

SUPPORTING INFORMATION

Amazonia is the primary source of Neotropical biodiversity

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Supporting Methods

Neotropical regions. We focused our analyses on the Neotropical realm (sometimes termed region) as defined by Morrone (7) along the northern and southern limits (ranging from northern Mexico to central Argentina) and including the whole Caribbean. Within the Neotropics, we then defined operational units for the subsequent biogeographic analyses. There is no consensus on how such regions should be defined, with sometimes large discrepancies between expert-based and data-driven schemes (8), as well as differences in the number and limits of biogeographic regions (bioregions) based on the same data but derived from different methods (9). In addition, there is probably no ‘universal’ set of bioregions that may be meaningful for ecologically and biologically disparate taxa (10, 11). We aimed at producing an adequate balance between biological relevance (reflecting major ecosystems), geological history, geographic separation, and an adequate number of regions in relation to the data and methodology available. We therefore departed from the terrestrial ecoregions and biomes proposed by Olson, *et al.* (12), which have been adopted by the World Wildlife Fund (WWF) and are widely used in ecology and biogeography. We reduced the number of biomes (Fig. S22) due to limitations in ancestral range estimation, in order to keep a reasonable number of species in the phylogenies for each region, and to reduce the risk of erroneous geographic coding of species into each region (e.g. due to the lack of georeferenced records in small ecoregions). In contrast, we split geographically disjunct biomes when separated by long distances, such as the dry regions of northern South America and the Cerrado and Chaco (currently separated by Amazonia), and the Atlantic Forests and Amazonia (separated by the South American Dry Diagonal) (13). Our primary classification includes 10 regions (Fig. 1). In order to test the robustness of our analyses to this classification, in particular how the broad definition of Amazonia by Olson, *et al.* (12) could affect the inference of dispersal events between Amazonia and Mesoamerica rather than between the Chocó and Mesoamerica, we also performed inferences based on a simpler, expert-based classification (Fig. S21).

Clades surveyed and species occurrences. We investigated the biogeographic history of two groups of plants (angiosperms and ferns) and four groups of vertebrates (birds, frogs, mammals, and squamates). We chose taxonomic groups for which large, relatively well-sampled time-calibrated phylogenetic trees were available. We downloaded occurrence records for all species from the Global Biodiversity Information Facility (Supporting References S1–S6). We only obtained georeferenced records and used the following filters: Scientific names (Pteridophyta,

Magnoliophyta, Anura, Squamata, Aves, Mammalia), location (a rectangle around Mesoamerica and South America, from c. 59° S and 125° W to 35° N and 25° W), and basis of records (specimens, literature occurrences). We only used data with no known coordinate issues and used the CleanCoordinates function of the package SpeciesGeoCoder v.1.8 (14) in R (15) for further automated cleaning of the occurrence records. We excluded records that were identified as invalid, containing plain zeros, in a rectangle of 0.2 degrees around capital centroids, and 0.1 degrees around country and province centroids, following Maldonado, *et al.* (16). We rounded coordinates to the fifth decimal. For the angiosperm dataset, we also conducted a taxonomic cleaning due to the large number of synonyms and subspecies ranks in this group. We excluded records of species only identified to genus level, excluded hybrids, and merged intraspecific ranks to species level. We used the Taxonomic Name Resolution Service (17) to merge known synonyms under accepted names and to exclude records with invalid or illegitimate names and those with unknown taxonomic status, keeping only those records that could be unambiguously matched to an accepted name.

We then limited the cleaned dataset to occurrence records within the Neotropics and used it to classify each species as present or absent in each of our studied regions using SpeciesGeoCoder. We only recognized a species as present in a region when at least 5% of all its occurrence records fell in the region, in order to minimize the effect of erroneous species identifications or georeferencing, and to decrease the occurrence of marginal distributions and geographic outliers. We assessed the impact of multiple thresholds on the species-to-region-classification with independent data on species ranges provided by the International Union for Conservation of Nature (IUCN; www.iucn.org), using frogs and mammals as test taxa. For this purpose, we performed a second region coding, classifying species as present in our study regions if their IUCN range intersected with the respective region. We then compared all presence and absence classification with our original classification based on GBIF data, using different filter thresholds starting from a filter of 0% exclusion (a species is coded as present if there is one or more occurrences in a region) to 50%, with multiple intermediate intervals. We then calculated the false positive and false negative rates in region classification for those species present in both datasets (Fig. S23). We did not impose an absolute minimum number of occurrences because of the low density of records for several groups, in particular plants where approximately 30% of all Neotropical species only have two or less georeferenced records (18).

Phylogenies. We retrieved large-scale time-calibrated phylogenies for all study groups available during the data compilation phase of this study. For ferns, we used the phylogeny of Lehtonen *et al.* (19), which includes 1,116 species representing over one-fifth of the extant global fern diversity. For angiosperms, we used the phylogeny of Zanne, *et al.* (20), which is the largest phylogeny of land plants published so far with 32,233 species (12.5% of the total diversity). For amphibians, we used the phylogeny of Pyron and Wiens (21), which includes 3,309 species, corresponding to about 43.2% of the known extant species (22). For squamates (lizards, snakes, and amphisbaenians or "worm lizards") we used the phylogeny of Pyron, Burbrink and Wiens (23), which includes 4,161 species representing all currently recognized families and subfamilies and 42.2% of the known species. For birds, we used the phylogeny compiled by Jetz, Thomas, Joy and Mooers (24), which includes 89.9% of all extant species. For mammals, we used the phylogeny of Rolland, Condamine, Jiguet and Morlon (25) which is based on the trees compiled by Kuhn, Mooers and Givnish (26), Fritz, Bininda-Emonds and Purvis (27), and Bininda-Emonds, *et al.* (28). This phylogeny accounts for 92.2% of all known extant mammal species (25). We only included species present in these phylogenies in the biogeographic analyses.

We used the CladeByTrait function now included in SpeciesGeoCoder v2 to extract predominantly Neotropical clades from the original phylogenies retrieved. This was necessary to limit the results to the study region and to exclude potential dispersal events from other regions outside the Neotropics. We defined the study clades to a minimum size of 9 species and a maximum size of 100 species (larger clades might have reduced the sample size of our dispersal models). We applied a monophyly threshold of 0.15, meaning that at least 85% of the species in the clade needed to occur within the study region. A summary of the number of species included in different steps of this analytical pipeline is provided in Table S9.

Dispersal events through time. Here we use the terms ‘migration’ and ‘dispersal’ interchangeably in a biogeographic context, meaning long-lasting establishment in a new region rather than e.g. annual bird migrations. We do not attempt to differentiate between vicariance and long-distance dispersal events, since this is notoriously difficult, and our goal here is to estimate when lineages entered different regions regardless of the underlying process.

We relied on the dispersal-extinction-cladogenesis (DEC) model (29) implemented in the R-package BioGeoBEARS (30) for inferring geographic range evolution of lineages. Although BioGeoBEARS allows the use of an extra parameter (“j”) for jump dispersal events at nodes, we considered the original DEC model to be more suitable for the predominantly

continental settings of the Neotropics. We developed two sets of analyses: one in which biotic connectivity among all regions was allowed at any point in time, and one in which we modelled connectivity based on current paleogeographic and geological evidence on the existence, position, and extent of each region (Table S3). We consider these two sets of analyses complementary: the unconstrained model carries fewer assumptions, thus decreasing the risk of manually influencing the results; while the time-stratified model takes into account the fact that some regions were not always available for migrating lineages at all times.

Analyses were run on all Neotropical clades identified to reconstruct shifts between regions in 5-million-year time bins; finer intervals would have increased precision but reduced power. To define a dispersal event between any pair of regions, we extracted the state with the highest log-likelihood at the beginning and end of each branch. Since we did not impose any particular order of dispersal routes, our methodology should avoid counting dispersal events ‘passing through’, but not remaining in intermediate regions. Widespread ancestral reconstructions and extant distributions were also included in the calculations.

We computed the absolute number of dispersal events through time by extracting the regions and ages of all nodes from each phylogeny. The number of branches and total amount of branch lengths in any phylogeny of extant species increase with time, potentially increasing the number of dispersal events towards the present even under a constant dispersal rate (31). We therefore also calculated relative numbers of dispersal events by dividing absolute numbers by the total length of all branches within each time bin (32, 33).

Dispersal events between regions could involve shifts in major biome types, shifts into another region within the same biome type, or both. We made an approximate estimation of each scenario by first classifying all regions in our biogeographic analyses into three major categories of biomes: ‘Open/Dry’, ‘Forested/Wet’, or ‘Mixed’ (Fig. 1, see color legend). We then scored all dispersal events between each pair of regions as either involving *shifts in region and major biome type* (between ‘Open/Dry’ and ‘Forested/Wet’ or vice-versa), or *region-only shifts* (staying within ‘Open/Dry’ or within ‘Forested/Wet’ biomes). Since we could not confidently determine the nature of shifts into or out of the ‘Mixed’ regions, we coded those as *ambiguous*. The dispersal categorizations are provided in Table S6.

Predictors of emigration and immigration. We tested the dependence of the number of dispersal events estimated for each region on six predictor variables related to biotic and abiotic features of the regions defined, as well as on phylogenetic sampling intensity. As abiotic predictors, we included current area and perimeter (calculated from the region’s polygons), and current

geographic isolation (calculated as median distance of the region's centroid to all other centroids). As biotic predictors, we calculated the total time that lineages spent in each region. This was estimated as the total branch length per region, using stochastic character mapping {Huelsenbeck, 2003 #3405} for each phylogeny in each region, based on the transition matrix with dispersal and extinction rates as estimated by BioBeoBEARS (30). To evaluate the possible effect of sampling biases, we also computed the total number of occurrence records per region, and computed a proxy for phylogenetic sampling by calculating the fraction of species sampled out of all species occurring in a region included in our analyses. This total species richness was approximated by the total number of species in the cleaned GBIF datasets. We transformed the response and all predictor variables using a log transformation ($\log(x+1)$) for constant residual variance and scaled all predictors to zero mean and zero variance for comparability among coefficients.

We tested the covariance of the predictors using the Variance Inflation Factor and Pearson correlations. The number of occurrence records and the total branch time were highly correlated (Pearson correlation = 0.8; Table S10), and we thus only used one of them in the models (branch lengths, since we considered them more biologically relevant). We fit two linear mixed-effect models in a Bayesian framework (one for emigration and one for immigration) using the INLA (34, 35) library in R. We excluded data from the two taxa with the fewest species sampled (ferns and frogs) as the number of dispersal events was zero for several regions in these clades. We evaluated the models visually by assessing constant residual variance and residual-predictor dependence. We used the default priors as recommended by Zuur, *et al.* (36), corresponding to a normal distribution ($\mu = 0$, $\sigma = 31.62$) for the fixed effects, and a LogGamma distribution for the log precision ($a = 1$, $b = 5e-6$) of the random intercepts and the residuals.

Limitations of the data and approach

Biases and errors. Recent work has shown that natural history collections, databases of species occurrences, and molecular sequences are prone to spatial and temporal biases and errors (37, 38). These issues are also evident for the Neotropics, with several regions considerably less sampled than others, such as the Caatinga in Brazil, which is much less sampled in proportion to its area than some parts of Mesoamerica (Fig. S1, Table S1). In general, phylogenetic under-sampling should lead to a reduced representation in the measurements of biotic interchange. This effect should be most pronounced if species were randomly distributed across the Neotropics. However, several plant and animal subclades within the major clades analyzed are confined to particular biomes or regions, and in those cases the inclusion of a single clade

representative might allow a correct estimation of the direction and number of dispersal events to that region, while a correct timing would demand denser sampling.

Our explicit incorporation of phylogenetic sampling aimed at directly assessing the impact of sampling in our analysis. We found no significant correlation between the number of dispersal events and phylogenetic sampling in the general model that included all regions and modelled clades (Fig. S18), but taking each clade separately we did find strong correlations (Figs. S14, S17). A similar result was obtained for the relation between total branch lengths and phylogenetic sampling, with no correlation in the general analysis but clade-specific correlations (Fig. S15); as well as between the number of occurrence records in each region and phylogenetic sampling, with an overall negative relation but clade-specific variation, from positive to neutral trends (Fig. S16). These results indicate that while the general results do not seem primarily controlled by sampling, we cannot exclude sampling biases at the level of individual clades and regions, and general biases beyond what our models could detect. Qualitatively, the overall congruence in the dispersal patterns obtained for well-sampled *vs* low-sampled clades (e.g., birds and mammals, as compared to angiosperms) suggests that uneven phylogenetic sampling is unlikely to alter the main conclusions of this study. Further sampling across the Neotropics will be crucial to further refine the results presented here.

In terms of errors (such as erroneous geo-referencing or identification), the various automated data verification and cleaning steps performed here do not replace manual verification by specialists, but our previous empirical evaluations show that they should have led to substantial improvements in data quality for the spatial scale of our analyses (16, 39).

Spatial scale. We could have chosen to perform our analyses on finer, more ecologically relevant units such as ecoregions (40) or vegetation types such as pockets of gallery forest within the Cerrado (41). However, this would lead to additional problems in terms of phylogenetic sampling (which would be very low for smaller regions, such as the Chocó, and patches of savanna scattered across Amazonian and Mesoamerican rainforests); accurate geographic coding (due for instance to the lack of precision in many species records, and unclear or complex limits between regions); and biogeographic analyses (since the DEC model used here is unable to handle a high number of regions in the geographic range evolution analyses). We expect our relatively coarse region delimitations to retain accuracy but decrease in precision as compared to a more fine-scale analysis. In addition, our delimitations preclude us from a definite differentiation between dispersal events involving shifts in major biome types from those remaining within a similar biome type, implying that our quantification of those

variables require further exploration with finer-scale data. This is particularly clear for dispersal events involving Mesoamerica and the West Indies, which comprise mosaics of different habitats and biomes, in relatively small areas. For instance, a lineage in the Andean Grasslands that disperses into Mesoamerica may remain confined to the Páramos of Panama and Costa Rica, while an Amazonian lineage may instead colonize the lowland rainforests of these countries, but none of these outcomes can be currently tested with our region classification.

Biome evolution. Our attempt to model the evolution and connectivity of Neotropical biomes through time should be seen as provisional and subject to improvements. Although there have been large changes in the areas of tropical biomes over time (42, 43), there are also large uncertainties of how to accurately infer the history and diversity of past ecosystems in general (44), and Neotropical biomes in particular (45). Since the major patterns reported here are similar between the unconstrained and the time-constrained biogeographic analyses, we do not expect these results to change at any significant degree even if ages of the regions analyzed, or their connectivity patterns, were to change moderately.

Extinction. Taxonomically and spatially uneven species extinctions could influence the inferred dynamics of regional sources and sinks of lineages, especially among large terrestrial mammals and birds, as well as in insular habitats such as the West Indies (46). However, the congruence in patterns of regional interchange across the six major clades analyzed indicates that differences in recent extinction across groups have not influenced the overall results.

Phylogenetic uncertainty. Although it would have been desirable to perform similar biogeographic reconstructions on tree samples rather than single phylogenies to take into account topological and branch length heterogeneity, the complexity of the analytical steps performed here rendered this unfeasible. Given the large number of species analyzed, and the cross-taxonomic congruence in most results, we expect that ambiguities due to phylogenetic uncertainty are surpassed by biogeographic signal.

Overall approach. Large-scale analyses based on data mining have been criticized, in favor of carefully controlled studies focused on single clades (44). We argue that synthetic, ‘top-down’ approaches and fine-scale, ‘bottom-up’ studies are complementary, mutually beneficial, and crucial for better understanding evolutionary history across multiple temporal, spatial, and taxonomic scales. By performing separate analyses on multiple taxonomic groups with different

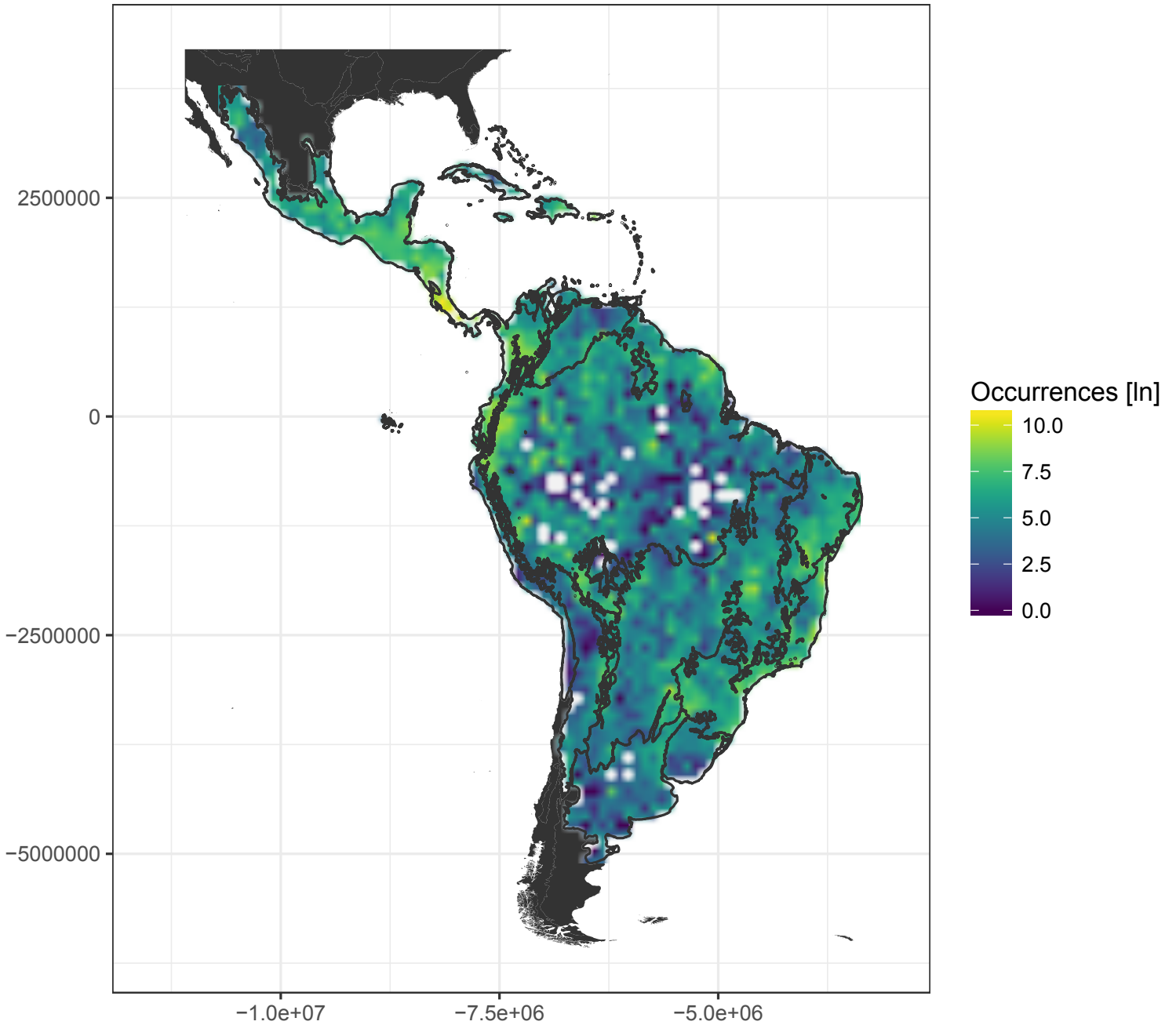
diversification rates and biogeographic histories, and using independent phylogenetic and distribution datasets, we are more likely to have taken into account clade heterogeneity, and obtained biologically realistic signals out of any underlying noise. Although further biological sampling in all Neotropical regions will be beneficial in many ways, these considerations suggest that our conclusions are not flawed by the data and methodology applied here.

Data availability

All original datasets of occurrence records are available through the DOIs provided in references 1–6 of this Supporting Information. The cleaned records used for the analyses, the resulting subclades pruned from the original phylogenies, as well as all analytical scripts based on these, are freely available from <https://doi.org/10.5281/zenodo.1149127>

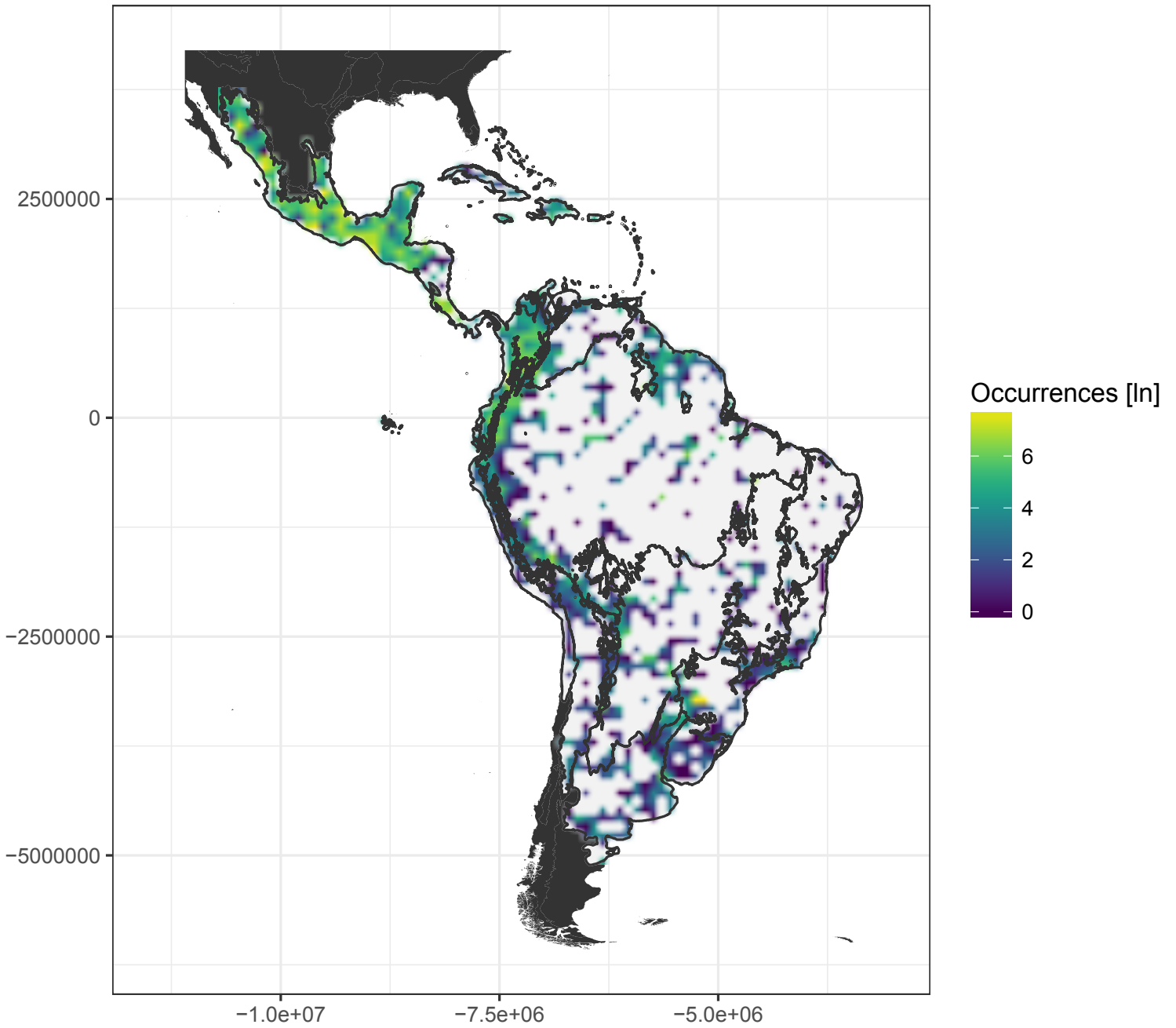
Angiosperms

Figure S1: Occurrence records per grid cell



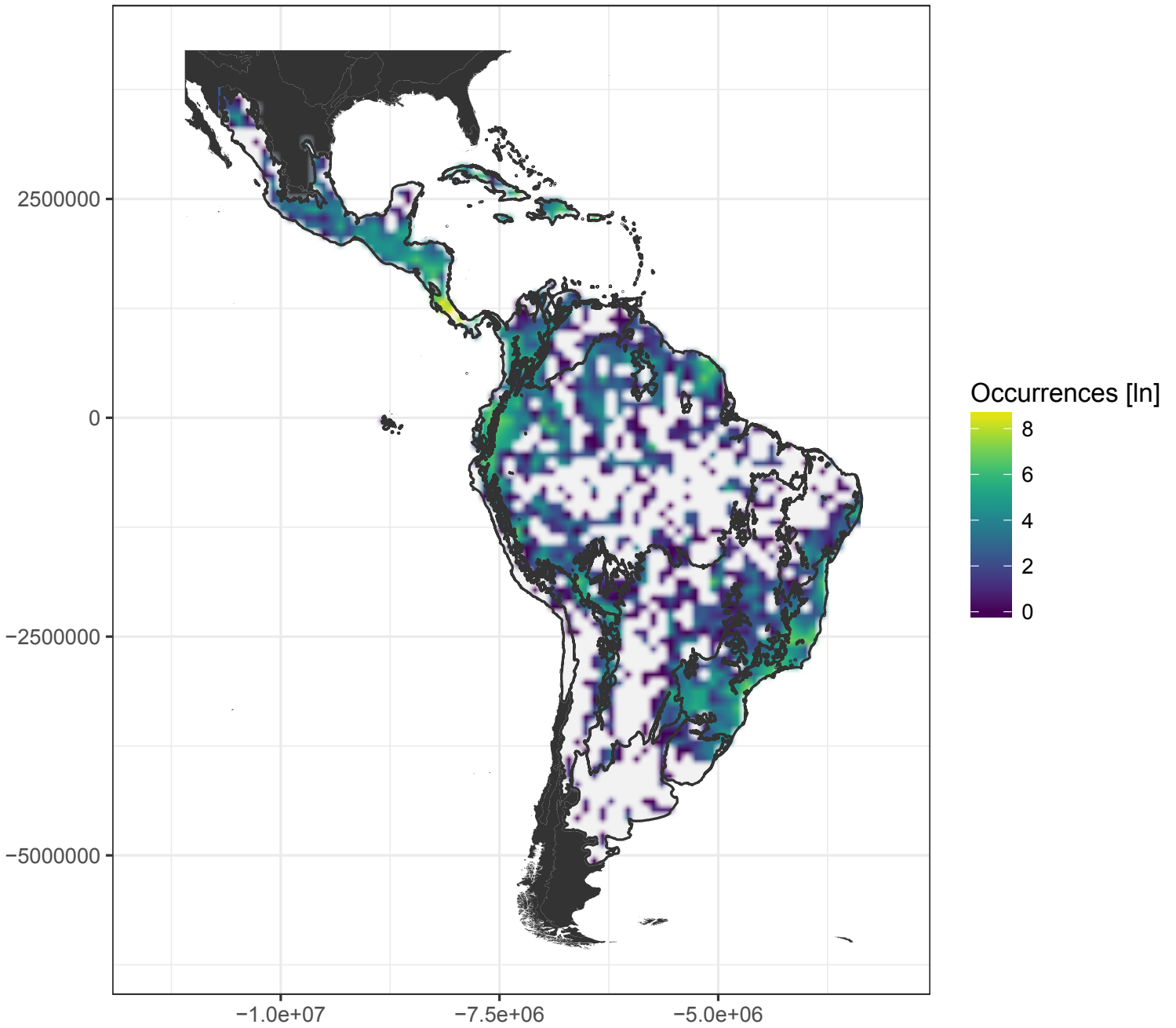
Birds

Figure S1: Occurrence records per grid cell



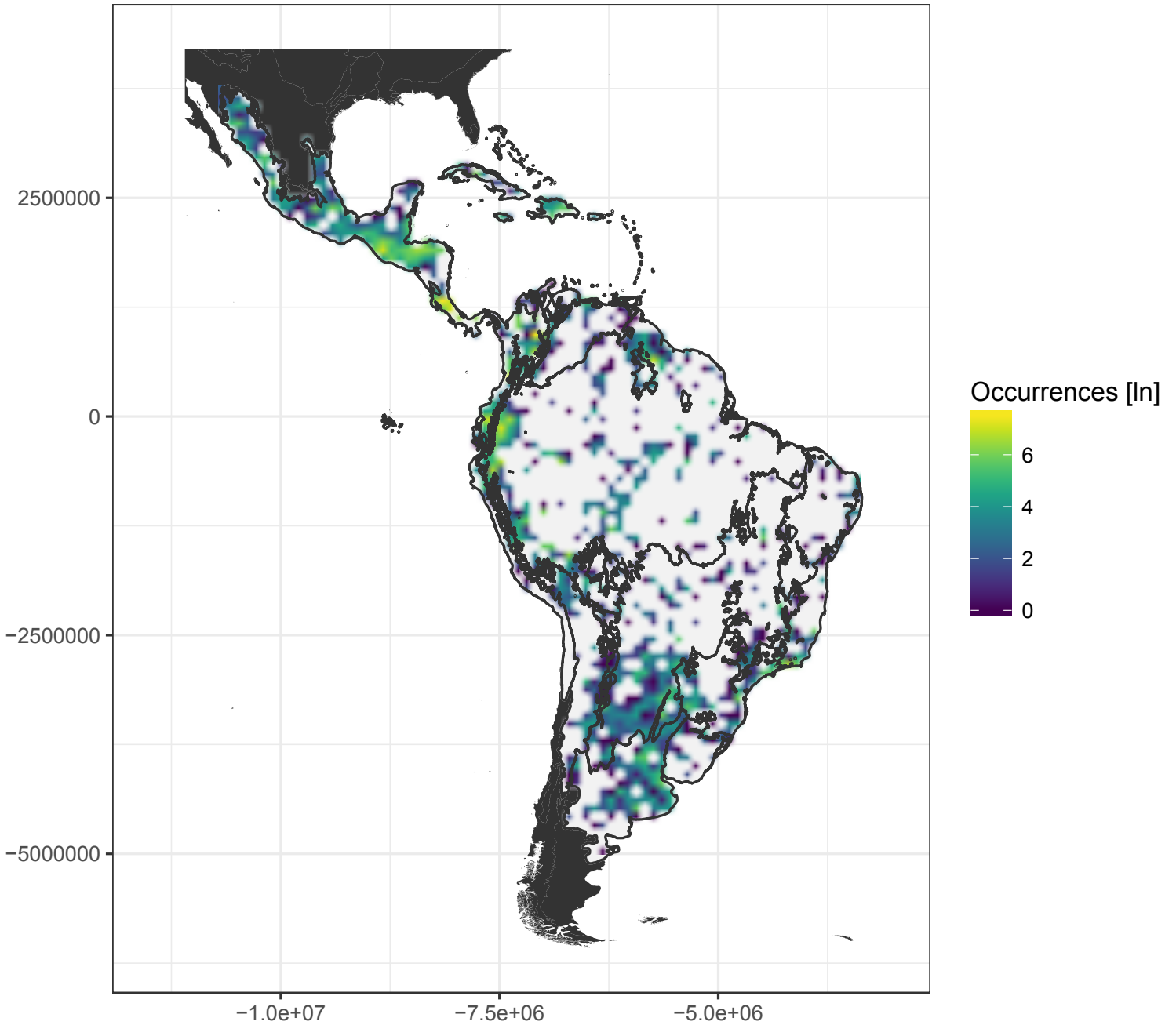
Ferns

Figure S1: Occurrence records per grid cell



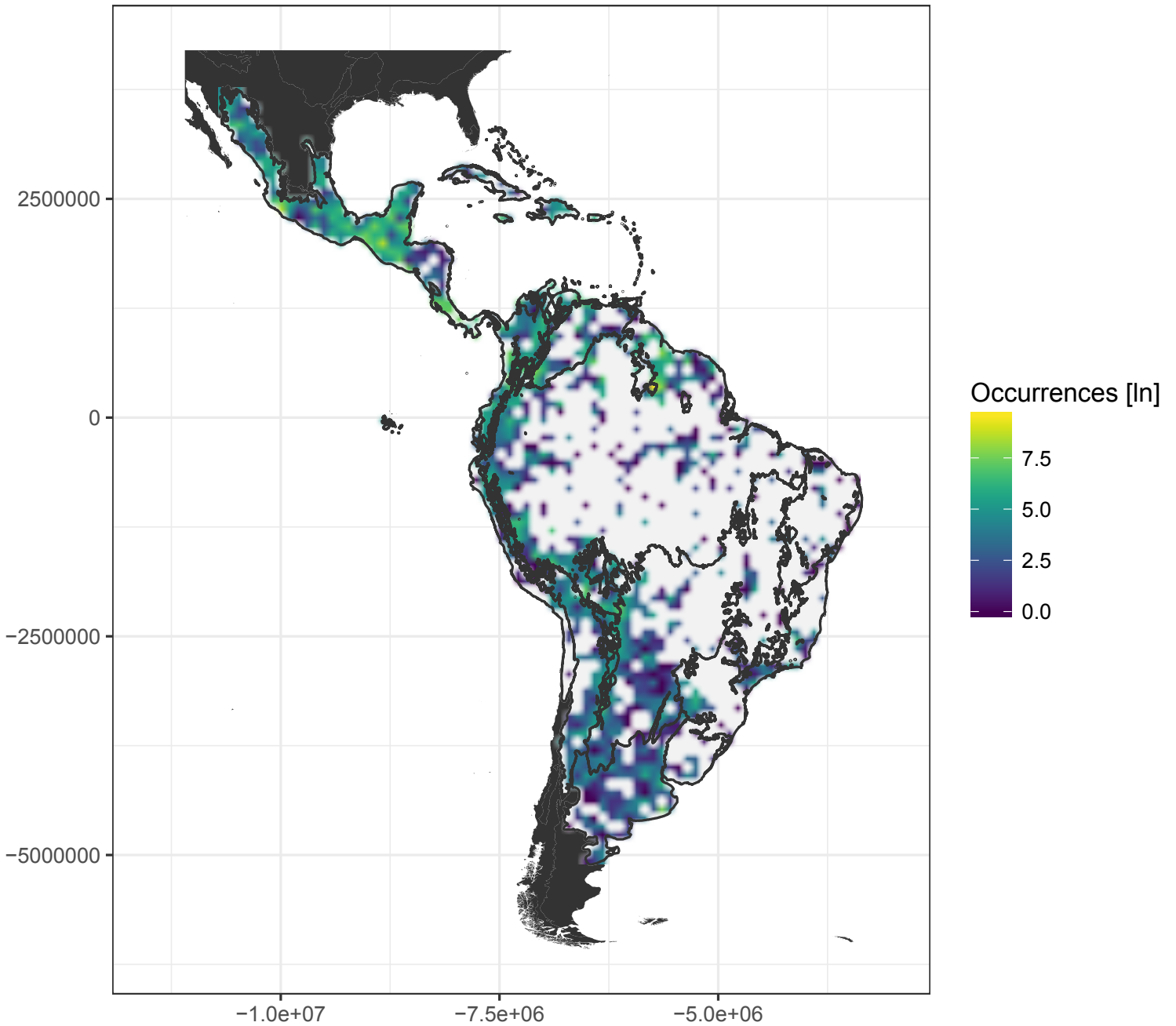
Frogs

Figure S1: Occurrence records per grid cell



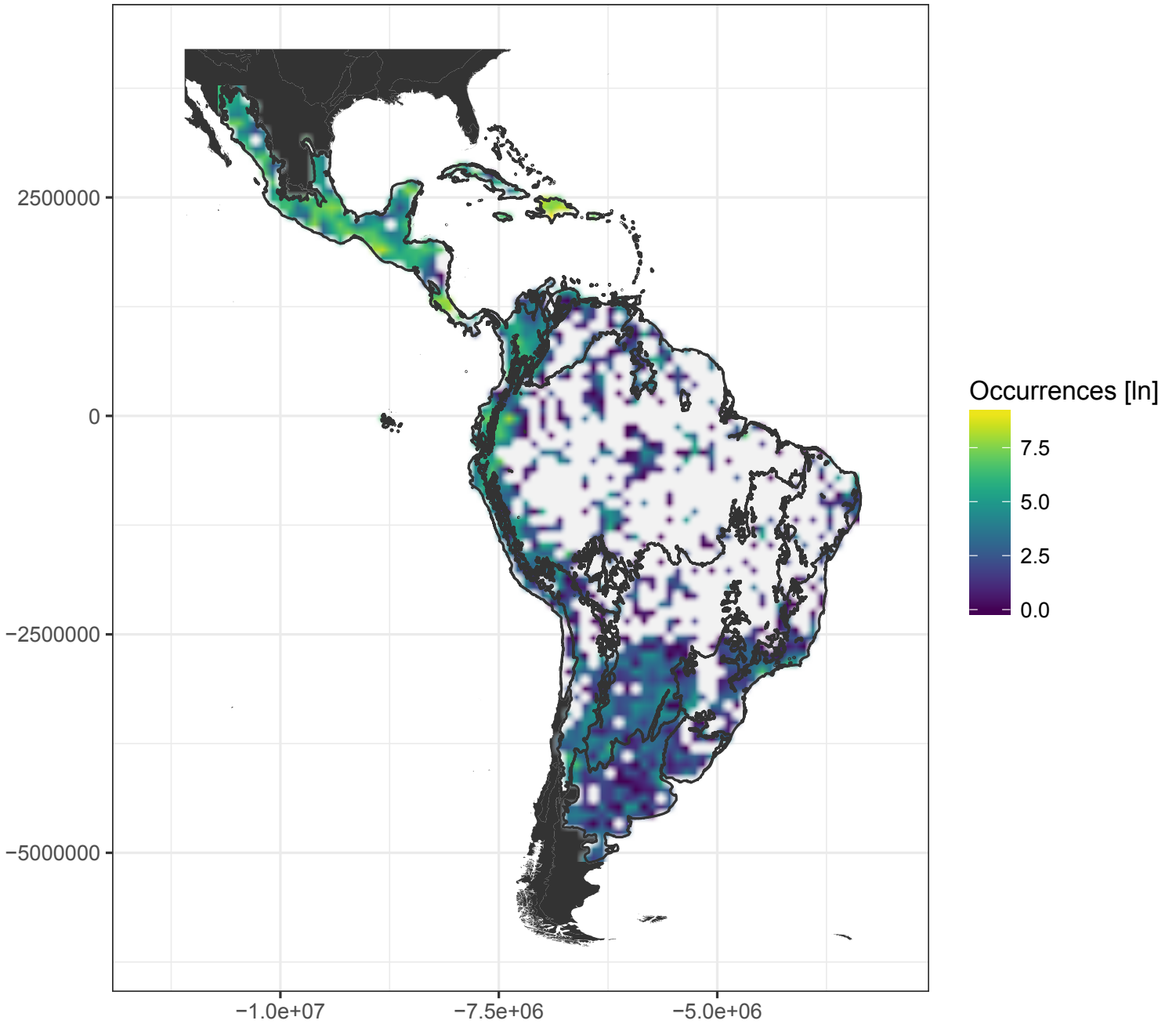
Mammals

Figure S1: Occurrence records per grid cell



Squamates

Figure S1: Occurrence records per grid cell



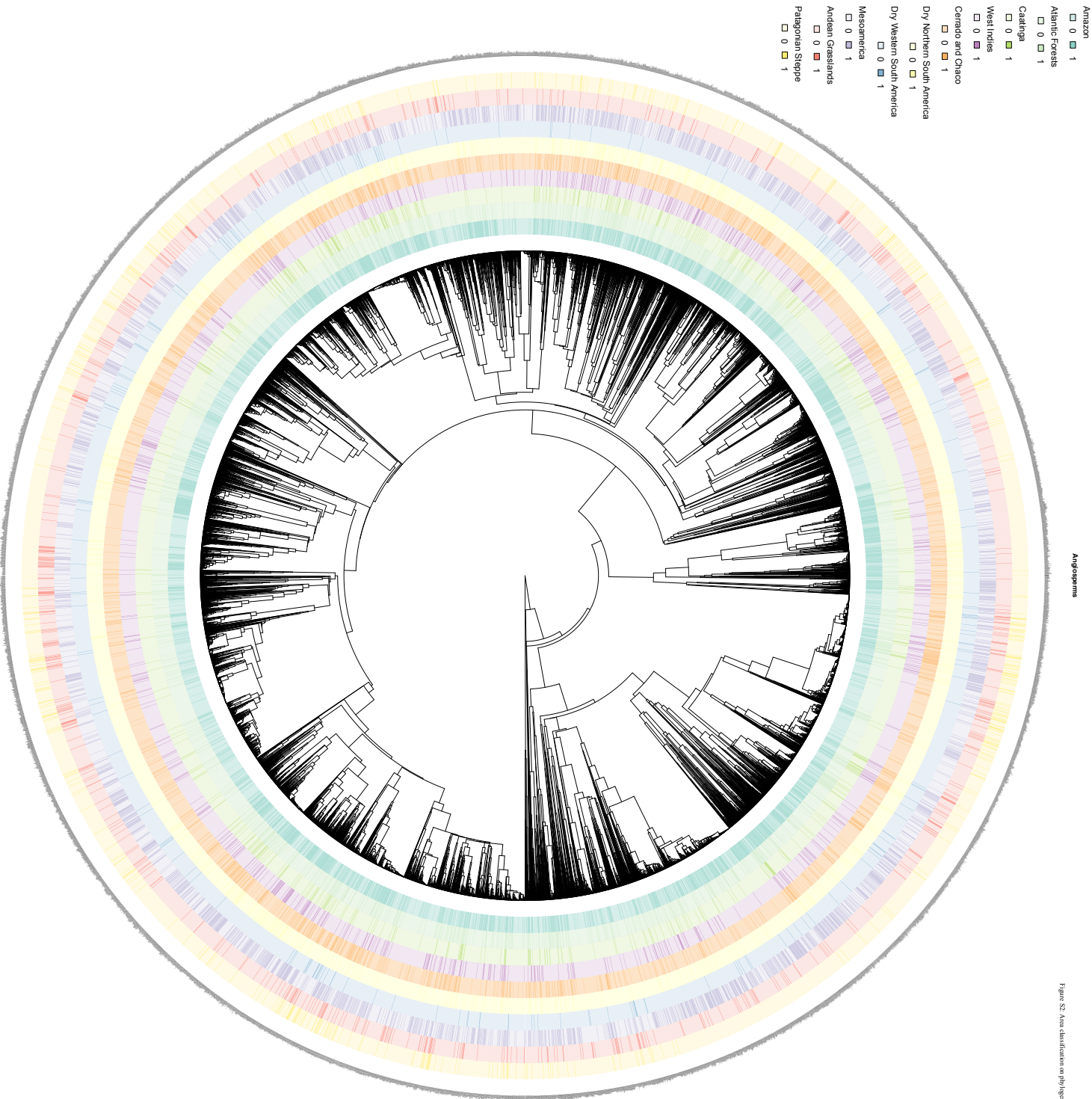
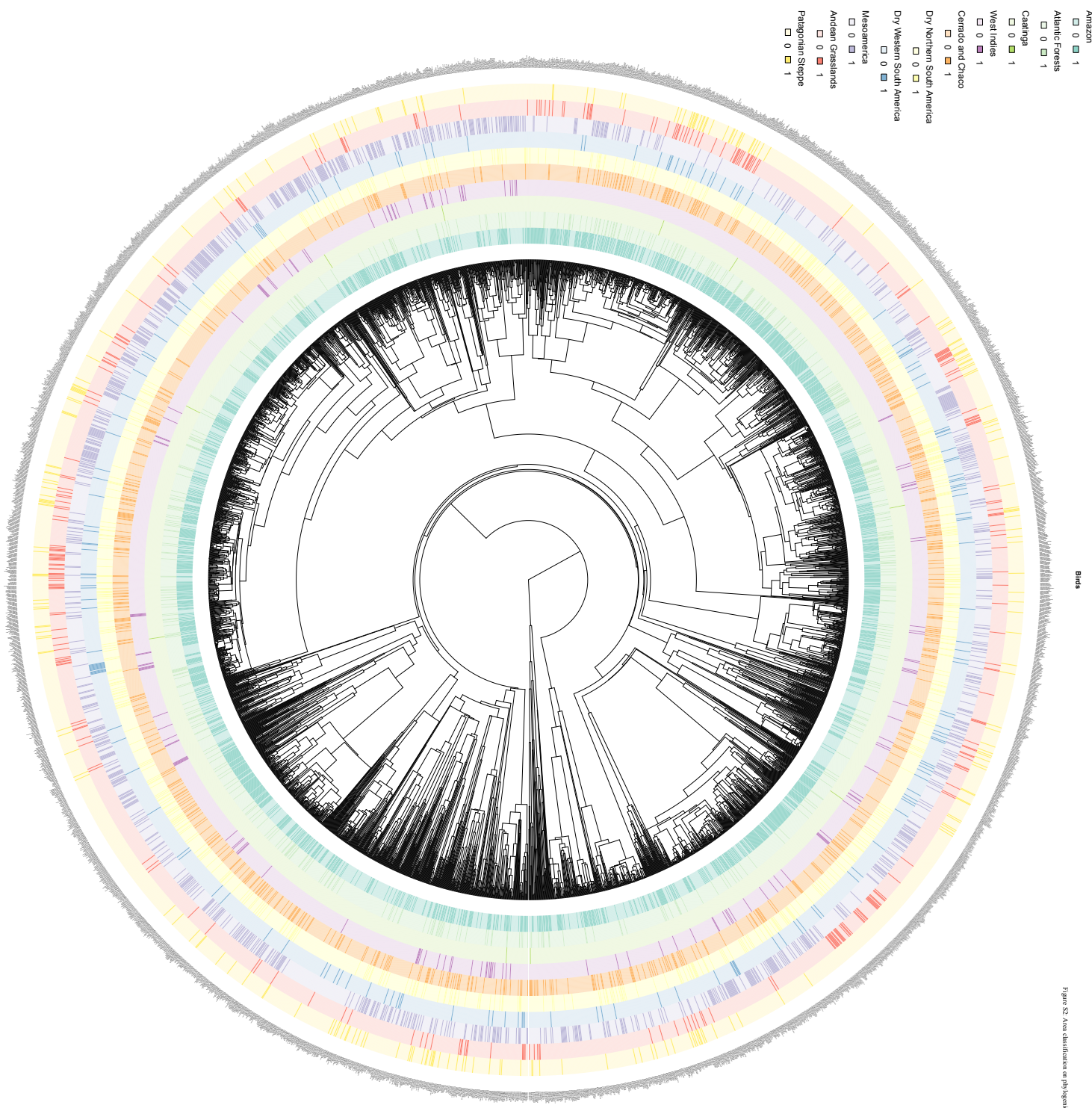
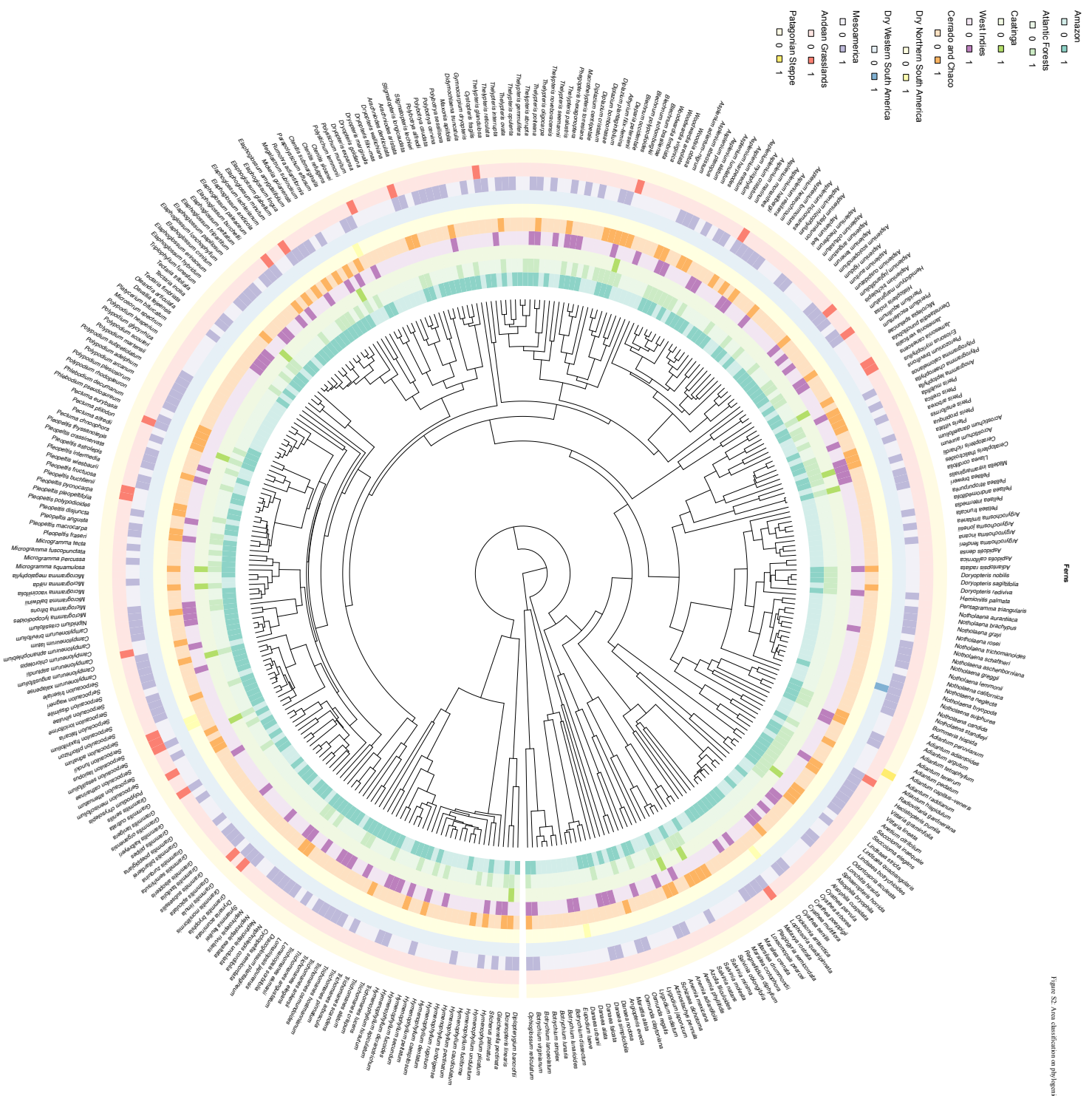


