-dependence (DD). Furthermore, two of these three lineages supported Himalayan-orogeny-dependence, and none supported C4-plant-expansion-dependence, respectively.

Diversification rate shifts were inferred for 13 lineages, and 12 of them were found to occur in Neogene, as shown in Fig. 3. Also, nine lineages among the 12 lineages above showed diversification rate shifts within the geological period that experienced a mid-Miocene intensification of aridification, and monsoons and expansion of C4-plants in PI. Four lineages showed rate shifts younger than 3 Mya, and 2 lineages showed rate shifts in the late Neogene. Sharp declines in global temperatures from around 2 Mya to the present are concurrent with

these recent rate shifts in these lineages, all of which are also declines in diversification rates (Fig. 3, SI Fig. 3b).

In FAMD analysis, 36% (Fig. 4 - Axis 1: 19.1%, Axis 2: 16.9%) of the total variation was explained by the first two dimensions. Majorly, diversification scenarios, species richness, temperature-dependence and diversity-dependence contributed to dimension 1 and biogeographic origins, taxonomic groups and clade ages contributed to dimension 2 (SI Fig. 4). Additionally, species richness and net diversification rates were associated. However, clade ages did not show any relationship with species richness (supplementary figure SI Fig. 4 and Fig. 4), similar to the PGLS analyses (Fig. 5).

Boxplots and the Wilcoxon test reconfirmed the association between TD, DD, species richness and net diversification as the lineages showing Temperature-dependent and Diversity-dependent diversification had significantly higher species richness and net-diversification rates (SI Fig. 4c). Additionally, among diversification scenarios, gradual accumulation favoured lower species richness and net-diversification rates (SI Fig. 4c), reconfirming the association between scenarios, species richness and net-diversification rates, as indicated by the FAMD.

Convex hulls around clusters pertaining to diversification scenarios illustrating time-varying diversification were predominantly concordant with that temperature- and diversity-dependence. Also, clusters of lineages pertaining to different biogeographic origins showed very little overlap in the multidimensional space. Additionally, all arthropod (n=5) and mollusc (n=3) lineages were found to form distinct clusters, with no overlap with clusters composed of amphibians, reptiles and plants (Fig. 4.b). *P-values* of PERMANOVA tests, indicating the significance of overlaps between clusters pertaining to each categorical variable, have been provided in SI Table 4.

The relationship between species richness and clade age was not significant across lineages in PGLS regression analyses (Fig 5.a, R^2 = 0.1, p = 0.141) as well as for different biogeographic and habitat affinities (SI Fig. 5), except for lineages distributed across both wet and dry habitats (SI Fig. 5, Wet+Dry habitat - R^2 = 0.47, p = 0.02). On the other hand, species richness and net-diversification rates showed a significant association (Fig 5.b, R^2 = 0.31, p = 0.002) across lineages and biogeographic and habitat affinities, except for lineages from wet and dry habitats (SI Fig. 5, Wet+Dry habitat - R^2 = 0.28, p = 0.887). Also, a statistically significant negative relationship was observed between net diversification rates and clade ages across lineages with a high phylogenetic signal (Fig. 5.c, SI Fig. 5).

4. Discussion:

Our multi-clade analyses examining the tempo and mode of diversification using birth-death models suggested that more than 50% of lineages show gradual species accumulations through time with high speciation rates accompanied by low extinction rates, suggesting that the historical stability of the landscape played an important role. However, we also showed that time-varying diversification patterns were evident among the other lineages, and paleotemperature, Miocene aridification, ecological limits, and species traits influenced them. Also, the biogeographic and taxonomic affinities impacted diversification and diversity dynamics. For the first time, we demonstrate that the diversification of peninsular biota follows idiosyncratic patterns and is influenced by multiple factors, including regional biogeographic and phylogenetic history, historical stability, and habitat heterogeneity. Notably, the disparity in diversification rates is the primary driver of differences in species diversity among peninsular-Indian lineages, driven by speciation rates as extinction rates remained low across lineages.

4.1. Disparities in the tempo of diversification in PI biota: Differences in speciation rates drove the disparities in the net diversification rates, as extinction rates remained low across PI lineages (Fig. 2). Among the 34 lineages studied, angiosperms (flowering plants) from five different clades had higher diversification rates than other faunal lineages. Angiosperms are known to have higher diversification rates, primarily because they typically have larger clade-level range sizes [71], polyploidy [72] and higher dispersal ability [73]. This means that angiosperms can occupy a wide range of ecological niches and are more likely to colonise new areas, promoting their diversification. On the other hand, soil arthropods, specifically centipedes and scorpions, were found to have the lowest net diversification rates among the studied lineages. This could be attributed to several factors, including their specialisation for fossorial (burrowing)

habits, predatory nature, and relatively low dispersal abilities [24,74]. Specialisation for a specific ecological niche may limit the opportunities for speciation, and low dispersal abilities could restrict their ability to colonise new areas and diversify [75]. The taxonomic identity highlights the importance of factors which are clade-specific, such as range size, dispersal abilities, and ecological niches, that can have a significant impact on speciation and extinction rates, ultimately influencing net diversification rates among lineages as seen across the Tree of Life [50].

The complex biogeographic history of peninsular India offered us a unique opportunity to explore the role of biogeographic affinities on diversification rates. Peninsular India has species assemblages with distinct biogeographic origins, sometimes even in the same taxonomic groups, such as amphibians, where ancient Gondwanan and younger Asian lineages co-exist [11]. We found that ancient Gondwanan lineages (n=13) diversified at lower rates than younger Asian lineages. Interestingly, most Gondwanan lineages are wet-zone specialists and show less dispersal and more vicariance-mediated diversification than Asian lineages. Gondwanan lineages also show a high degree of ecological specialisation and retention of their ancestral niches, such as fossoriality by arthropods, blind snakes and caecilians and preference for freshwater habitat by molluscs. Ecological specialisations or niche conservatism may limit diversification rates, leading to lower diversification rates among Gondwanan lineages [75–77]. On the other hand, many Asian lineages occupy diverse ecological and climatic niches, contributing to higher diversification rates. This indicates that biogeographic affinities and ecological specialisation influenced the diversification rates in peninsular India.