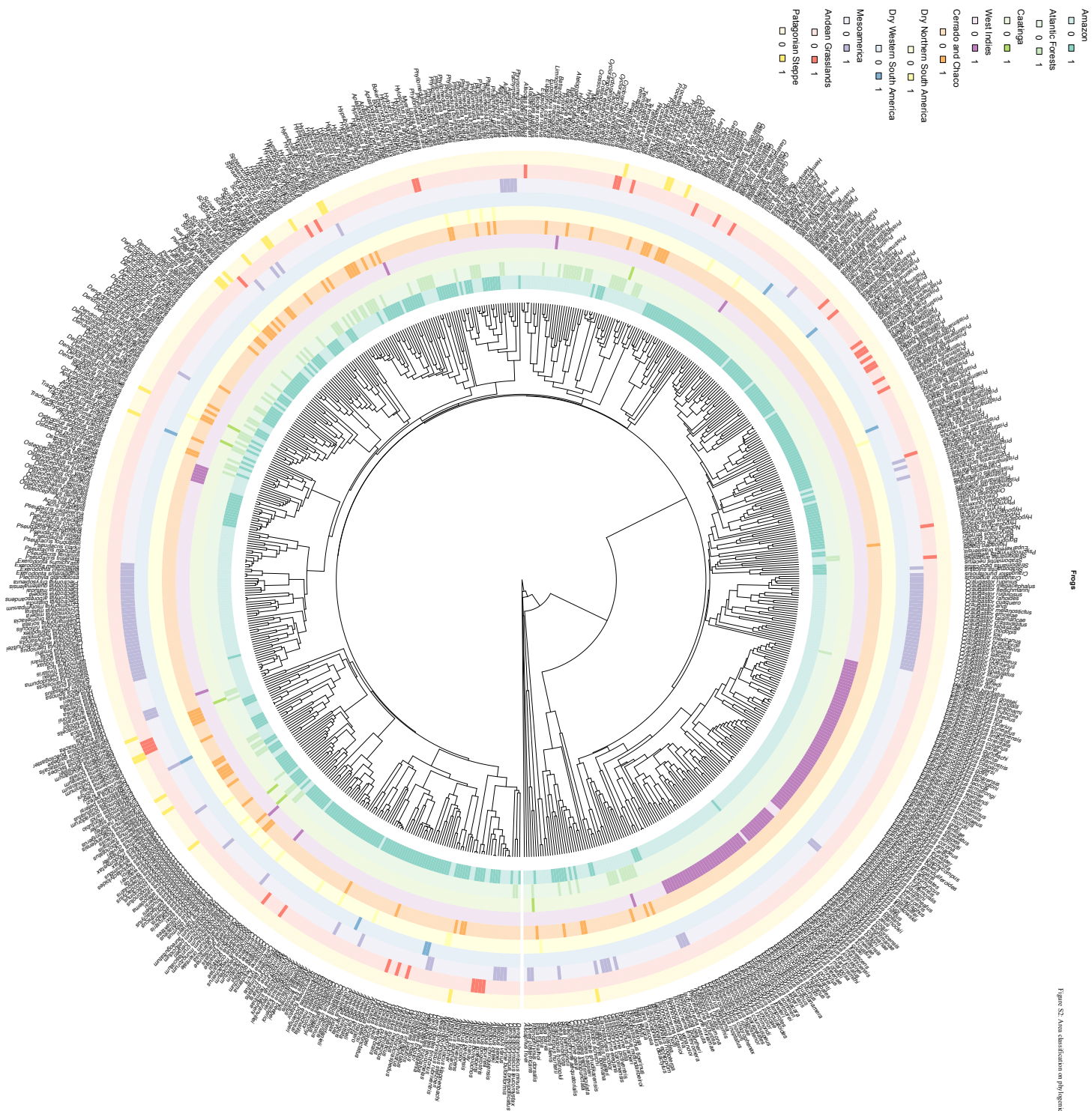
Figure S1. Area identification on phylogenies