Another important factor thought to influence the diversification rates is habitat preference [78,79]. Although wet and dry forests are well characterised by their distinct climatic conditions, wet and dry forest dwelling taxa remained relatively similar in their diversification rates [10,18]. On the

other hand, freshwater lineages (n=4) showed significantly lower diversification rates than terrestrial lineages, and three out of these four lineages are molluscs. Hence, species traits could have influenced the diversification rate more than habitat preference. However, a larger sample size is required to strengthen this claim.

4.2. Climatic stability, paleotemperature, ecological limits and biogeography: More than half of the studied lineages (approximately 53%) supported the constant-rate pure-birth model, indicating a gradual accumulation of diversity over time. This gradual diversity increase is attributed to the stable climate in regions of diversity expansion [7,28,29], especially in tropical biomes like the tropical forests of peninsular India. This is an intriguing pattern given that peninsular India (PI) has experienced significant climatic changes throughout the Cenozoic era, during which diversity has accumulated [13,14]. Therefore, we suspect some areas in peninsular India may have served as refugia, and it would be worth identifying them in the future through spatially explicit diversification analyses. Exploring how diversification rates vary across space in peninsular India would be worth exploring. In the Neotropics, 50–67% of endemic plant and tetrapod lineages were supported by gradual diversity expansions [7]. This suggests that stable climate refugia supporting diversity accumulation is not unique to peninsular India but may have global relevance in tropical regions, which need further exploration.

A large proportion of the current species diversity in peninsular India is of Asian origin, except for a few small vertebrates and soil arthropods [11]. The plant fossil record suggests diverse Gondwanan flora in the region until at least the late Paleocene, which now has extant relatives in Southeast Asia [12,80,81]. Relictual Gondwanan floral lineages are yet to be identified in peninsular India or all have gone extinct. Despite the potential role of peninsular India as an "evolutionary graveyard" for floral lineages [81], our results indicate a predominant historic stability in the

landscape. One potential way to provide this stability is through rapid turnover of the forests where ecologically similar species of Asian origins replace Gondwanan lineages. This prediction can be tested using extensive South and Southeast Asian plant clades. Also, similar assessments across other tropical biomes and more taxa from peninsular India would be necessary to assess the generality of stability in tropical forests.

On the other hand, lineages with time-varying diversification rates show a complex interplay between climatic events, episodic rate shifts, and species traits. The Neogene period, especially during the mid-Miocene, witnessed intensified aridification and seasonality in the Indian subcontinent, which is believed to have significantly impacted diversification, particularly among lizards [14,15,38]. While previous studies suggested a connection between climatic events and diversification, a robust statistical framework to test these hypotheses was lacking. Of the 14 lineages with episodic rate shifts, 12 occurred during the Neogene (23–2.6 Mya), and three occurred more recently, younger than 3 Mya. These shifts involve either an overall decline in diversification rates due to ecological limits or symmetrical episodic shifts (SES), which result from alternating periods of increased and decreased diversification. Nine of these lineages showed rate shifts that consistently overlapped with the temporal range of relevant climatic events, suggesting a potential link between climatic changes and diversification in these lineages. Additionally, four lineages with strict declines in diversification rates appear to be concurrent with drastic declines in global temperatures during the late Neogene and throughout the Quaternary.

Another important diversification pattern observed among multiple taxa globally and in tropical regions is the slowdowns in diversification rates [26,33]. A global study assessing the drivers of slowdowns inferred the role of diversity-dependence (or ecological limits) and declining global

paleotemperature [26]. As previously described, diversification slowdown and diversity dependence were observed in *Hemidactylus* geckos. Similar results were also found in two more lineages, namely scorpions and bush frogs (Heterometrinae and *Pseudophilautus*). And, these patterns were found to be linked to diversity dependence and temperature dependence, suggesting that changes in species diversity and temperature fluctuations play a role in diversification rates. In four lineages, waxing and waning (diversity declines) were detected and influenced by temperature fluctuations, and only two of these lineages showed equal support for diversity dependence. Again, variation in speciation rates contributed to diversity declines in these lineages, except in one where the extinction rate was relatively high (*Ophisops*).

Mid-Miocene intensification of aridification and monsoons have also been hypothesised to drive exponential species accumulation (SI Fig. 1) [15,38]. However, none of the lineages in our dataset supported a recent rise or exponential accumulation. Also, the role of Himalayan orogeny and the expansion of C4 plants in explaining diversification among PI biota remained limited. Only a few lineages showed dependence on these factors, and we suggest that their influence might have been episodic and not consistent throughout lineage history. Hence, derivative curves of these factors, highlighting periods of instability, can be utilised to check the dependence of diversification. Other factors, such as paleo-temperature, could have played a more significant role in diversification. Analytical methods to determine the dependence of diversification in each time interval (piecewise dependence) on factors like paleo-climate and existing diversity can be useful in these scenarios.

4.3. Drivers of diversification rates, clade ages and species diversity: Species diversity across taxa was strongly associated with their intrinsic diversification rates (net-diversification rate) rather than the evolutionary time for diversification (clade-age), supporting the expectation of the

diversification-rate hypothesis. The strong relationships between the diversification rates and species richness has been suggested in clade-specific studies (e.g., plant family Annonaceae) [51] as well as across the Tree of Life [50]. Interestingly, we also found a significant negative relationship between diversification rates and clade age, where older lineages have lower diversification rates. Older lineages, persisting in a region for long, are expected to have limited ecological niches to diversify further. Further, regional-level processes could also impose ecological limits on speciation with increasing diversity [72]. Therefore, in peninsular India, old lineages, mainly of Gondwanan origins, are expected to show diversity-dependent diversification. However, only six out of 34 lineages showed strong evidence for diversity-dependence, of which only three had Gondwanan (total n=13) affinity, indicating that other factors may also be at play in shaping diversification patterns.

Phylogenetic niche conservatism (PNC) could also explain low diversification rates among older lineages. Given most old lineages are terrestrial Gondwanan lineages (except Heterometrinae and *Cnemaspis*) and are distributed solely in the wet zones (i.e. they exhibit PNC), ecological speciation would be limited by high niche saturation [75,77]. In contrast, high diversification rates for young PI lineages, which are of Asian origins, can be explained by higher dispersal rates allowing lineages to occupy diverse ecological and climatic niches (many have Pan-PI and SL distribution) [11,23,82].

Phylogenetic relatedness also contributed significantly to the negative relationship between diversification rates and clade ages, as indicated by Pagel's lambda values in the PGLS analyses. In our dataset, young lineages (geckos, frog and plants) share biogeographic and ecological (climatic niche, range, dispersal ability, trophic levels, etc.) similarities and so do old lineages (centipedes and scorpions), among themselves. It is because the ecology and evolutionary history

of biota are strongly tied in PI, which may pose ecological constraints on diversification for young and old lineages and hence, disparities in diversification rates are also very pronounced.

It is also likely that the biomes and ranges that comprise the old lineages constitute museums of biodiversity, whereas the ones comprising young lineages constitute cradles of biodiversity. A recent study on endemic woody plants suggests that the Western Ghats is both a museum and a cradle of diversity [83]. Given many endemic lineages (e.g. - centipedes, scorpions, geckos) found in the WG are not restricted to the biodiversity hotspot but have pan-peninsular distributions, the entirety of PI may potentially be a museum and a cradle of biodiversity. The old lineages studied here follow the museum model where they have low diversification rates, longer persistence times and constant diversification, whereas younger lineages show characteristics of the cradle model of more dynamic and higher diversification rates. This could potentially explain the negative relationship between diversification rates and clade ages (Fig 5). It would be worth exploring this further to validate this relationship with more lineages with distinct ages, richness patterns and ecologies in peninsular India and tropical regions.

4.4 Understanding diversification in tropical areas: limitations and way forward

There has been tremendous growth in methods that infer the diversification tempo and mode in the recent past. However, one of the limiting factors to applying these across taxa and regions has been the requirement of large datasets, where the number of tips analysed in each lineage should be high. Many clades studied in our study are species-poor; therefore, we used multiple methods, including summary statistics (□-statistics) and birth-deaths models implemented in different frameworks. Also, a default sampling fraction of 1 was kept in the AICc-based birth-death model fitting and the CoMET analyses across all lineages for simplicity. We acknowledge

that this might contribute to erroneous assessments in diversification models, especially in slowdowns when taxa are incompletely sampled. Hence, future studies should incorporate more precise sampling fractions for each lineage for robust results. Additionally, comparing these canonical rate estimates with pulled diversification rates (PDR) would be helpful in avoiding the issue of non-identifiability among many congruent models and provide robust estimates for extinction rates [84]. Nevertheless, simulations through our parameter estimates were able to significantly recover the branching patterns and the number of tips of the empirical phylogenies (SI Fig. 6).

Our dataset comprising 633 endemic peninsular Indian species is strongly biased towards small vertebrates (~70 % - 437 species), and birds, freshwater biota and soil arthropods are among the most underrepresented groups. However, it is worth noting that the endemicity among birds (~5%) and mammals (~15%) itself is low in peninsular India (IUCN maps) as compared to the soil arthropods (~ 90%) [74,85], small vertebrates (~ 52% - amphibians and reptiles) and flowering plants (~ 26%) [86]. This could be because bird and mammal assemblages in PI are mainly dispersal-driven and haven't undergone in-situ speciation like soil arthropods, small vertebrates and angiosperms.

Furthermore, speciation rates drove diversification rates among peninsular Indian taxa, as extinction rates remained low across peninsular Indian lineages. Given the current peninsular India biota largely comprises groups which have evolved post the K/T mass extinction event (ca. 66 Mya), we do not find the signature of extinctions in our dataset [12,87]. The current diversity estimates could be underestimated for soil arthropods, herpetofauna and freshwater biota, as many new species are still being described [24]. Also, many studies have explicitly focused on the Western Ghats, the known biodiversity hotspots, and other regions of peninsular India remain

unexplored and understudied. Even in global datasets, soil and freshwater habitats are poorly represented, urging us to focus on unexplored taxa and habitats for a holistic understanding of the tempo and mode of diversification across tropical forests. Additionally, phylogenetic reconstructions using more sophisticated tree priors like the fossilised birth-death (FBD) model or the cladogenetic diversification rate shifts (ClaDS) model are ought to influence the estimates for the diversification dynamics, and need to be integrated in future studies.

The role of historical stability in the biotic diversification in tropical forests has been recognised for a long time [7,88]. In addition, species traits and geoclimatic events influencing diversification have also received support across taxa and regions [8,89]. We show that diversification in Peninsular India has a signature of historical ecosystem stability as well as paleotemperature, Miocene aridification and intensification, and existing diversity, the known global drivers of time-varying diversification. The complex tempo and mode of diversification shown in our results suggest that regional biogeographic, geoclimatic and phylogenetic history needs to be examined across tropical regions, including peninsular India. Furthermore, exploring among-clade rate-heterogeneity within endemic lineages using methods like - BAMM and ClaDS can provide insights on the intricacies of their cladogenesis and possibly shed light on the bioregionalisation of diversification within a biome. Studies like this, where multi-taxa comparisons are carried out from different tropical areas, are critical for gaining insights into the evolution of biodiversity in a tropical biome.