Ferns

Figure S5. Area distribution on phylogenies



Phylo

Figure S2. Area classification on phylogenies

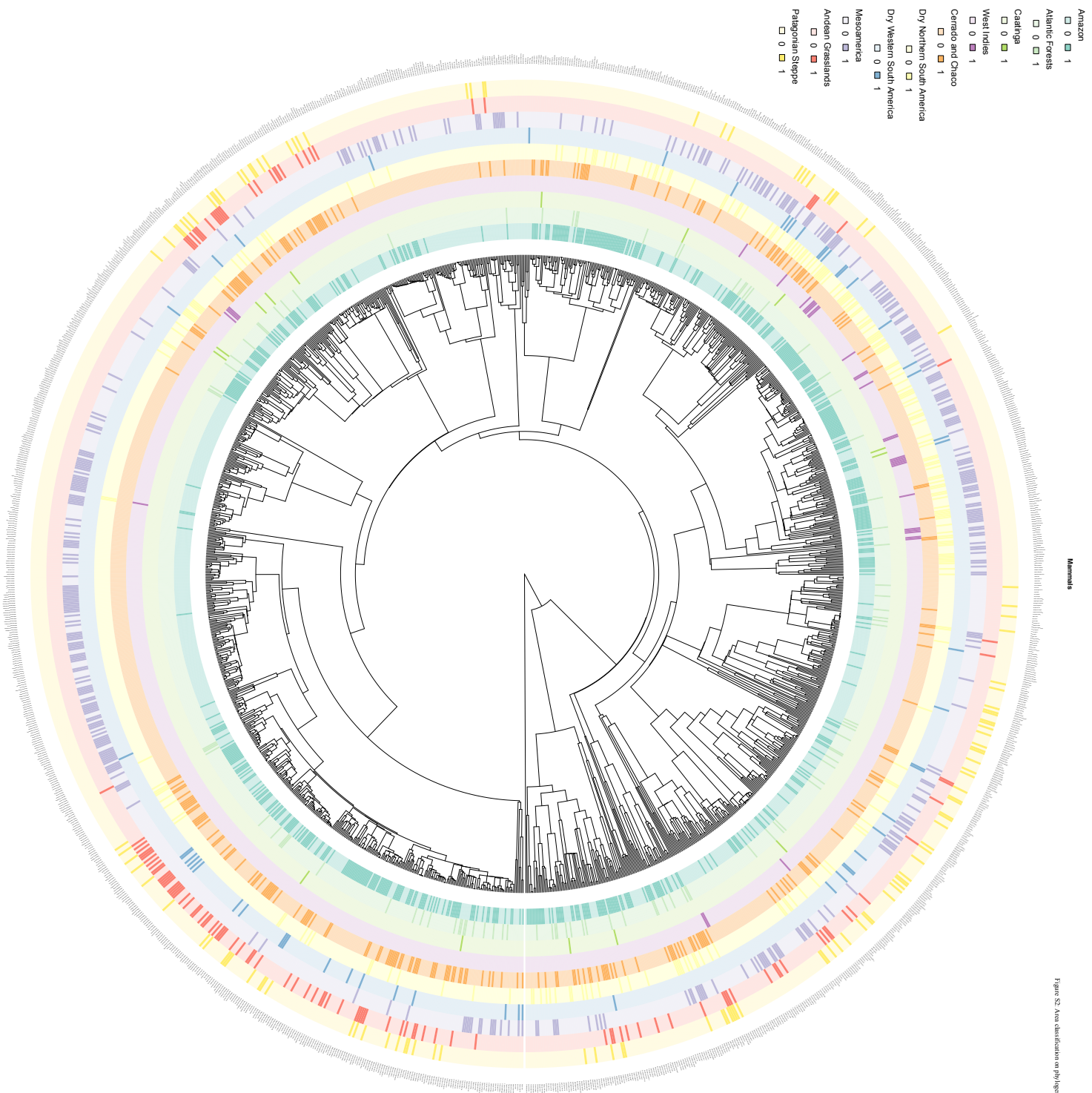


Figure S2. Area classification on phylogenies

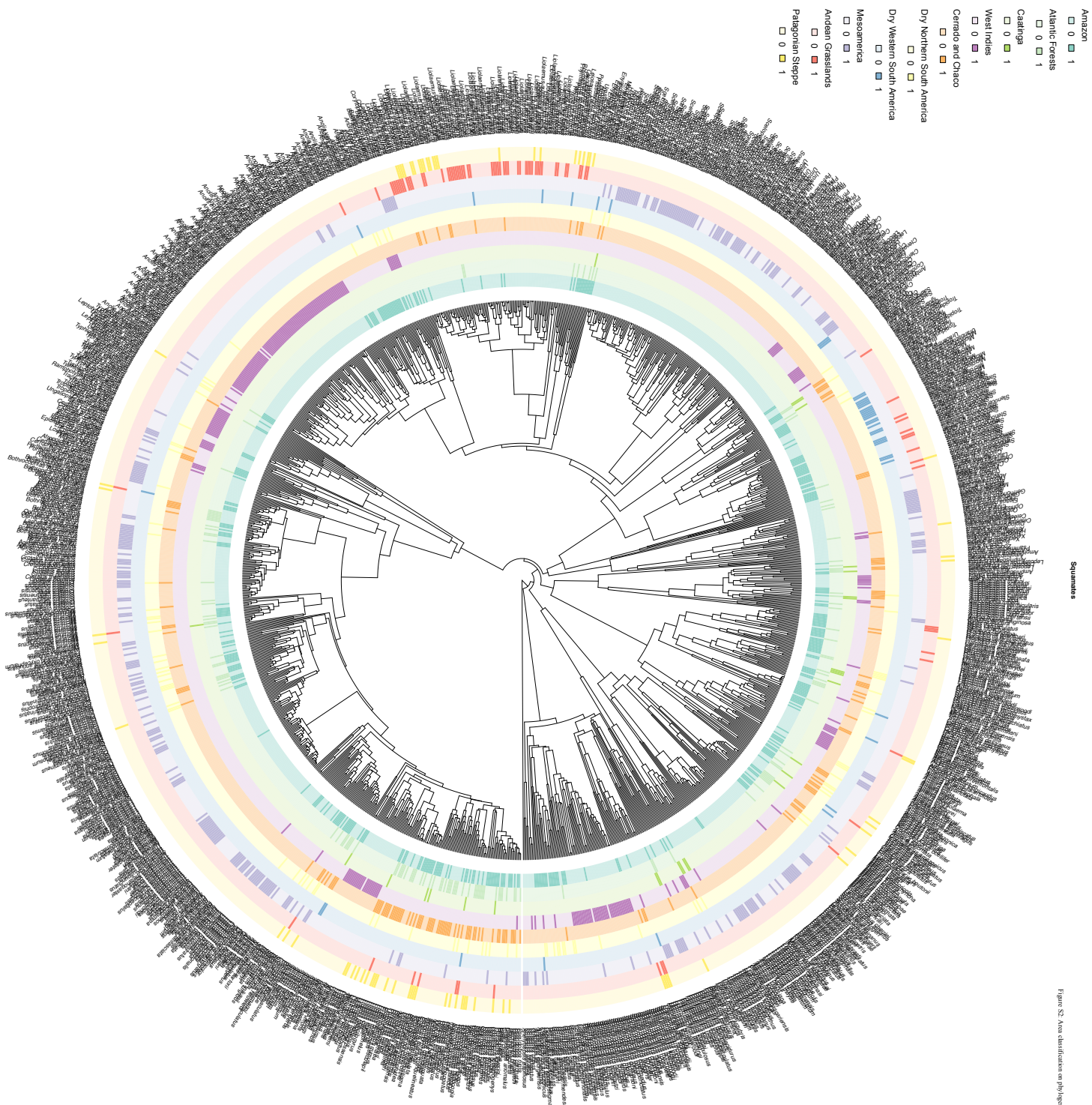


Figure S3: Clades of angiosperms

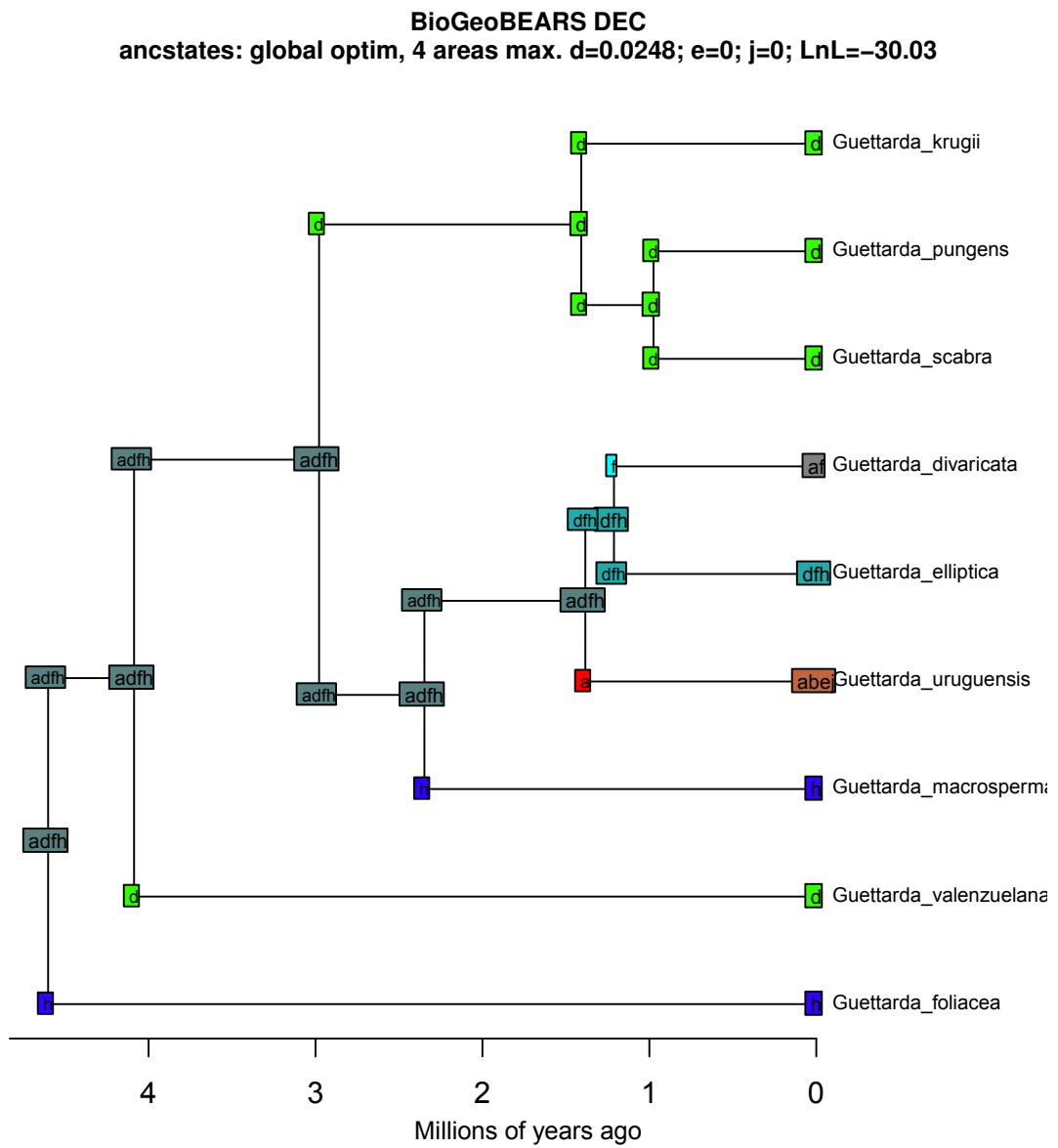


Figure S3: Clades of angiosperms

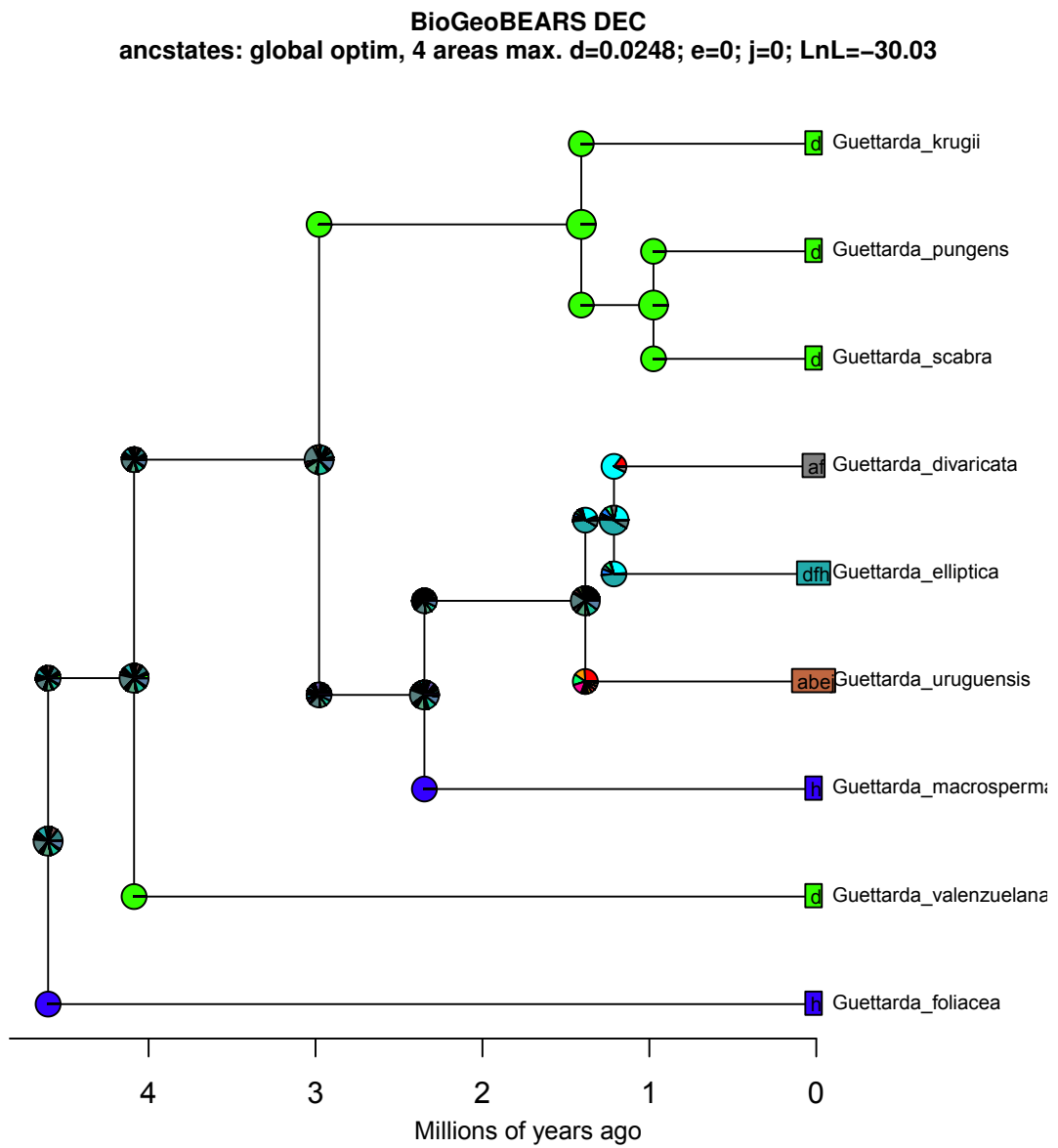


Figure S3: Clades of angiosperms

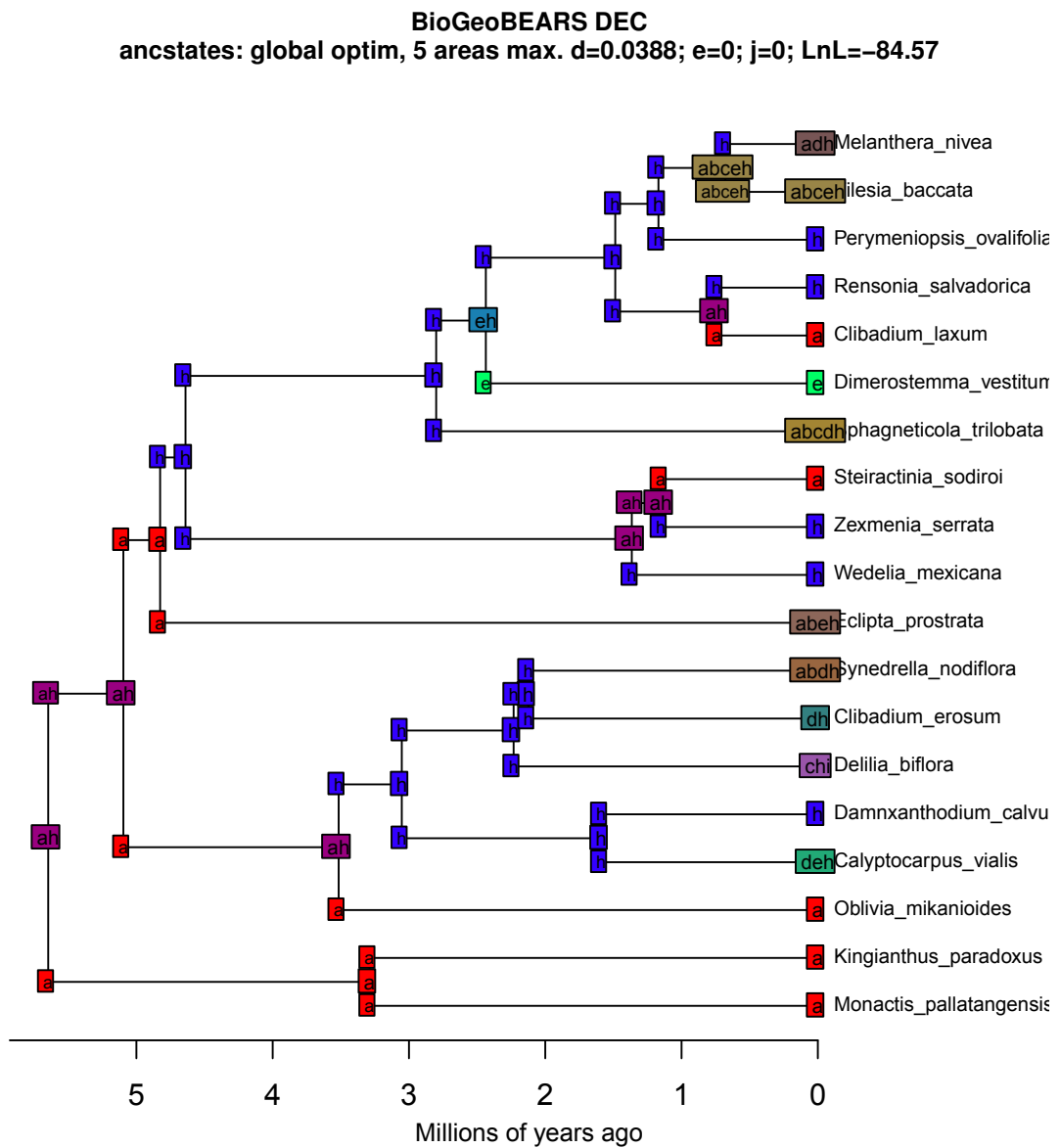


Figure S3: Clades of angiosperms

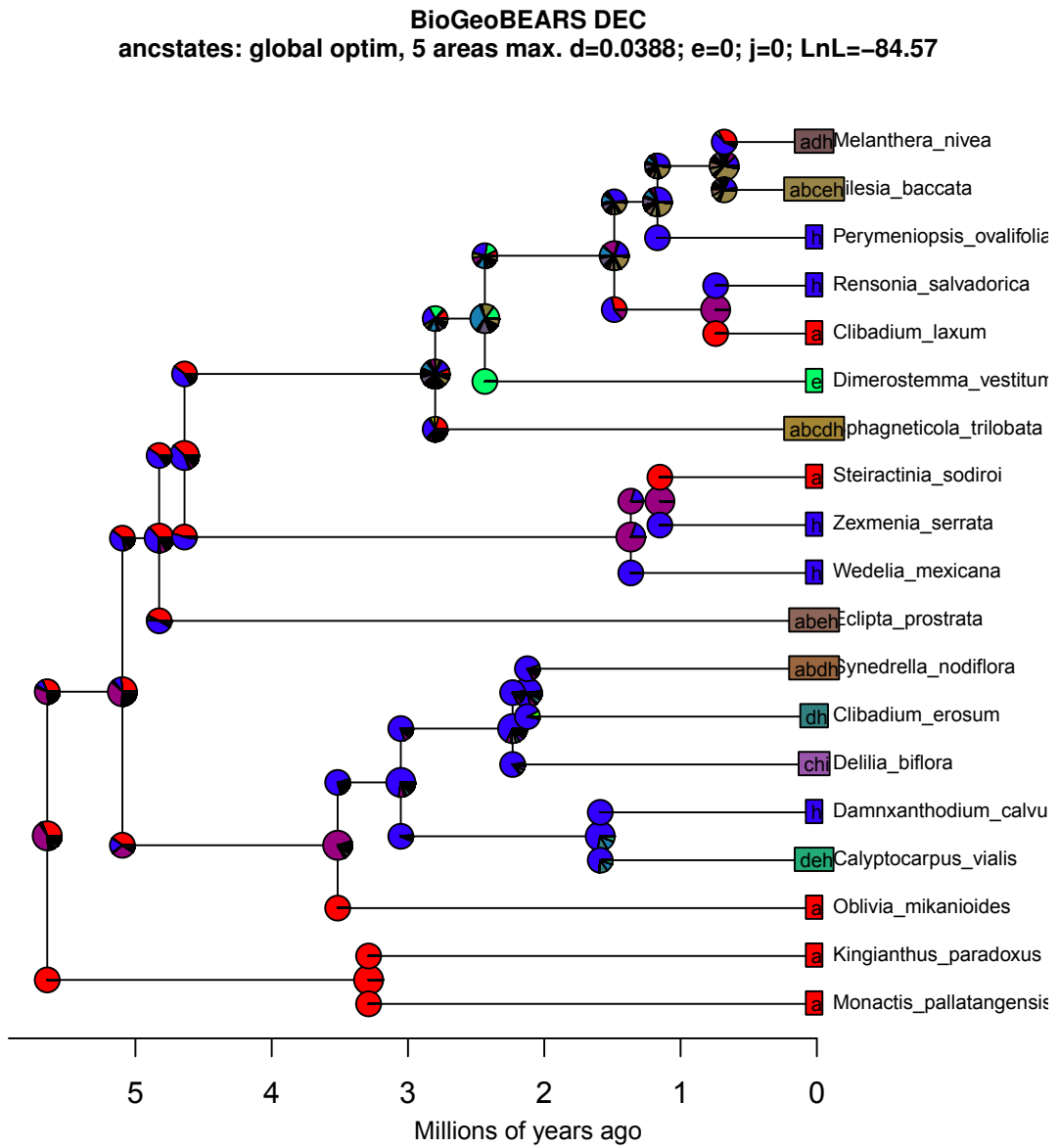


Figure S3: Clades of angiosperms

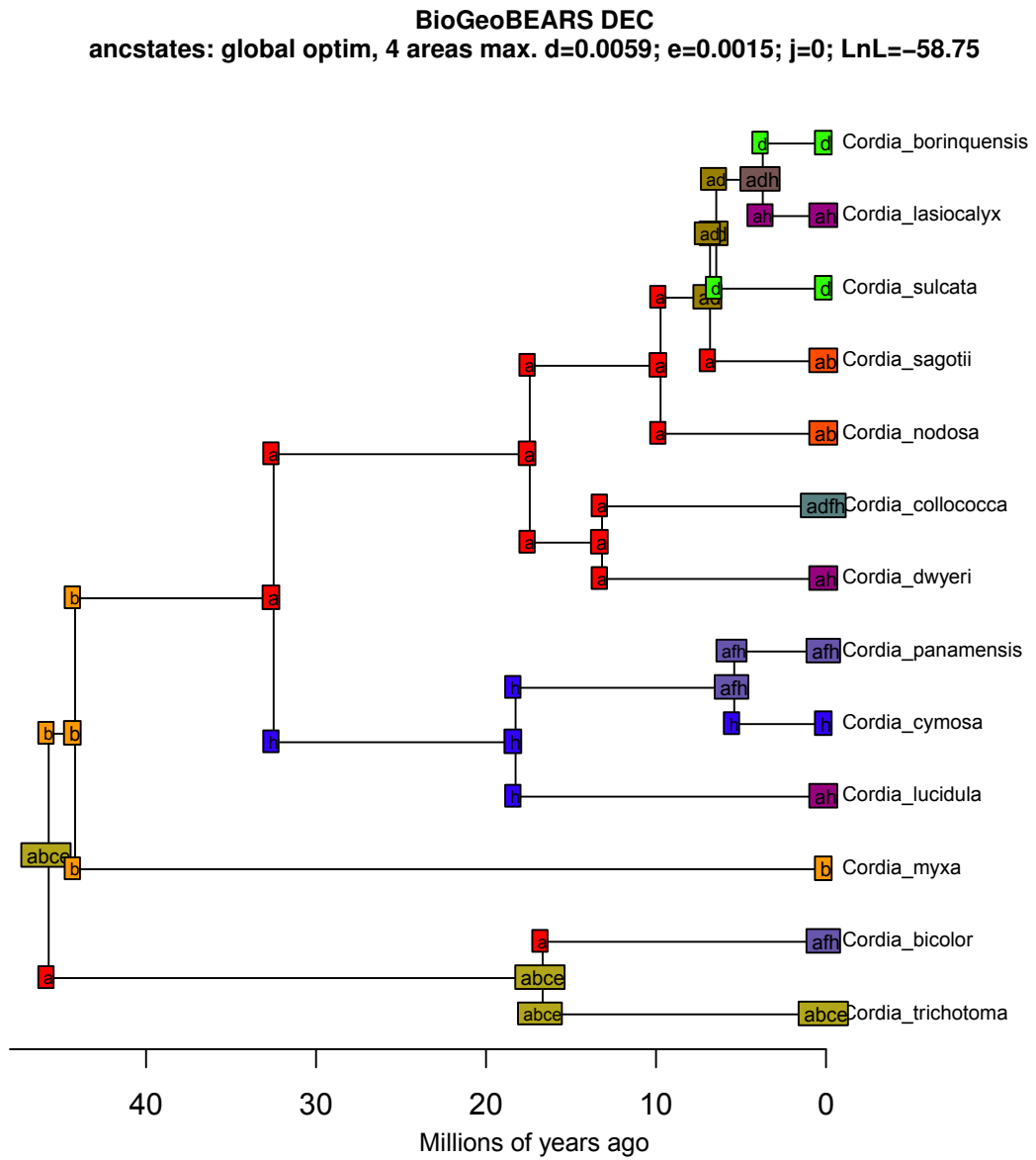


Figure S3: Clades of angiosperms

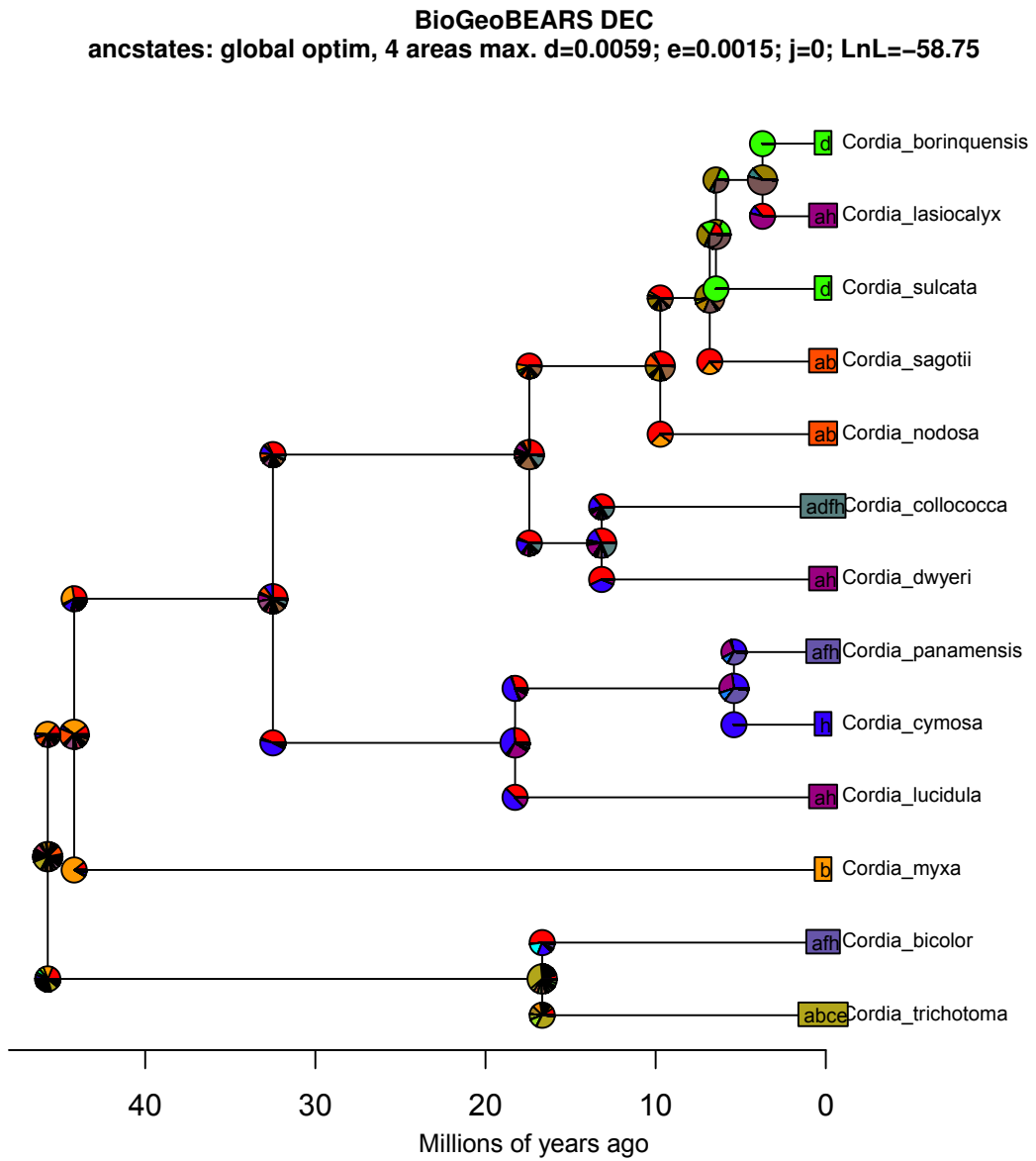


Figure S3: Clades of angiosperms

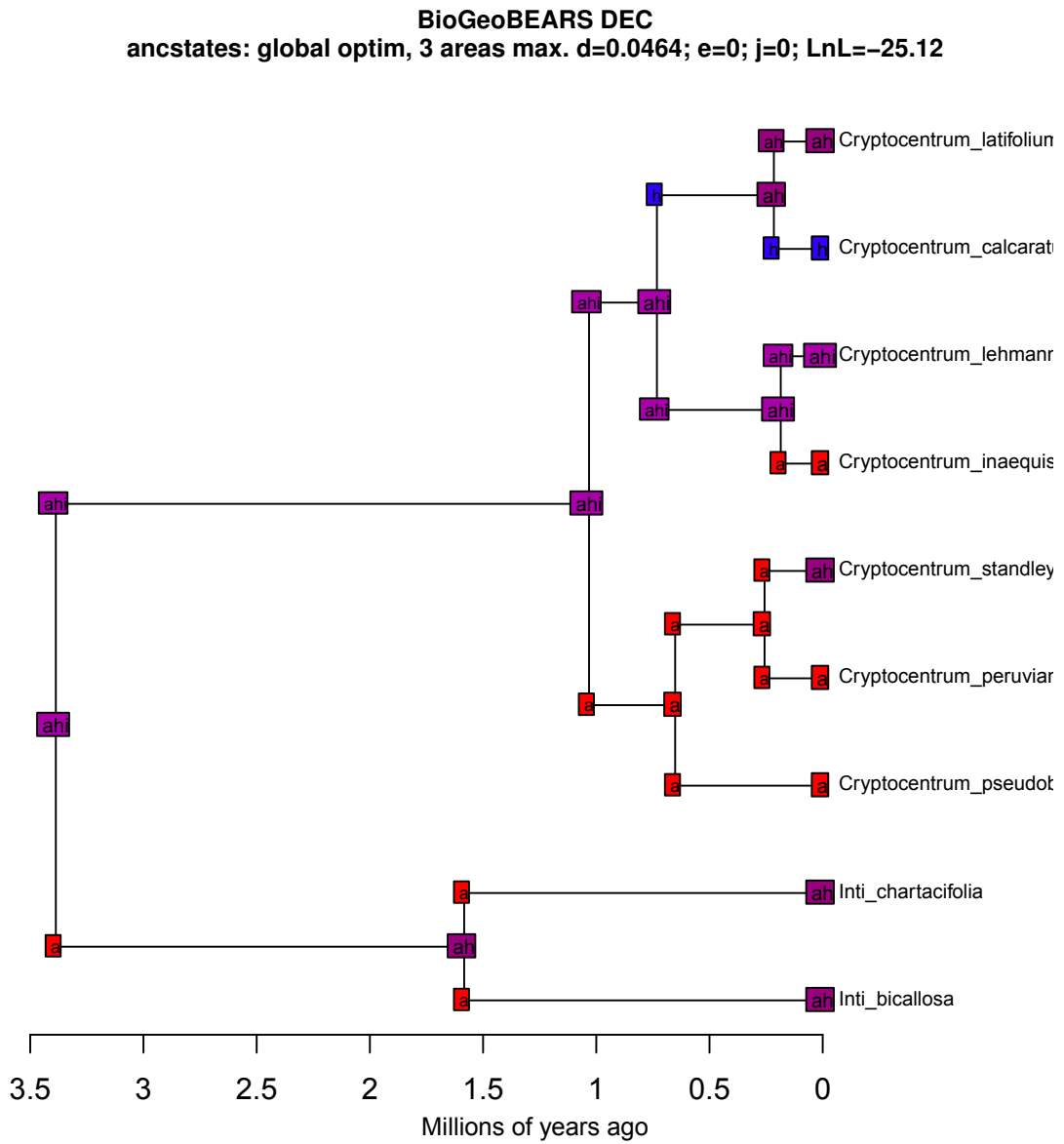


Figure S3: Clades of angiosperms

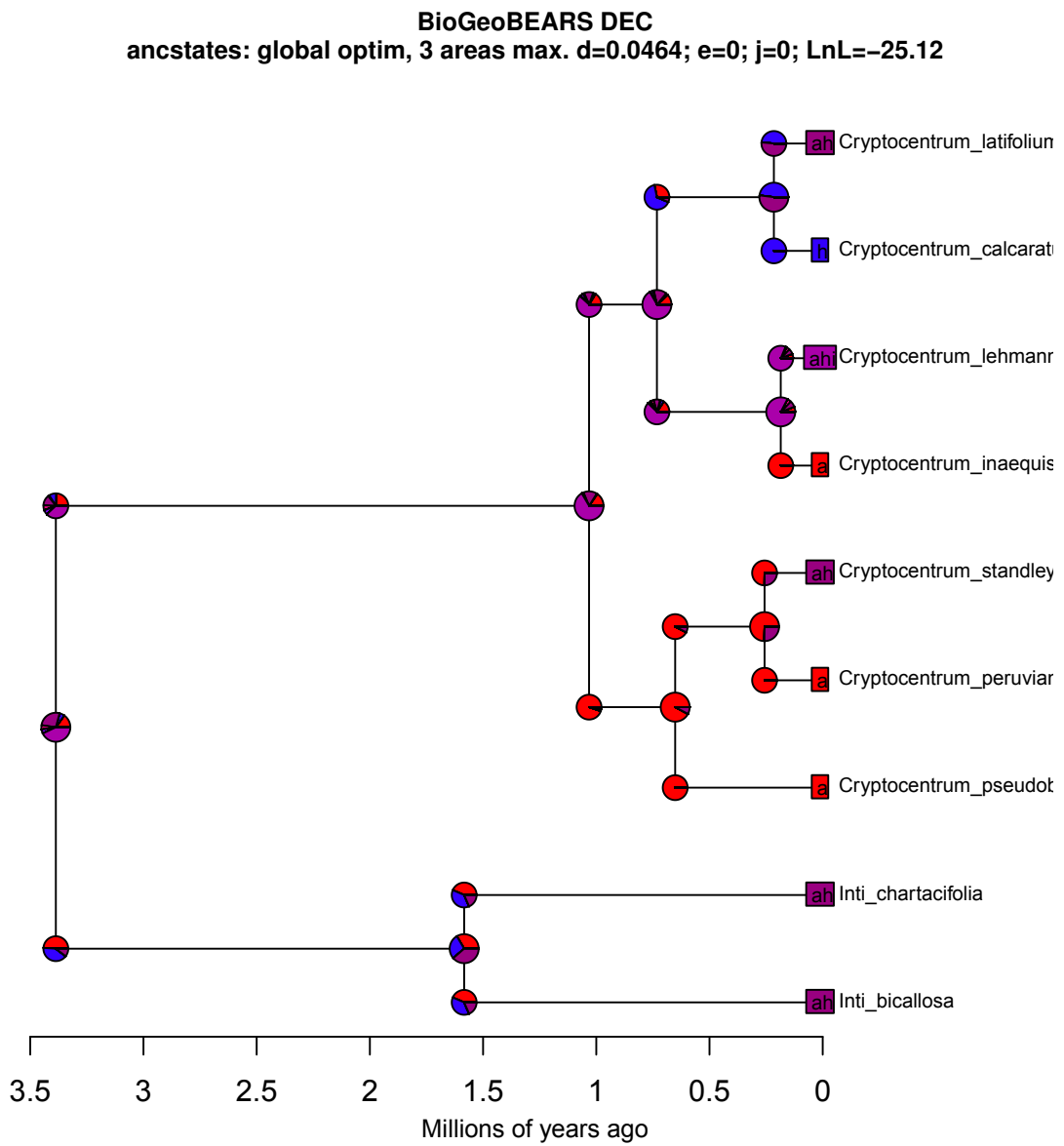


Figure S3: Clades of angiosperms

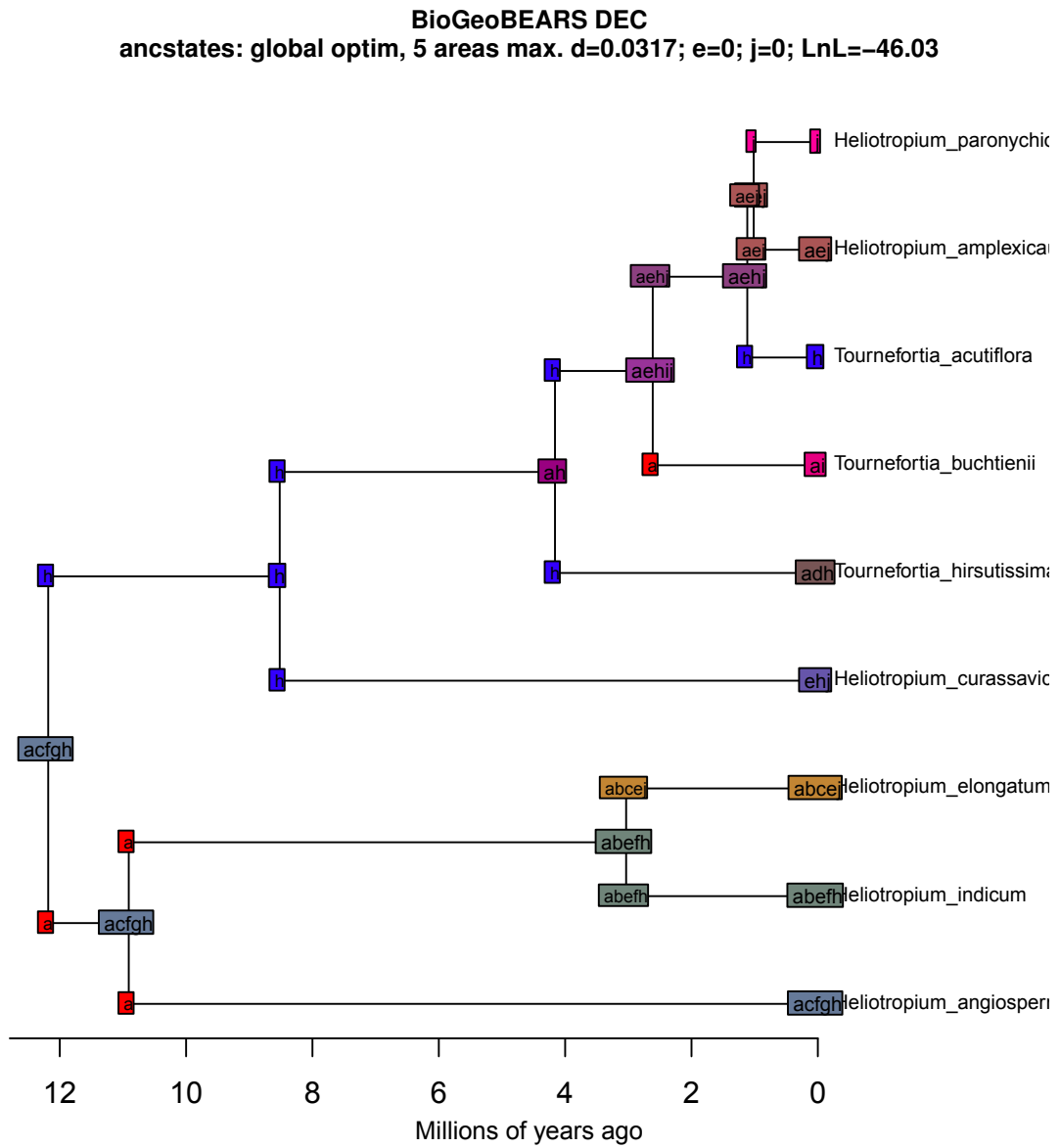


Figure S3: Clades of angiosperms

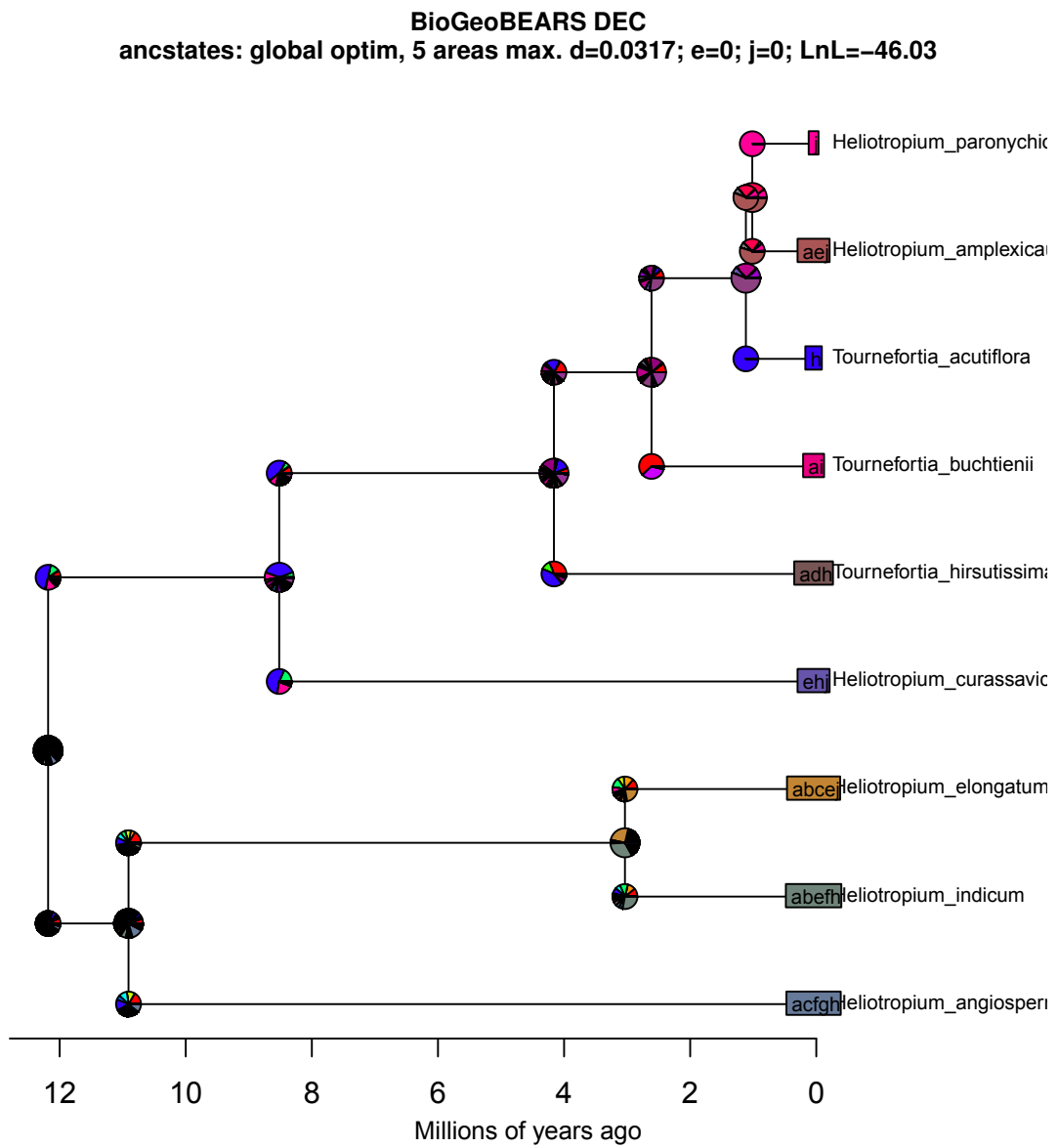


Figure S3: Clades of angiosperms

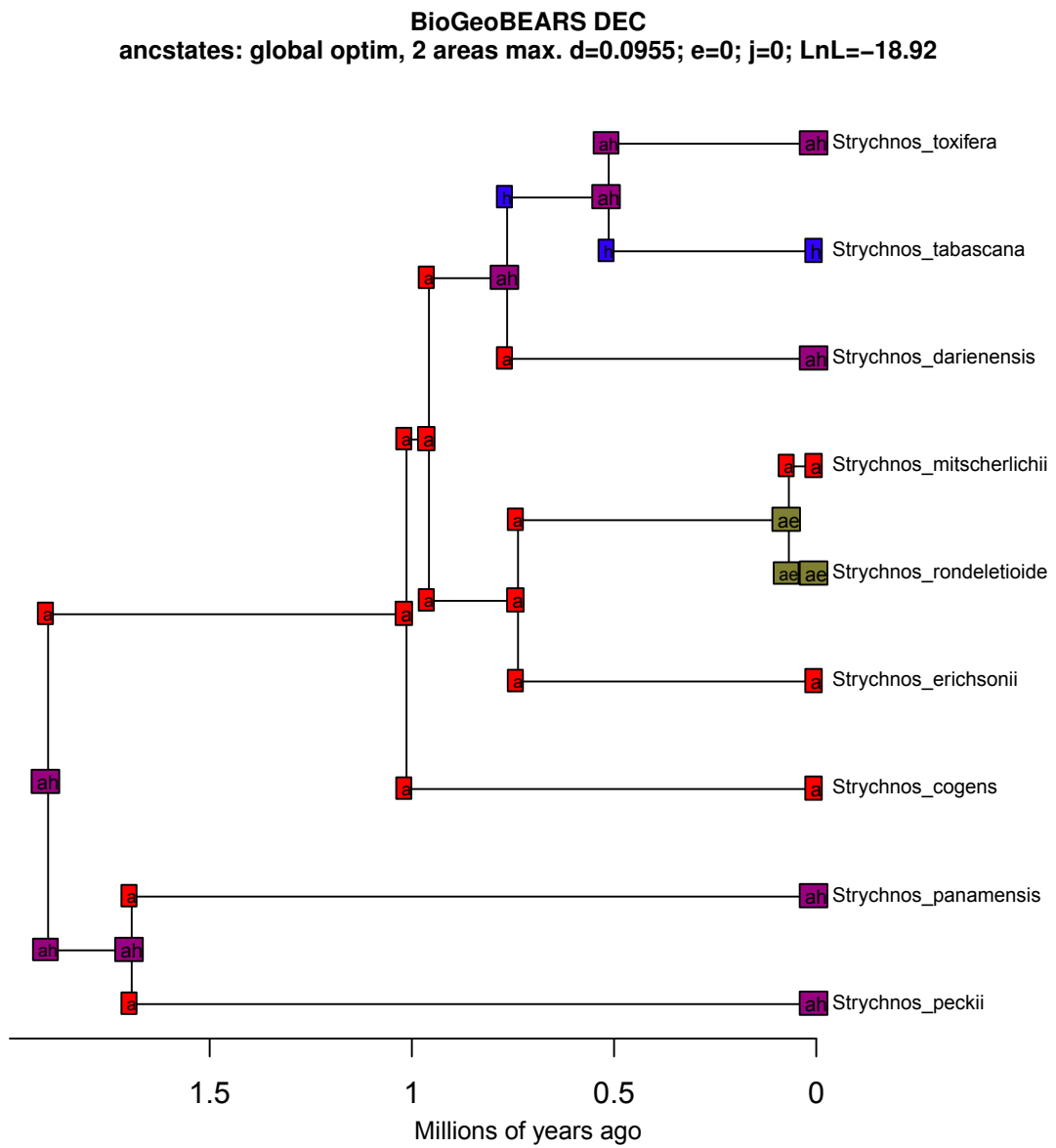


Figure S3: Clades of angiosperms

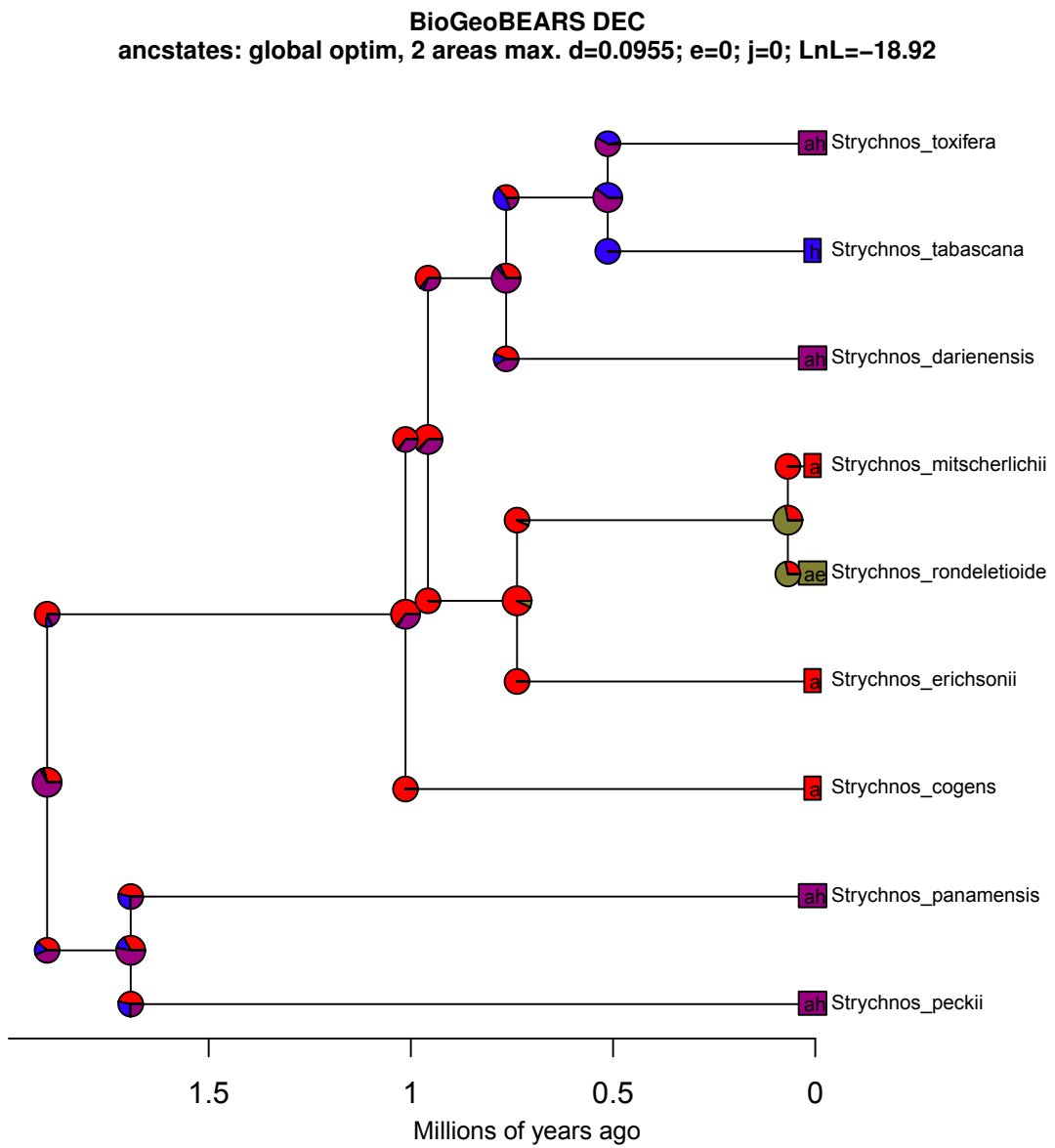


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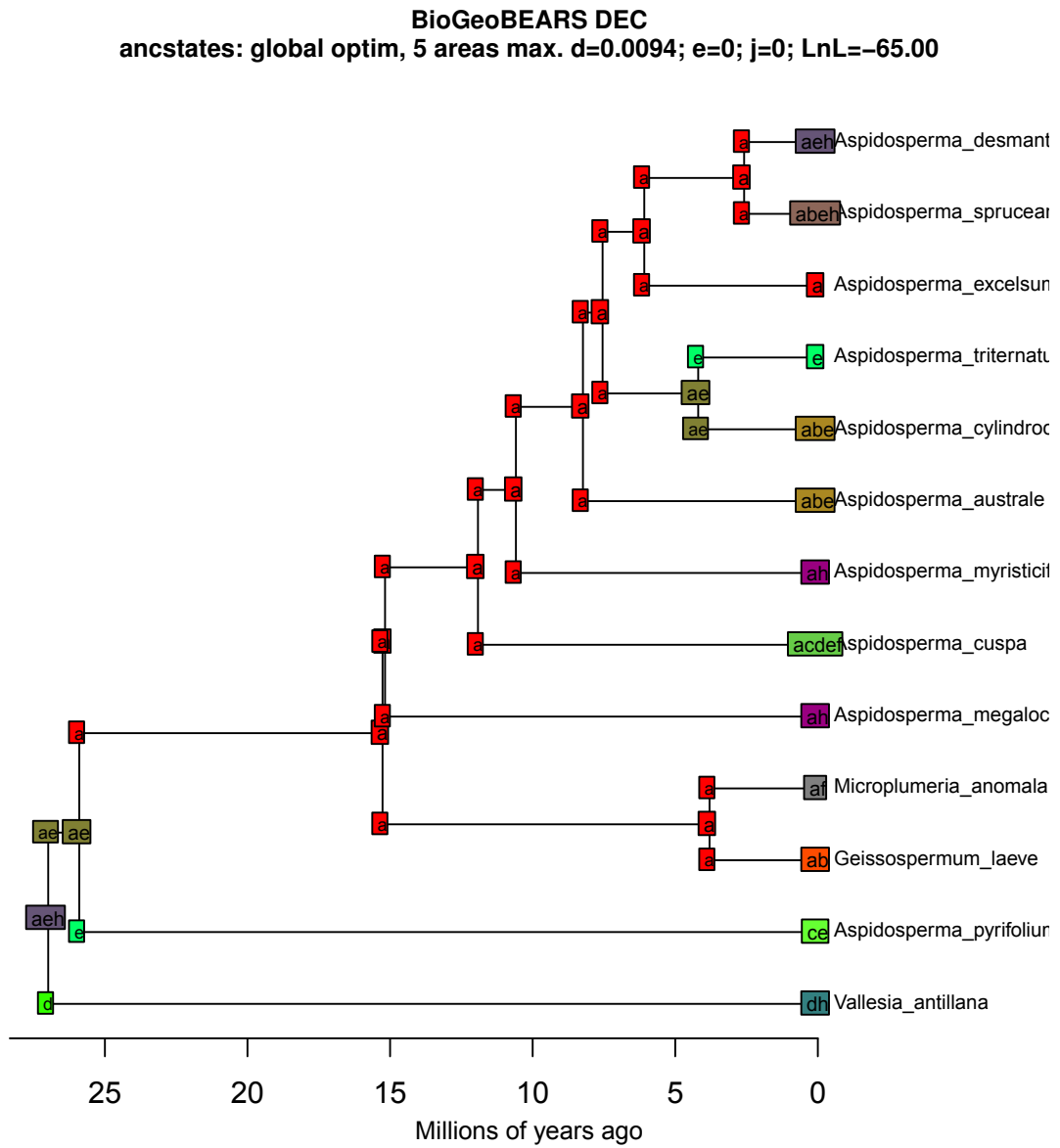


Figure S3: Clades of angiosperms

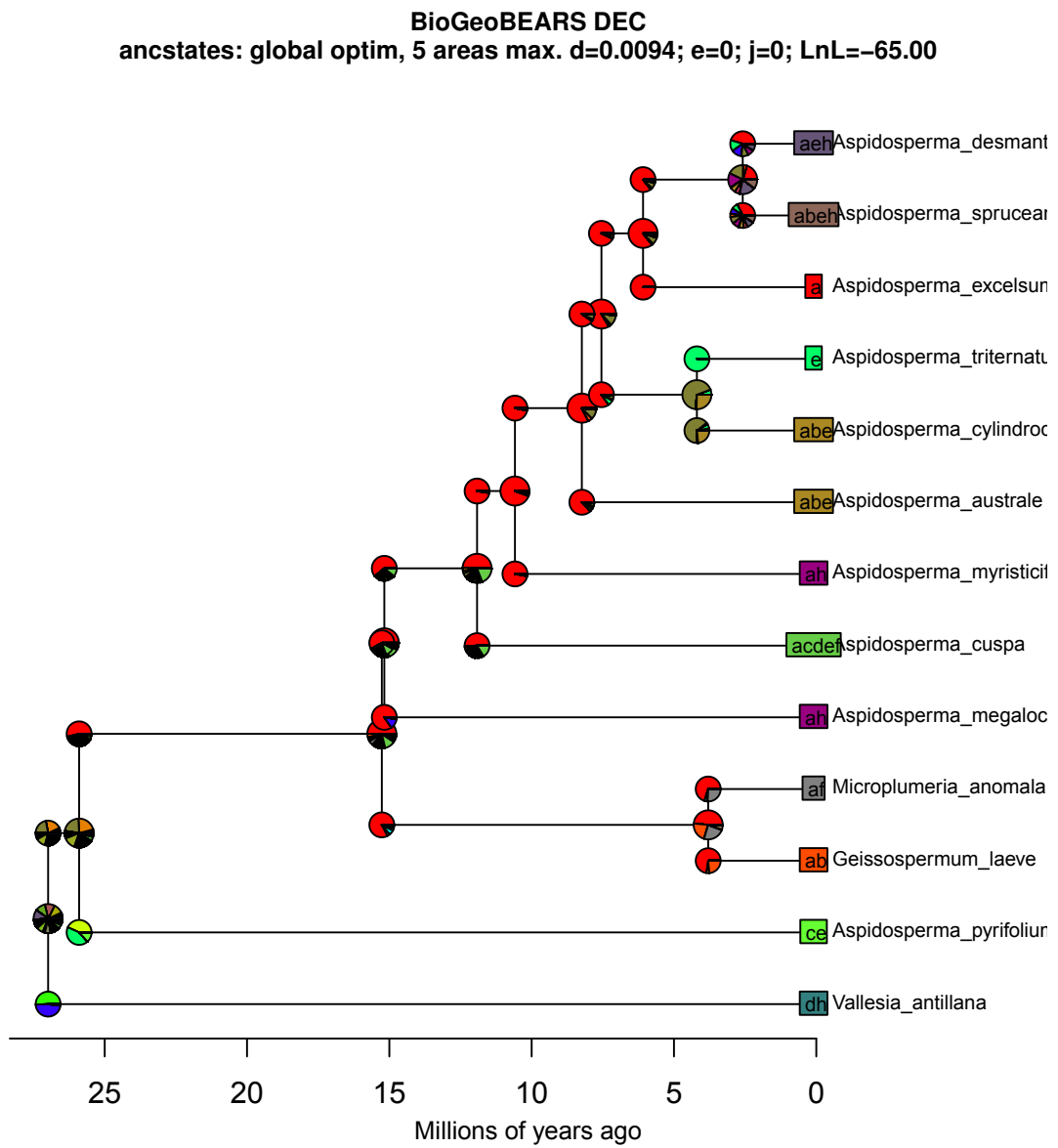


Figure S3: Clades of angiosperms

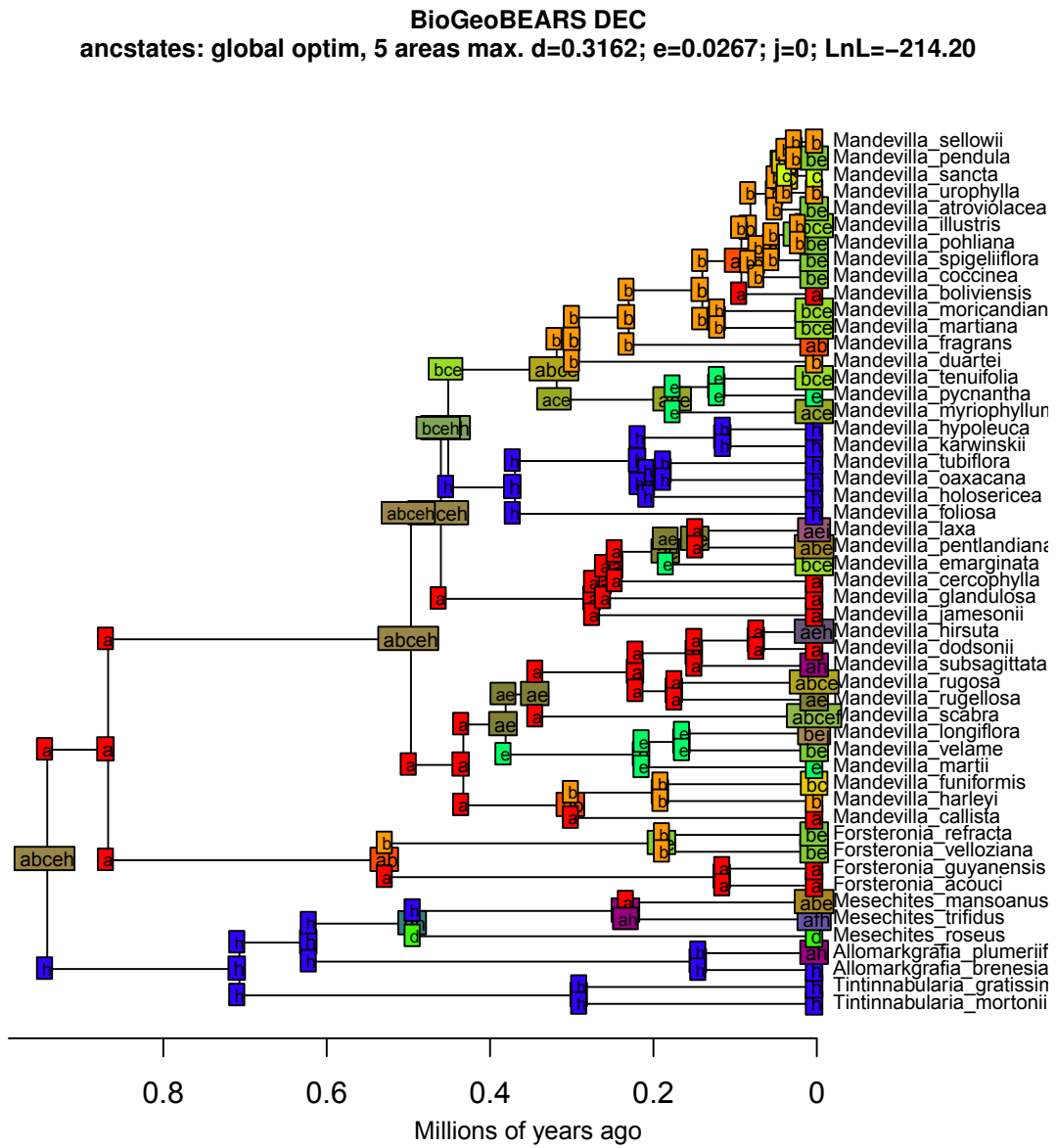


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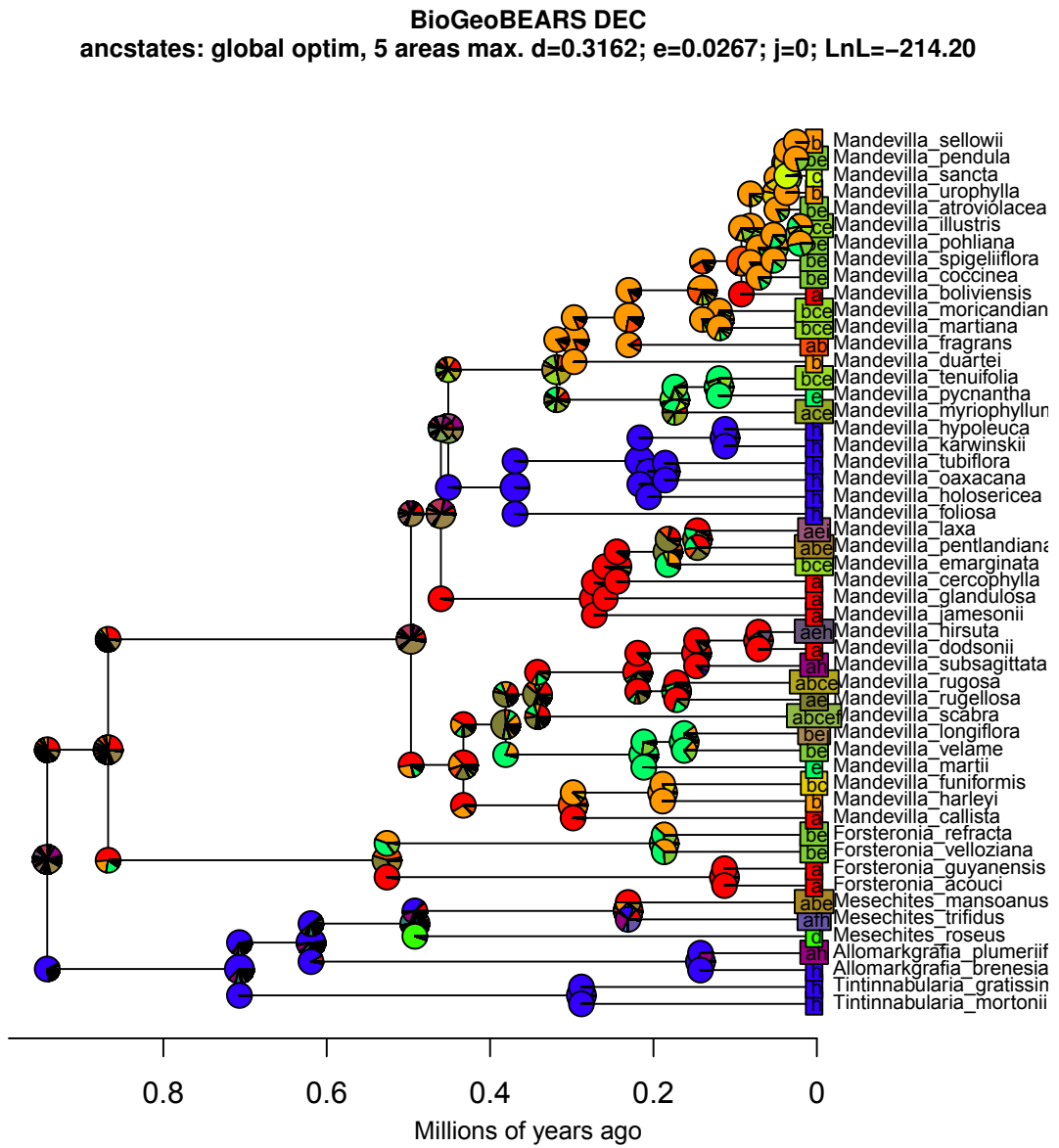


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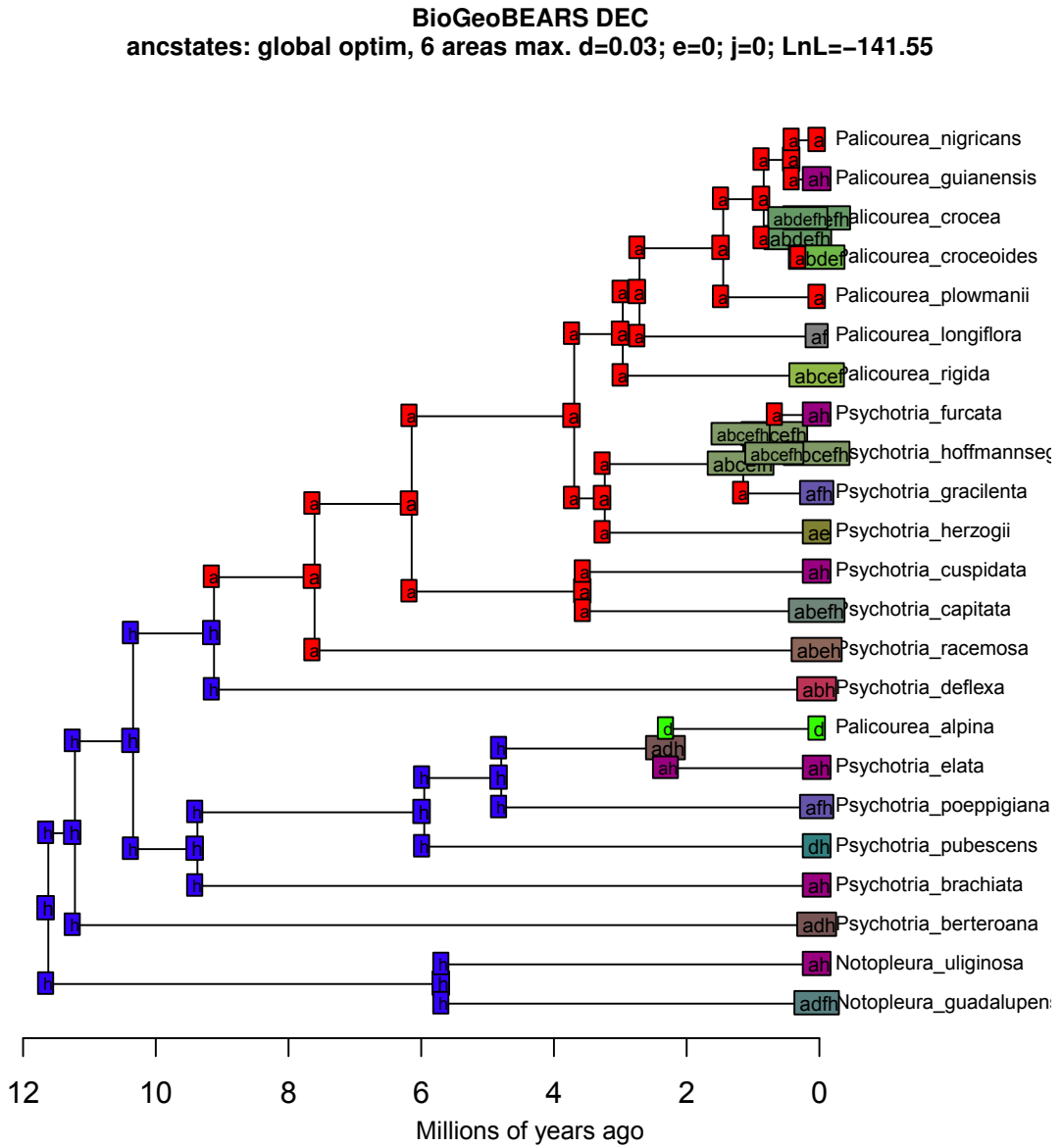


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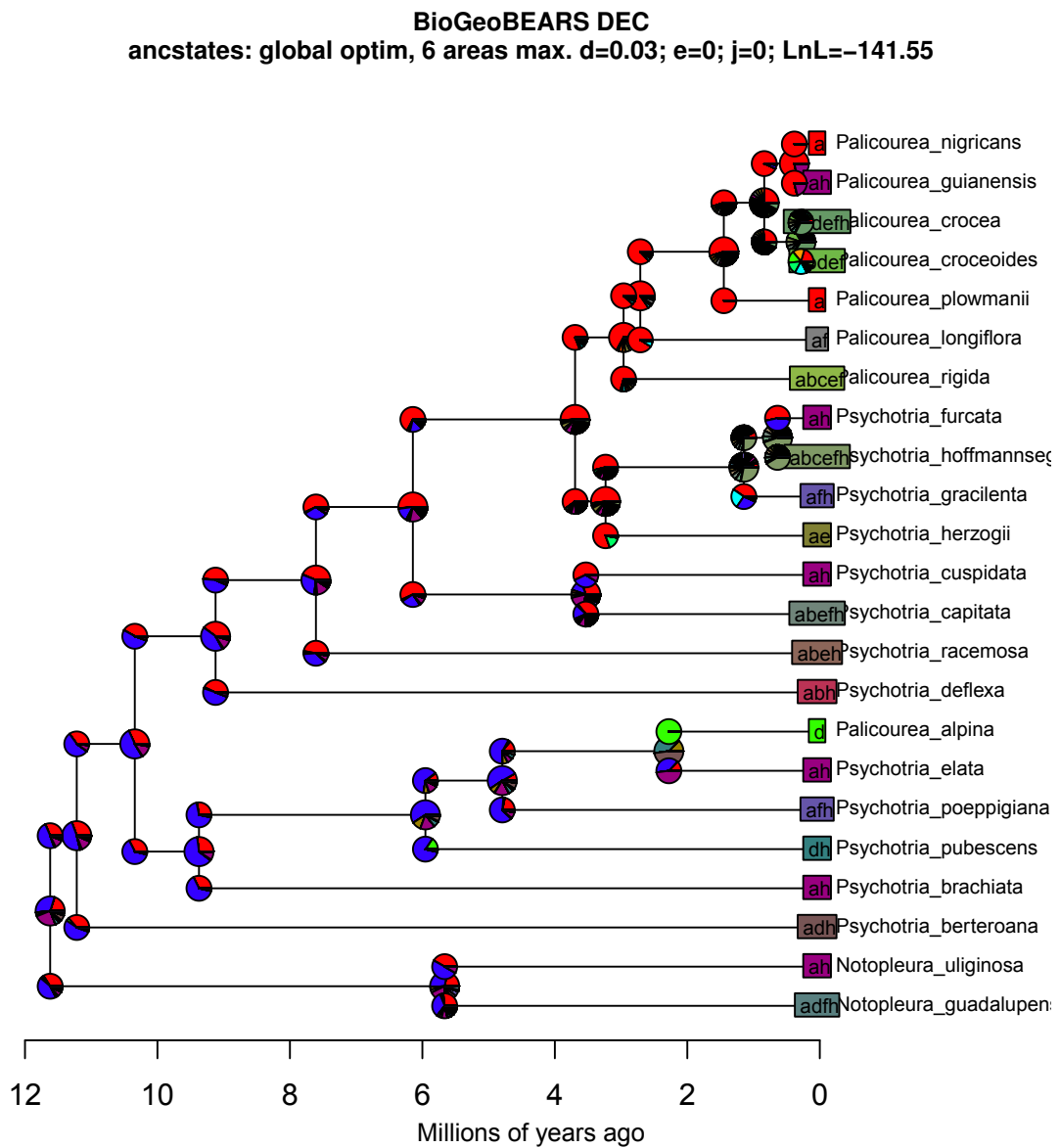


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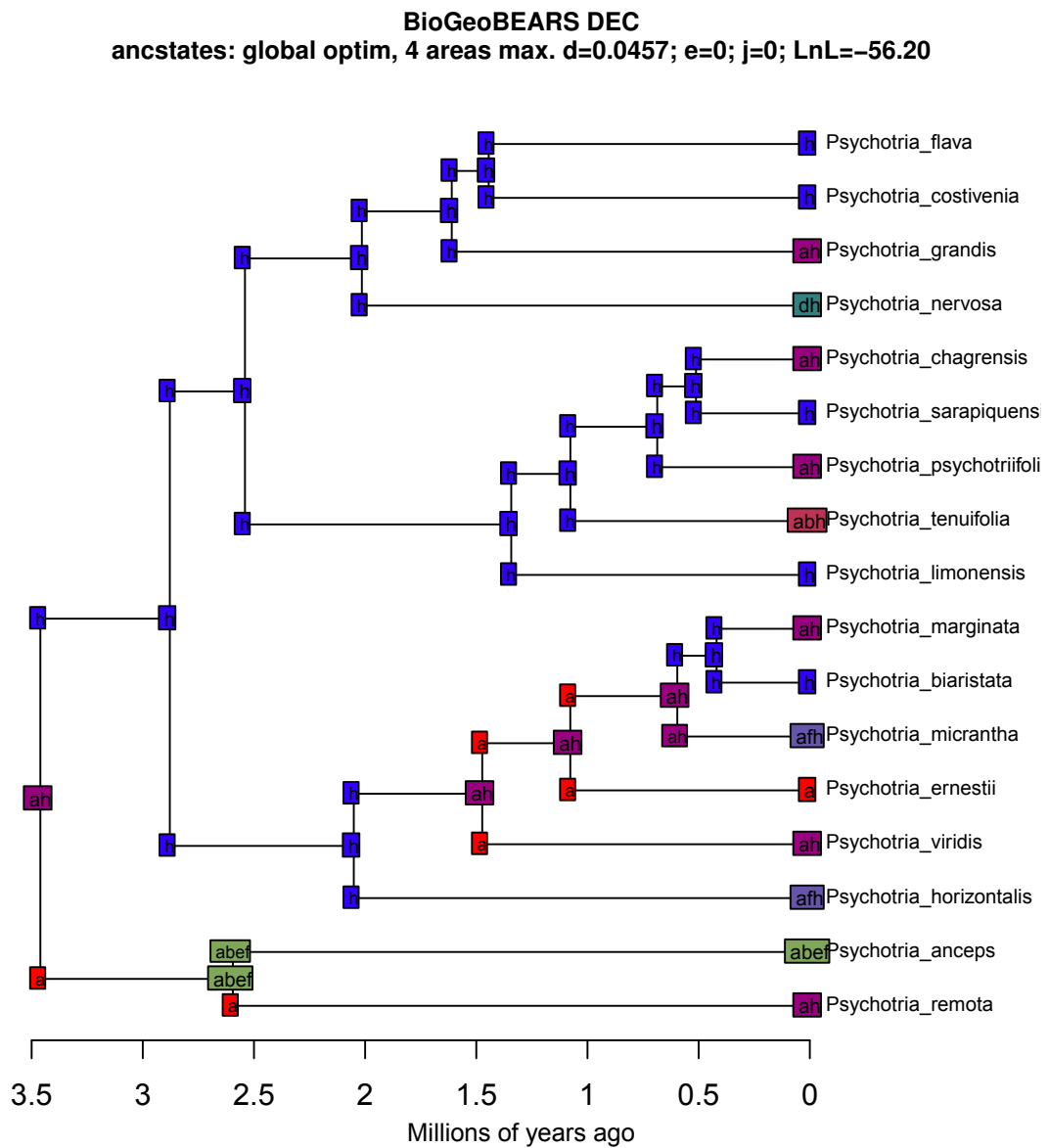


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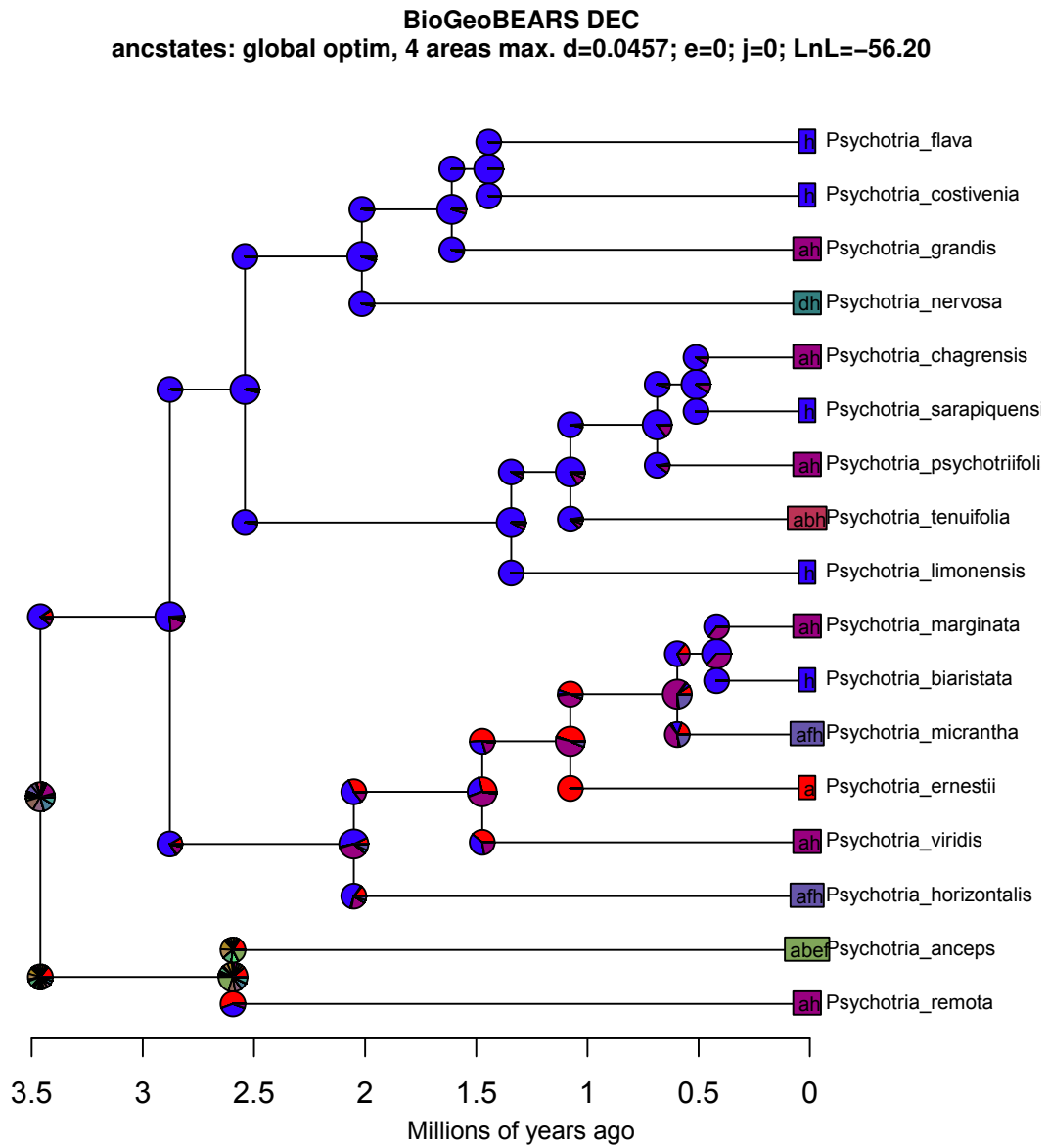


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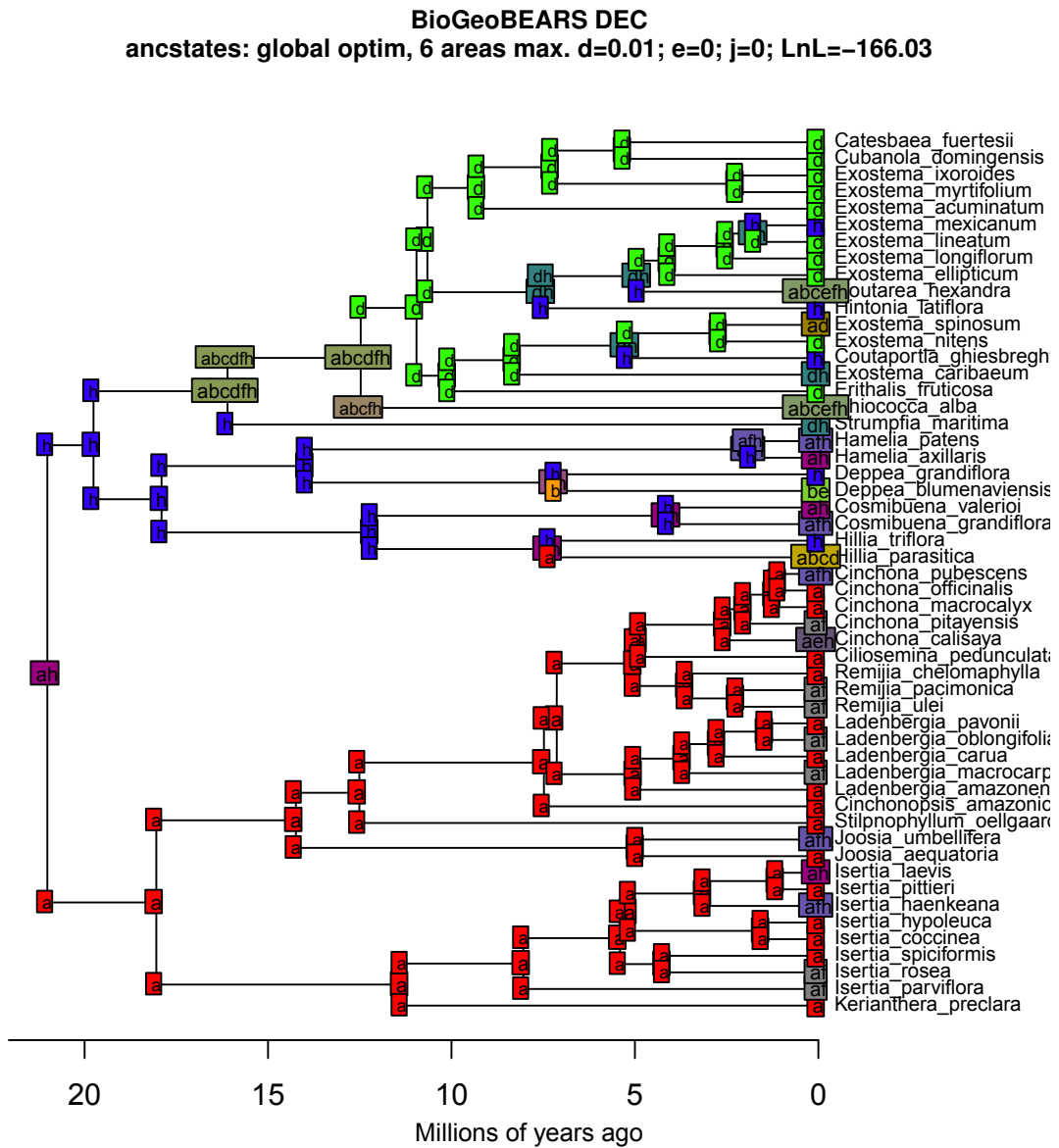


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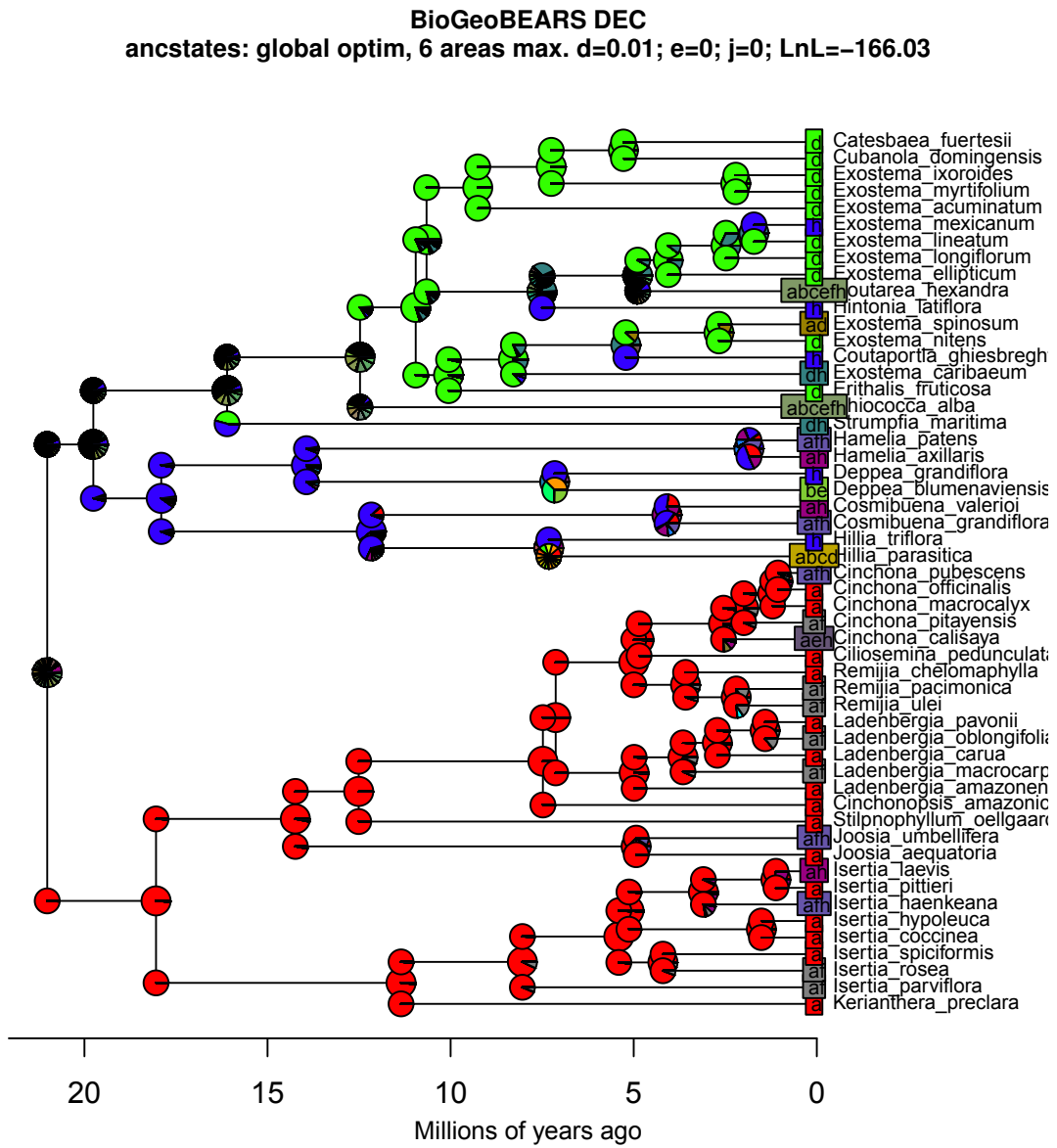


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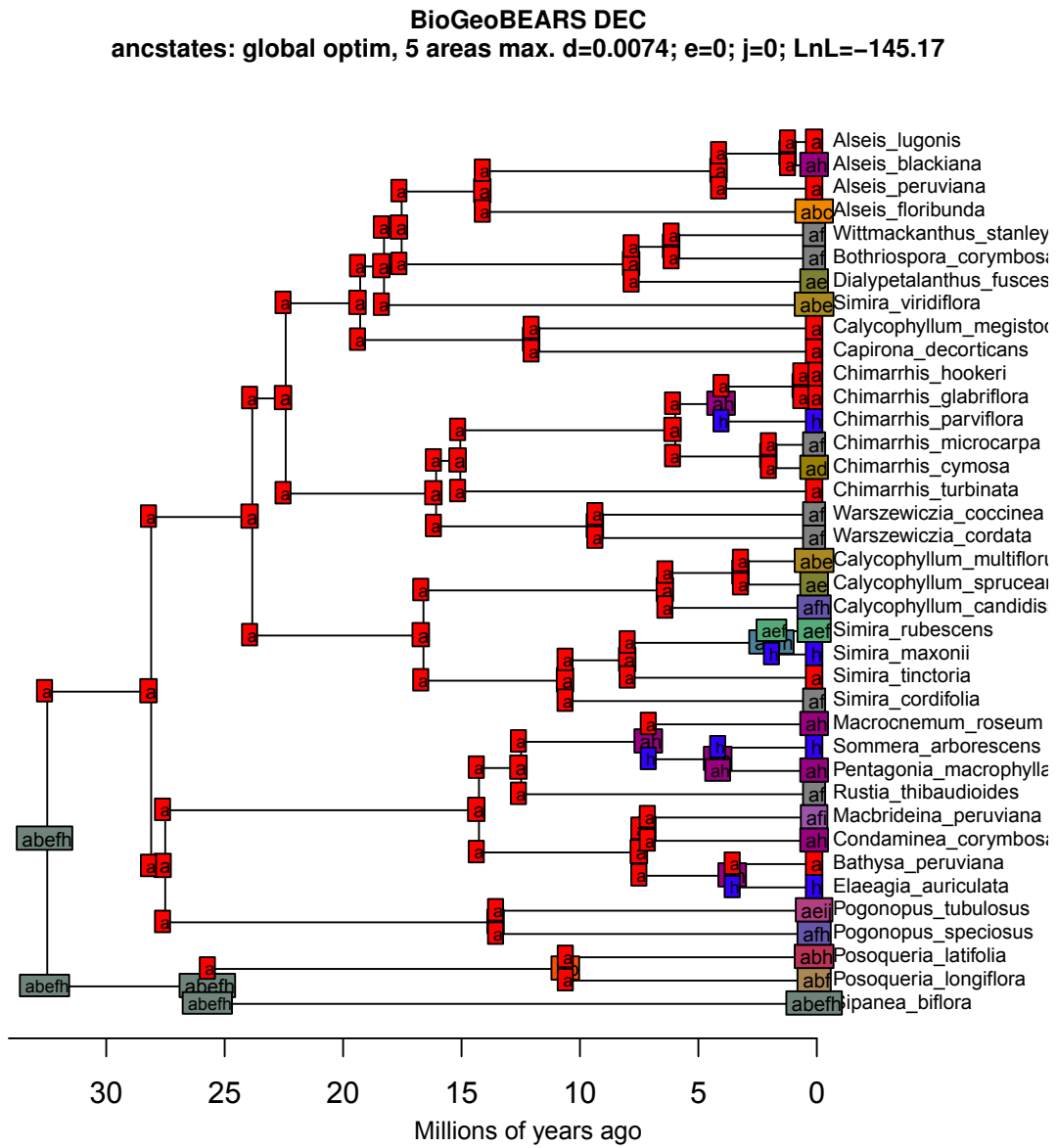