Figure captions

Fig. 1. Clade age, number of species and endemicity, biogeographic and habitat affinities for 34 endemic lineages from peninsular India (PI) along with Paleoclimate data. a. i. The illustration of 34 endemic lineages of plants and animals from peninsular India with their divergence times. The numbers indicate the number of endemic species from PI by number of species present in the respective group. Key geological events (Table 2) have been highlighted using grey vertical bars. **a. ii)** A map of peninsular India showing a global biodiversity hotspot, the Western Ghats (denoted as WG), the Eastern Ghats (denoted as EG), and dry plains (DZ), **a. iii)** Barplots indicating habitat type and biogeographic affinities for each lineage, **b.i)** Global paleotemperature (in °C) [42] for the Cenozoic era. **b.ii)** Pedogenic carbonates (δ^{13}) [43] indicating the type of vegetation cover, **c.iii)** Reconstructed elevations of the Himalayan-Tibetan Orogen (in metres) [45].

Fig. 2. The pace of diversification. Comparisons of speciation **(a)**, extinction **(b)** and net-diversification rates **(c)** across taxonomic groups **(i)** (arthropods, molluscs, amphibians, reptiles, birds, plants), habitat types **(ii)** (FW - Freshwater habitat, Wet - Wet forests, Wet+Dry - Wet and dry habitats) and biogeographic origins **(iii)** (Asian and Gondwanan) in 34 lineages. Shown are the median (thicker lines within the box plots), the 25th and 75th interquartile range (the extremes of boxes) and the 95% credible intervals (as shown by the lines extending above and below the boxes). Each dot represents the relevant diversification rate of each lineage and dots lying outside the 95% credible intervals are the outliers in each category. Asterisks on top of the

boxplots indicate statistical significance in comparisons (* - $p < 0.05$, ** - $p < 0.01$, non-significant comparisons haven't been highlighted) and numbers indicate sample size within each category. The dotted line indicates the overall mean rate of diversification and the red dot indicates that the rates of the corresponding category are significantly different from the overall mean, statistically.

Fig. 3. Diversification patterns and drivers. Horizontal bar plots indicate clade-ages of 34 lineages, circles indicate symmetrical rate shifts and triangles represent one-way episodic rate shifts and their positions indicate their time of occurrence. Multiple opposing one-way rate shifts (sudden increase followed by sudden decrease or sudden decrease followed by sudden increase) within a lineage, inferred by the CoMET analysis are indicated by multiple oppositely faced triangles. Text in blue indicates the diversification scenario favoured by a lineage, followed by the prevalence of temperature (TDD) and/or diversity-dependence (DDD) in the lineage. Key geological events (Table 2) have been highlighted using grey vertical bars. **(inset)** Vertical Bar plot indicates the prevalence of different diversification scenarios in PI lineages, SC1 - gradual accumulation, SC2 - slowdowns, SC3 - Waxing and Waning and Episodic Rate Shifts.

Fig. 4. Ordination (Factor Analysis of Mixed Data - FAMD) plots made using 13 relevant ecological and evolutionary parameters for 34 lineages. a) The first two dimensions of the ordination analysis explain that the variables positioned in the space represent their relative contribution to the relevant axes. The positions of the variables relative to each other represent the strength of their associations. Dimension 1 is majorly explained by variables relevant to lineage identity (Taxonomic group, Biogeographic Origin and Clade age) and Dimension 2 is majorly explained by diversification and diversity dynamics (Species richness, Diversification Scenarios, etc.), **b)** Each panel represents a categorical variable and the clusters within them

represent the categories. Clusters relevant to diversification scenarios are largely congruent with that of diversity-dependence and temperature-dependence. Check SI Table 4 for information relevant to PERMANOVA tests for inferring significantly distinct clusters within each categorical variable.

Fig 5. Drivers of species richness. Phylogenetically corrected linear regression analysis of species richness (log transformed) versus clade-age (log transformed) and diversification-rates (n=34 for all the three plots). Each point is relevant to one lineage, R^2 values indicate the goodness of fit of the regression lines, *p*-value indicates the significance of the regression and λ indicates the degree of phylogenetic non-independence of the correlation (i.e. the phylogenetic signal in the correlation). Solid and dotted lines indicate statistically significant and non-significant linear models (significance level - $p < 0.05$), respectively.

Table captions

Table 1: Parameters of time-varying birth-death models corresponding to each diversification scenario assessed in the study. □ and □ indicates the coefficient of gain or loss with time used in the birth and death models respectively. $\square_0$ and $\square_o$ are the speciation (birth) and extinction (death) rates at present time (t=0). Additional remarks define unique intricacies within the corresponding sub-scenarios; see the SI figure 1 for detailed scenarios and predictions.

Table 2: Major geoclimatic events relevant to peninsular India and their estimated periods of occurrence

Table 3. Patterns and drivers of diversification

Supplementary Information

SI Tables and Figures (Attached)

Code Availability: Custom codes used in the analyses would be made available upon acceptance of the manuscript.

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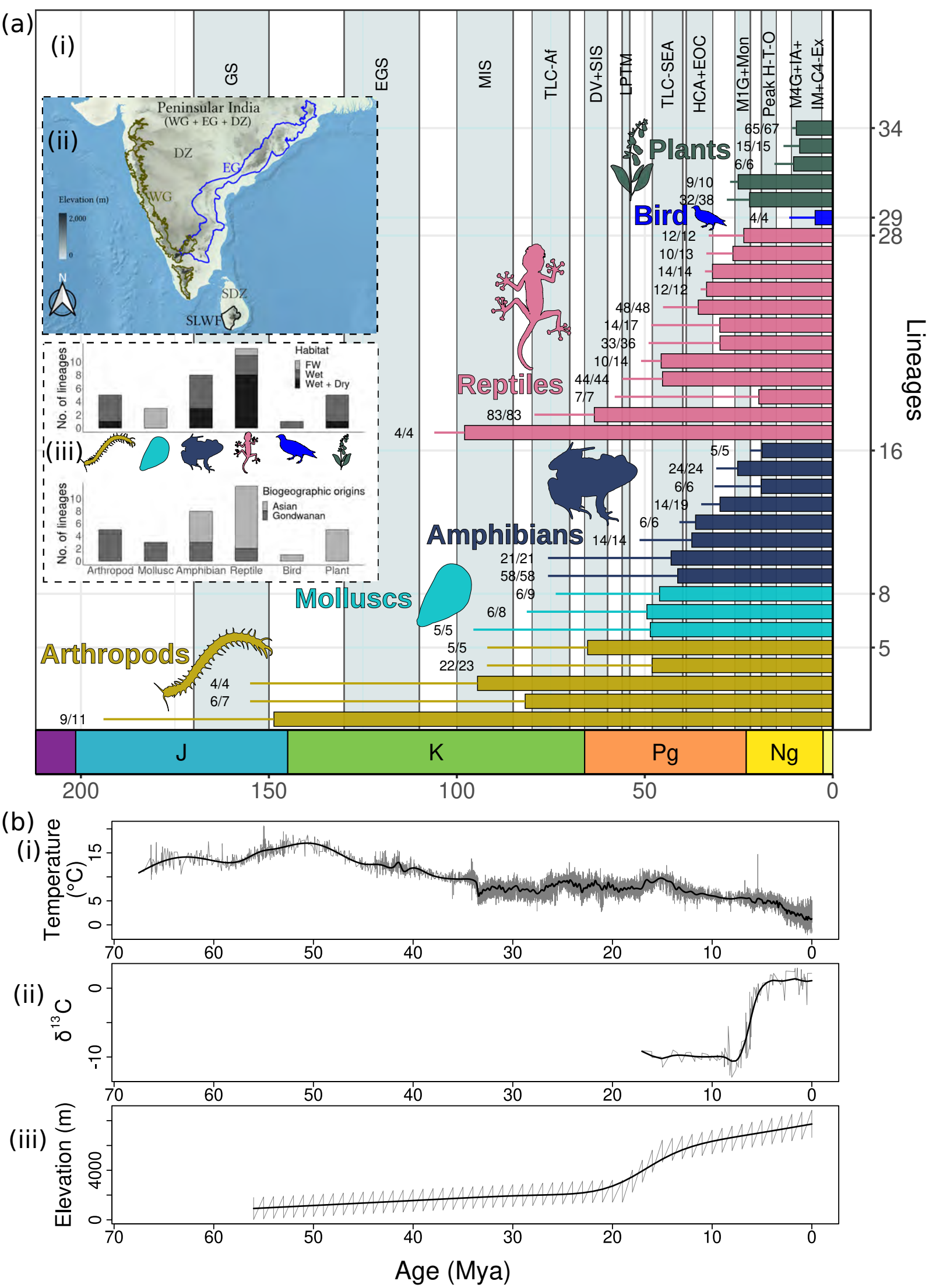
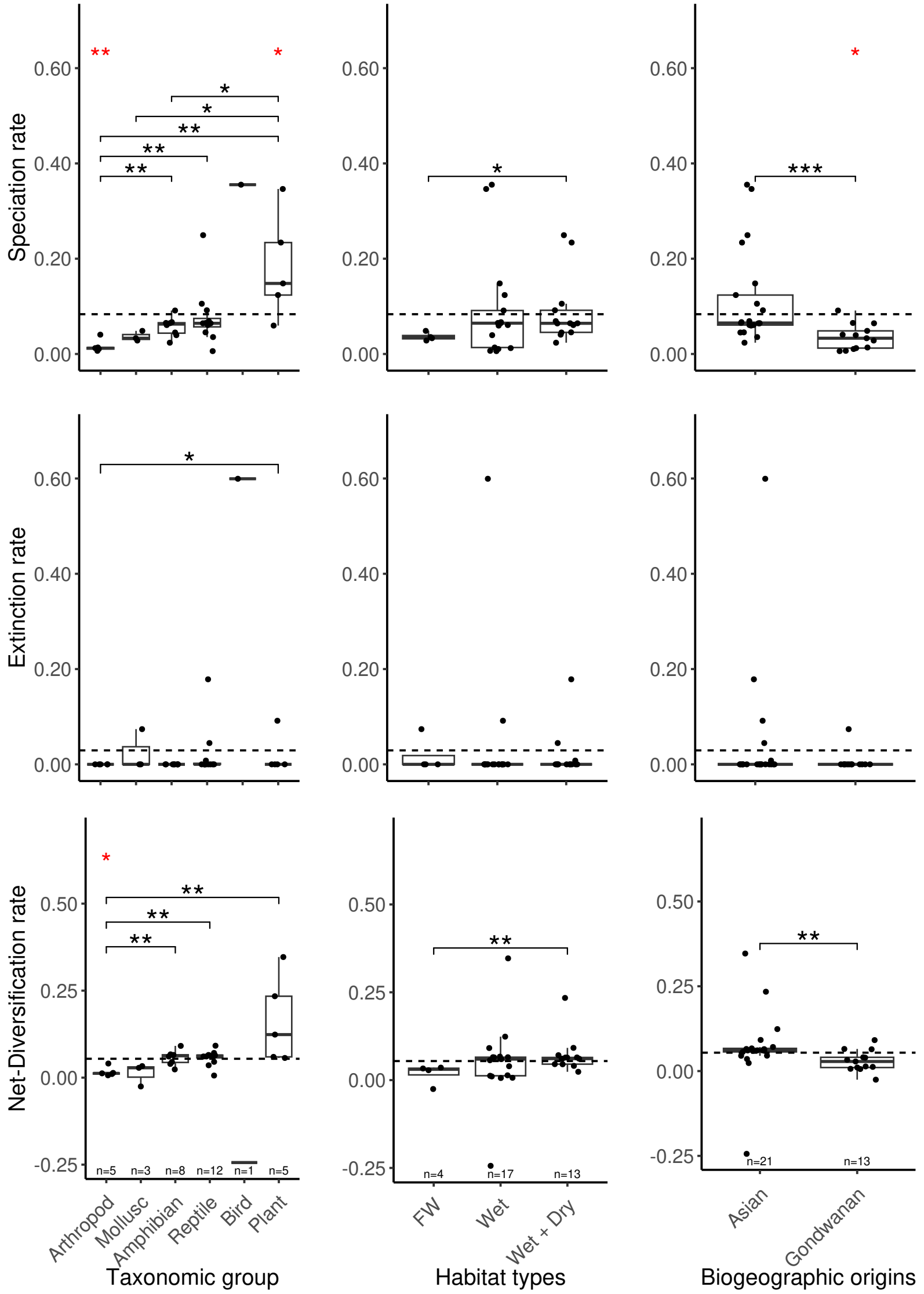