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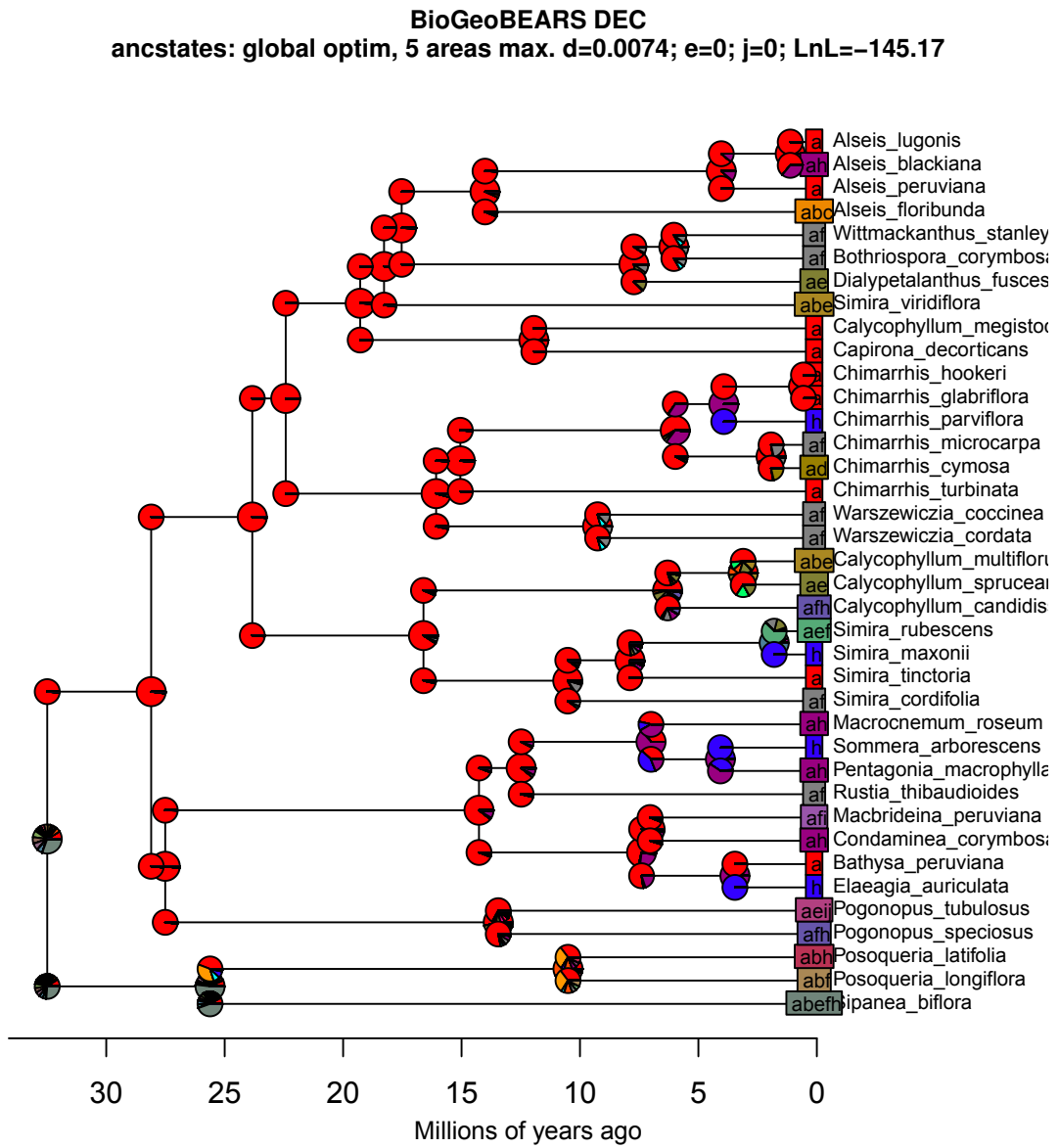


Figure S3: Clades of angiosperms

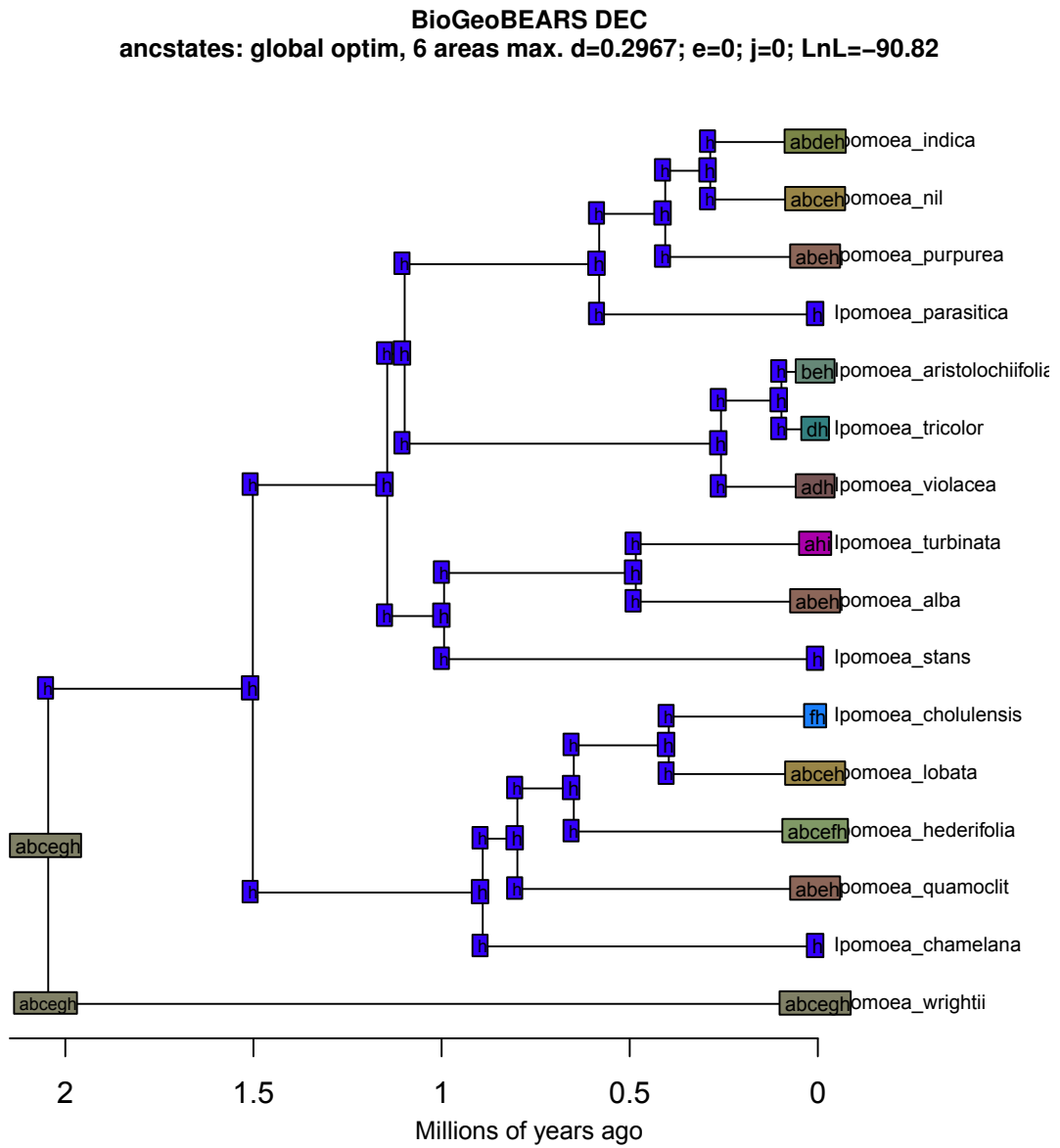


Figure S3: Clades of angiosperms

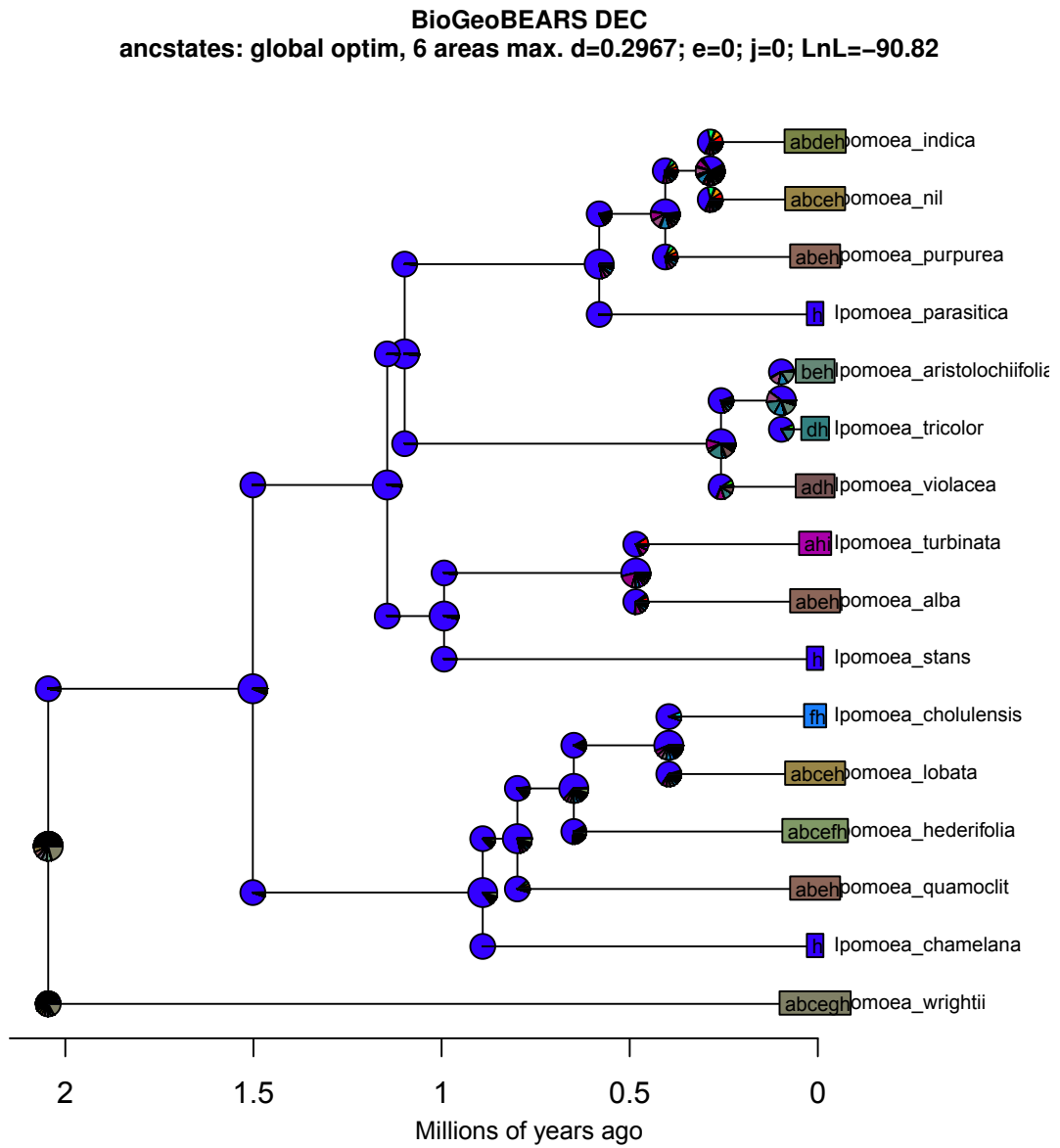


Figure S3: Clades of angiosperms

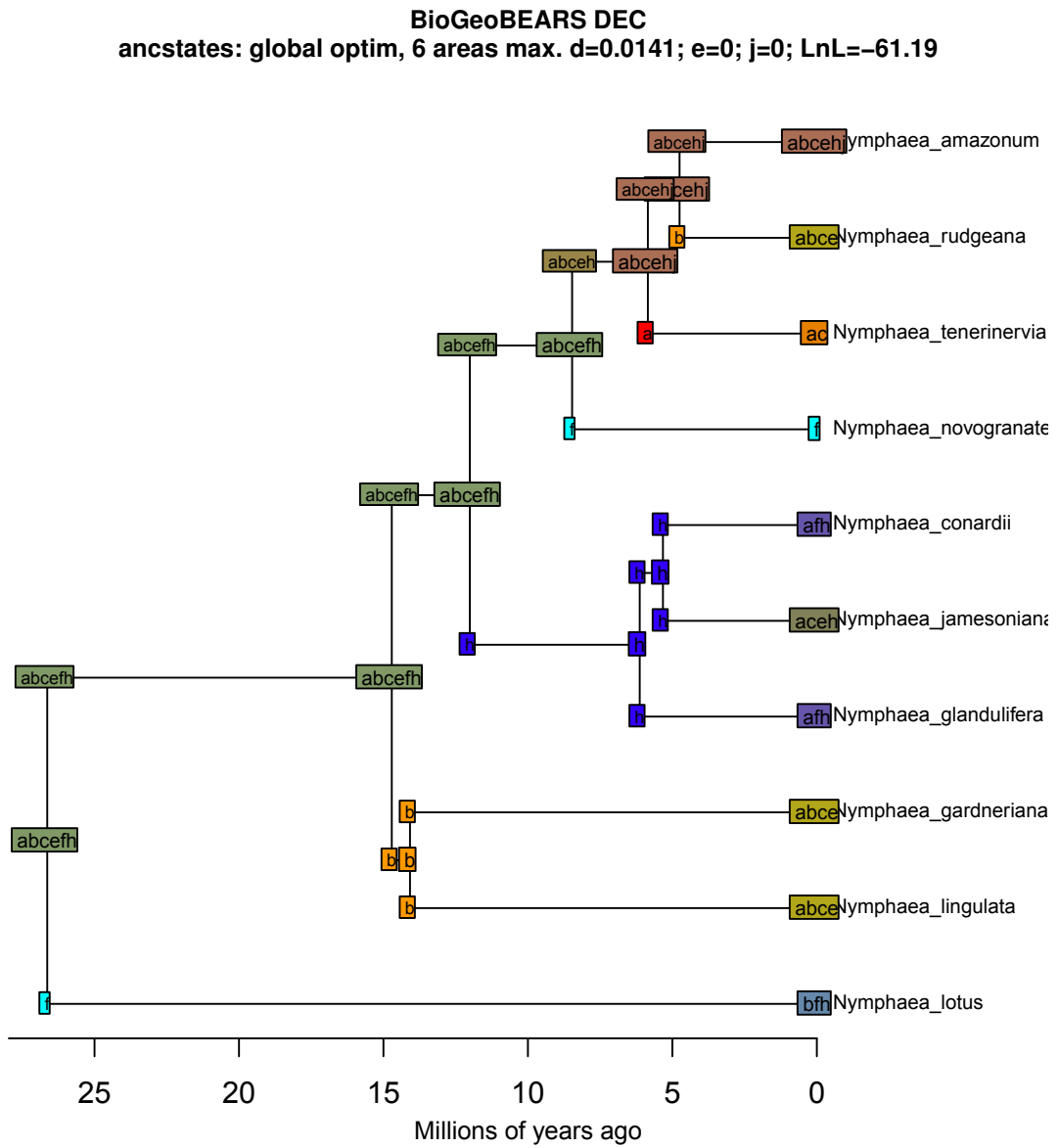


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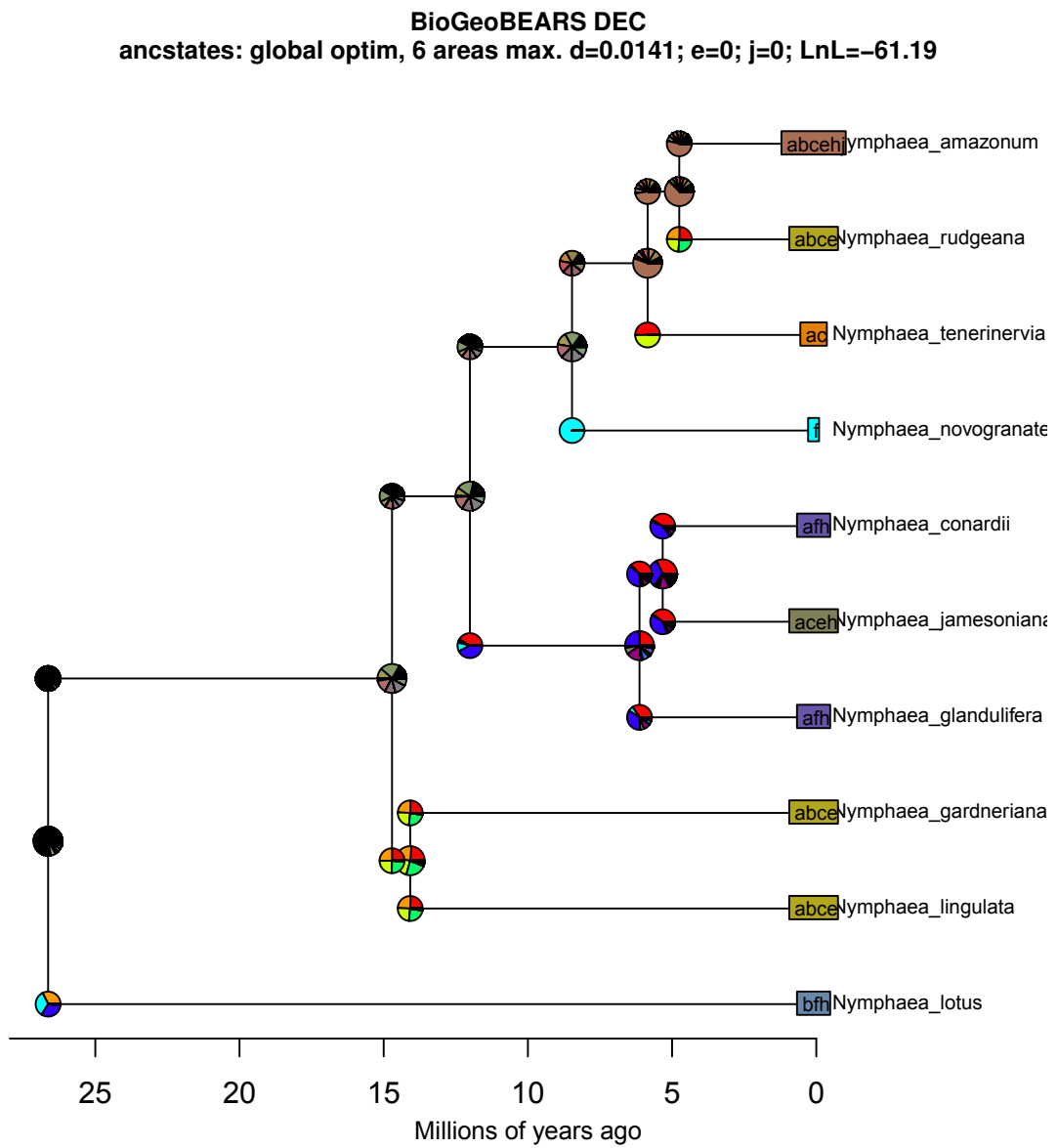


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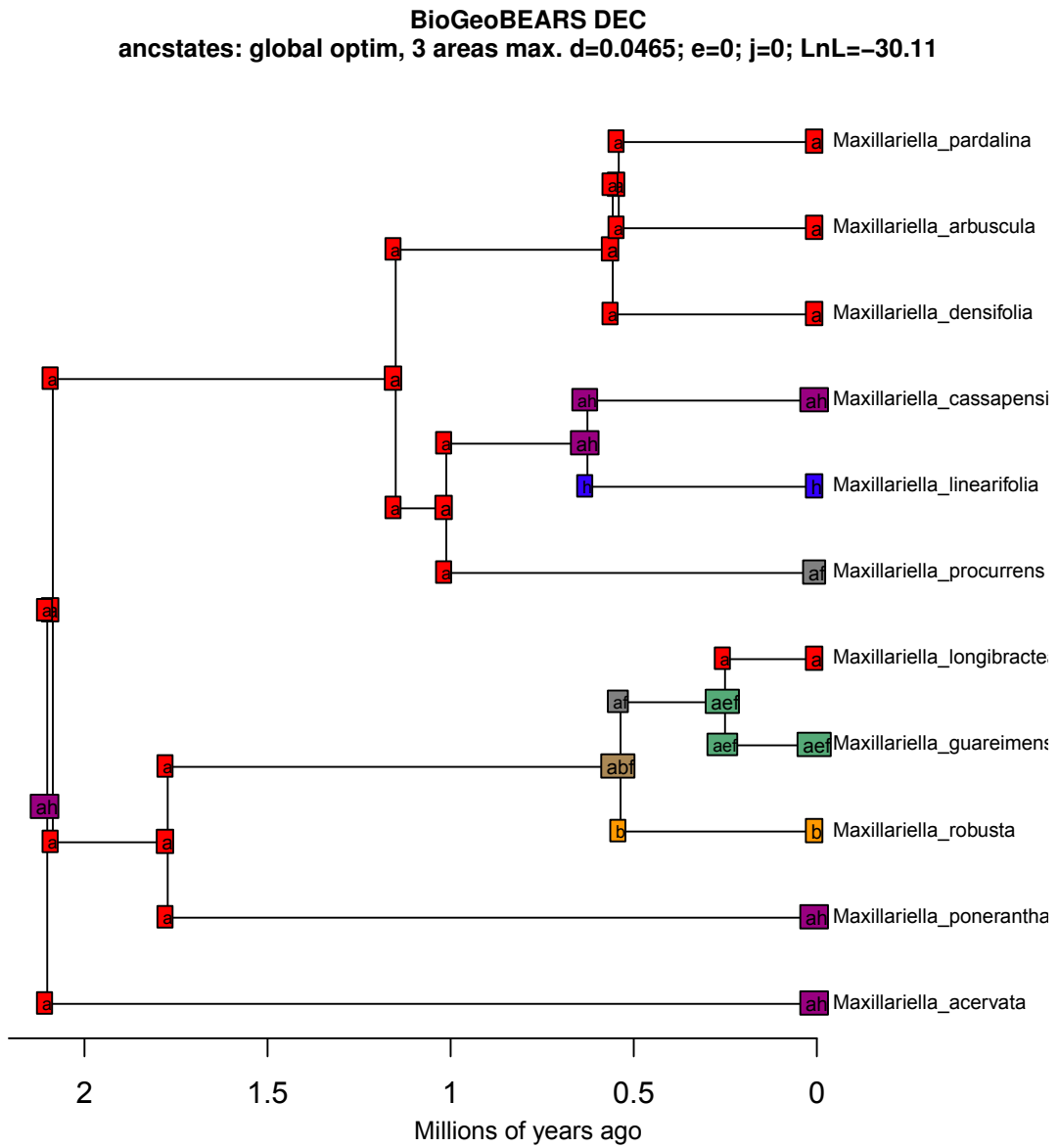


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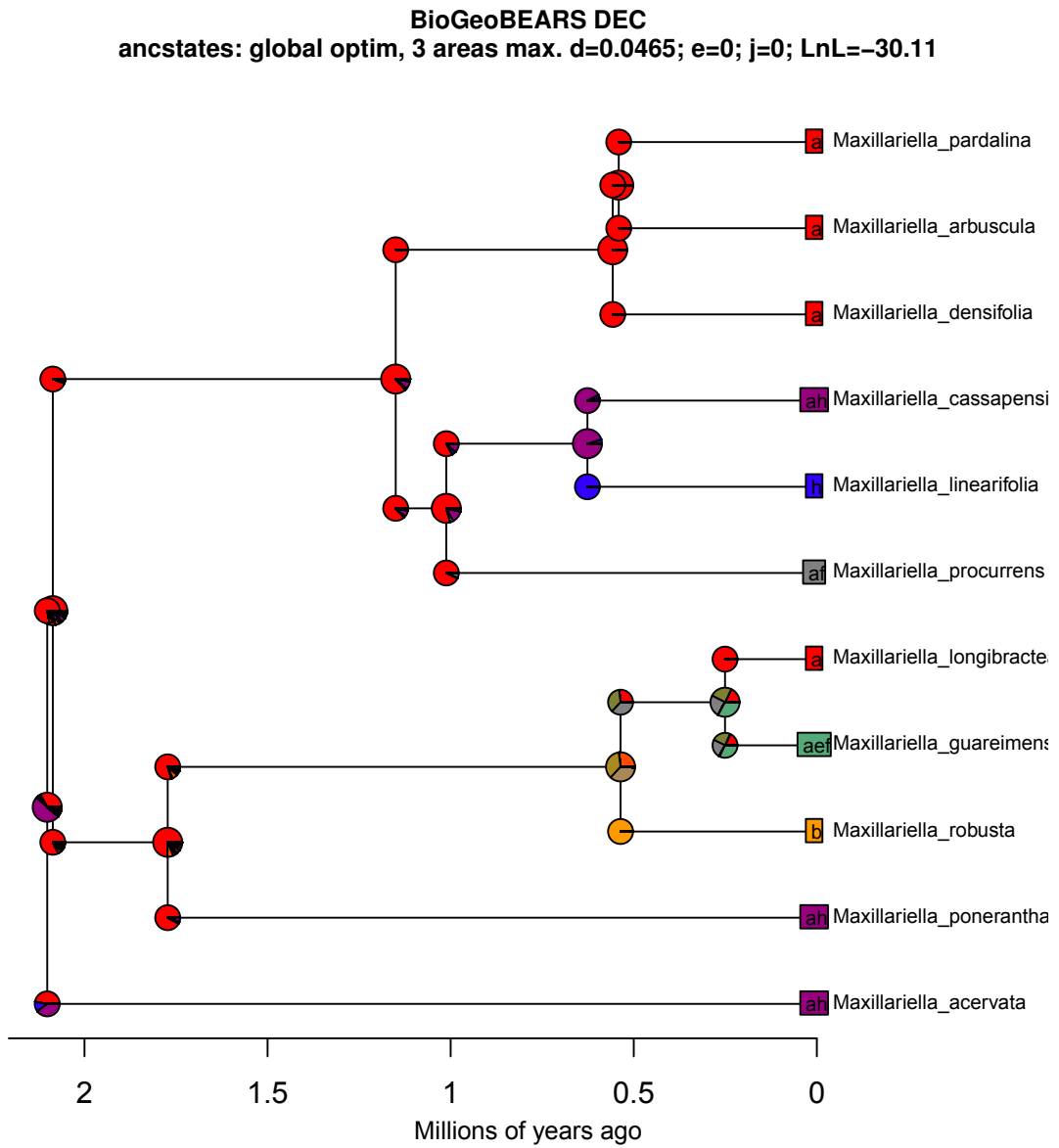


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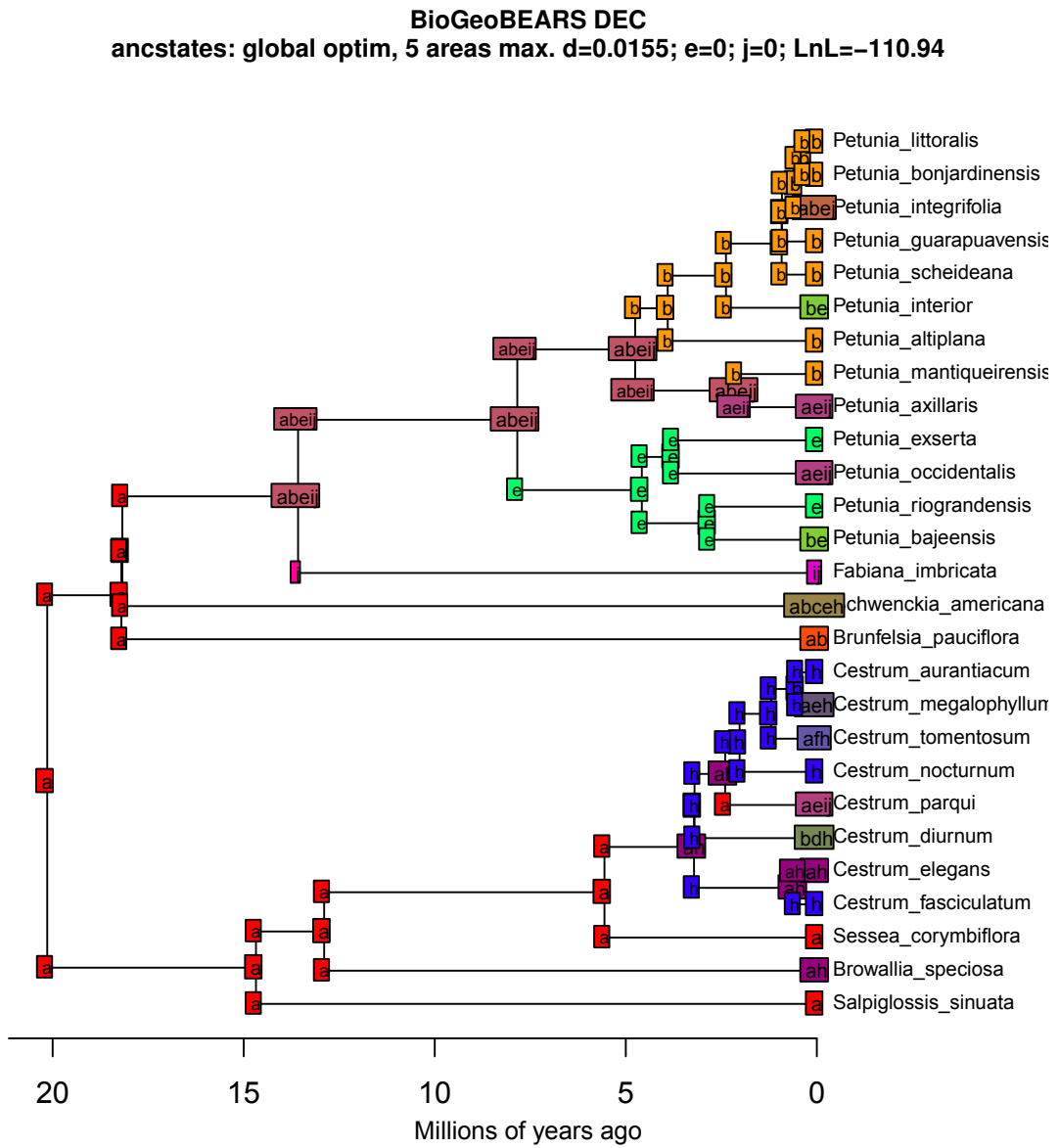


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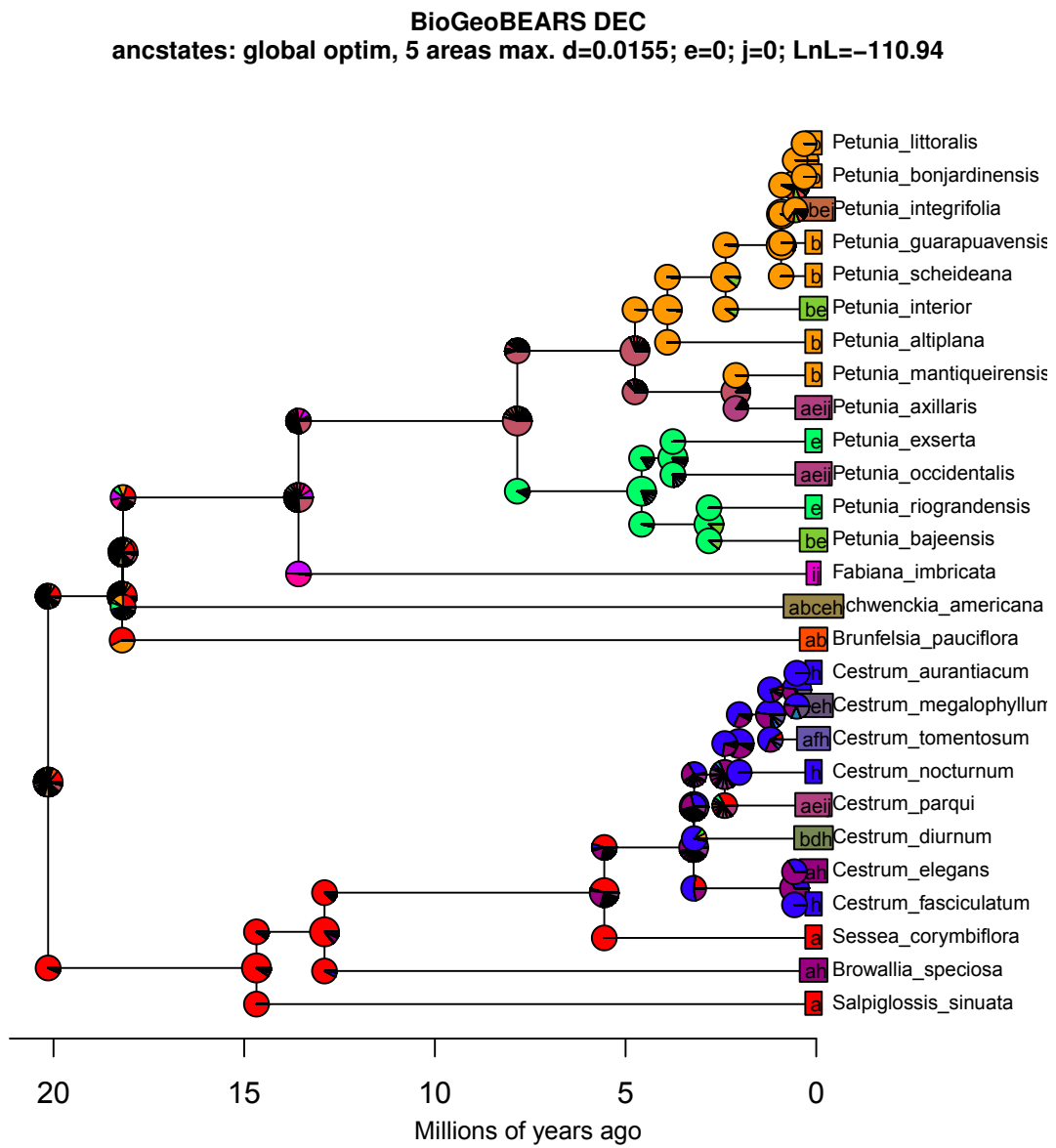


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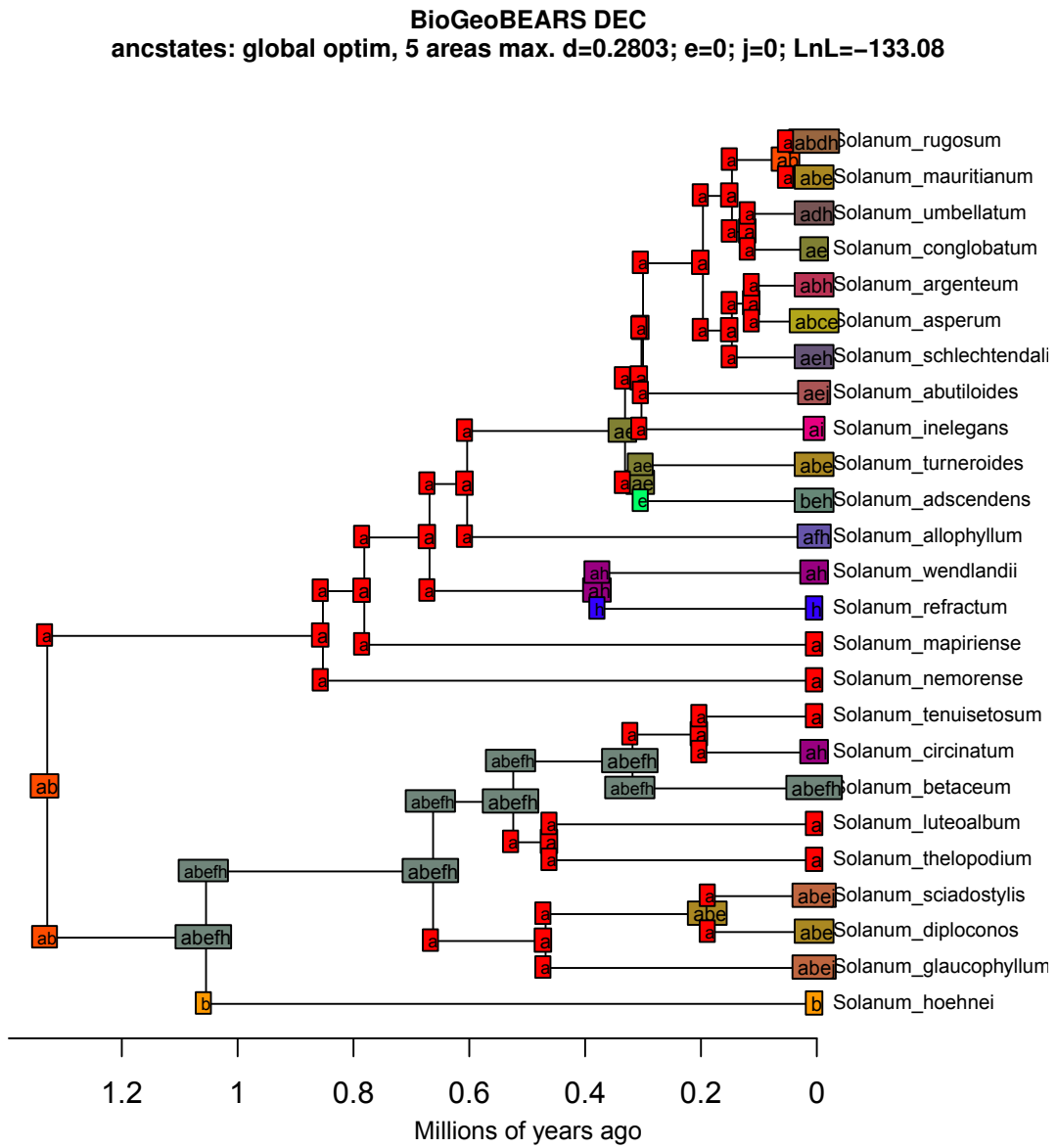


Figure S3: Clades of angiosperms

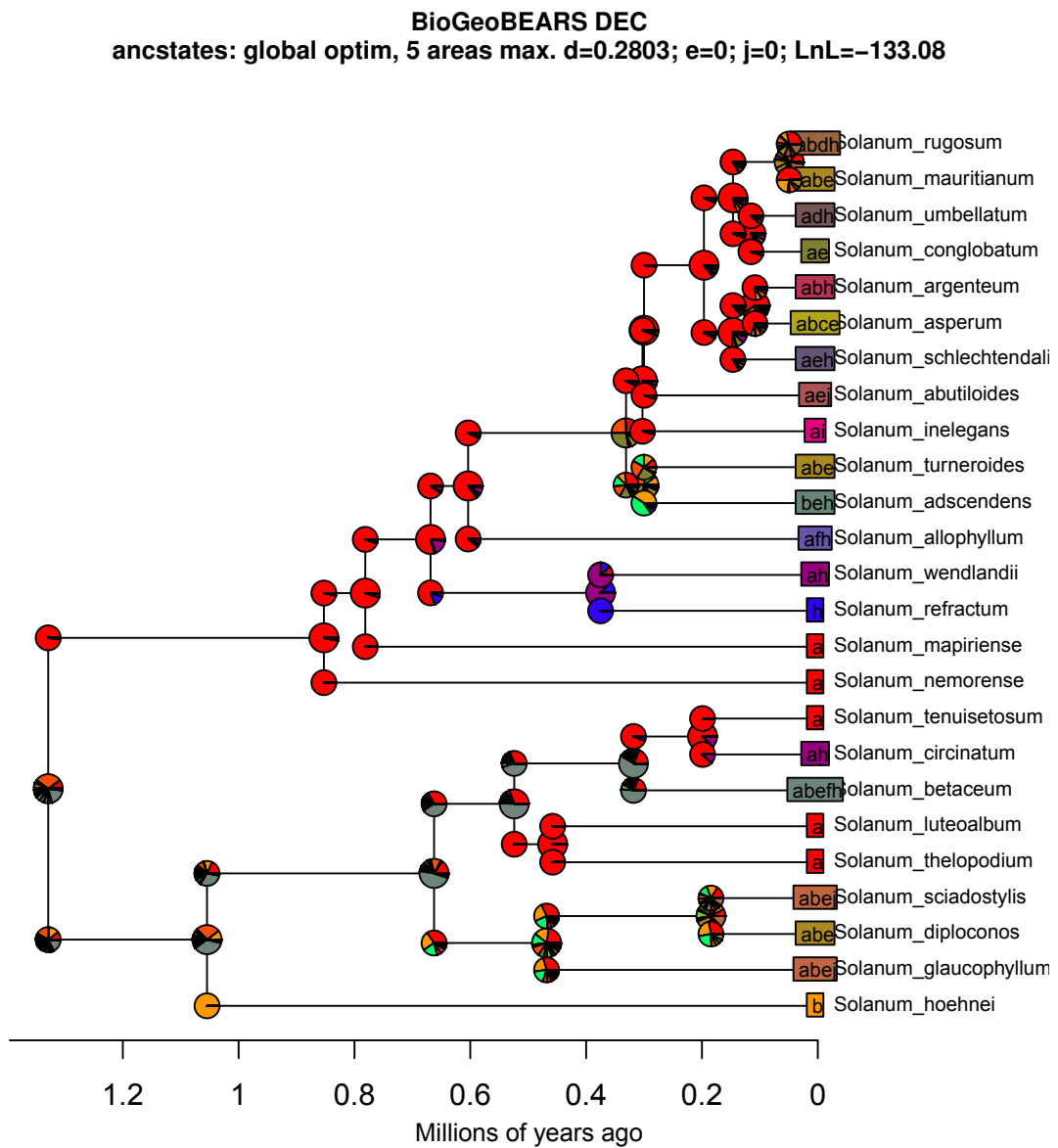


Figure S3: Clades of angiosperms

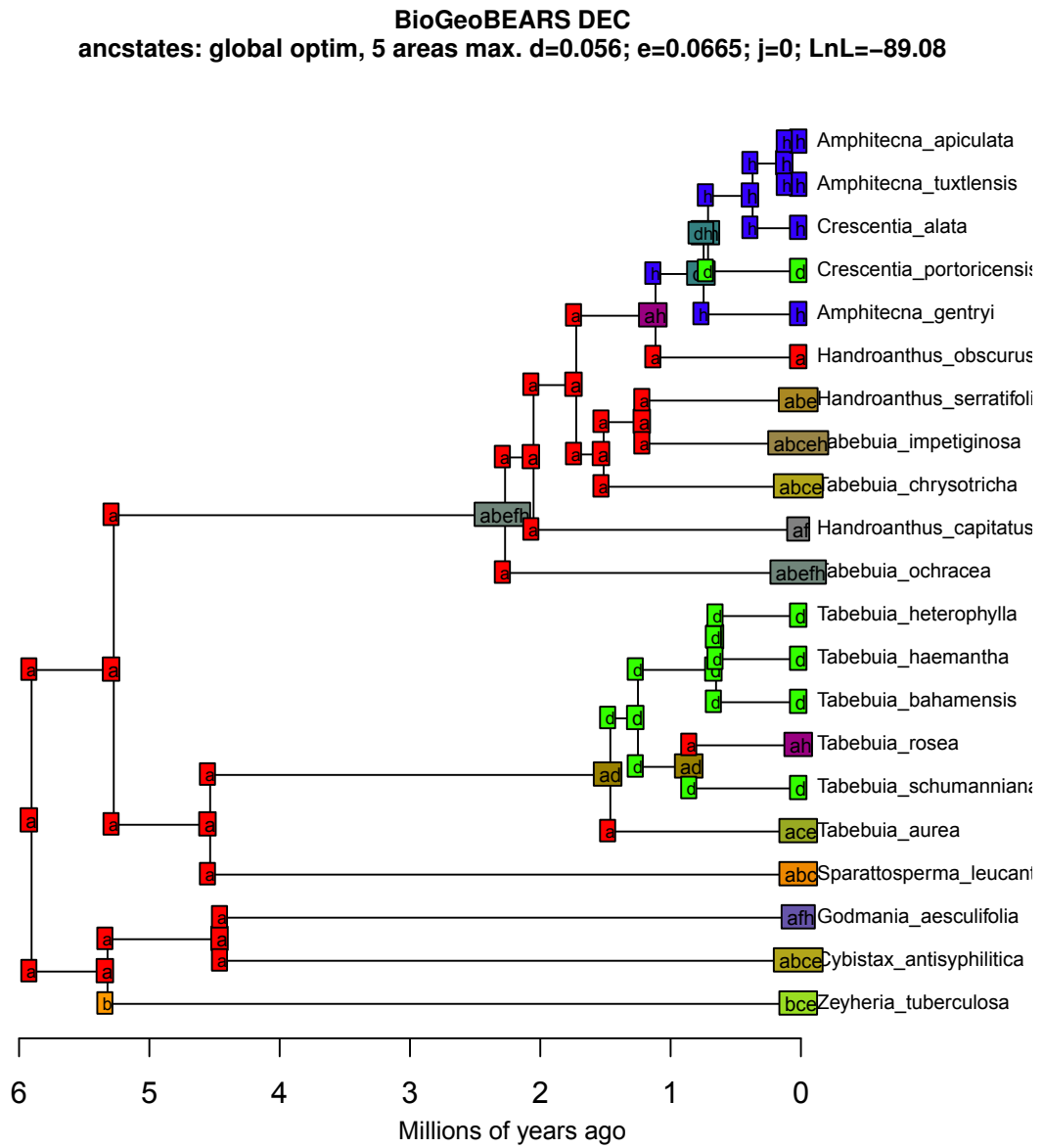


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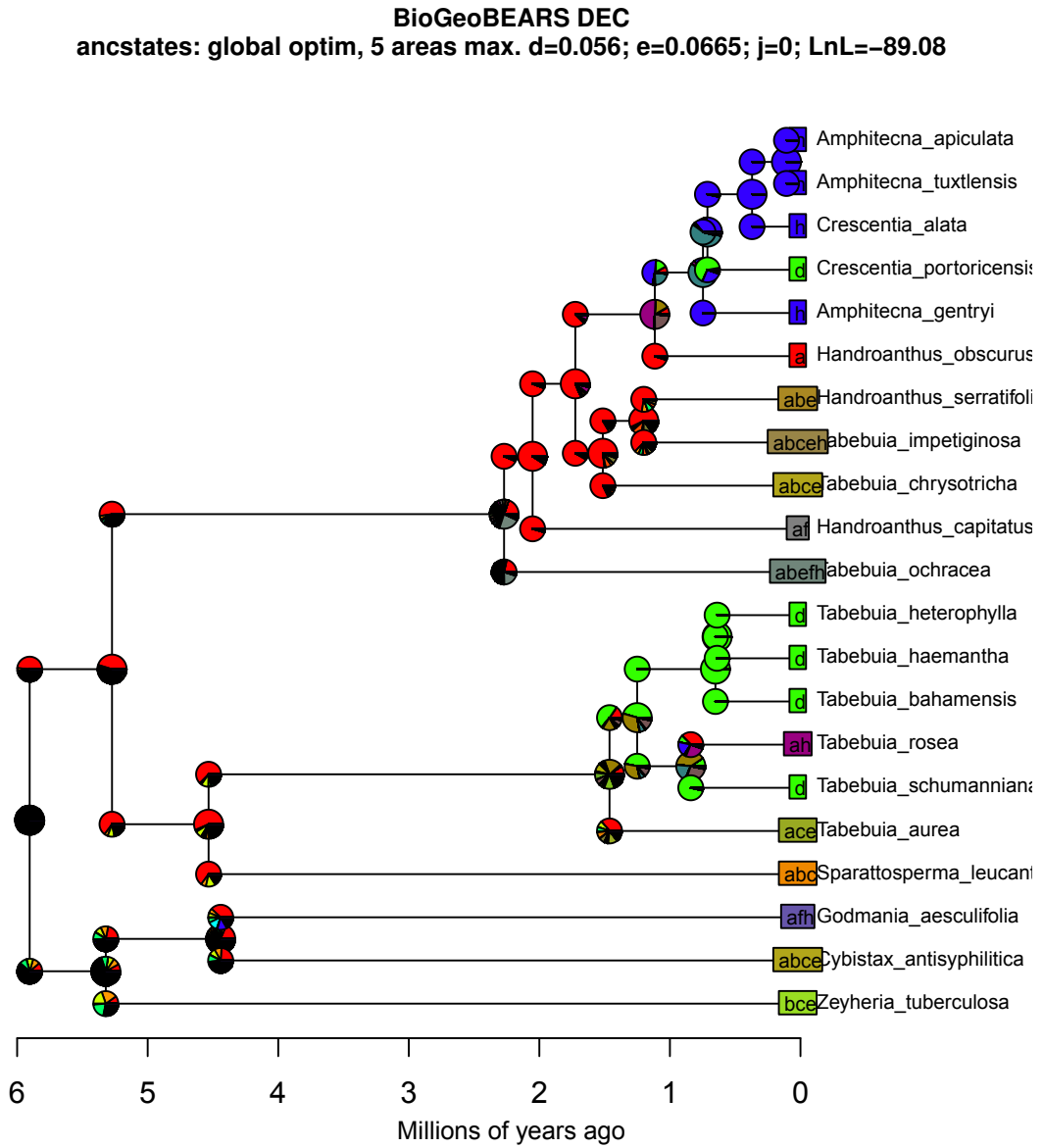


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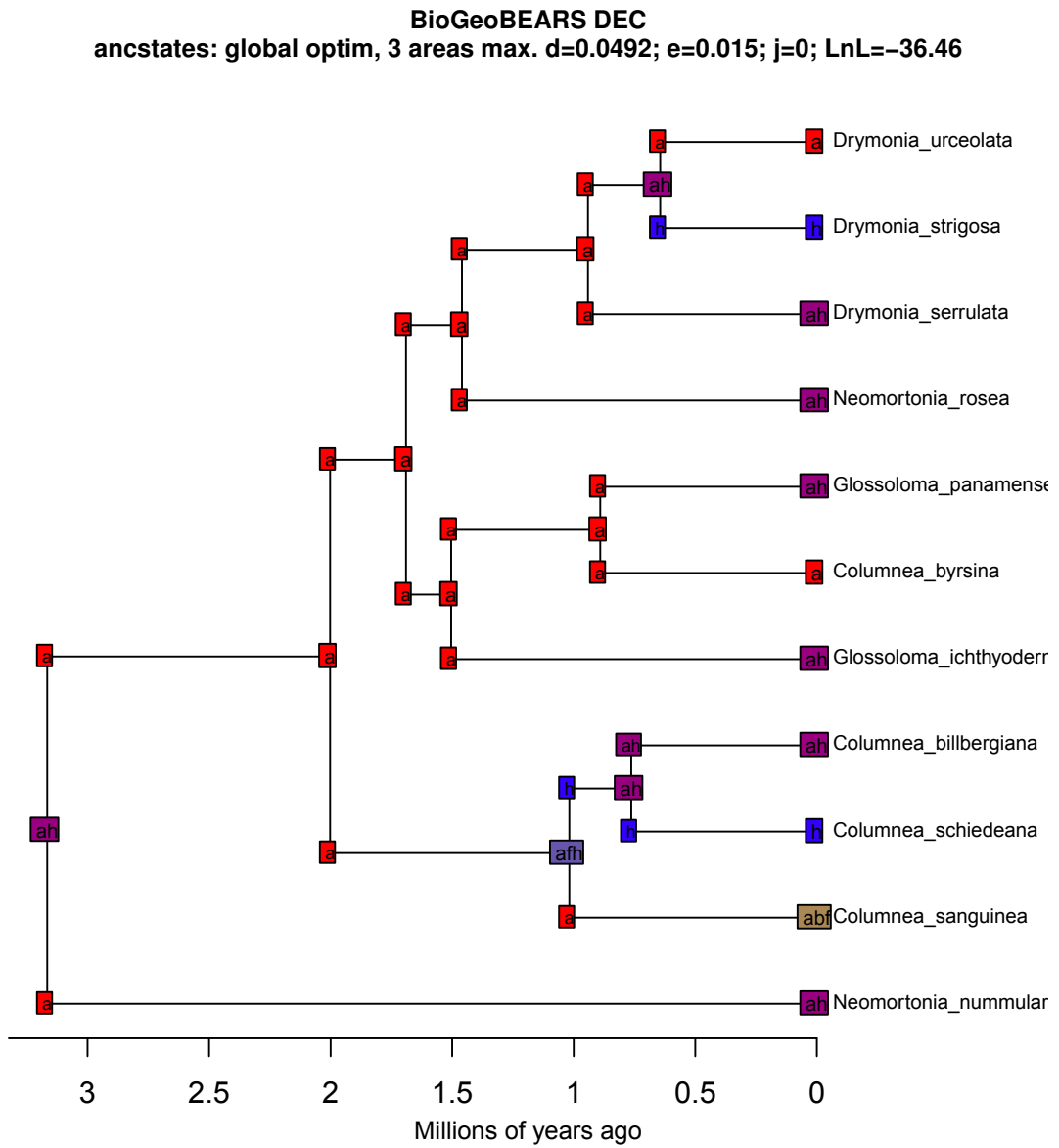


Figure S3: Clades of angiosperms

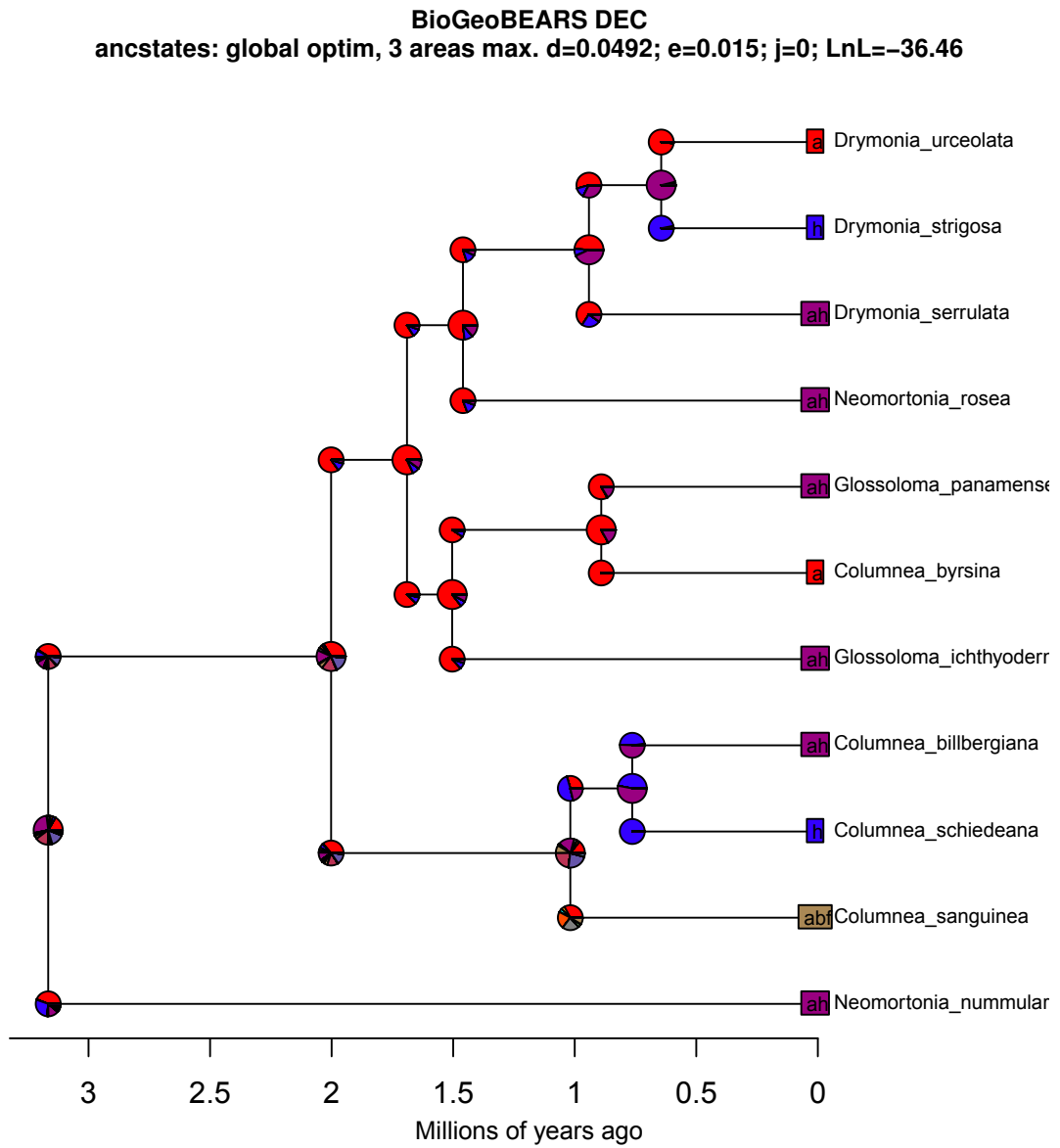


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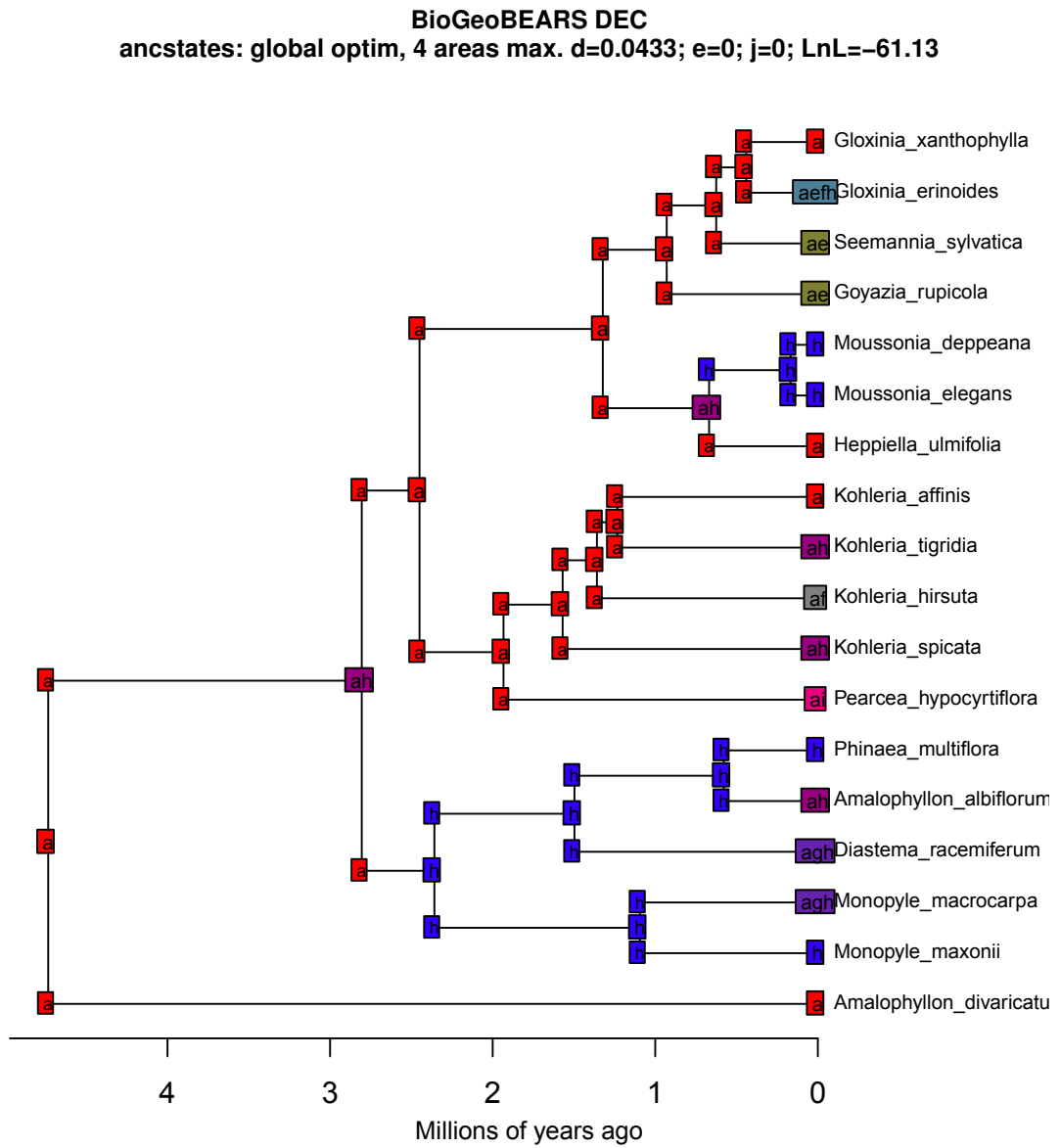


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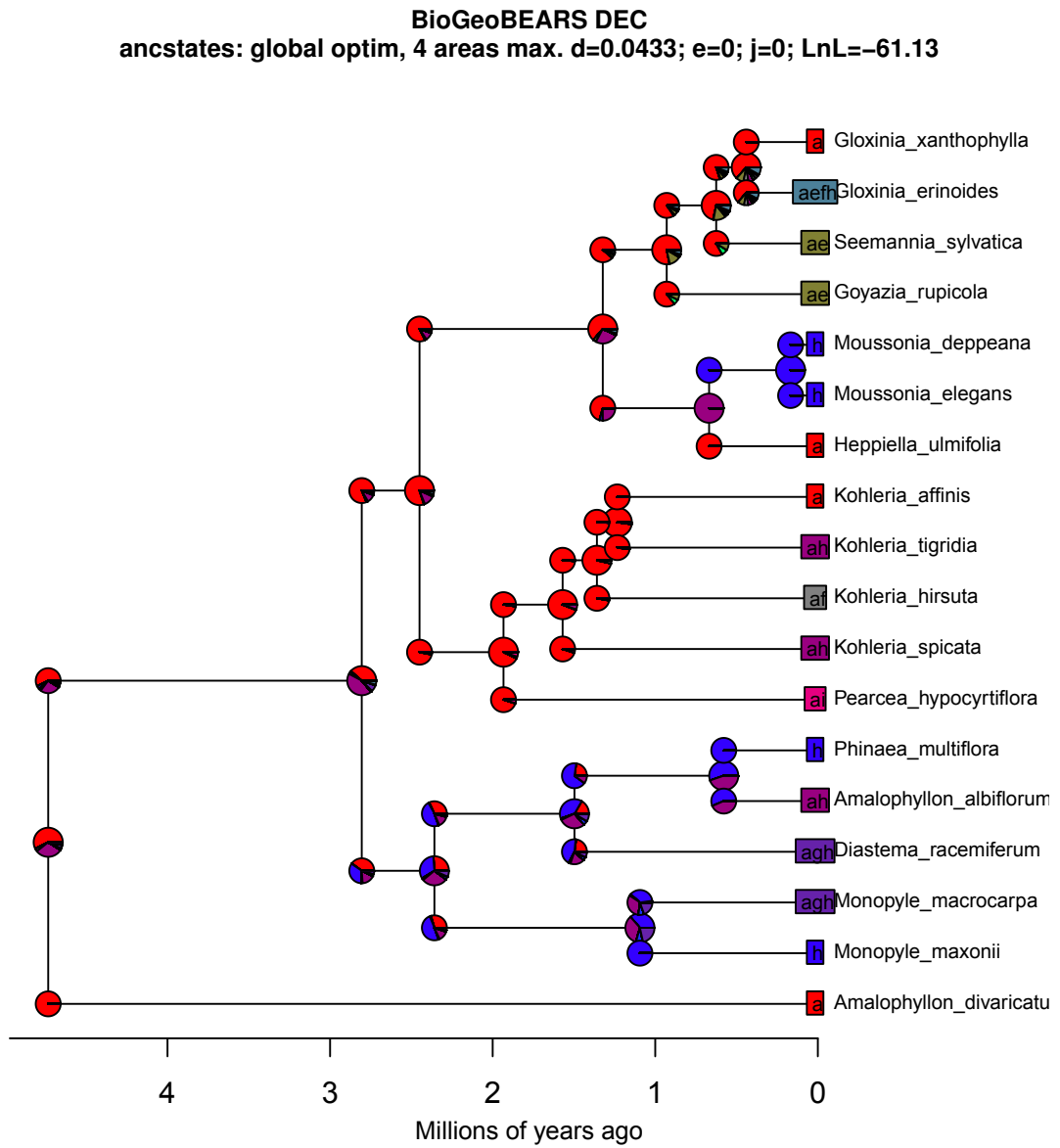


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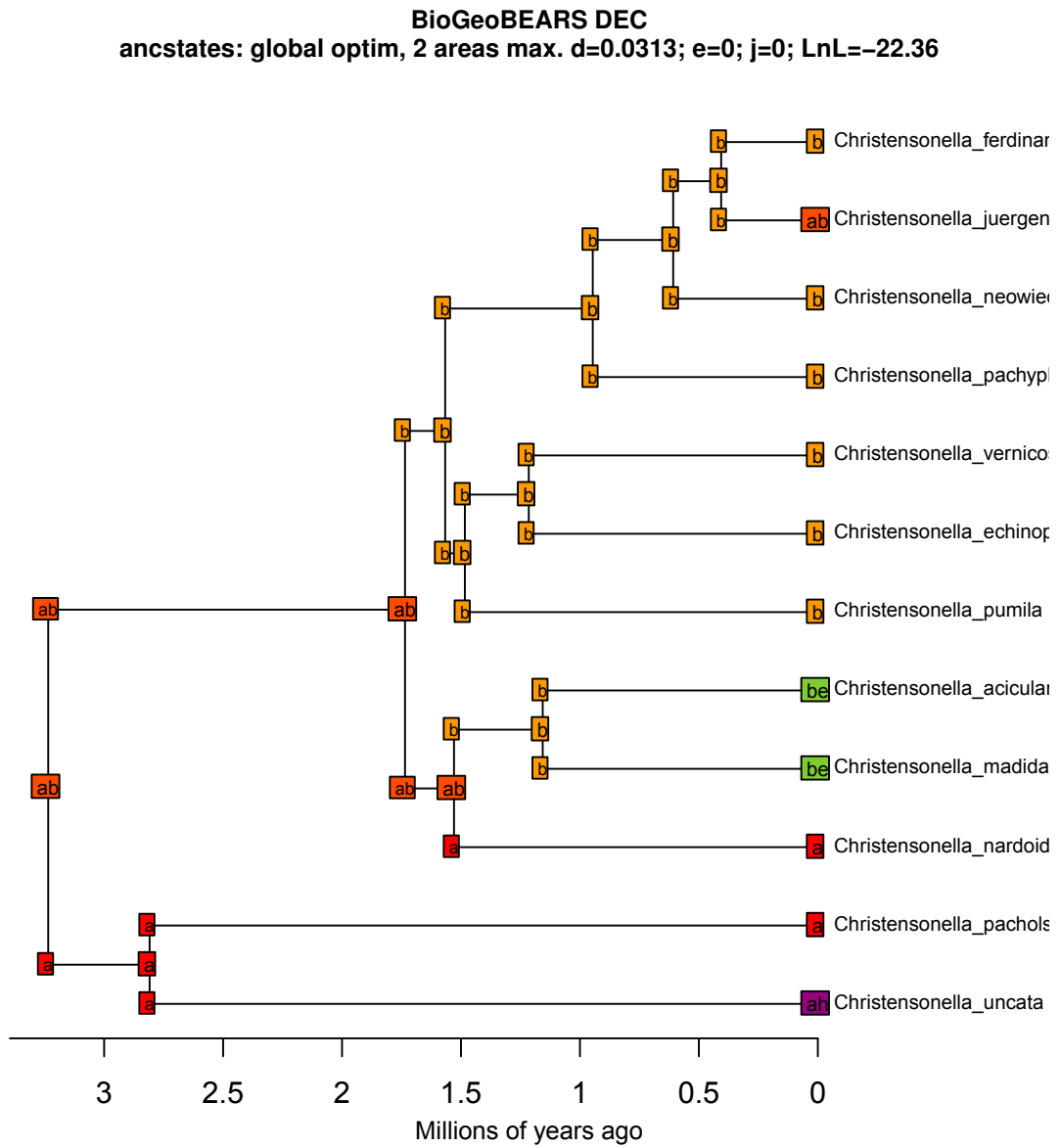


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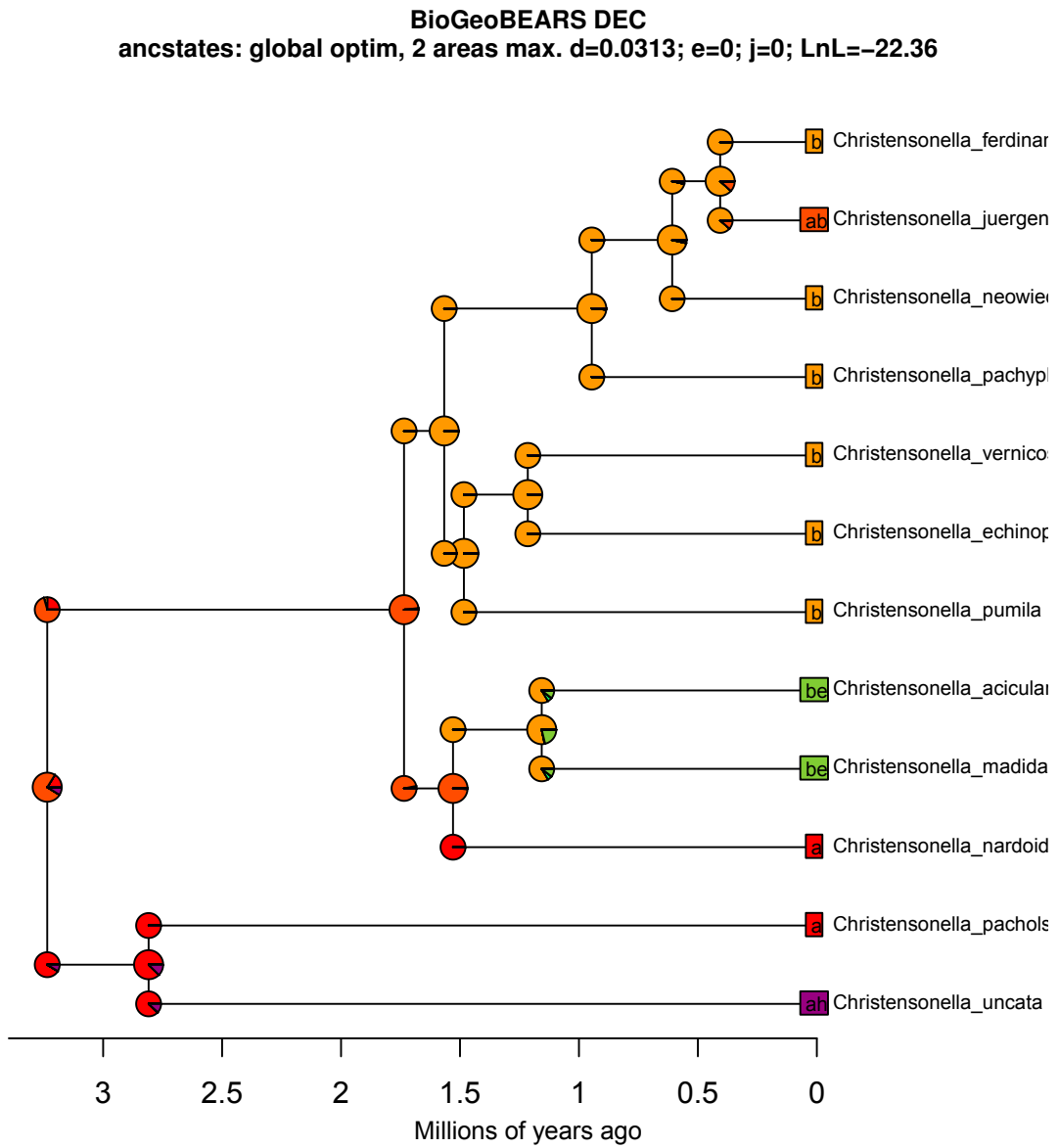


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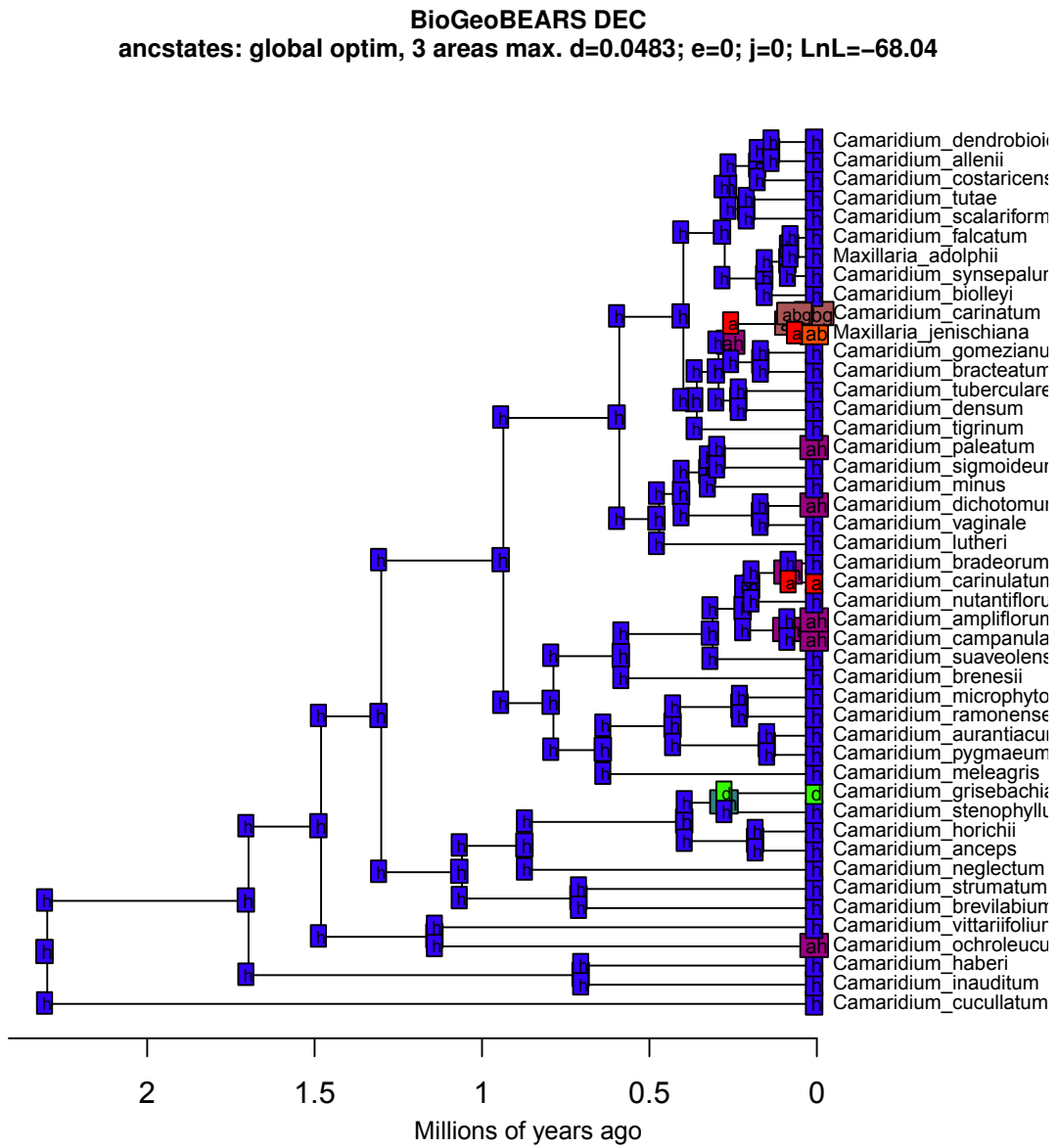


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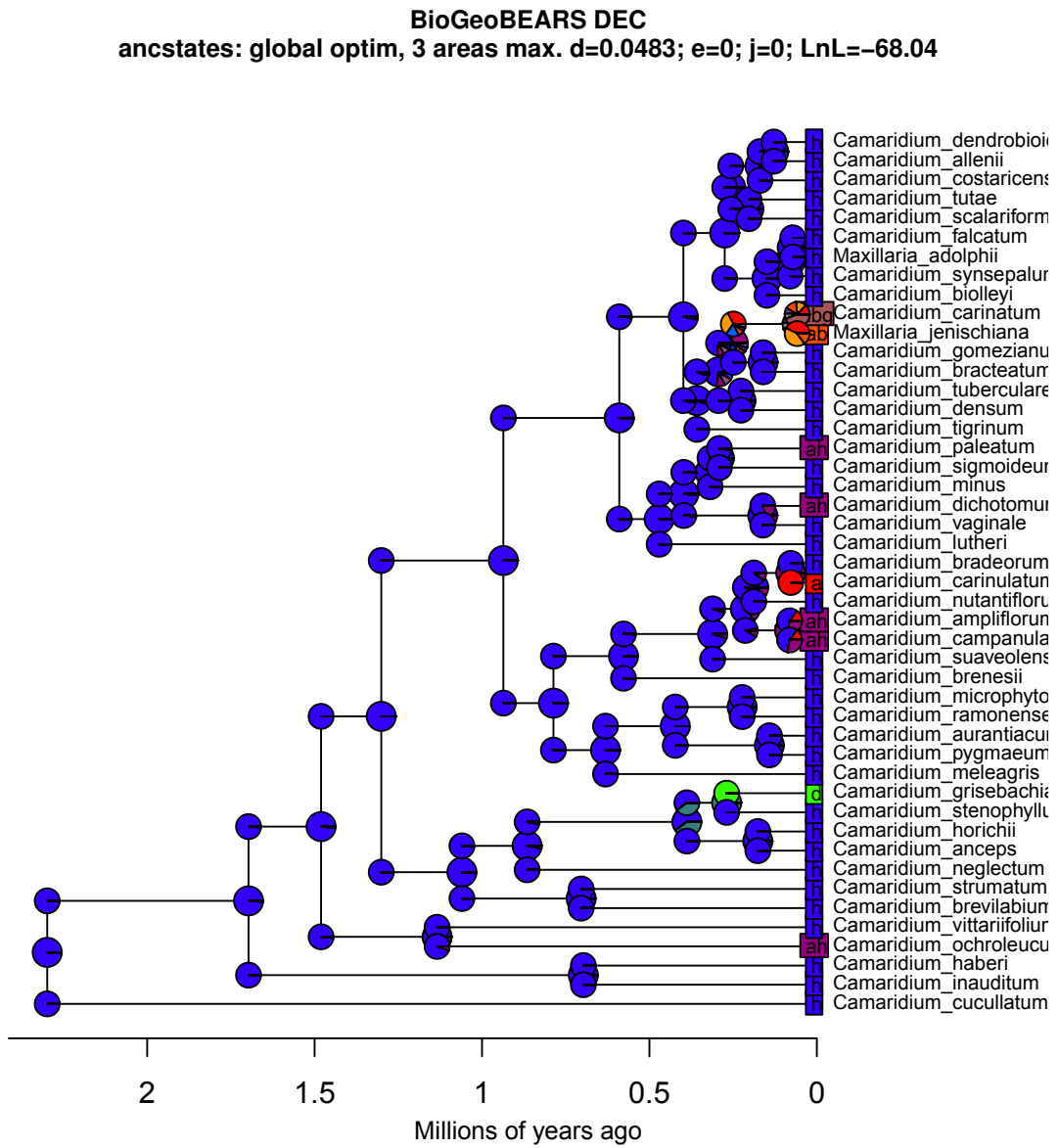


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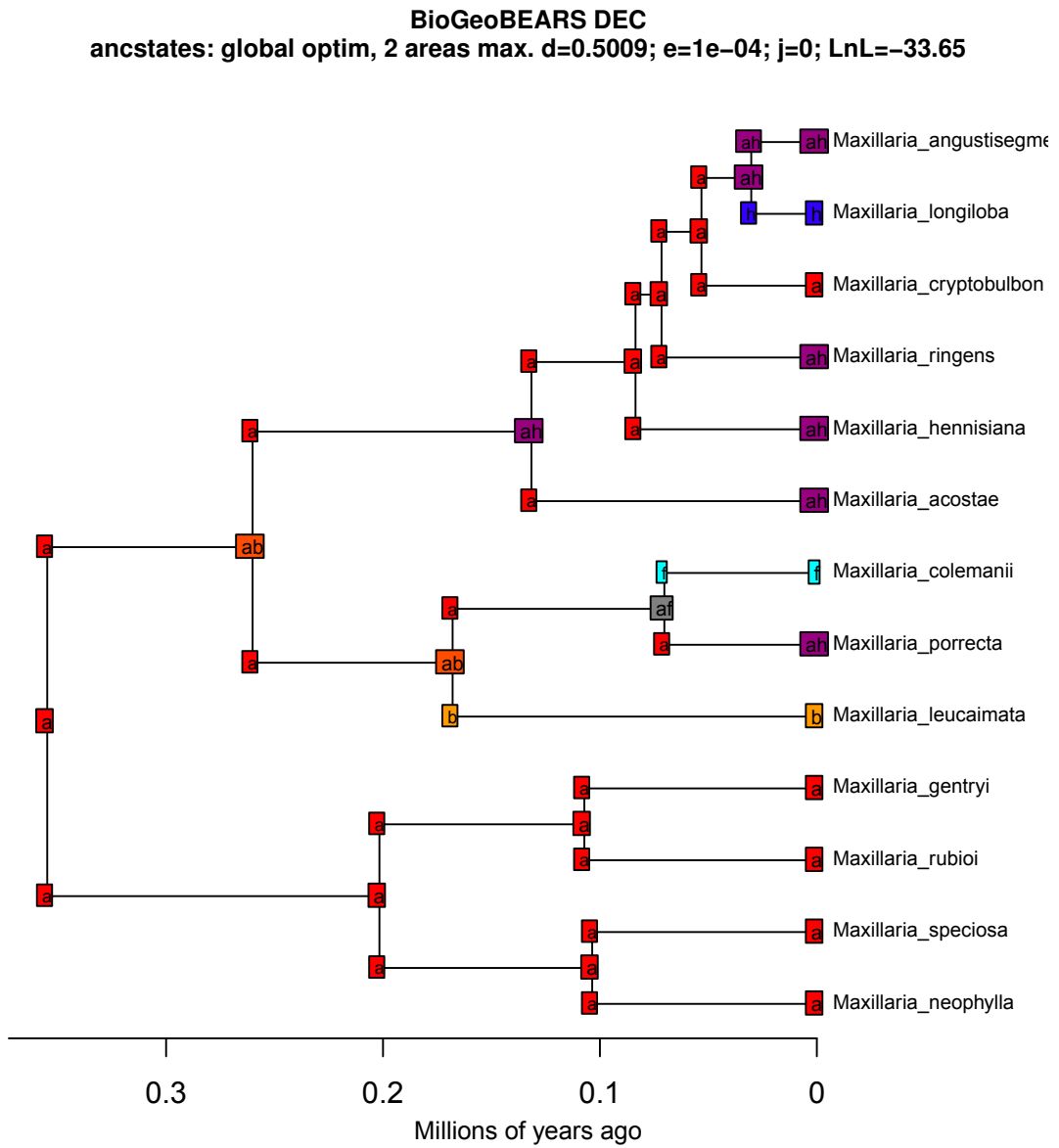


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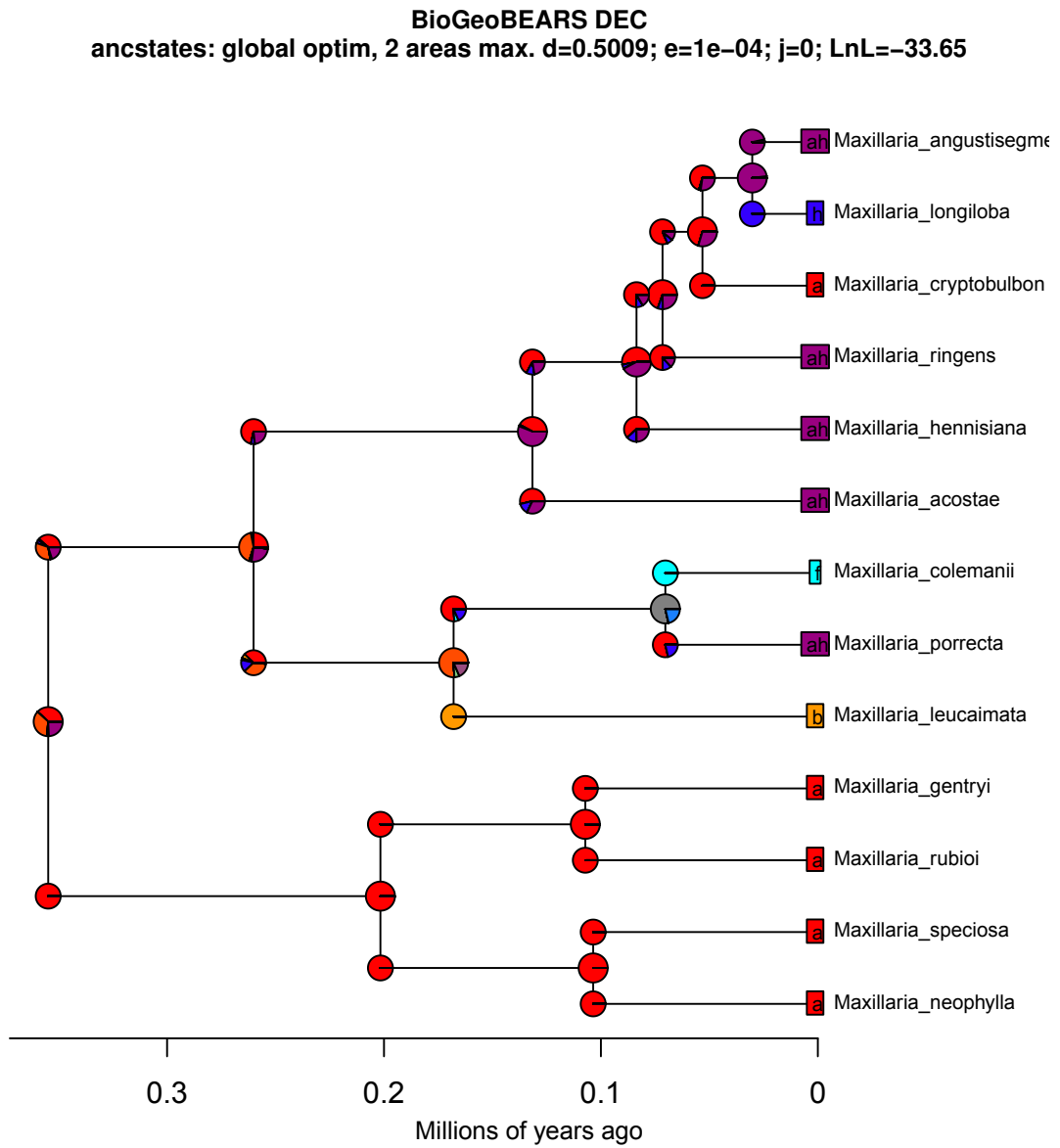


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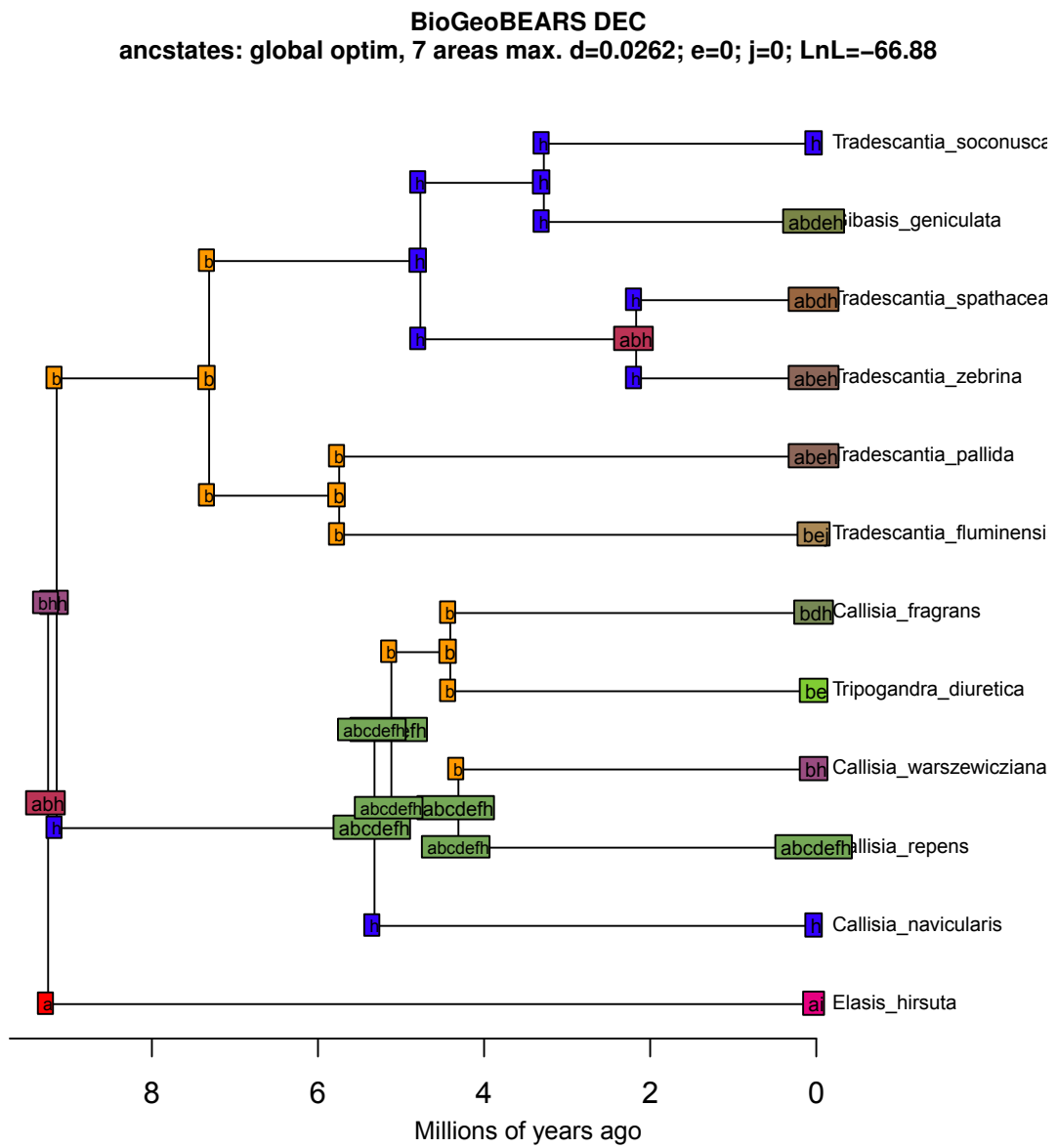


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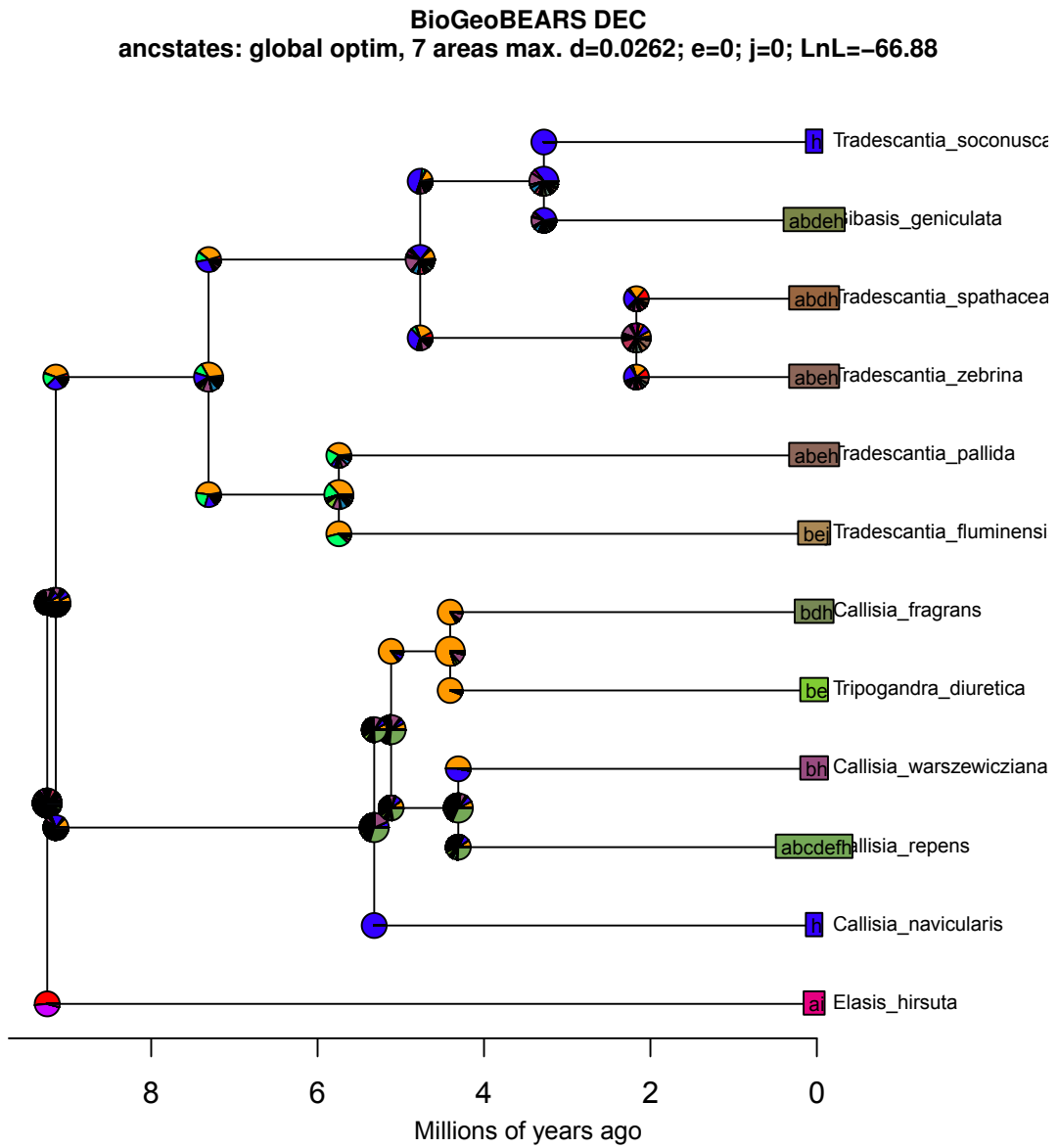


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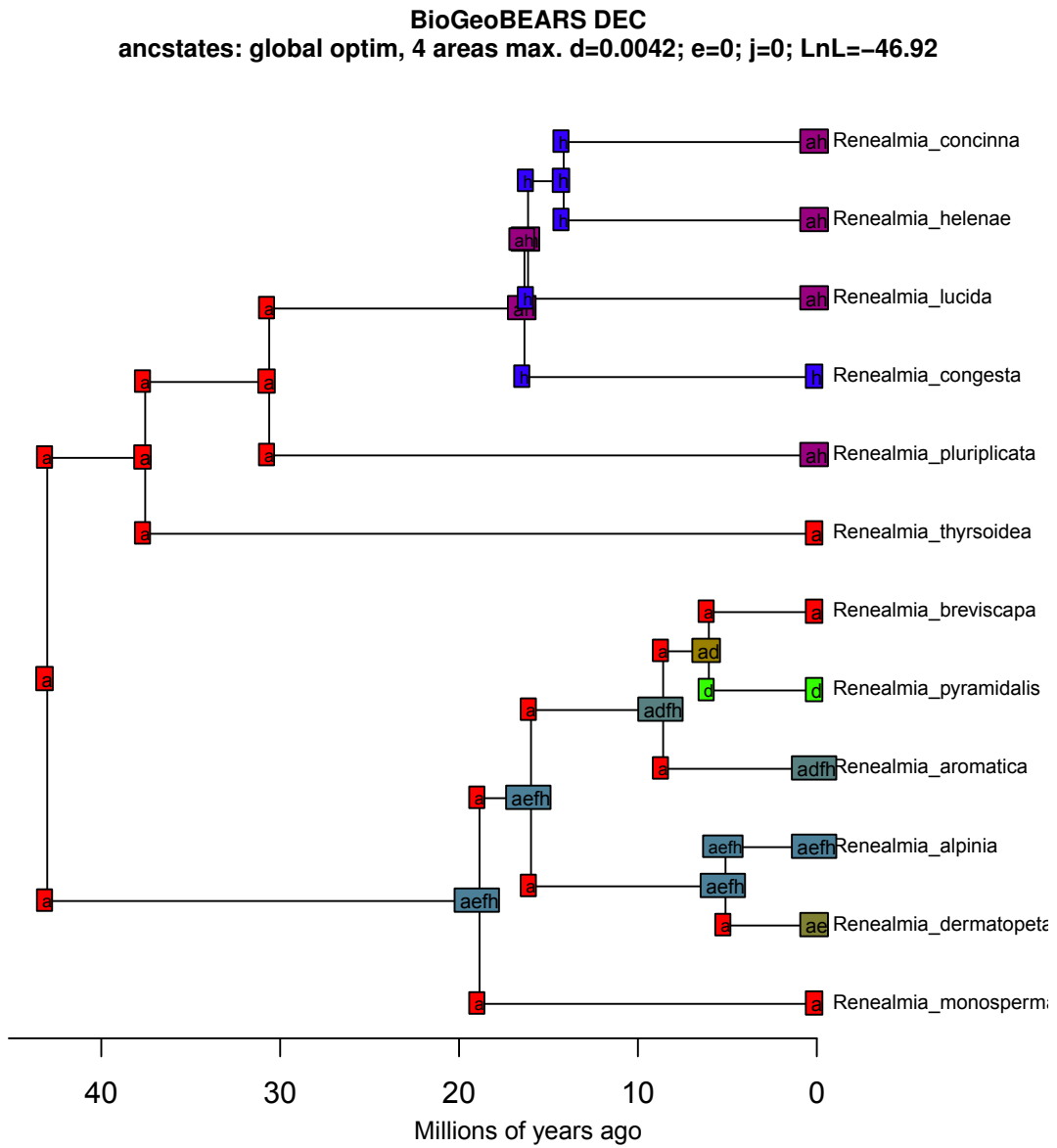


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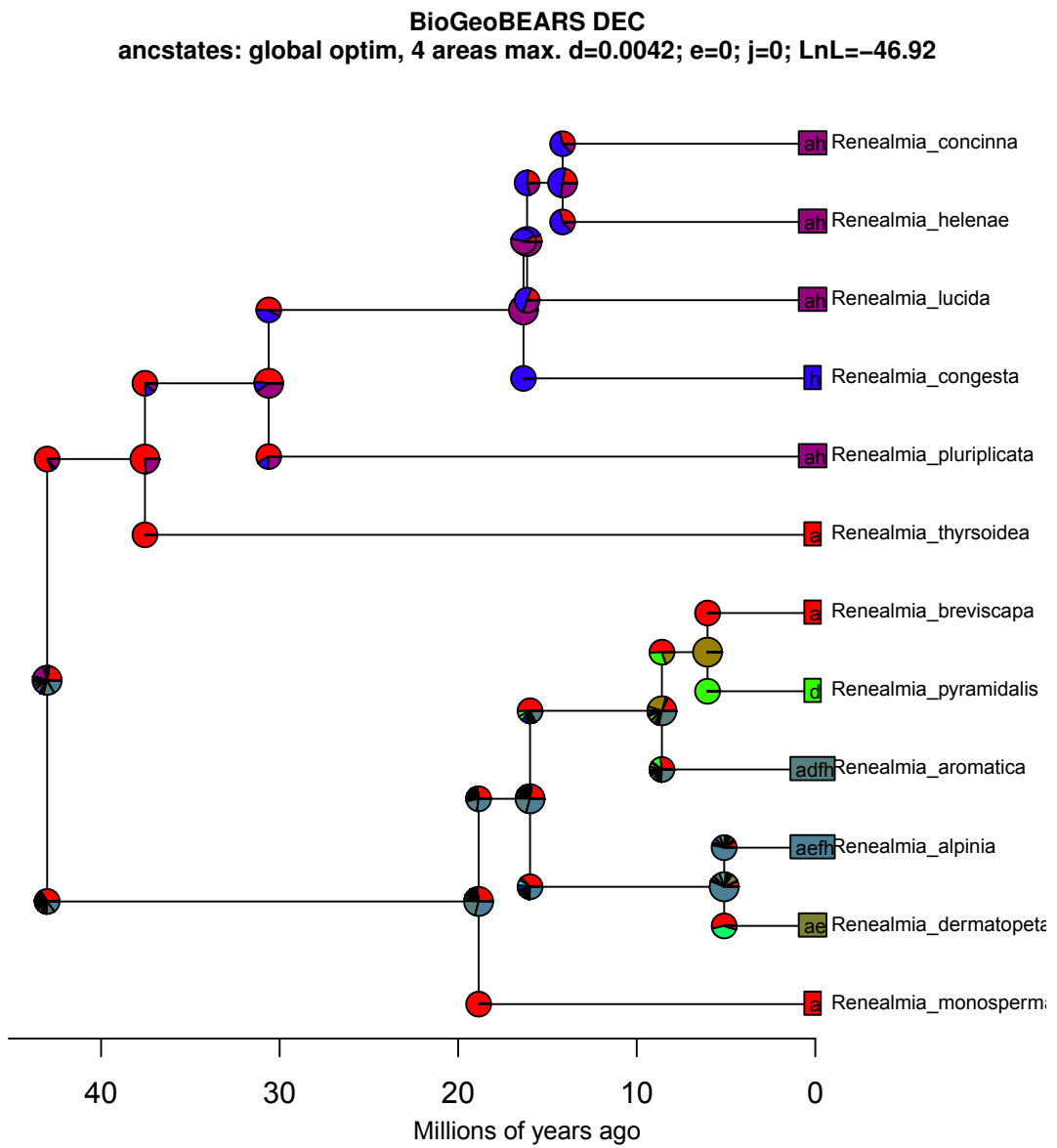