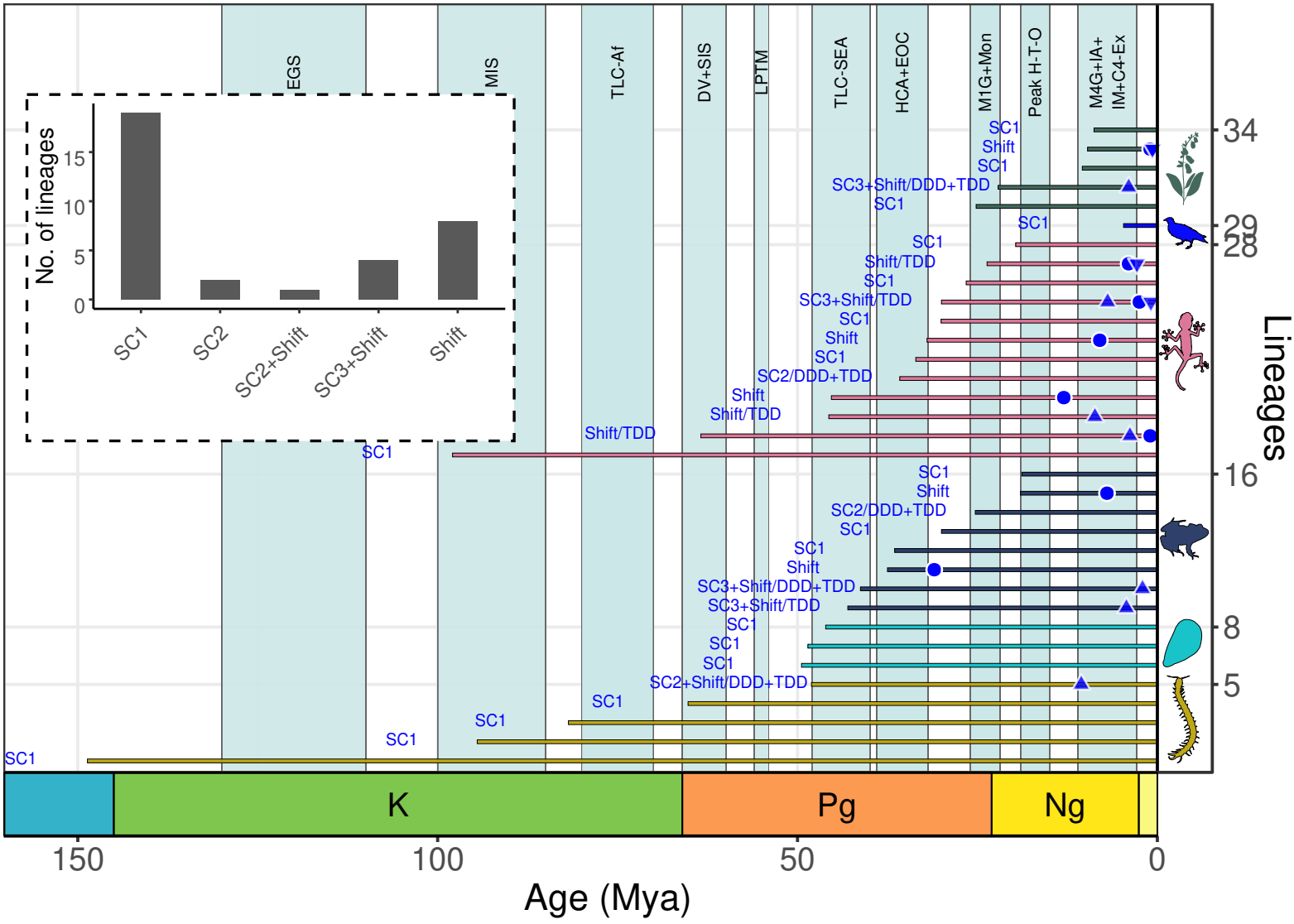
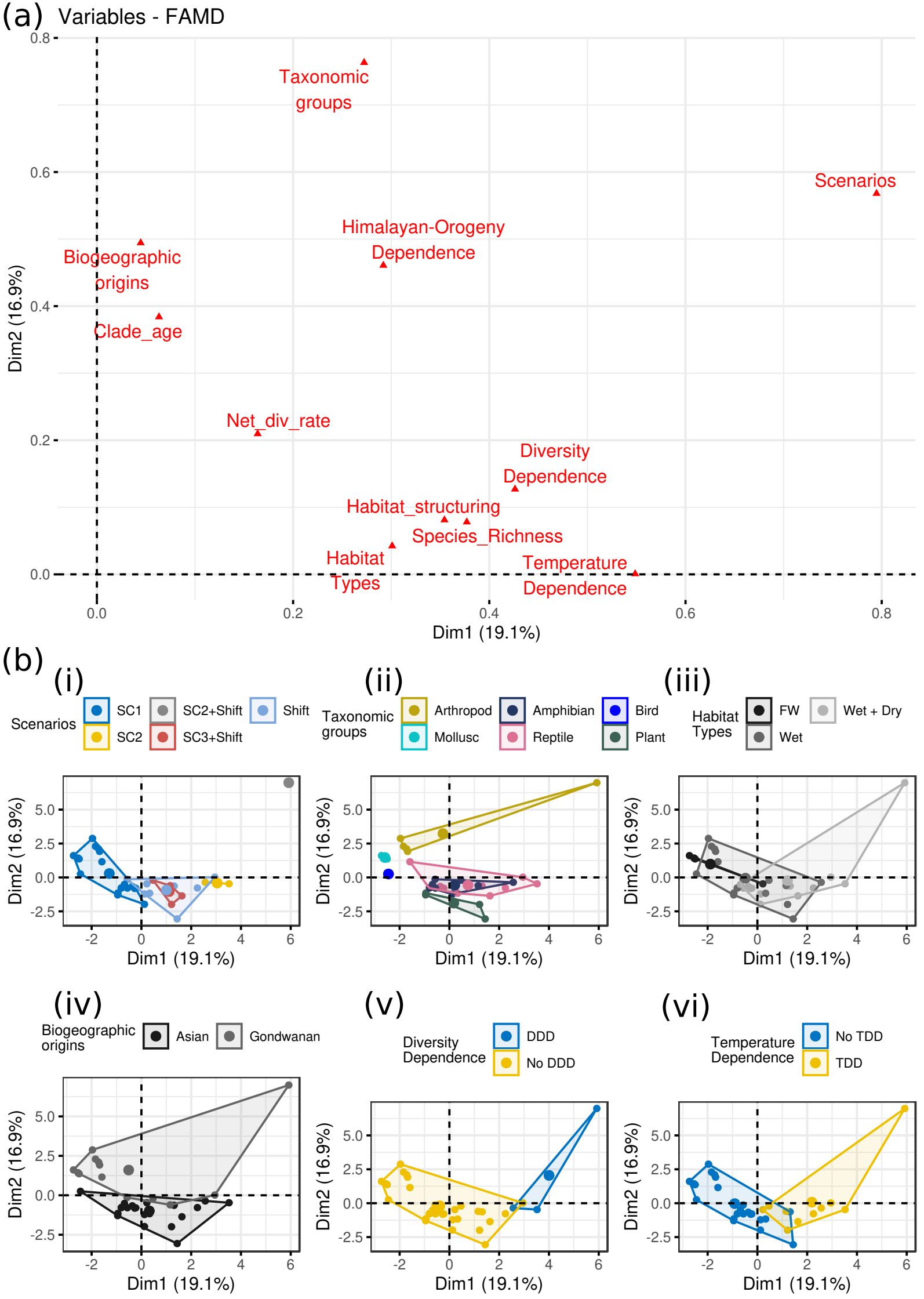
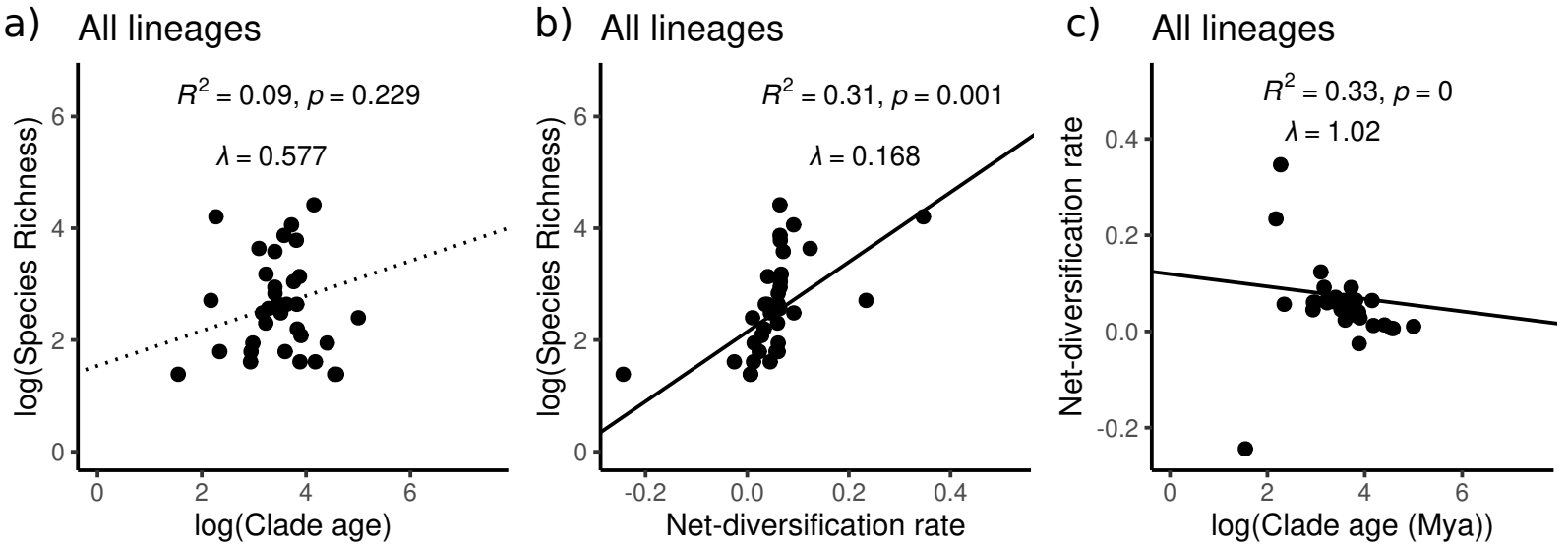