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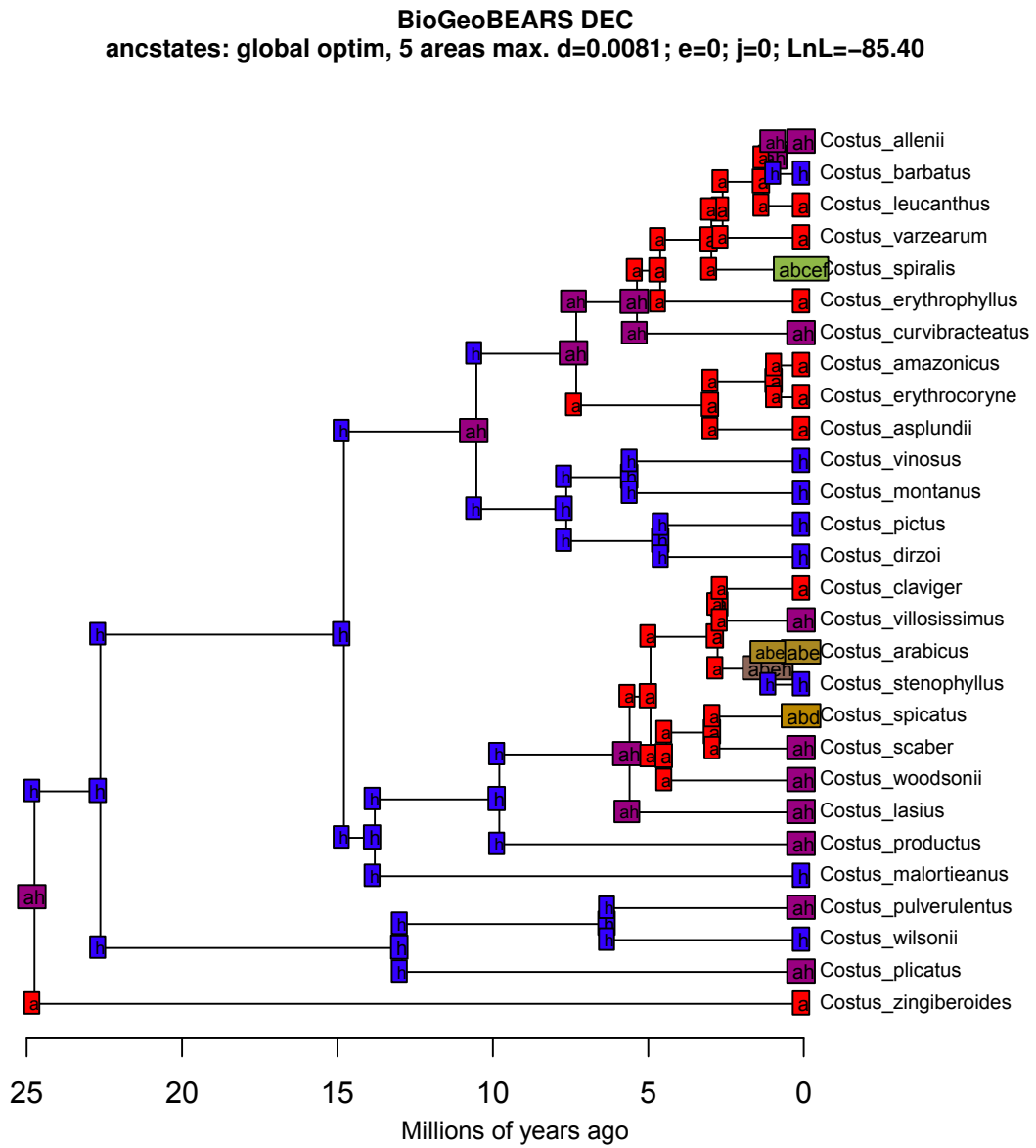


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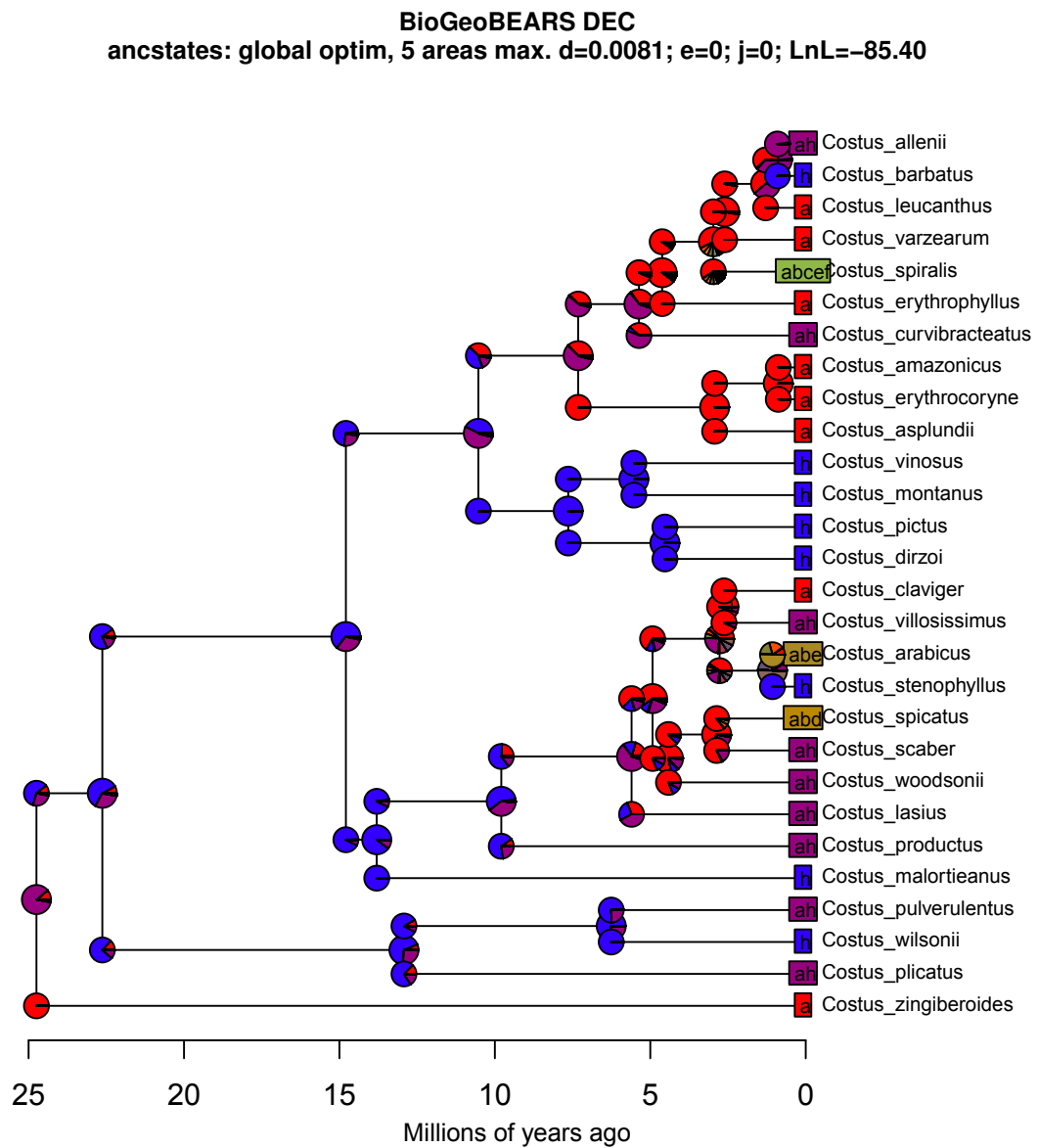


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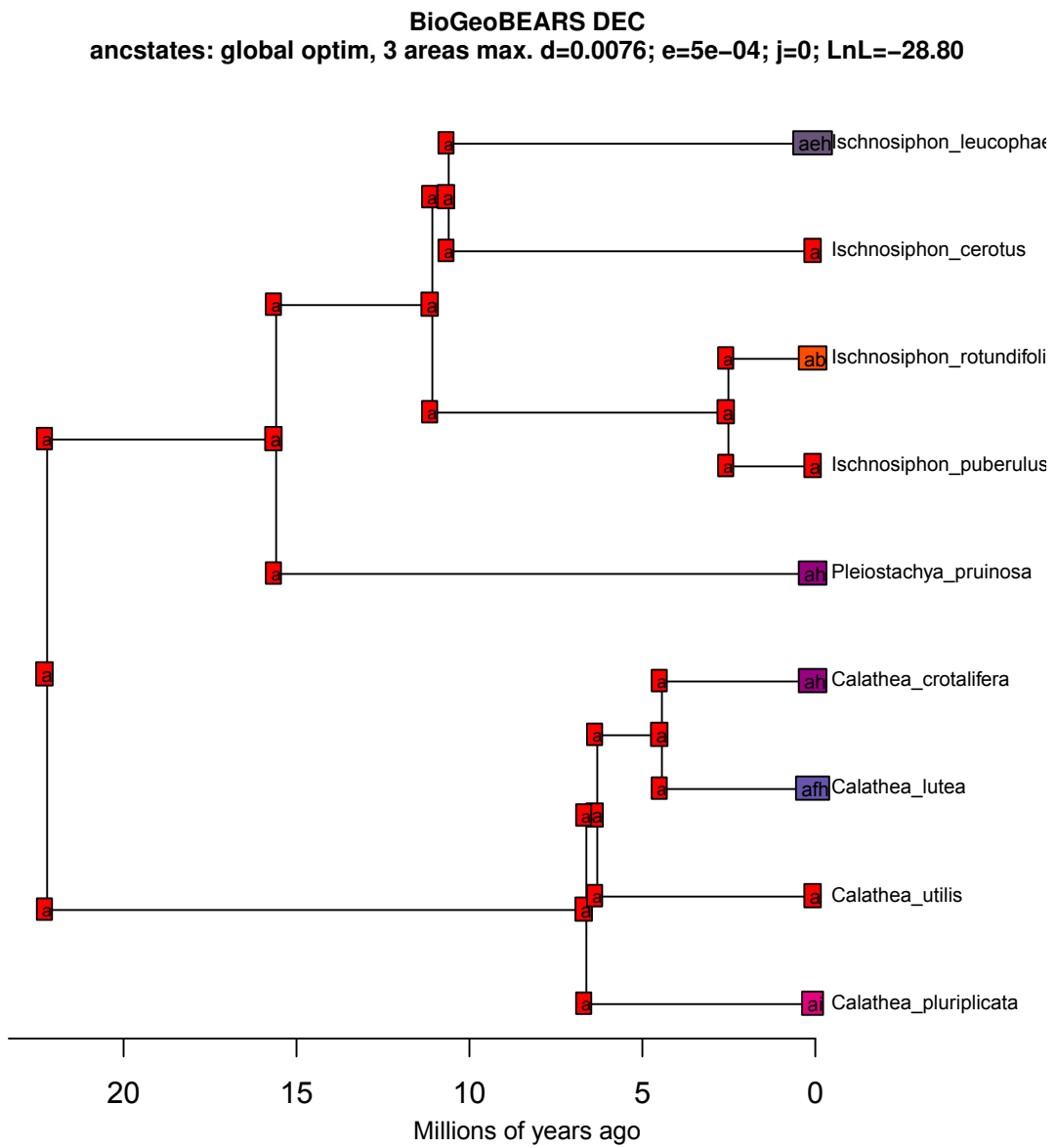


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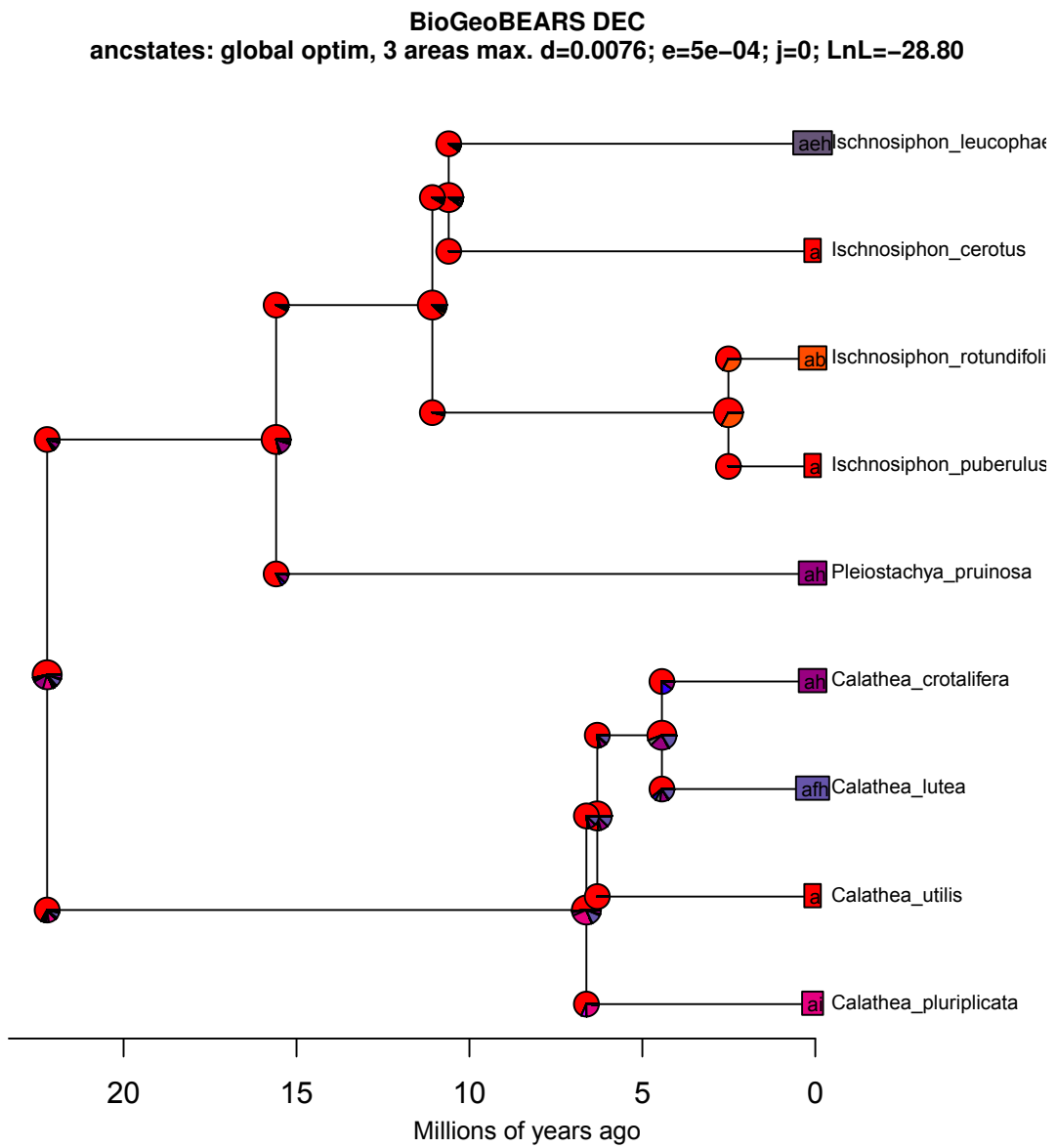


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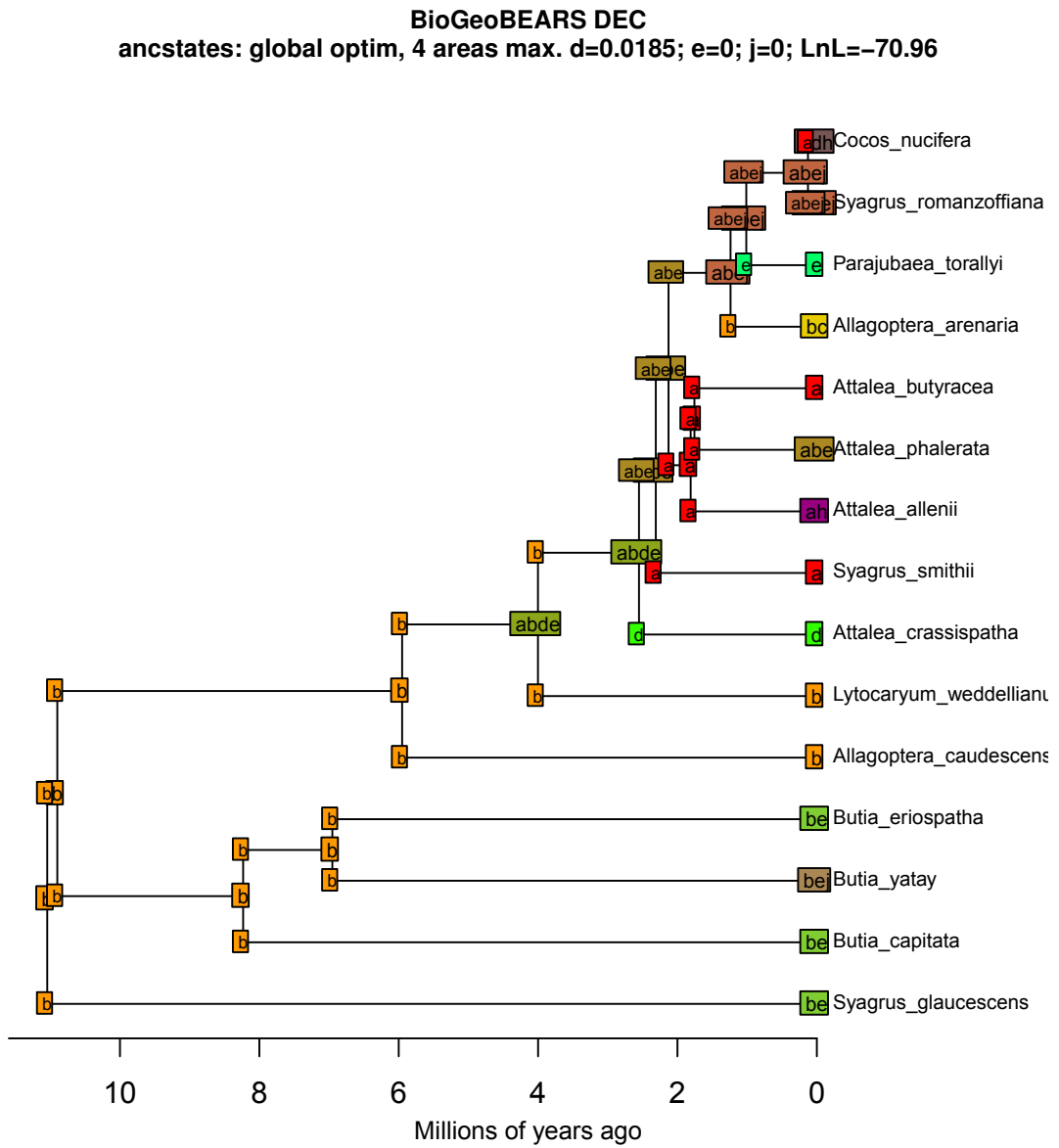


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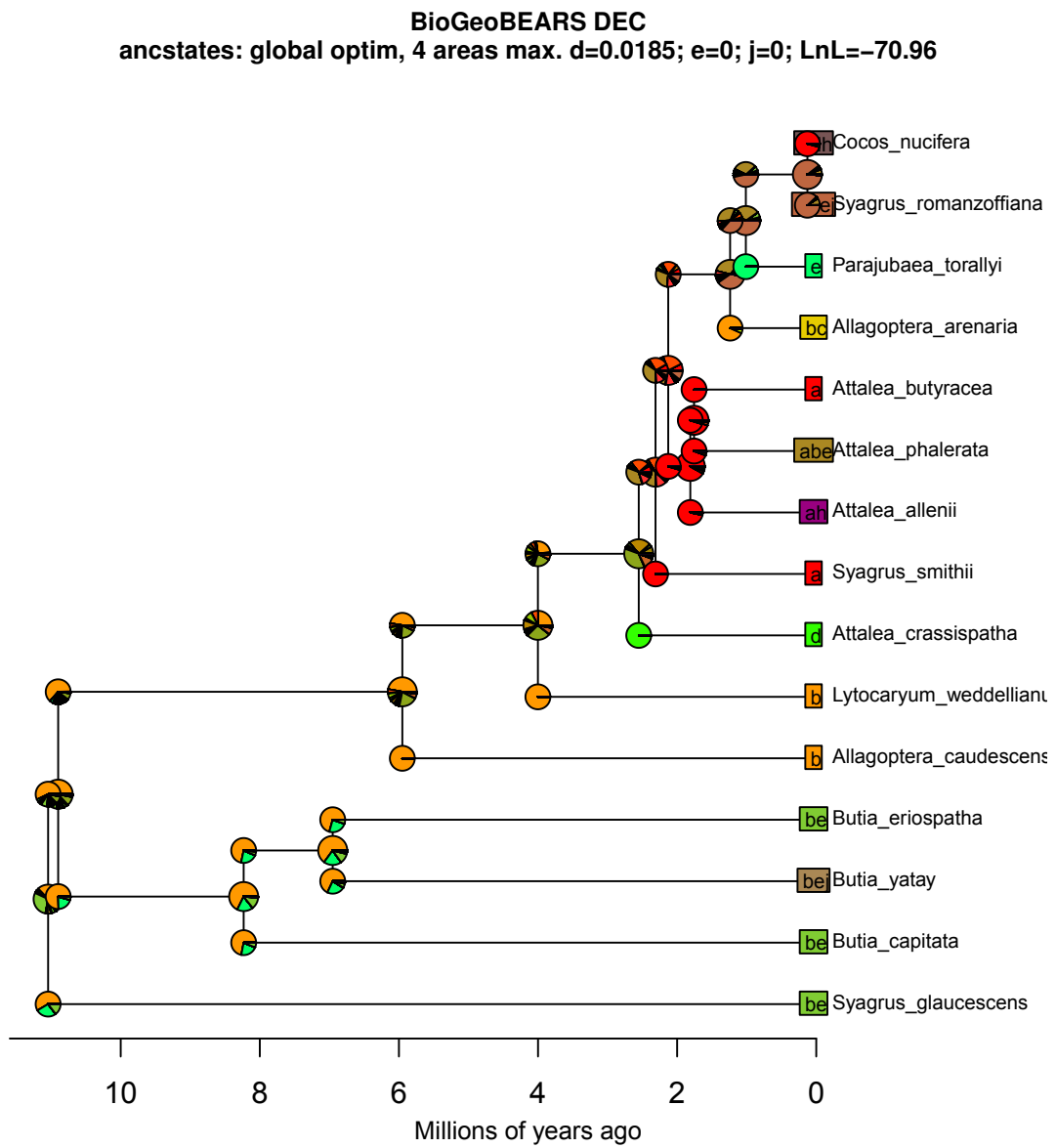


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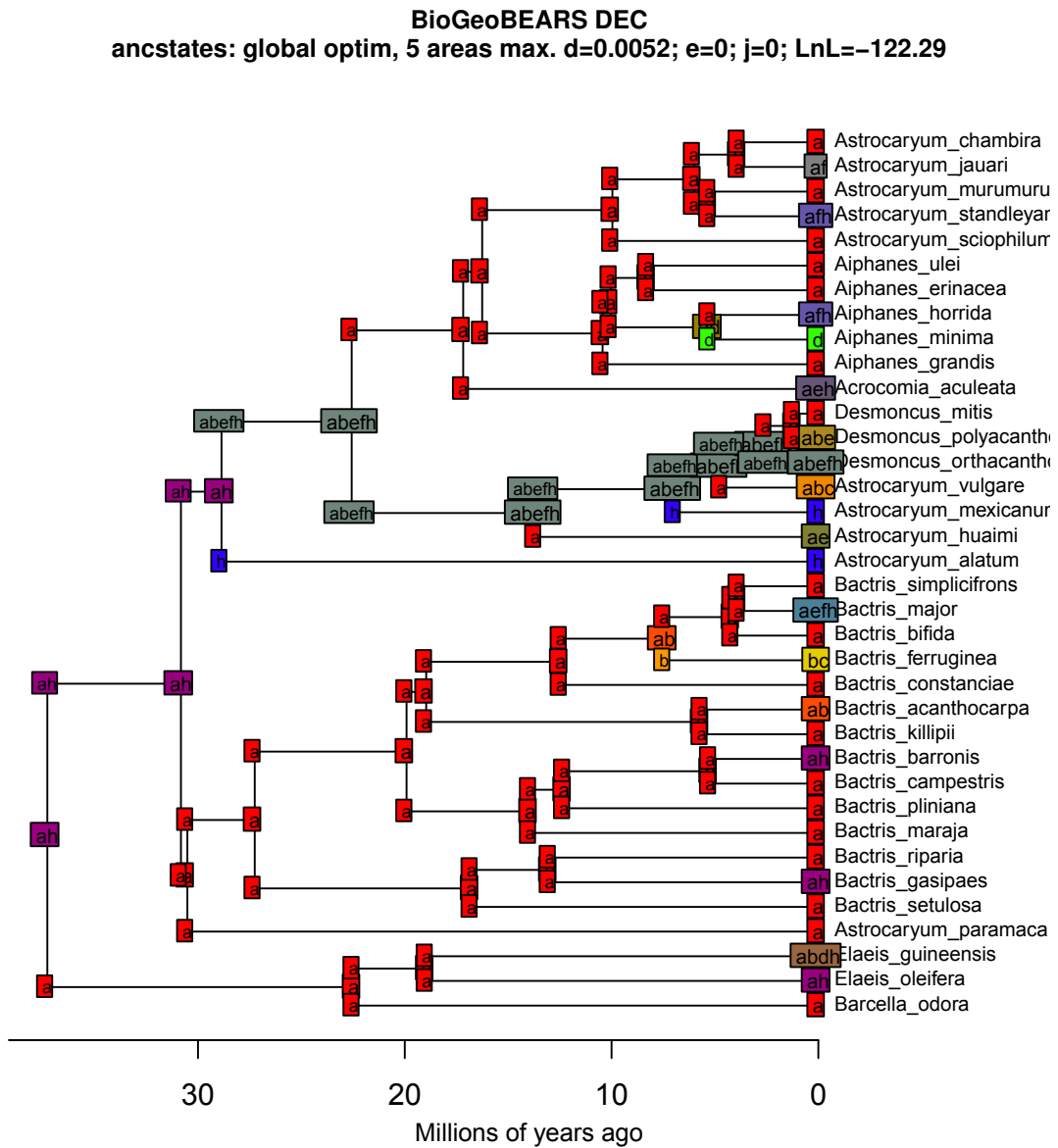


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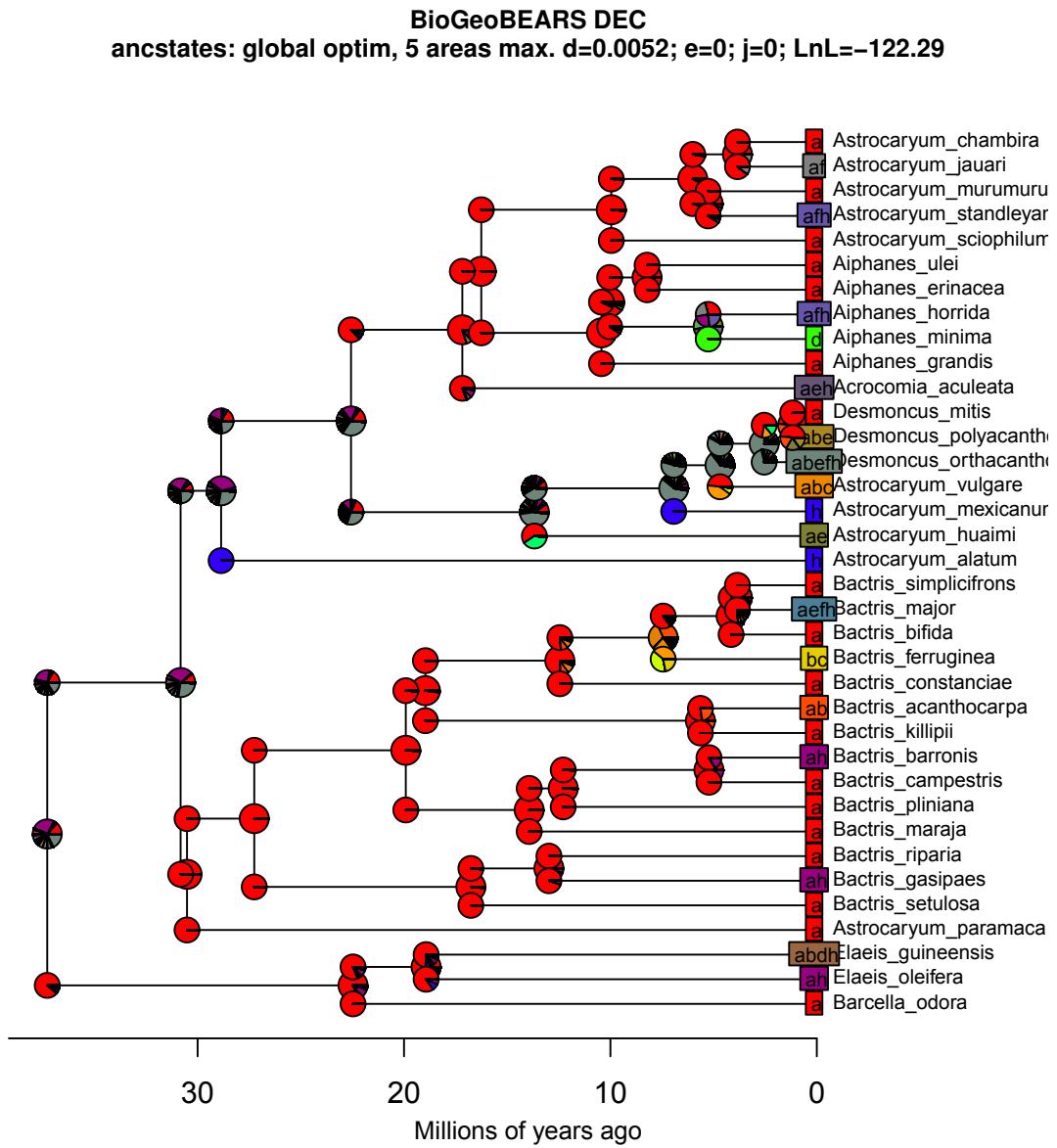


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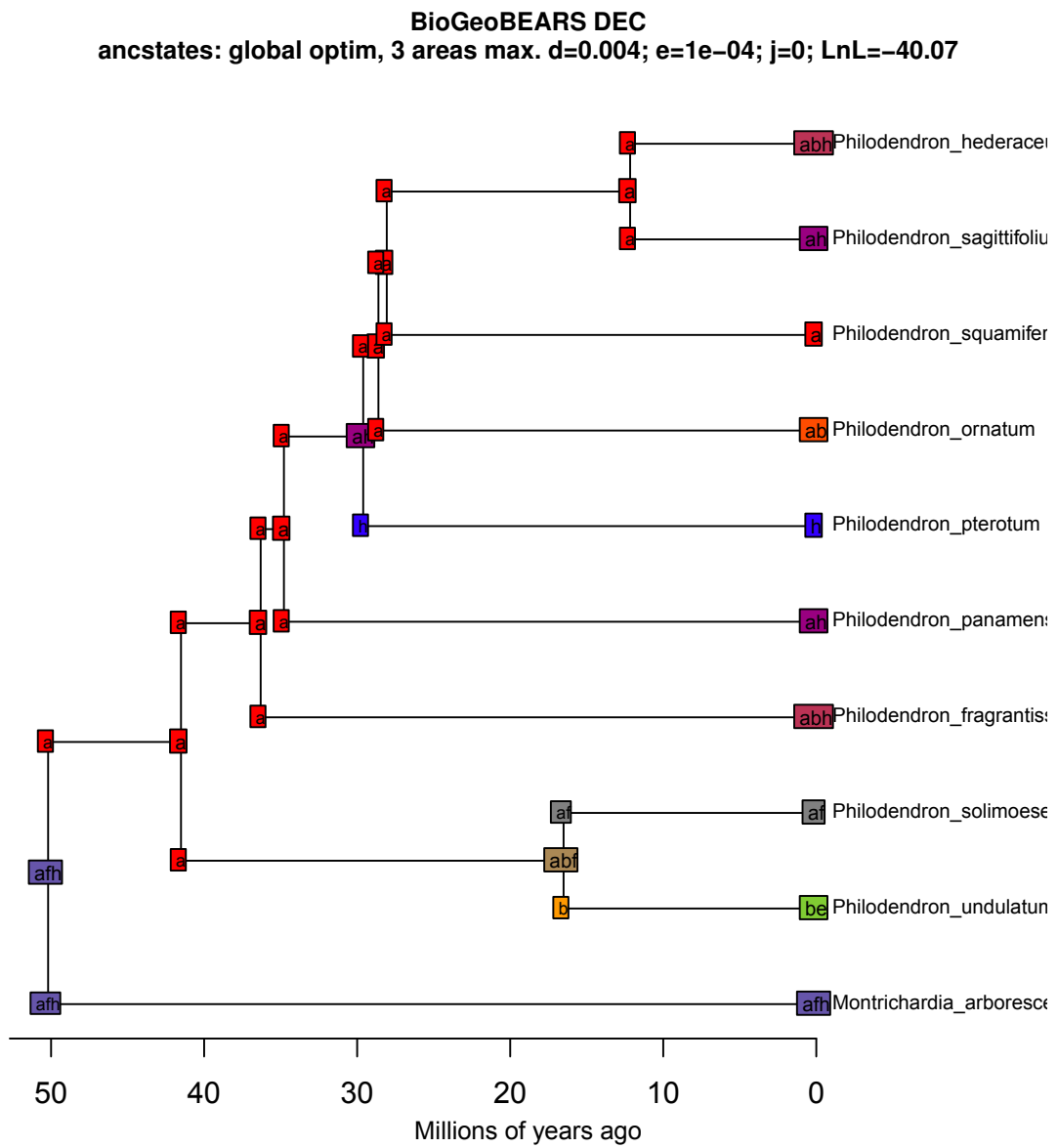


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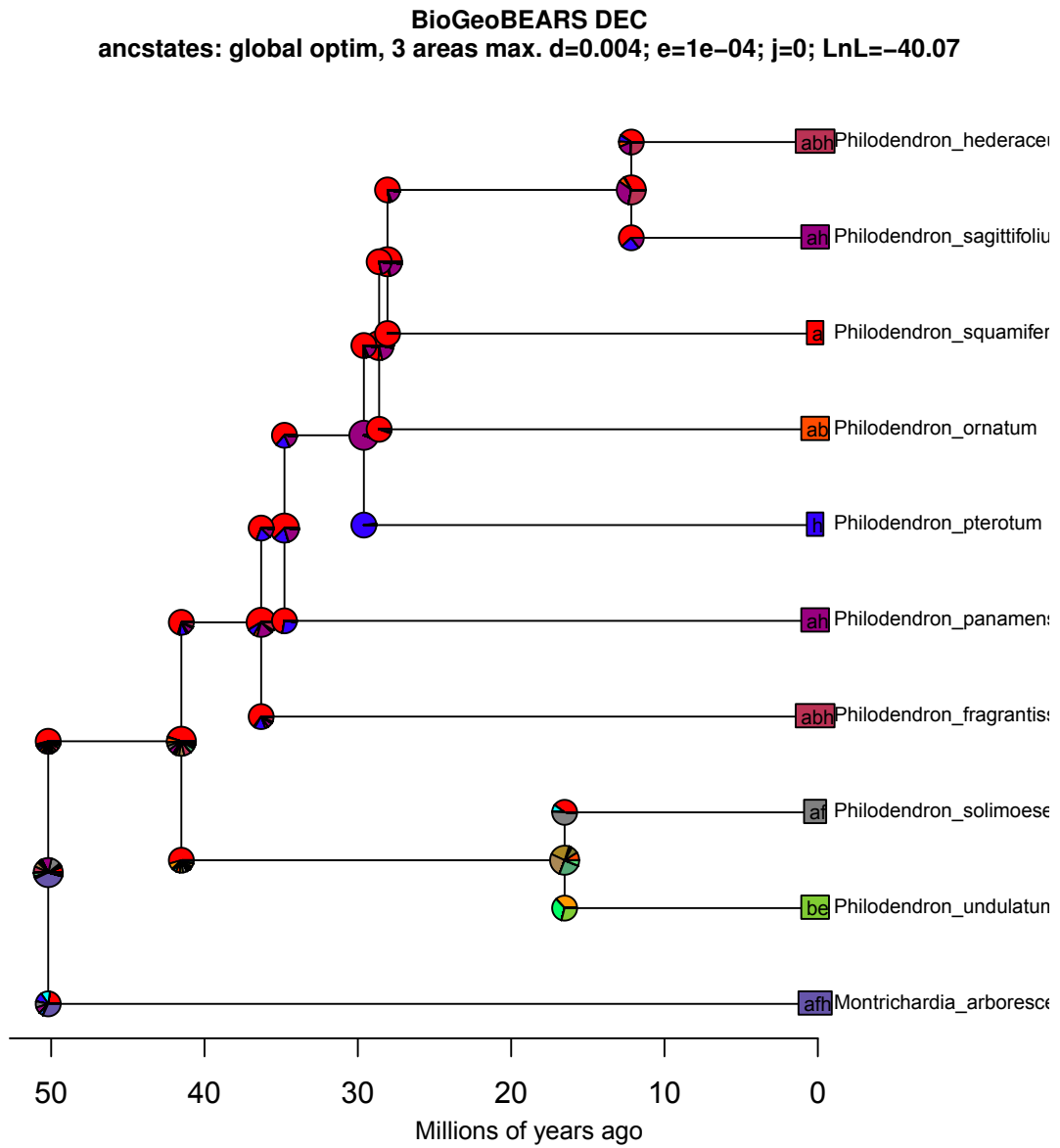


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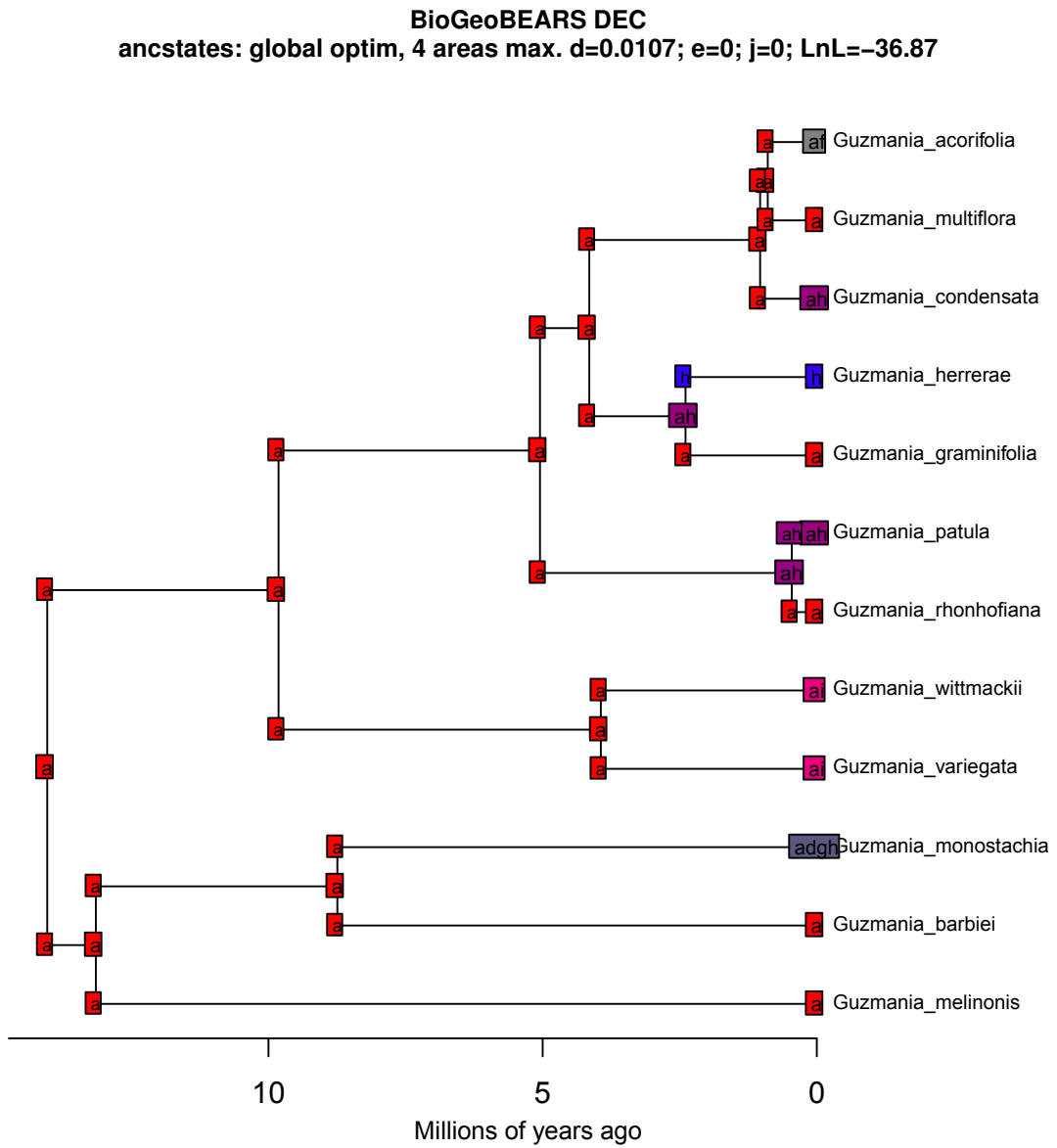


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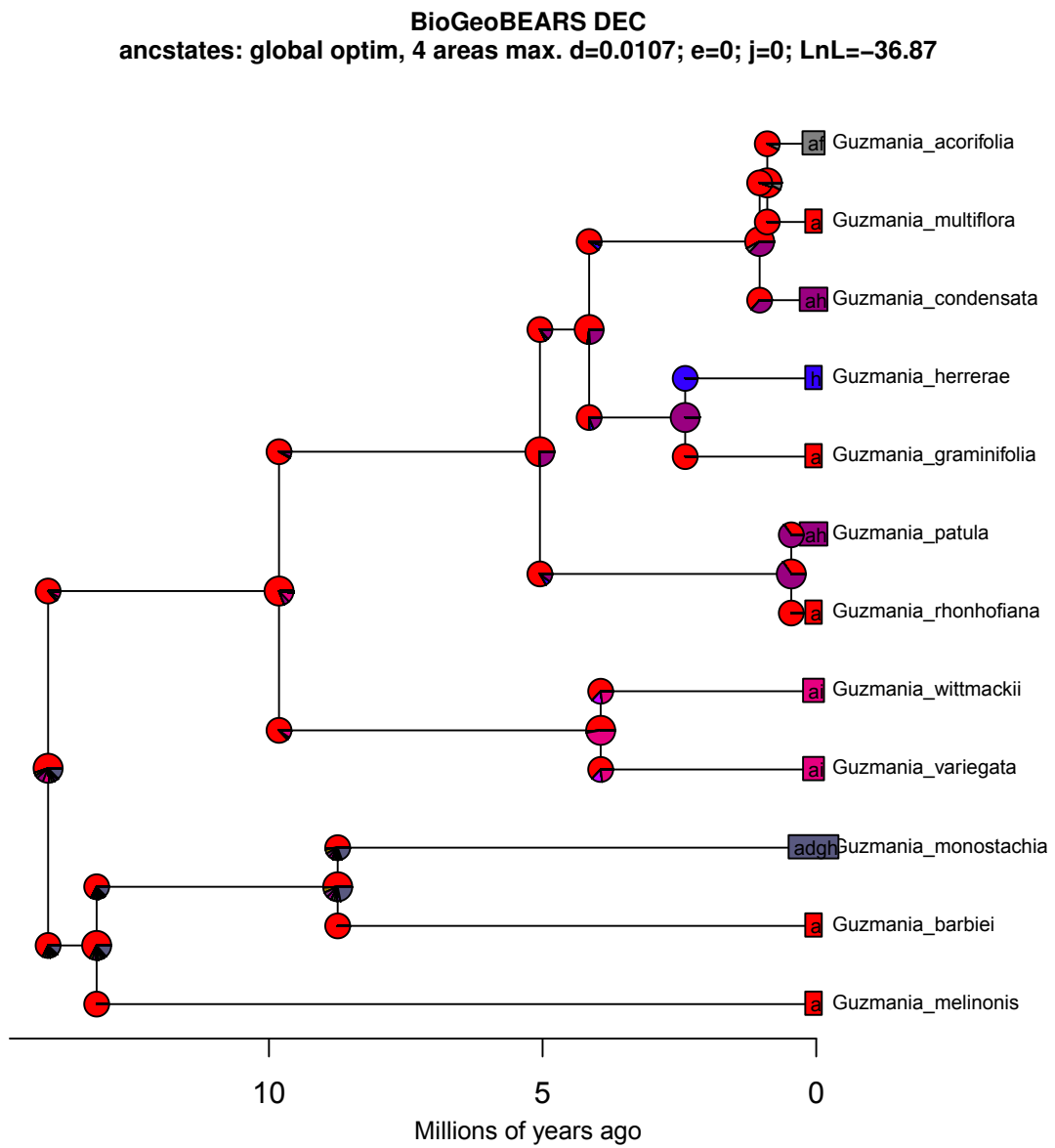


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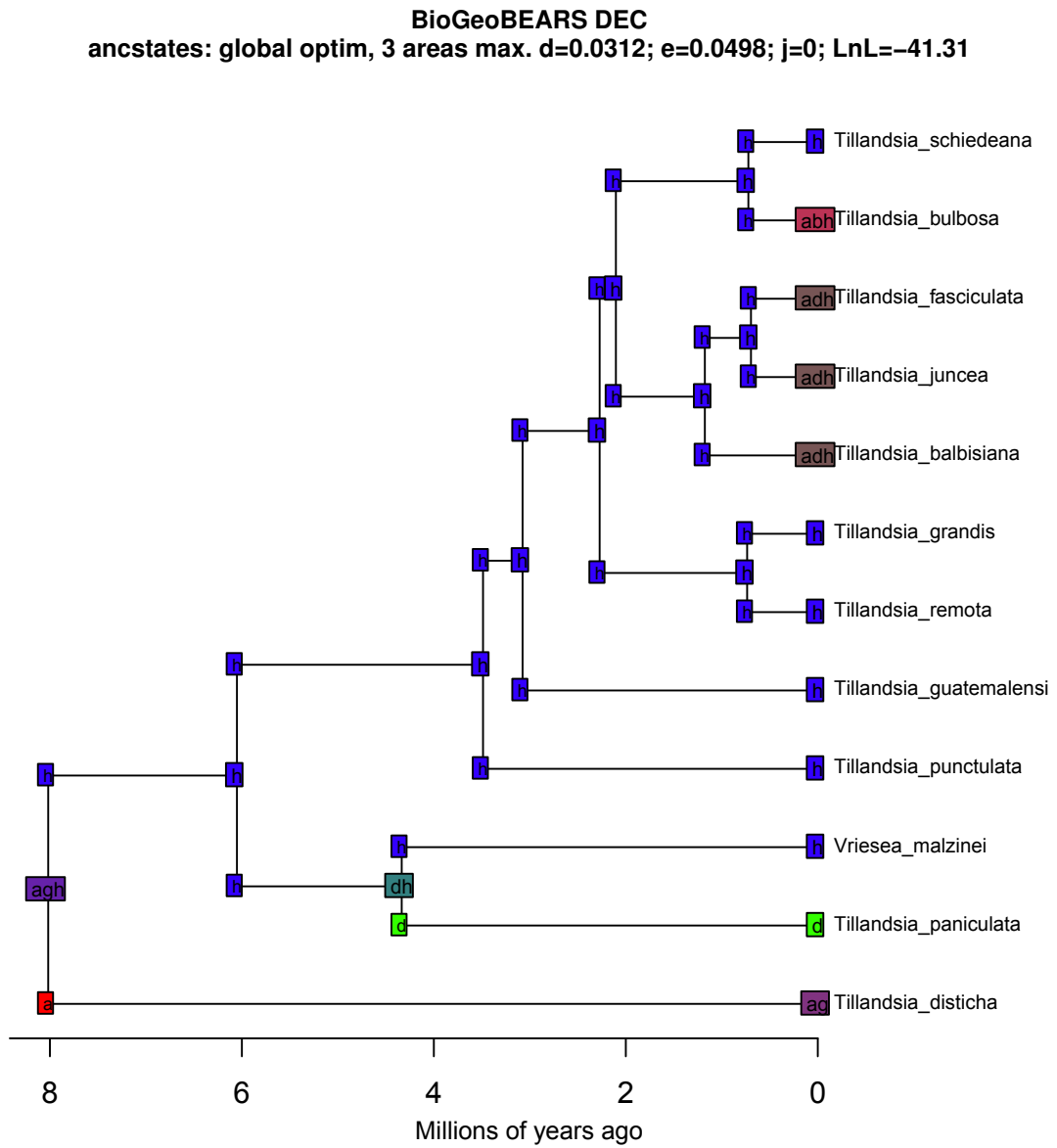