(a)
(i)
GS
EGS
MIS
TLC-Af
DV+SIS
LPTM
TLC-SEA
HCA+EOC
M1G+Mon
Peak H-T-O
M4G+IA+
IM+C4-Ex
Plants
Bird
Reptiles
Amphibians
Molluscs
Arthropods
Lineages
(ii)
Peninsular India
(WG + EG + DZ)
DZ
EG
WG
SDZ
SLWF
Elevation (m)
2,000
0
N
(iii)
No. of lineages
Habitat
FW
Wet
Wet + Dry
Biogeographic origins
Asian
Gondwanan
Arthropod
Mollusc
Amphibian
Reptile
Bird
Plant
J
K
Pg
Ng
200
150
100
50
0
(b)
(i)
Temperature (°C)
(ii)
δ13C
(iii)
Elevation (m)
Age (Mya)


Speciation rate
Extinction rate
Net-Diversification rate
0.60
0.40
0.20
0.00
0.50
0.25
-0.25
n=5
n=3
n=8
n=12
n=1
n=5
n=4
n=17
n=13
n=21
n=13
Arthropod
Mollusc
Amphibian
Reptile
Bird
Plant
FW
Wet
Wet + Dry
Asian
Gondwanan
Taxonomic group
Habitat types
Biogeographic origins