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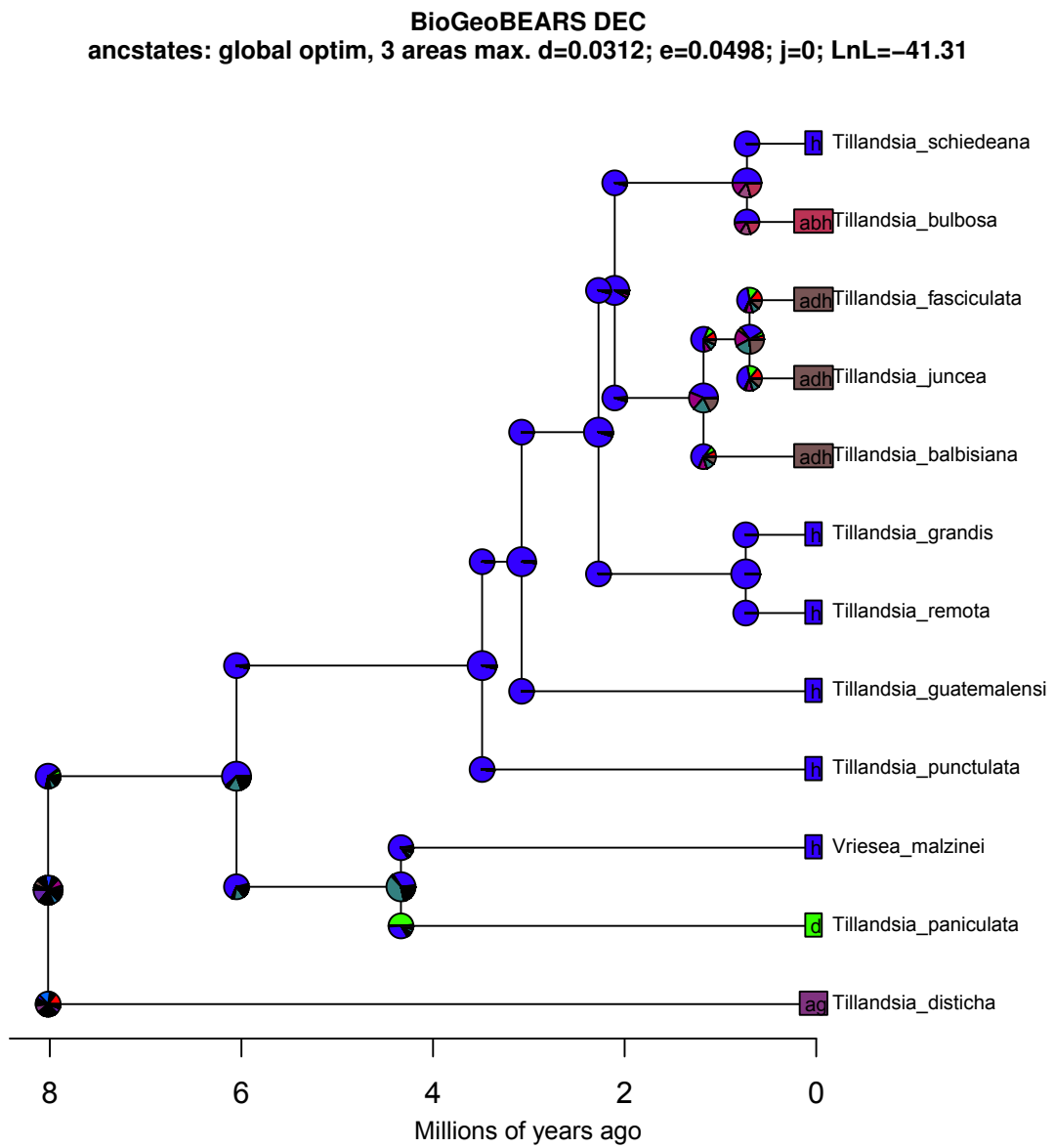


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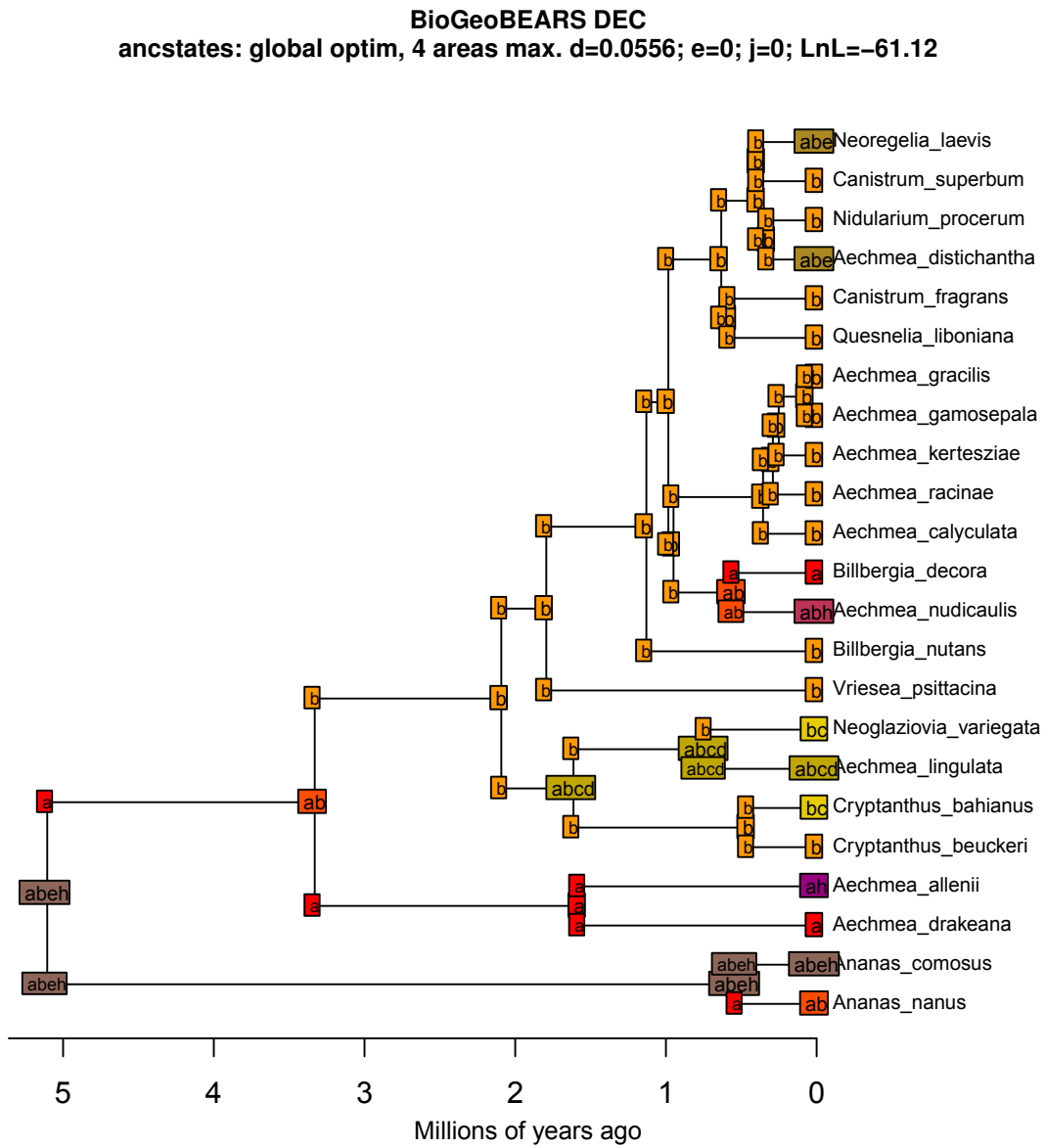


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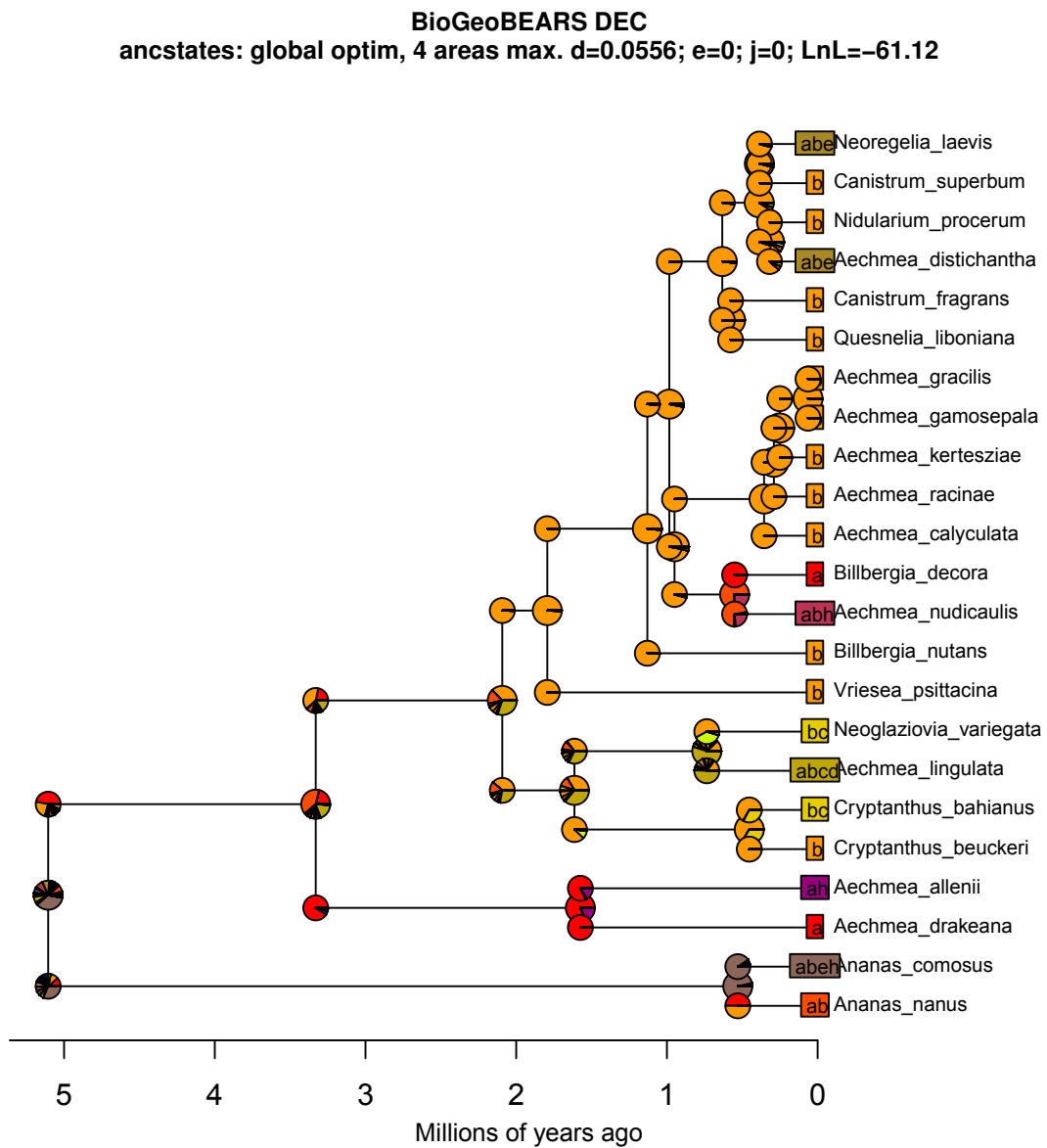


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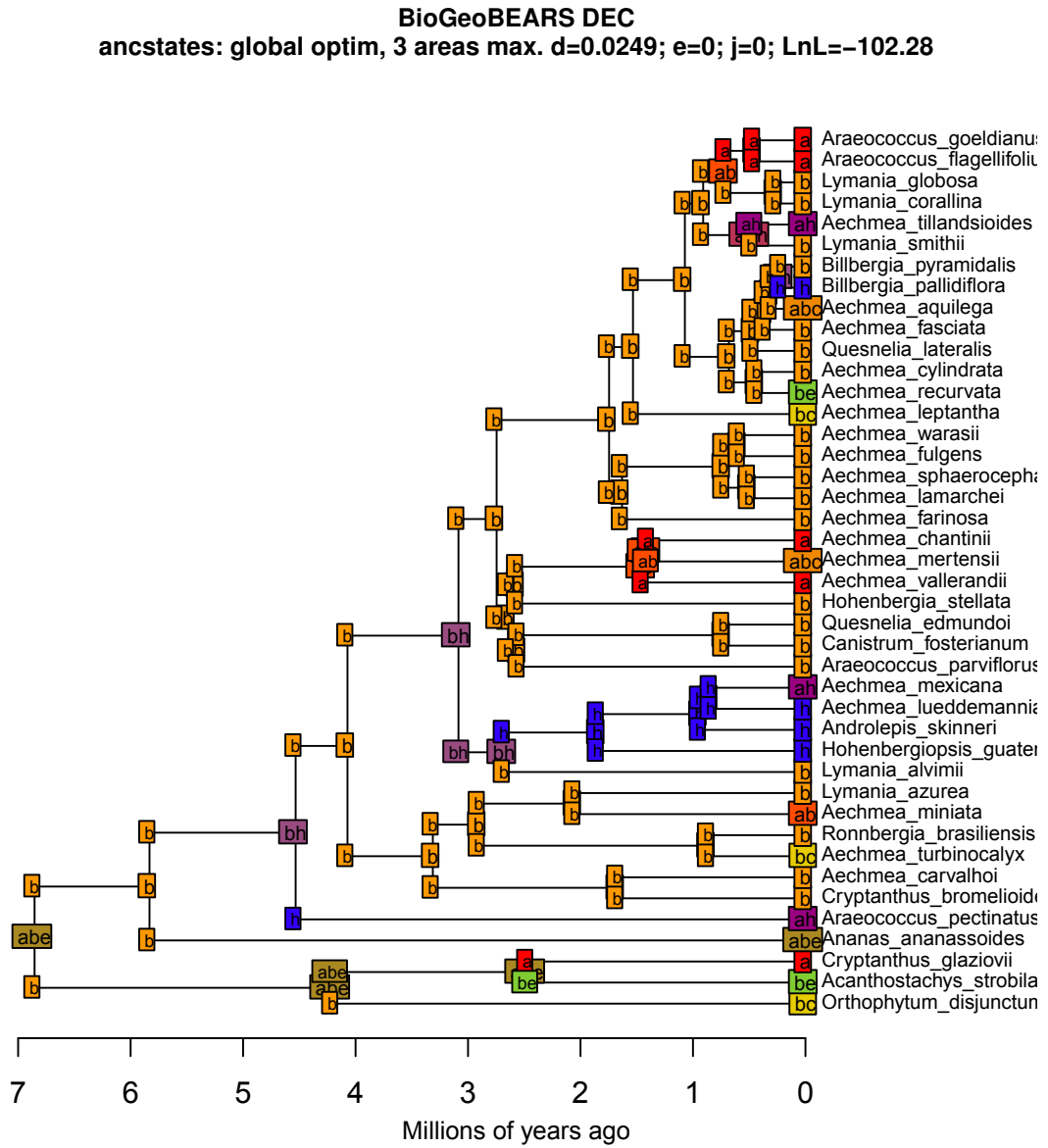


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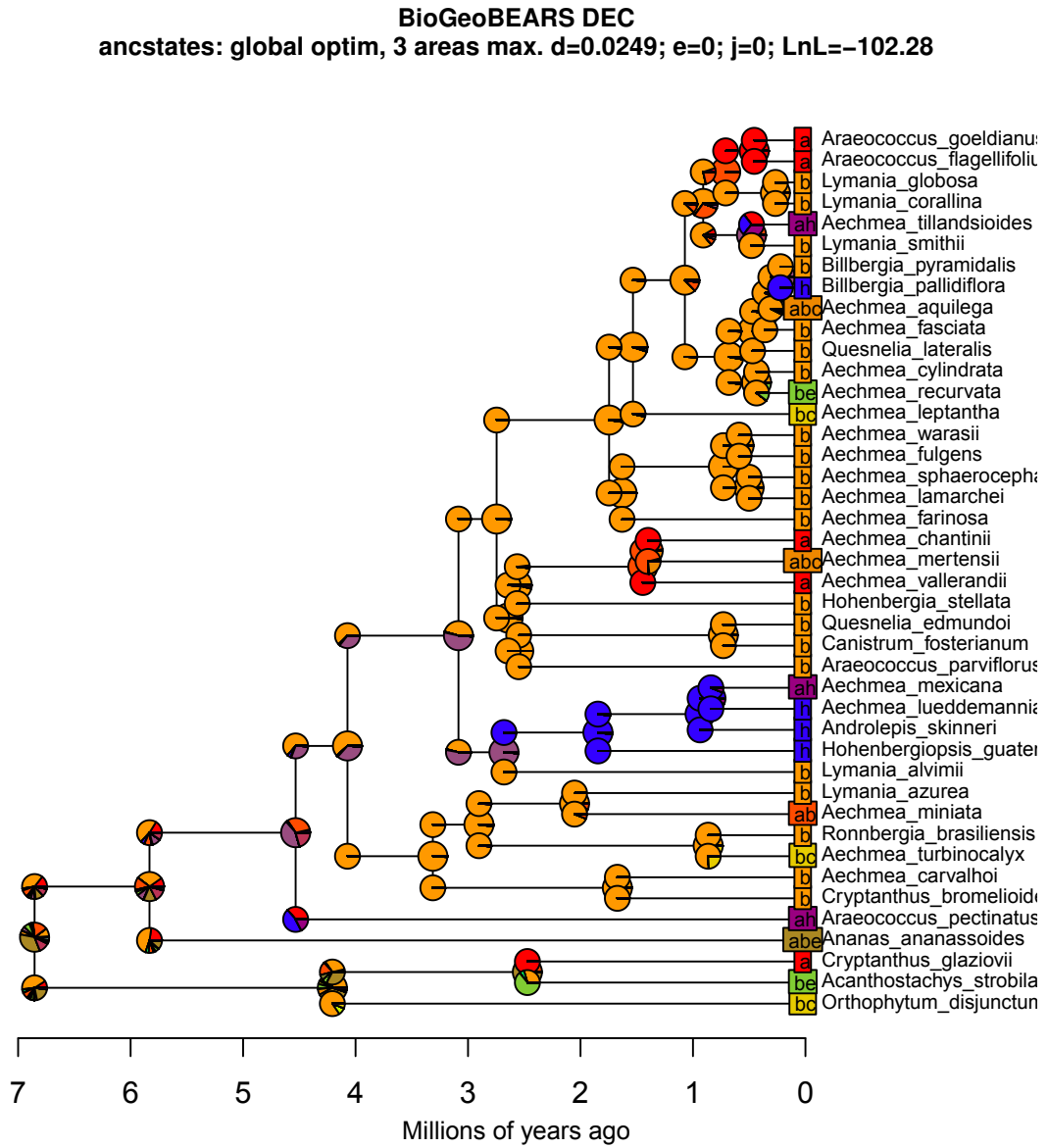


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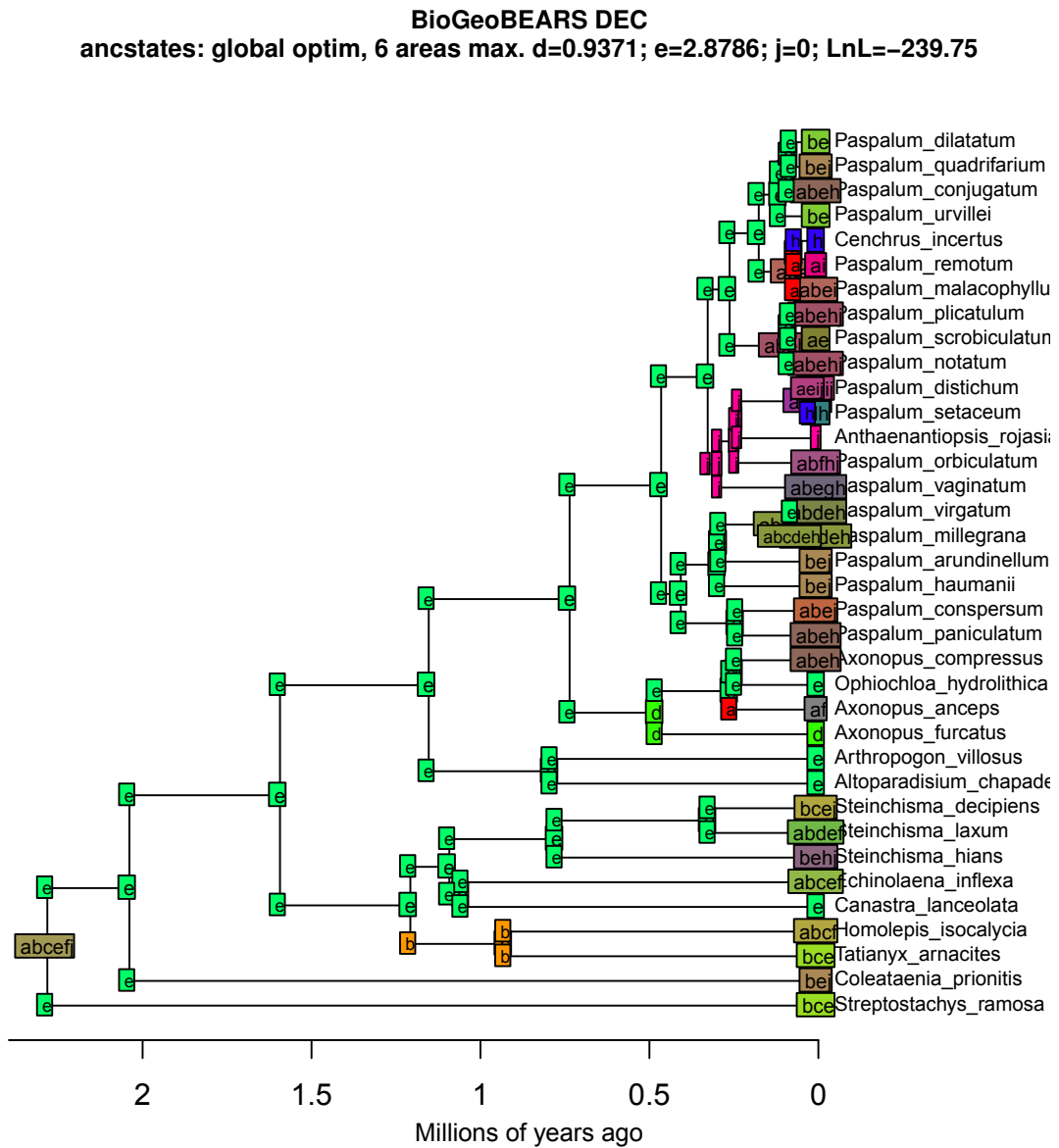


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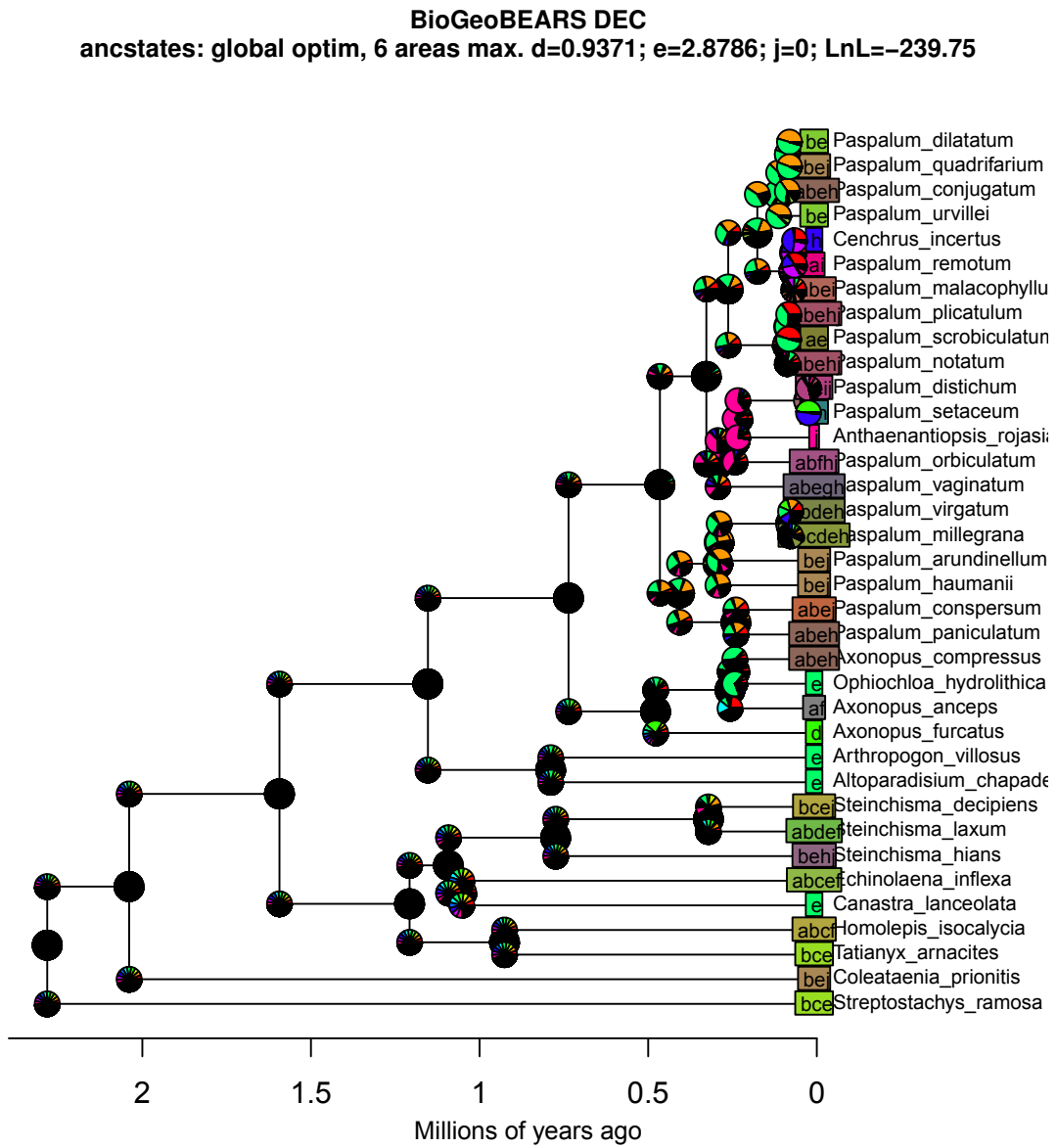


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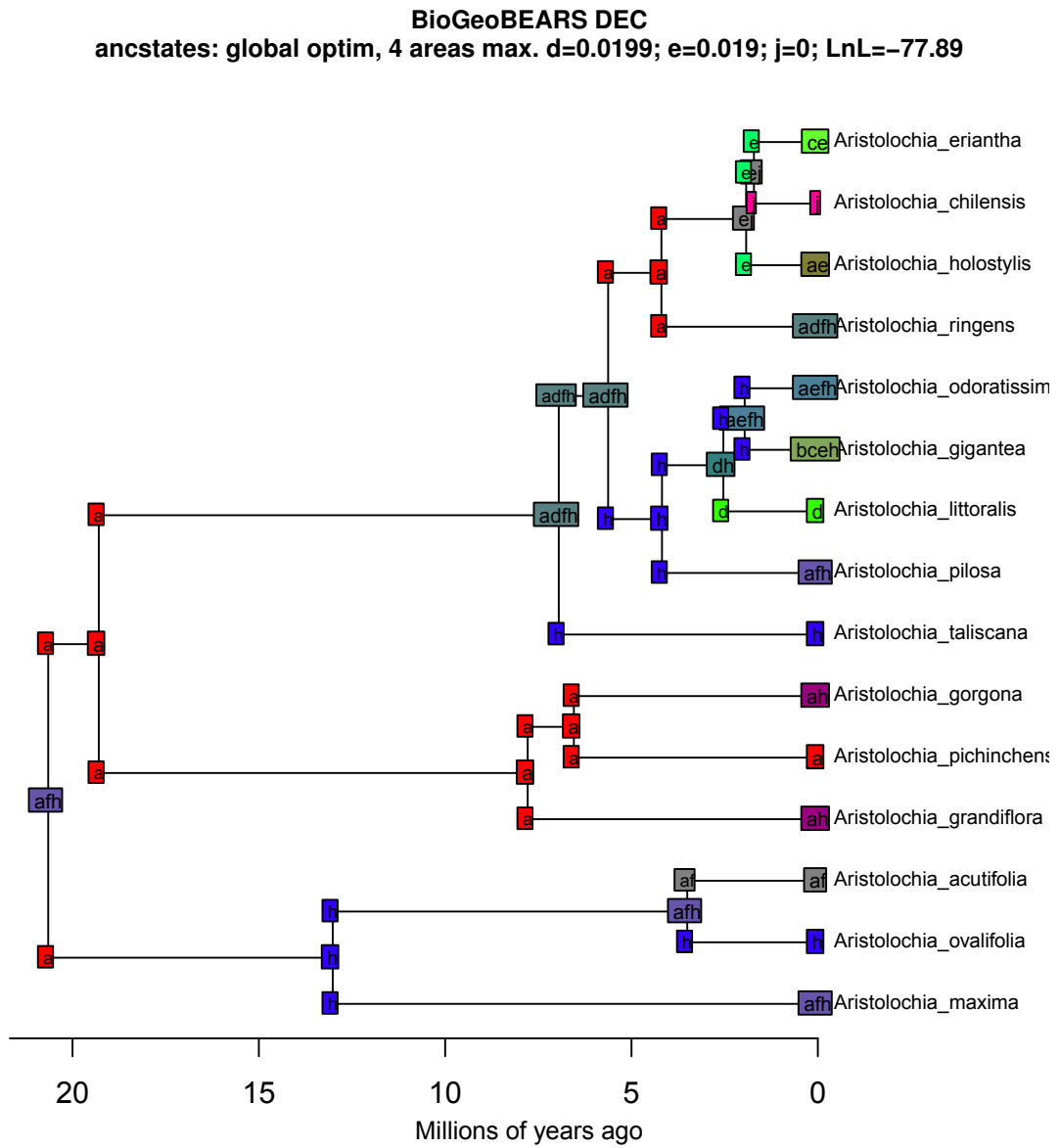


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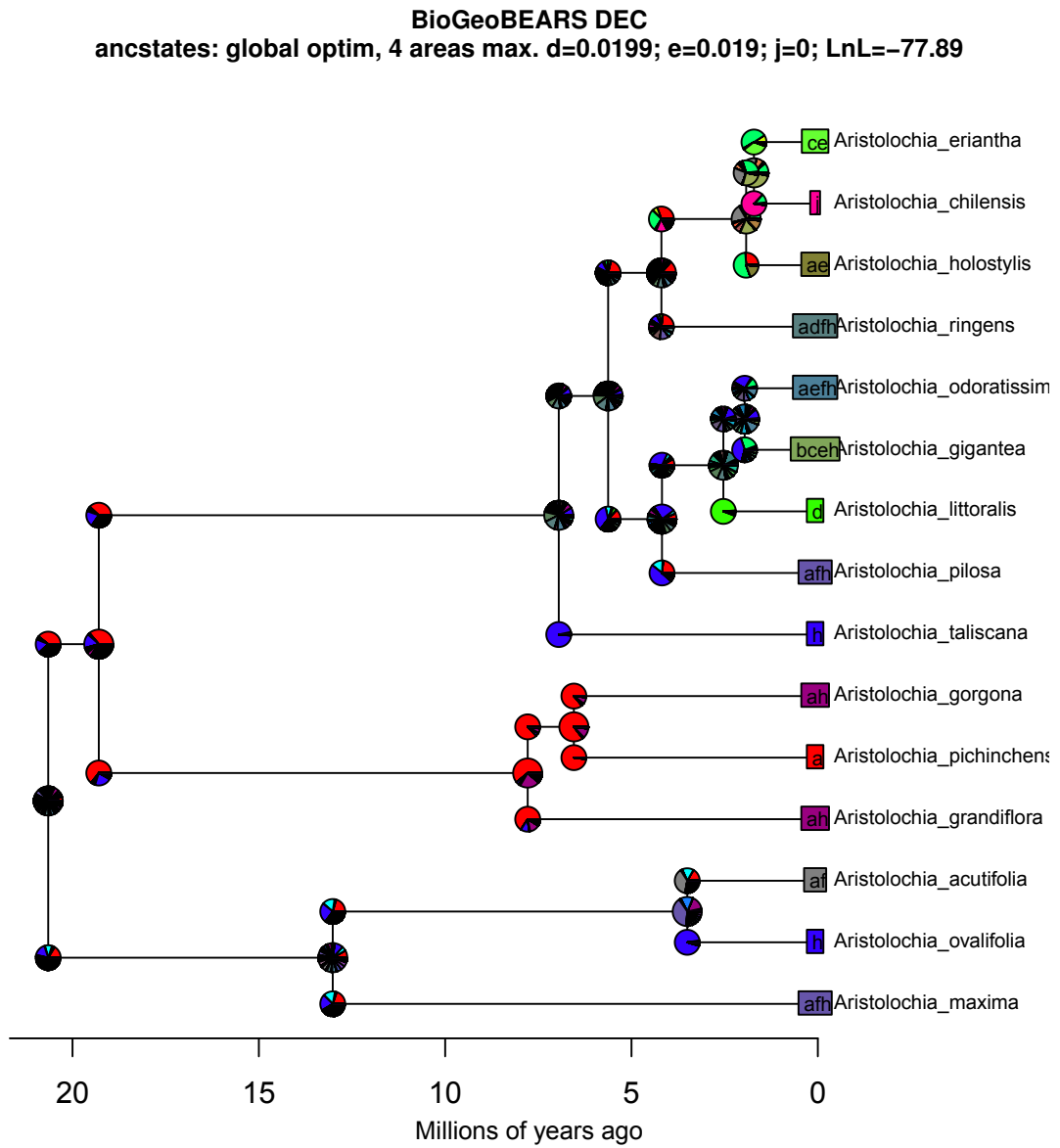


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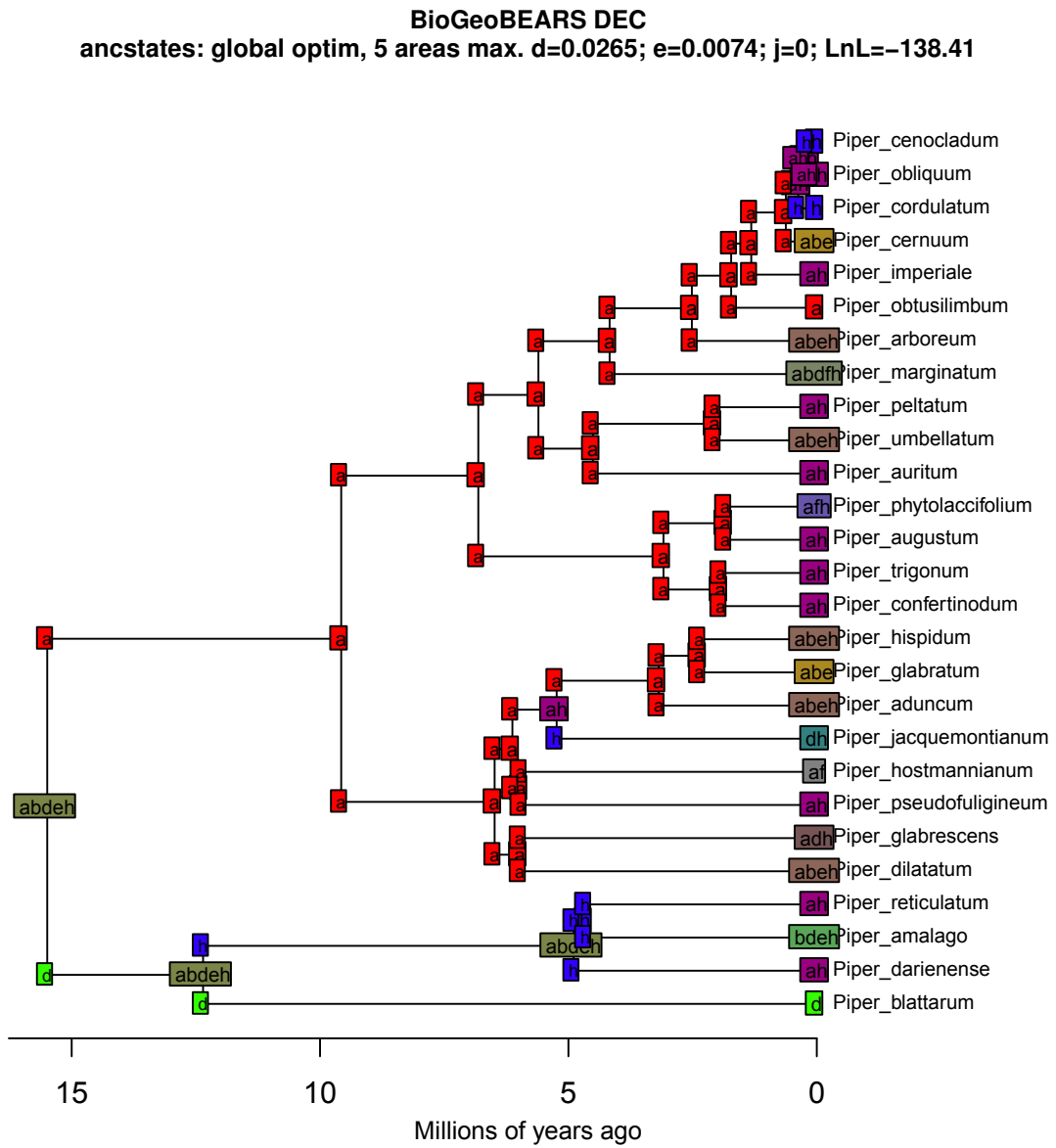


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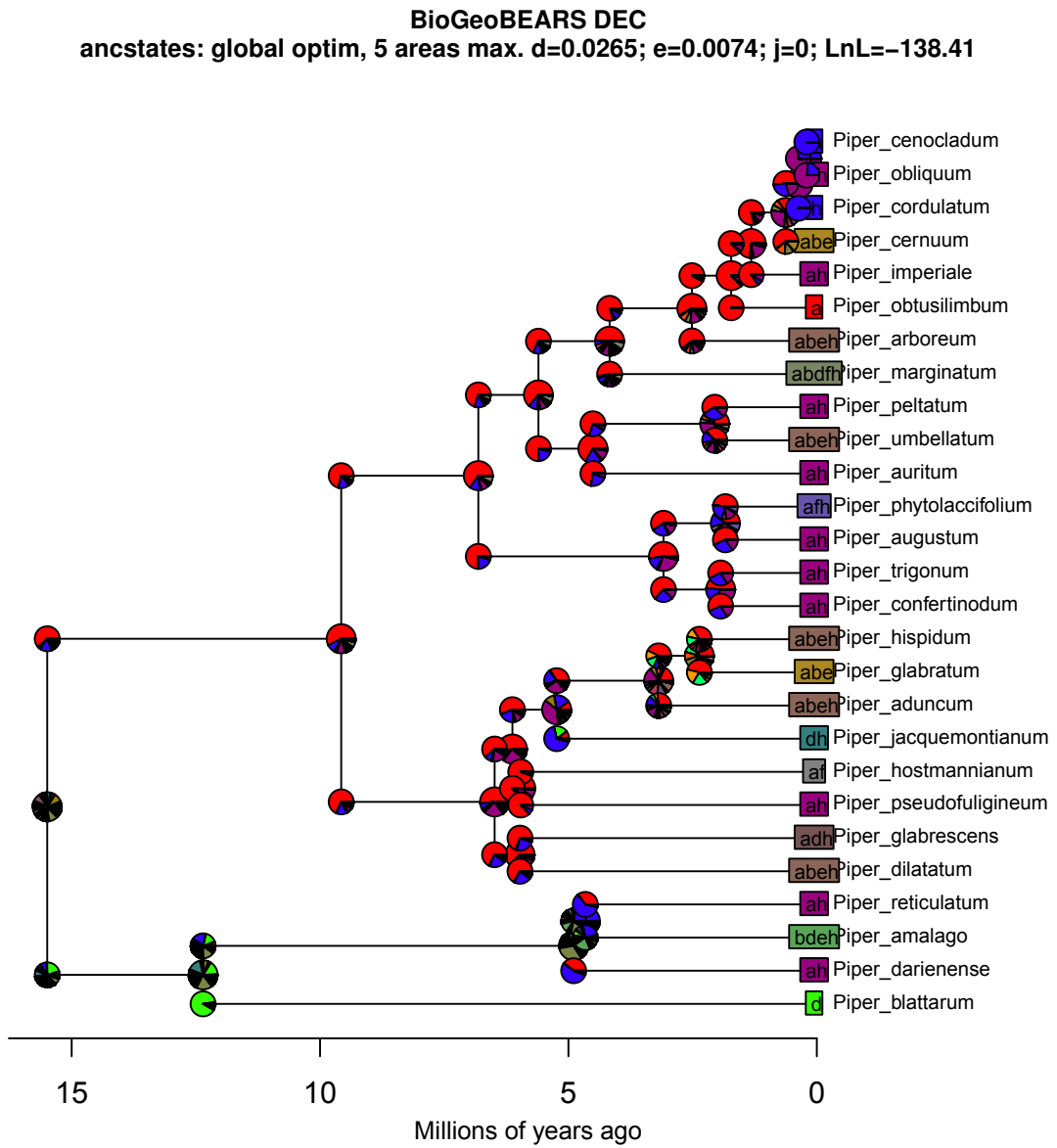


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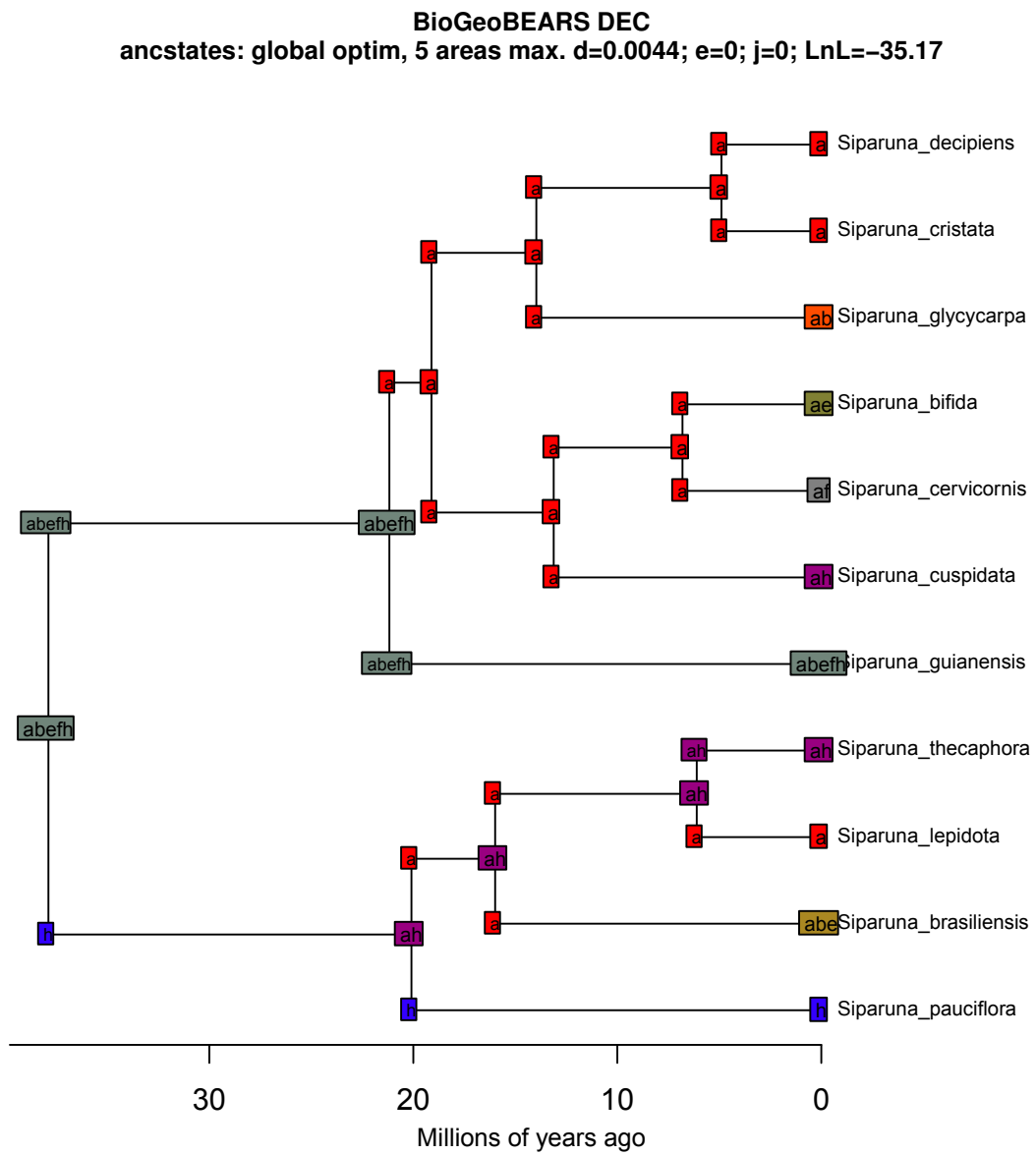


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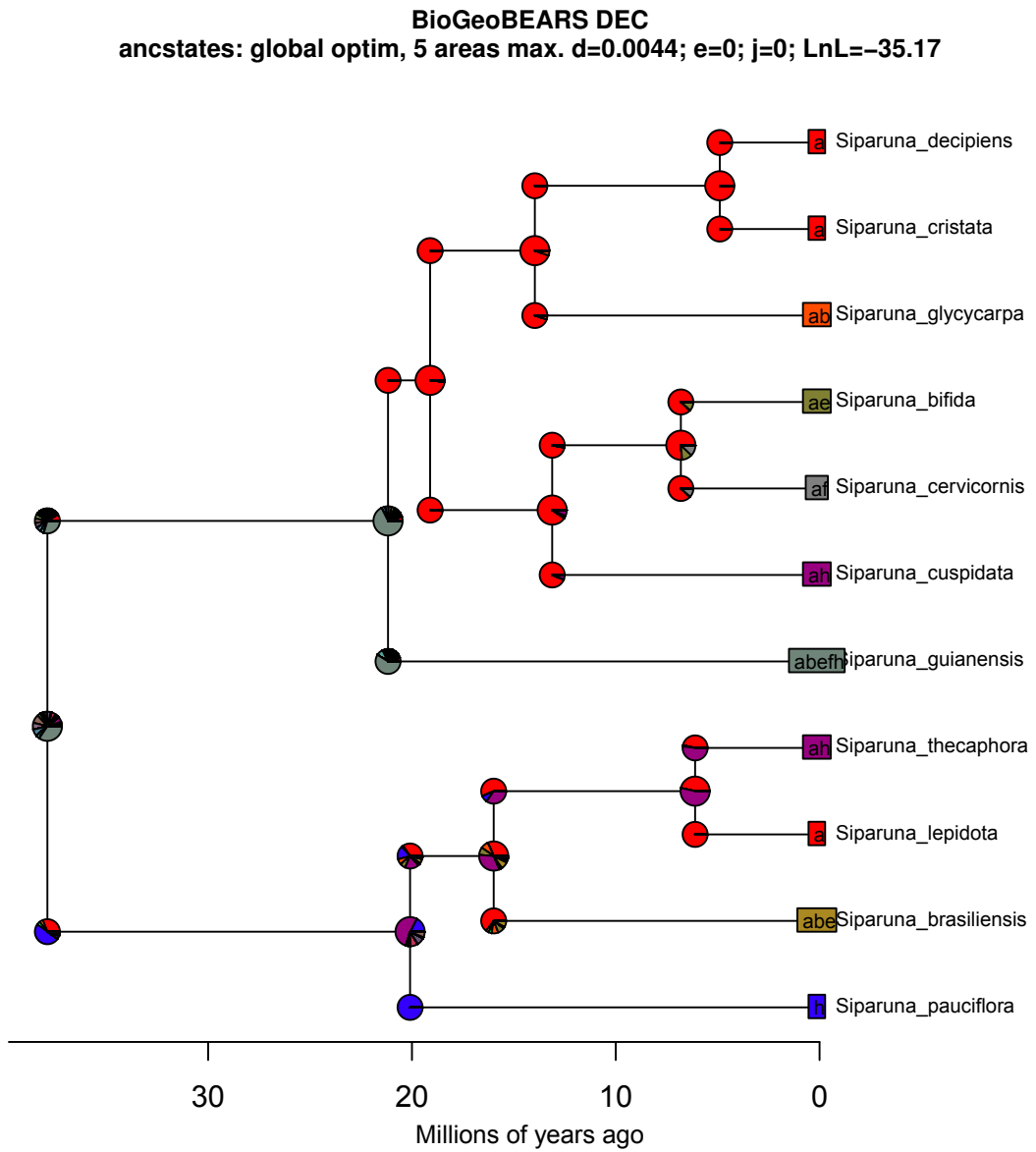


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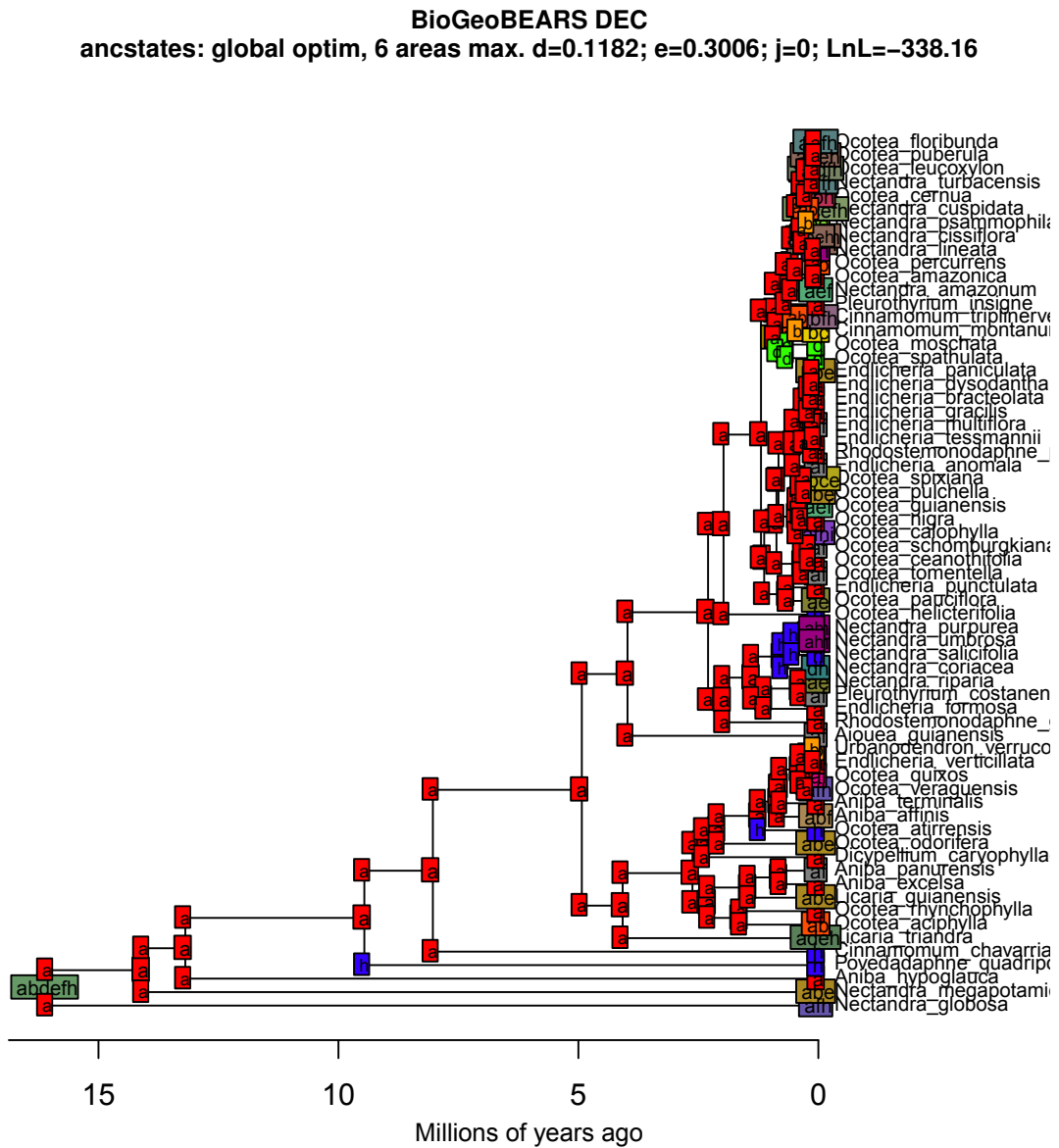