EGS
MIS
TLC-Af
DV+SIS
LPTM
TLC-SEA
HCA+EOC
M1G+Mon
Peak H-T-O
M4G+IA+
IM+C4-Ex
No. of lineages
15
10
5
0
SC1
SC2
SC2+Shift
SC3+Shift
Shift
SC1
Shift
SC1
SC3+Shift/DDD+TDD
SC1
SC1
SC1
Shift/TDD
SC1
SC3+Shift/TDD
SC1
Shift
SC1
SC2/DDD+TDD
Shift
Shift/TDD
Shift/TDD
SC1
SC1
Shift
SC2/DDD+TDD
SC1
SC1
Shift
SC3+Shift/DDD+TDD
SC3+Shift/TDD
SC1
SC1
SC1
SC2+Shift/DDD+TDD
SC1
SC1
SC1
SC1
34
29
28
16
8
5
Lineages
K
Pg
Ng
150
100
50
0
Age (Mya)


(a) Variables - FAMD
Taxonomic groups
Scenarios
Himalayan-Orogeny Dependence
Biogeographic origins
Clade_age
Net_div_rate
Diversity Dependence
Habitat_structuring
Species_Richness
Habitat Types
Temperature Dependence
Dim1 (19.1%)
Dim2 (16.9%)
(b)
(i)
Scenarios
SC1
SC2
SC2+Shift
SC3+Shift
Shift
(ii)
Taxonomic groups
Arthropod
Mollusc
Amphibian
Reptile
Bird
Plant
(iii)
Habitat Types
FW
Wet
Wet + Dry
(iv)
Biogeographic origins
Asian
Gondwanan
(v)
Diversity Dependence
DDD
No DDD
(vi)
Temperature Dependence
No TDD
TDD


a)
All lineages
$R^2 = 0.09$, $p = 0.229$
$\lambda = 0.577$
log(Species Richness)
log(Clade age)
b)
All lineages
$R^2 = 0.31$, $p = 0.001$
$\lambda = 0.168$
log(Species Richness)
Net-diversification rate
c)
All lineages
$R^2 = 0.33$, $p = 0$
$\lambda = 1.02$
Net-diversification rate
log(Clade age (Mya))

Scenarios	α	β	$\lambda 0 - \mu o$	**Additional remarks**
SC 1a	0	0	>0	$\mu o=0$
SC 1b	0	0	>=0	
SC 1c	<0	<0	>=0	$\alpha=\beta$
SC 1d	>0	>0	>=0	$\alpha=\beta$
SC 2a	>0	0	>0	$\mu o=0$
SC 2b	>0	0	>=0	
SC 2c	0	<0	>=0	
SC 2d	>0	<0	>=0	
SC 3a	>0	0	<0	
SC 3b	0	<0	<0	
SC 3c	>0	>0	<0	$\alpha>\beta$
SC 3d	>0	<0	<0	
SC 4a	<0	0	>0	$\mu o=0$
SC 4b	<0	0	>=0	
SC 4c	0	>0	>=0	
SC 4d	<0	>0	>=0	

Diversification scenarios	**Total**	**Temperature dependence**	**Diversity dependence**	**Himalayan orogeny dependence**	**Dependence on expansion of C4-plant**
Gradual accumulation (SC1)	19	0	0	0	0
Saturated accumulation (SC2)	2	2	2	0	0
Saturated accumulation + Episodic Shift (SC2+Shift)	1	1	1	1	0
Waxing-waning + Episodic Shift (SC3+Shift)	4	4	2	0	0
Symmetrical Shift (Shift)	8	3	0	0	0

Geological event	**Code used in further analysis**	**Period of occurrence (Mya)**
Gondwanan split	“GS”	Between 170 and 150
East-Gondwana split	"EGS"	Between 130 and 110
Madagascar-India separation	"MIS"	Between 100 and 85
Transient land connection with Africa	"TLC-Af"	Between 80 and 70
Deccan volcanism and Seychelles-India separation	"DV+SIS"	Between 67 and 60
Last Paleocene Thermal Maxima	"LPTM"	Between 56 and 54
Transient land connection with south-east Asia	"TLC-SEA"	Between 48 and 40
Hard collision with Asia and Eocene-Oligocene cooling	"HCA+EOC"	Between 39 and 32
Mi-1 glaciation and Monsoon kicks in	"M1G+Mon"	Between 26 and 22
Peak Himalayan-Tibetan Orogeny	"Peak H-T-O"	Between 19 and 15
Mi-2 glaciation, Intensified aridification, Intensification of monsoons, Expansion of C4 plants	"M4G+IA+IM+C4-Ex"	Between 11 and 3 (overlapping ranges of events, hence clubbed together)