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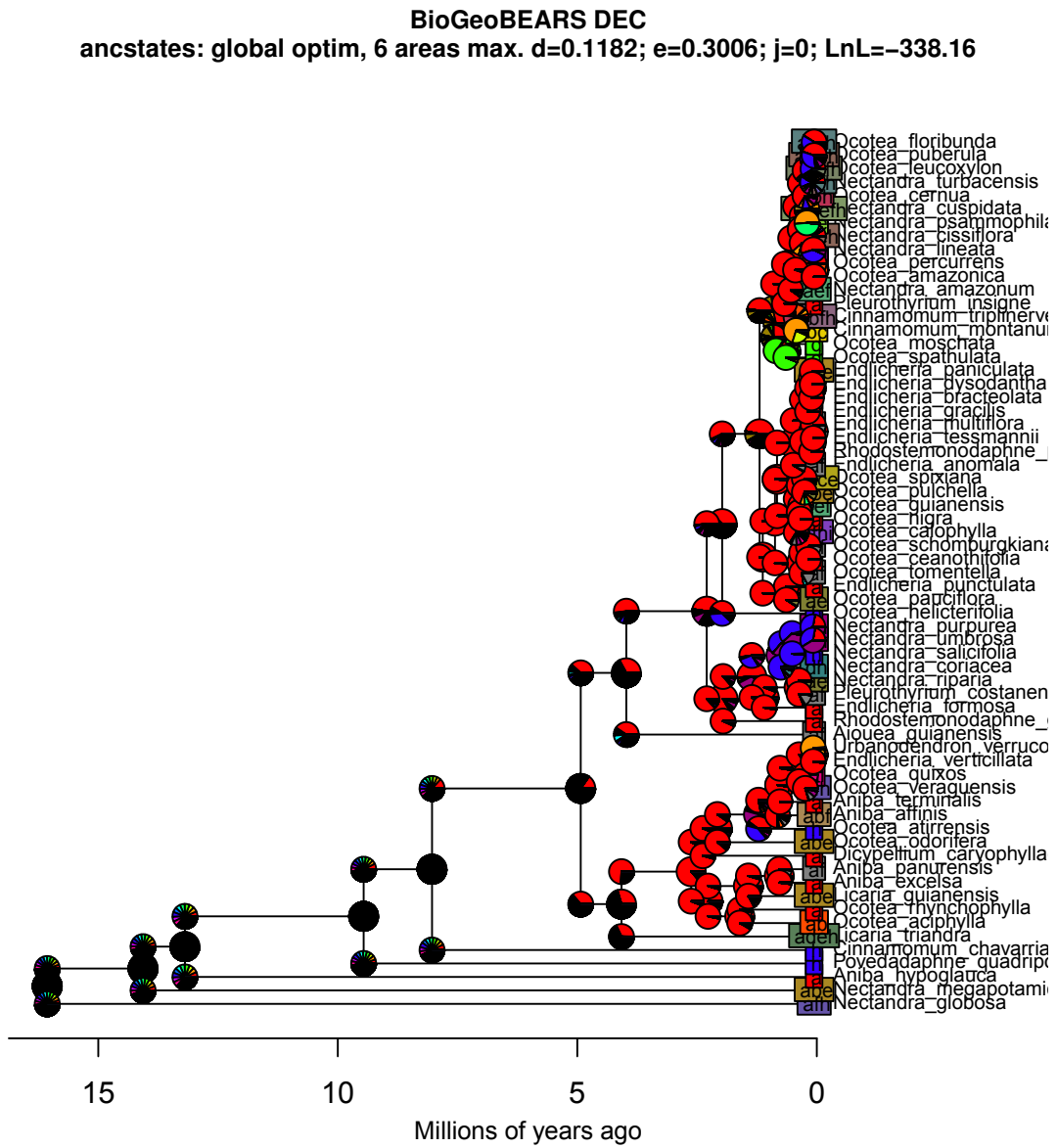


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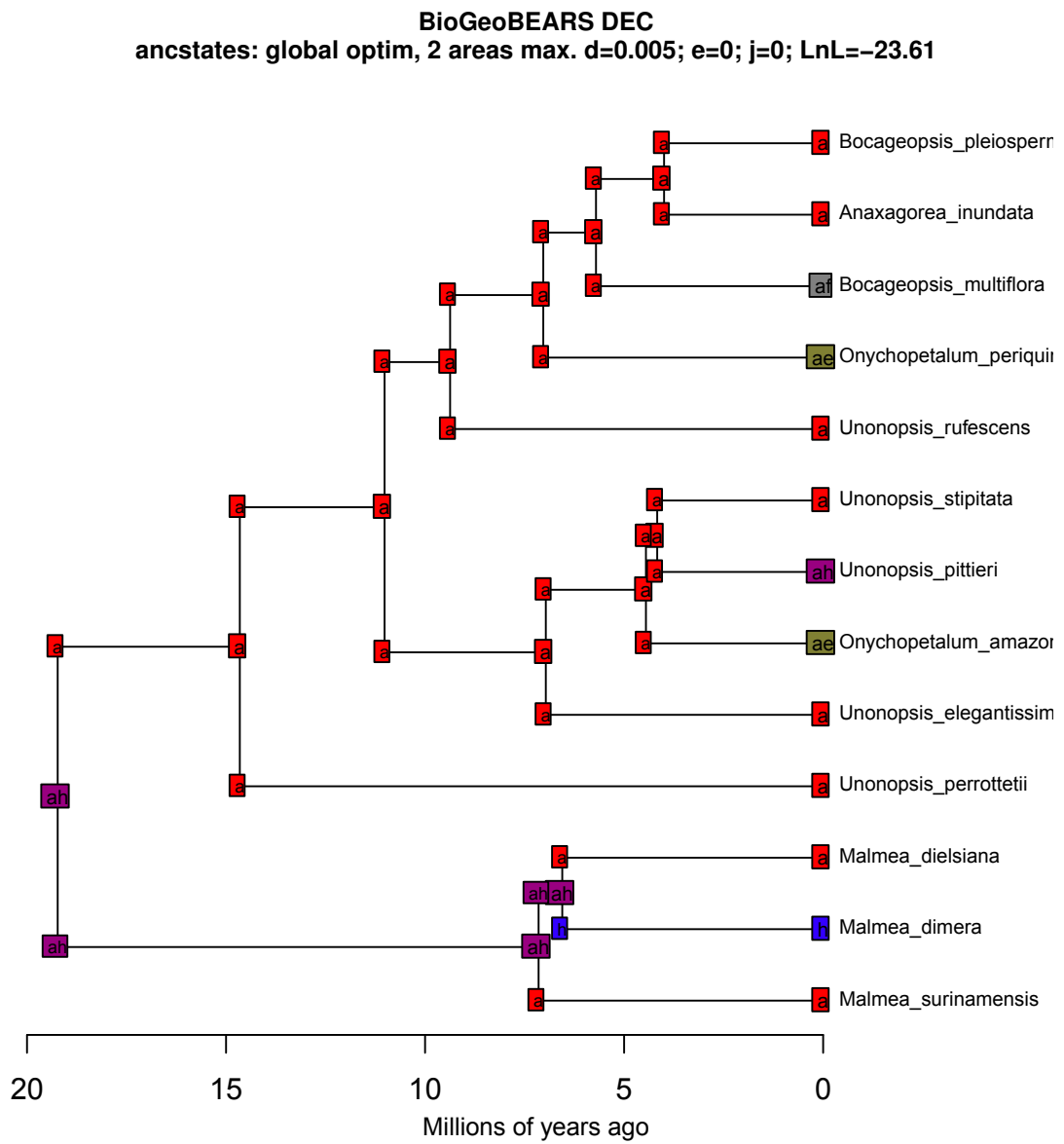


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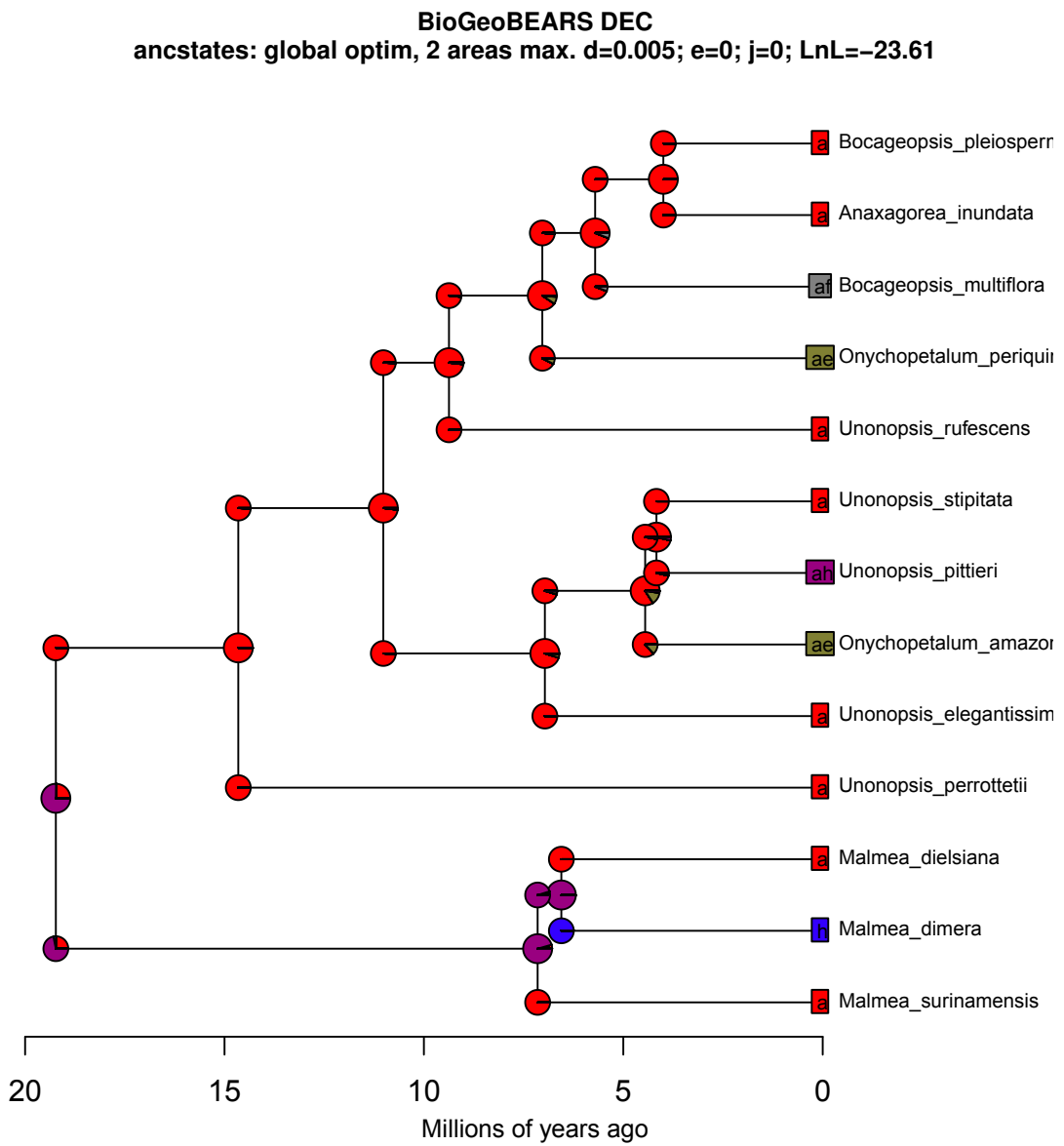


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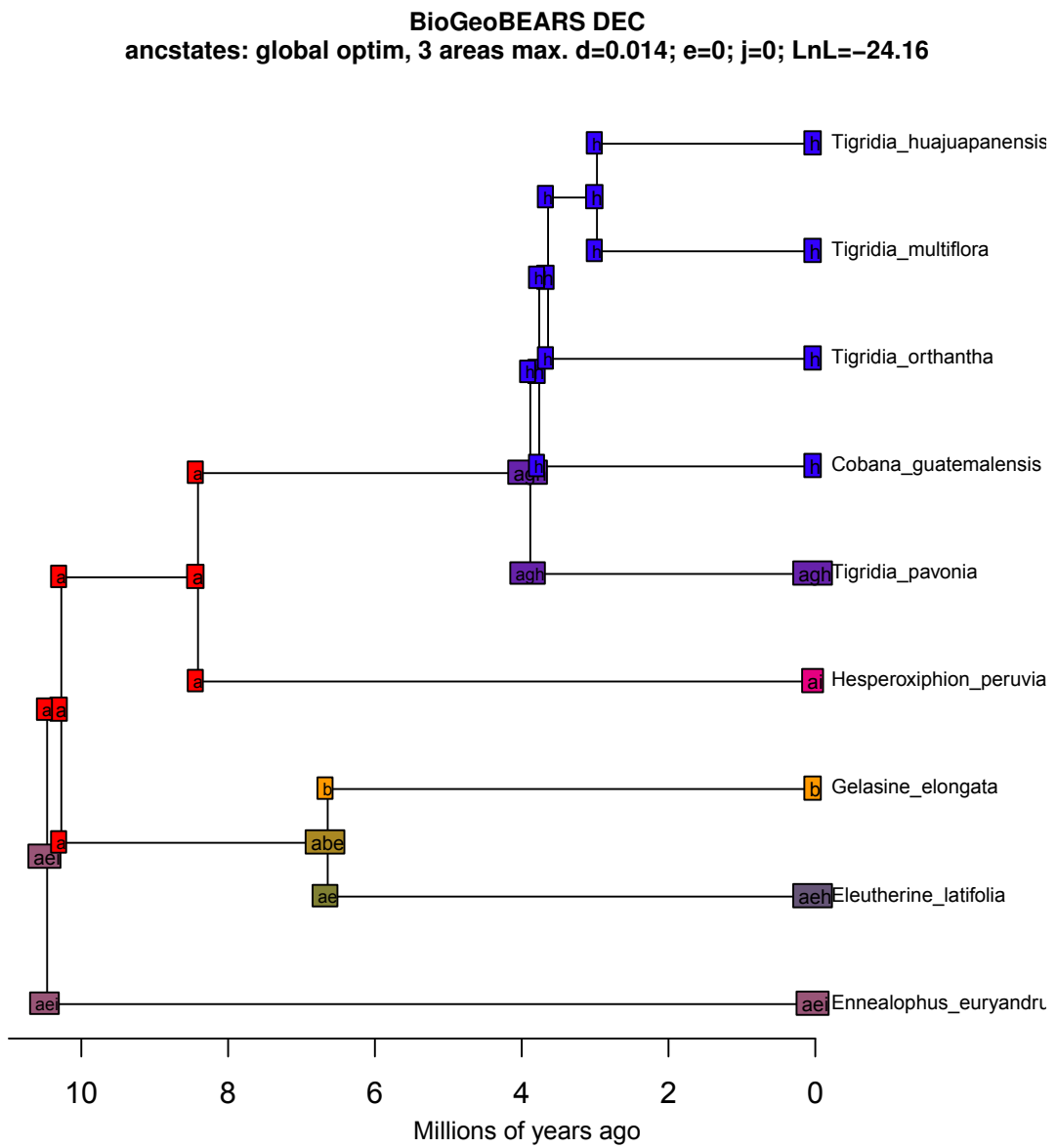


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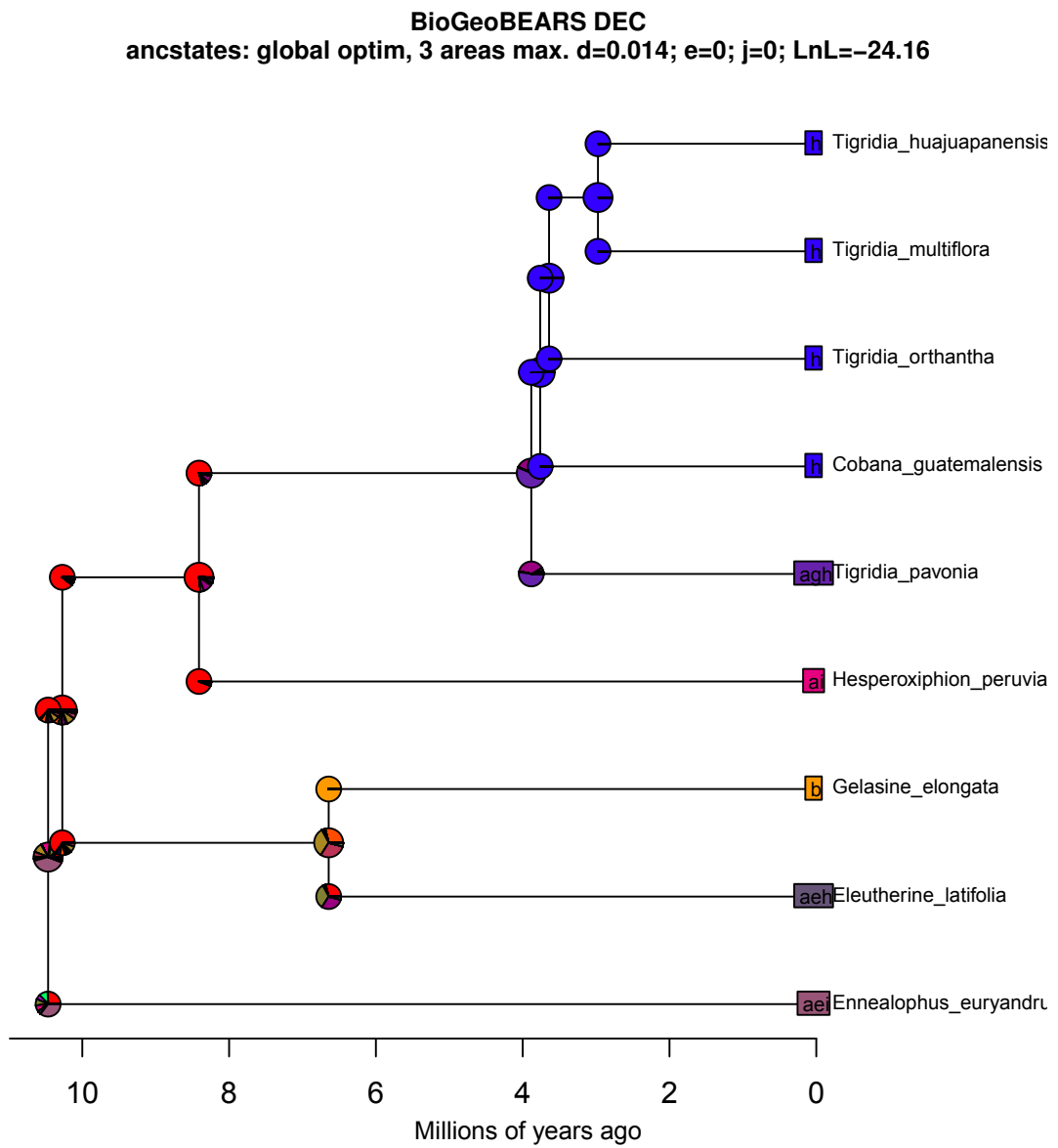


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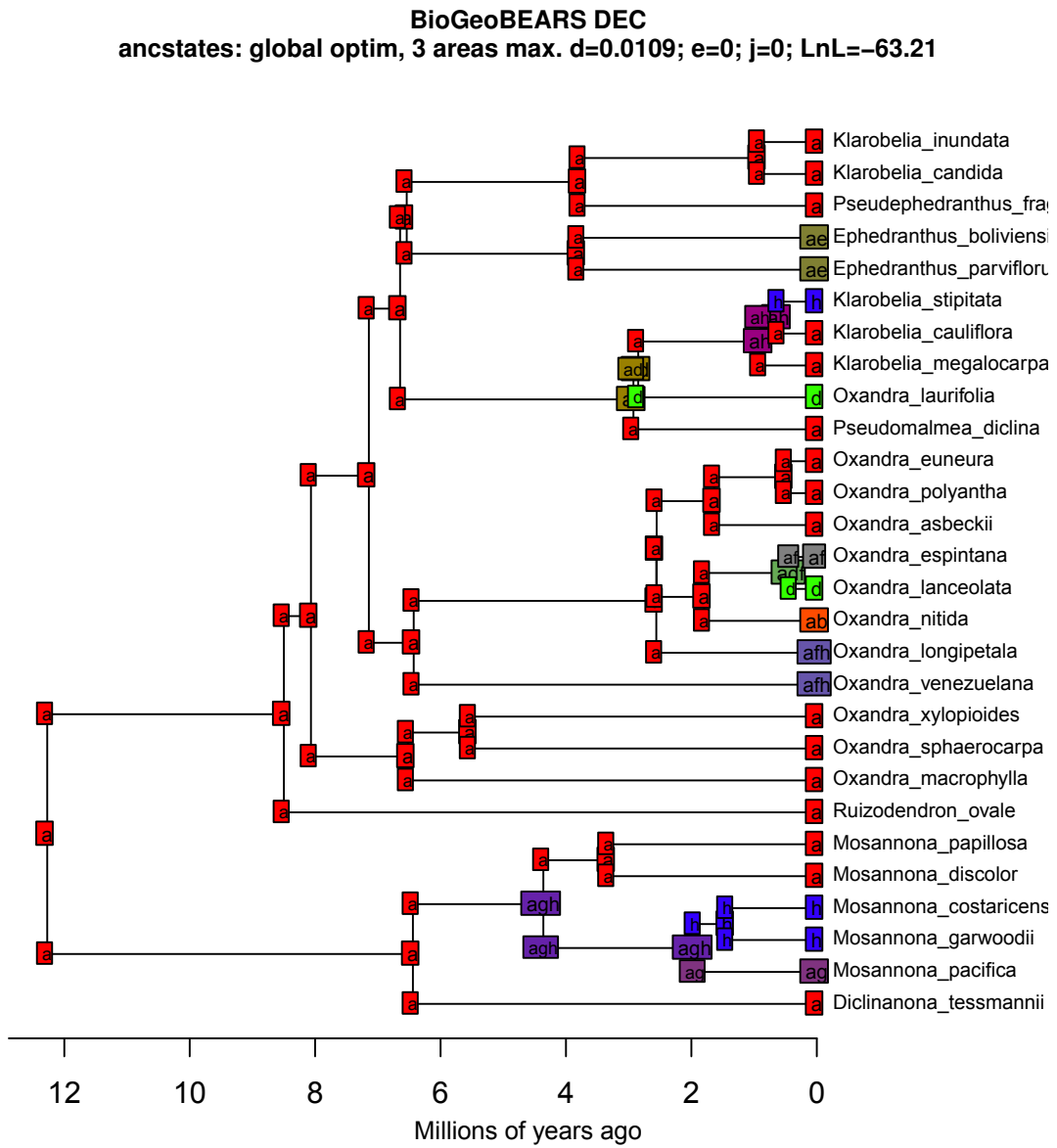


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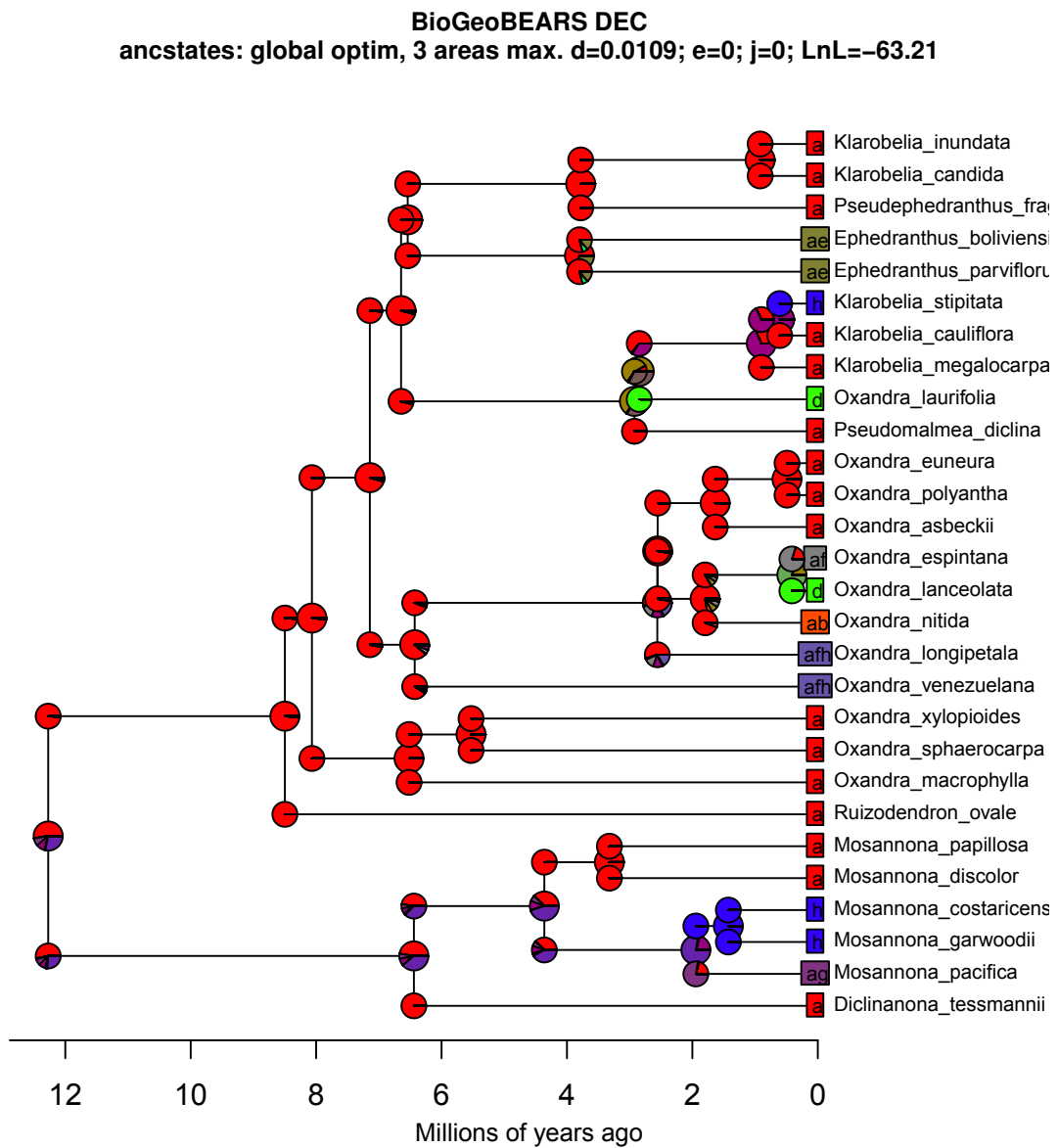


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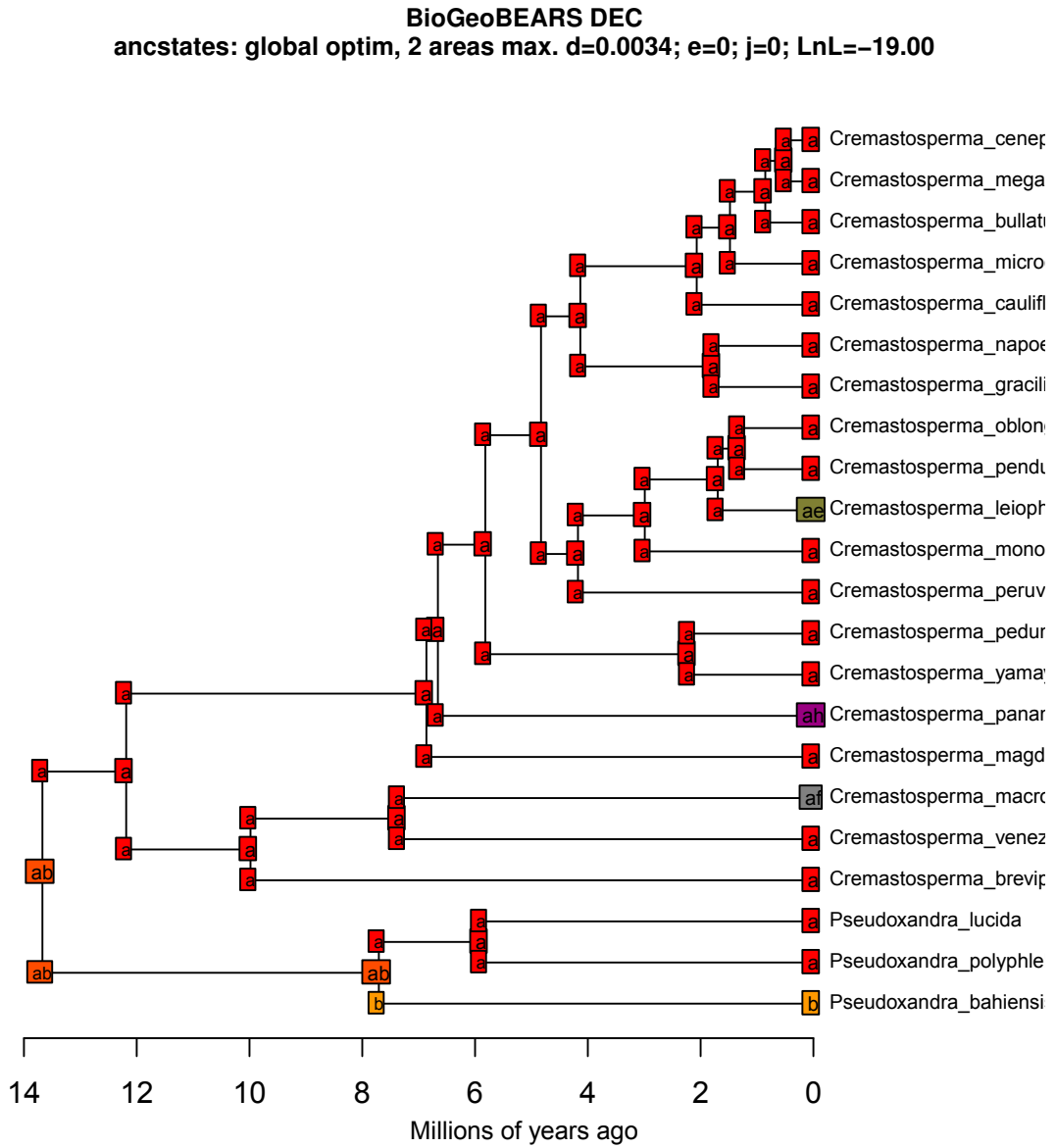


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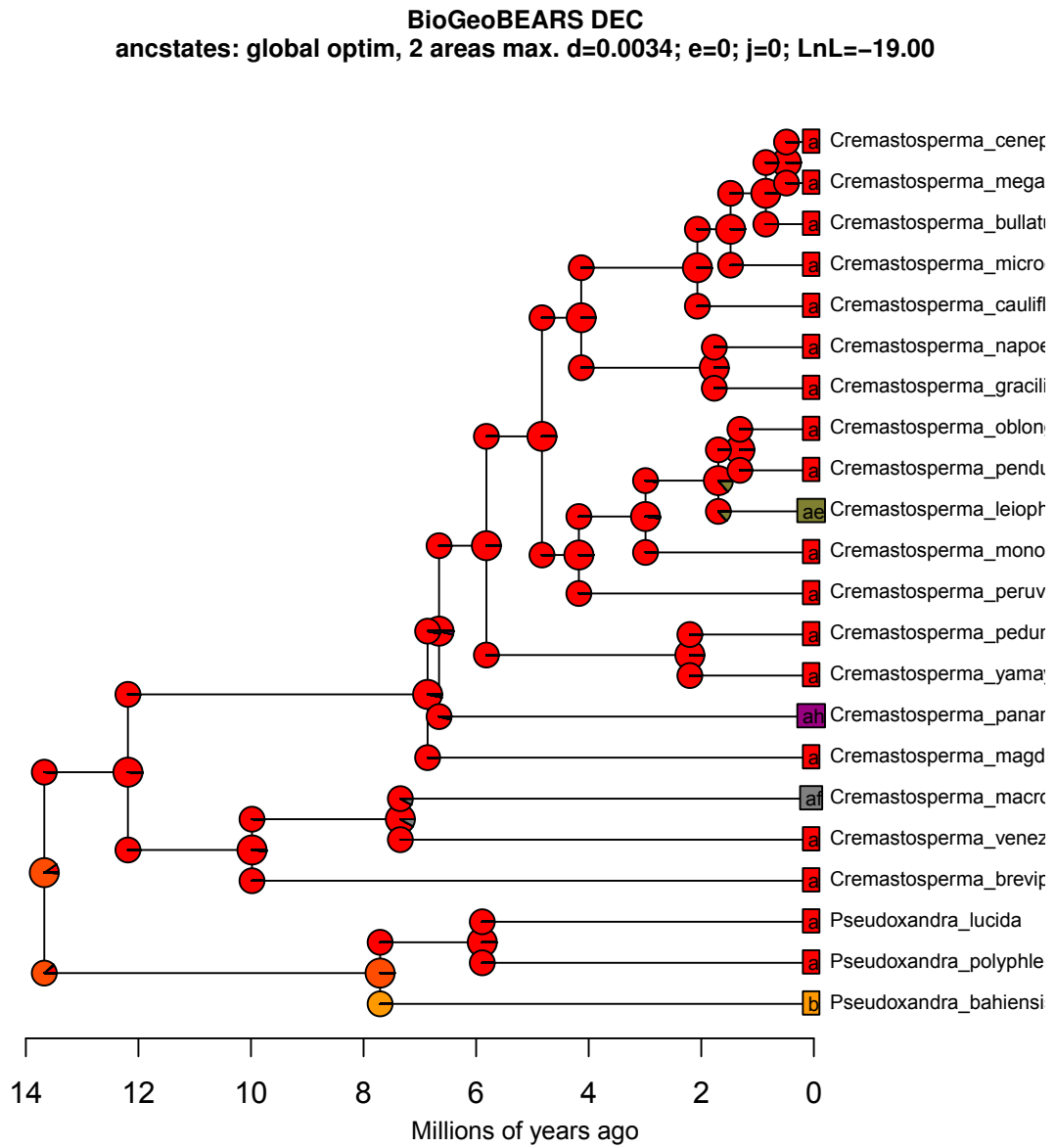


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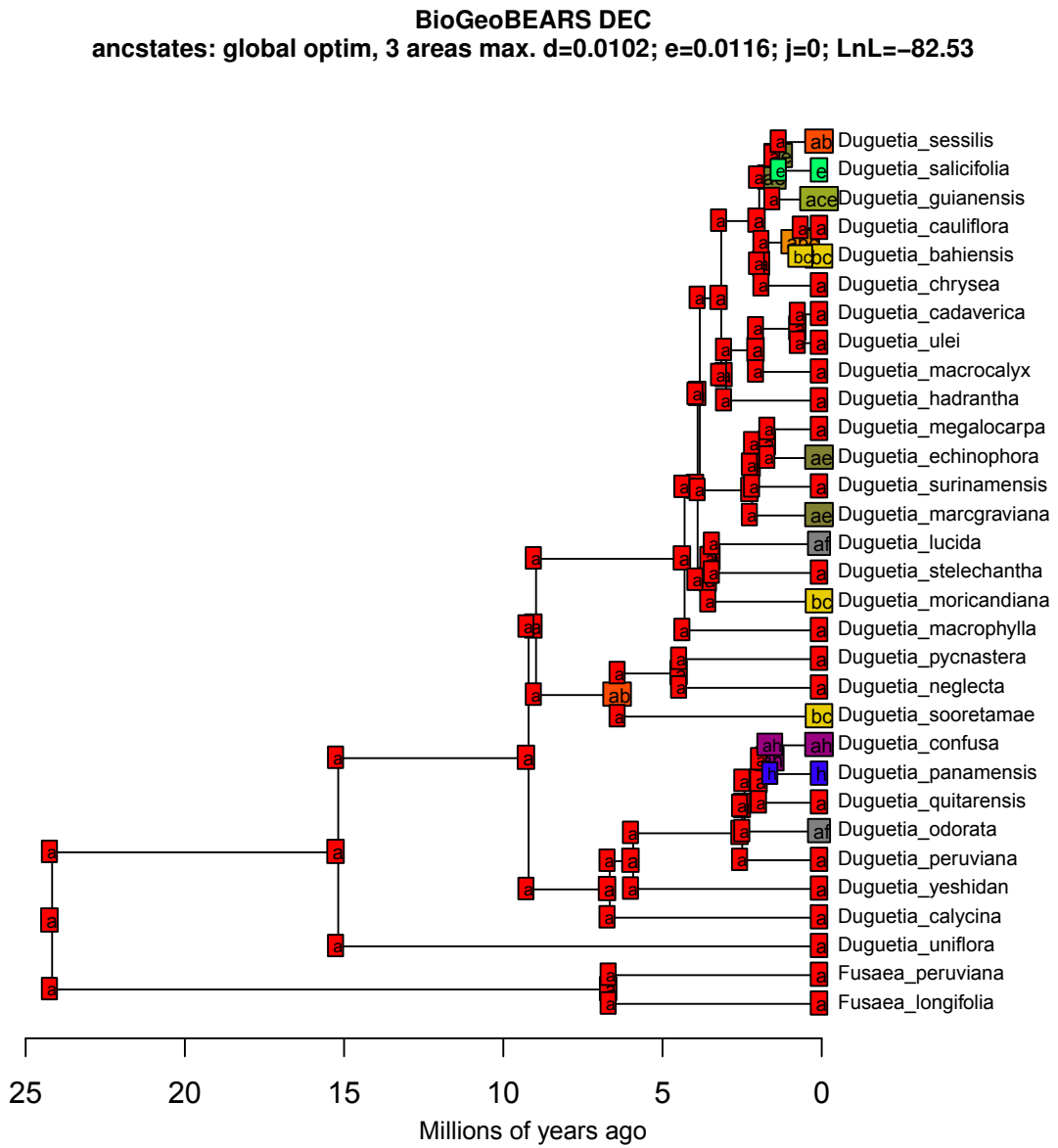


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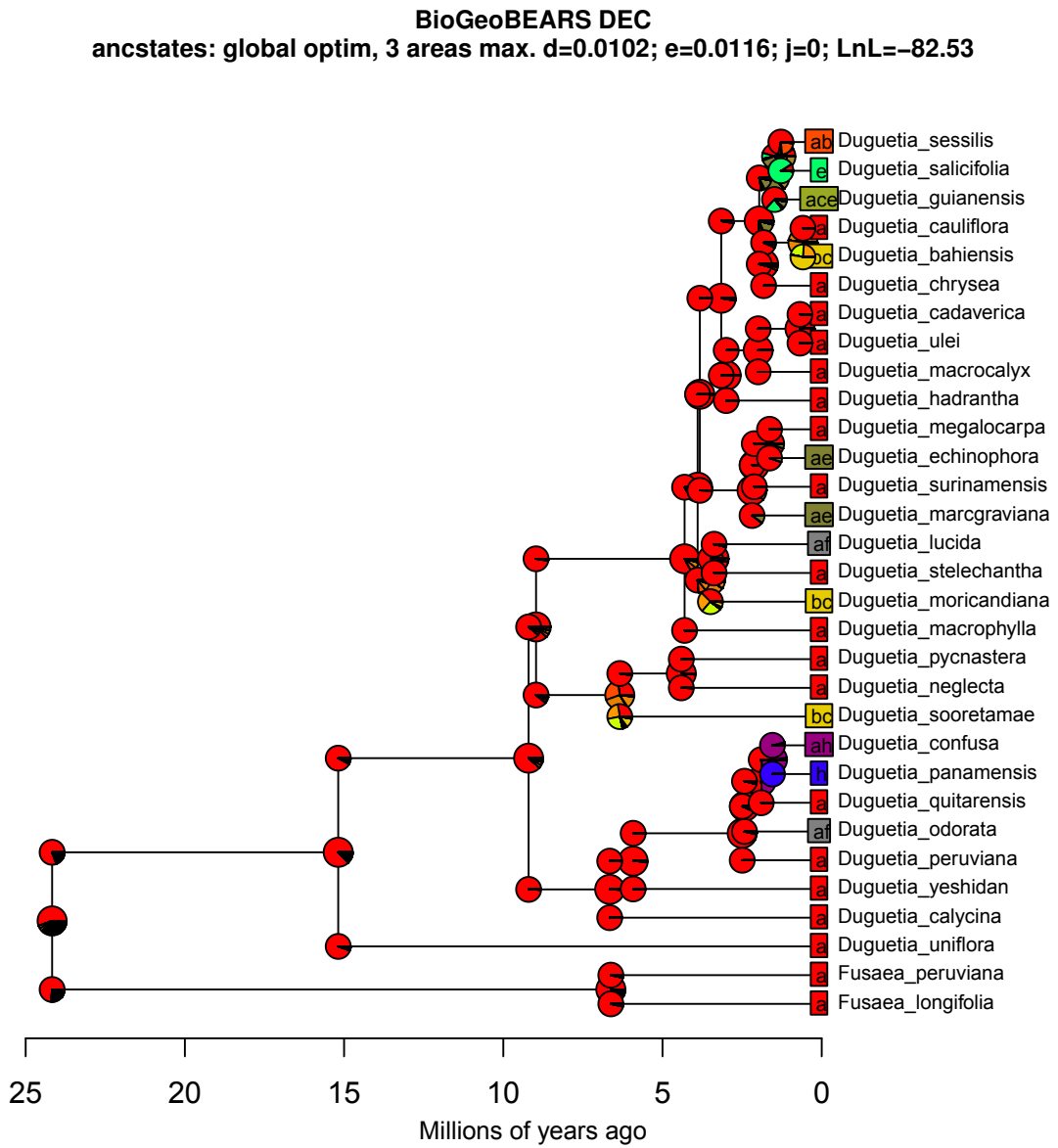


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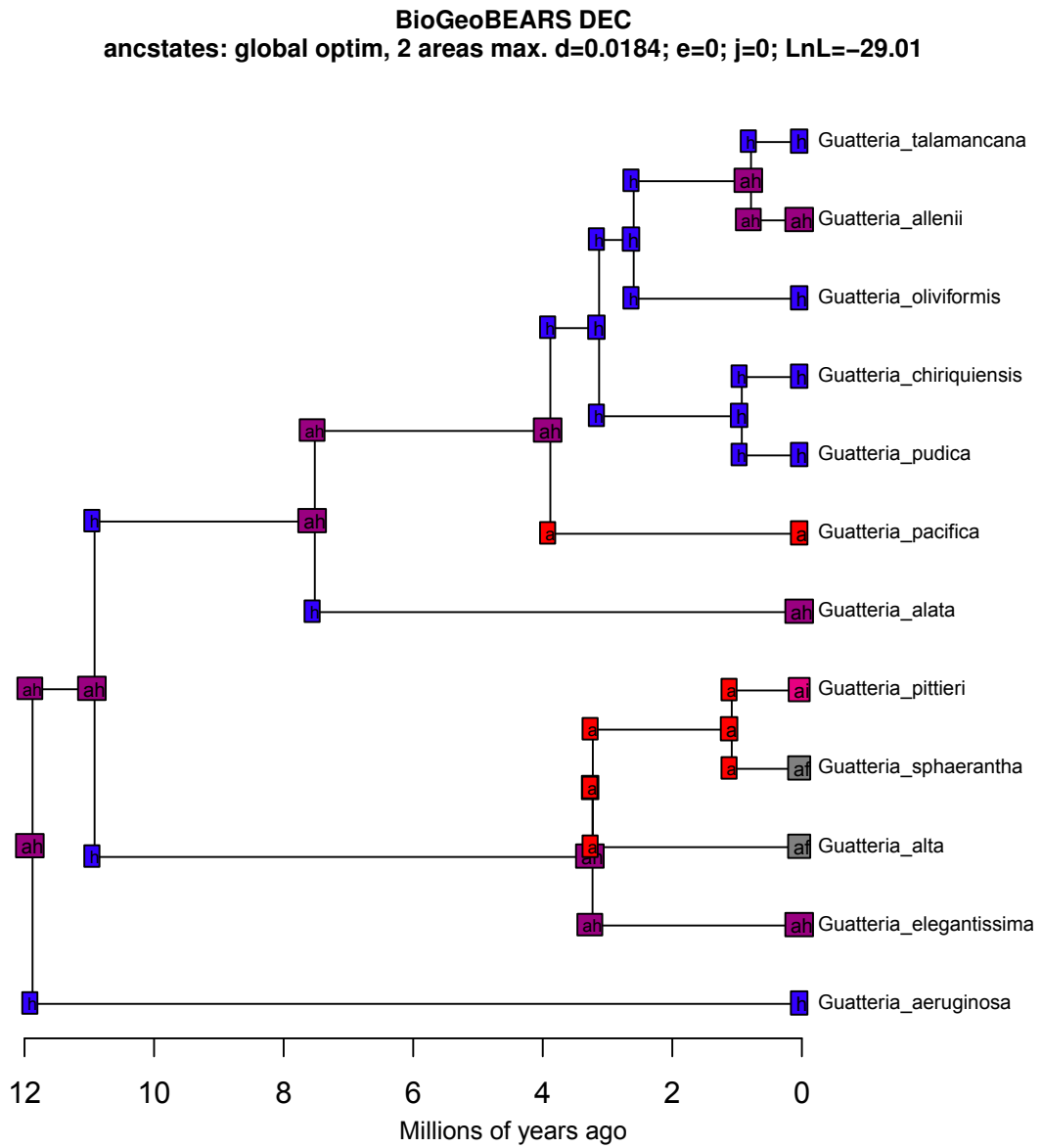


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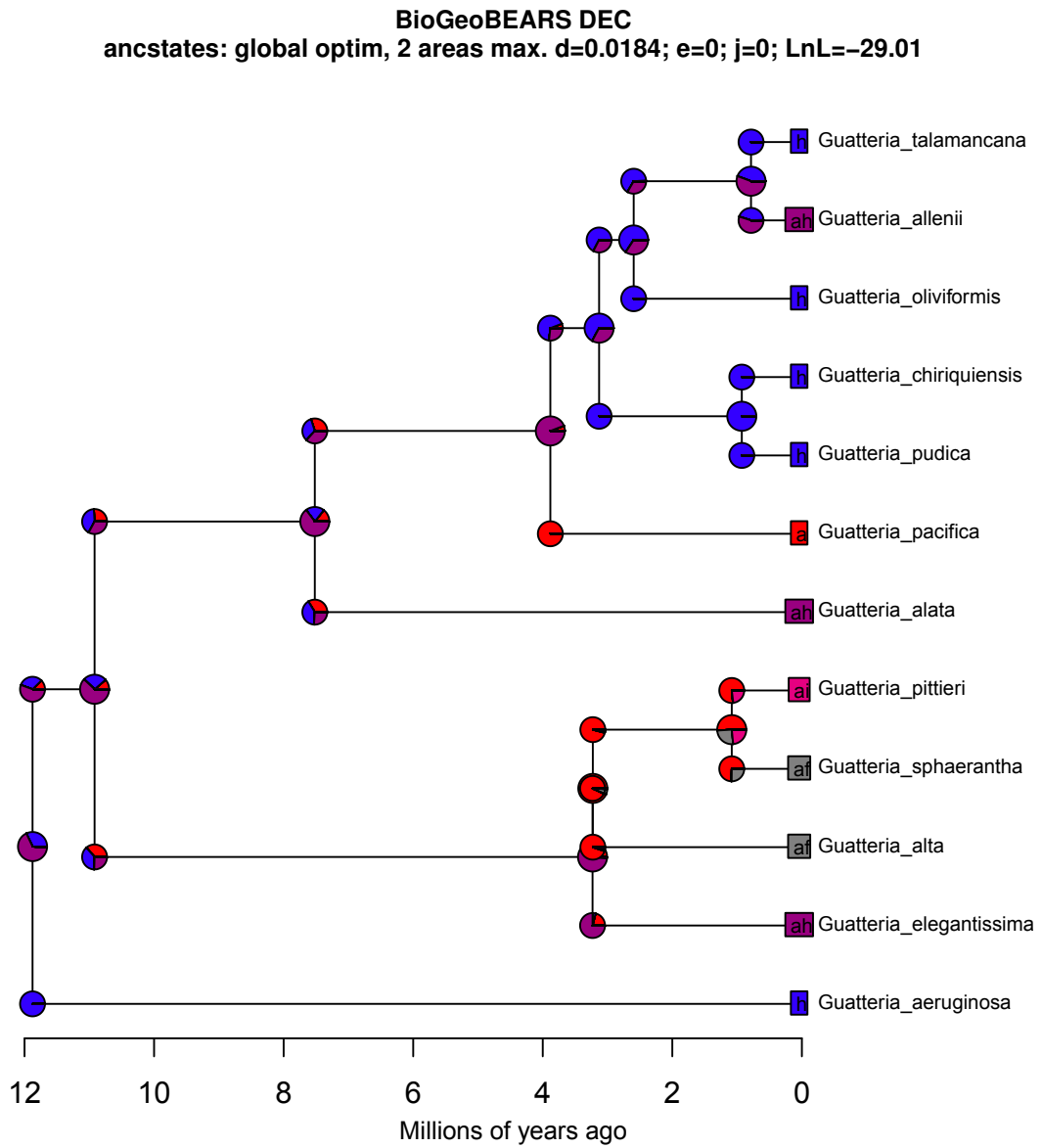


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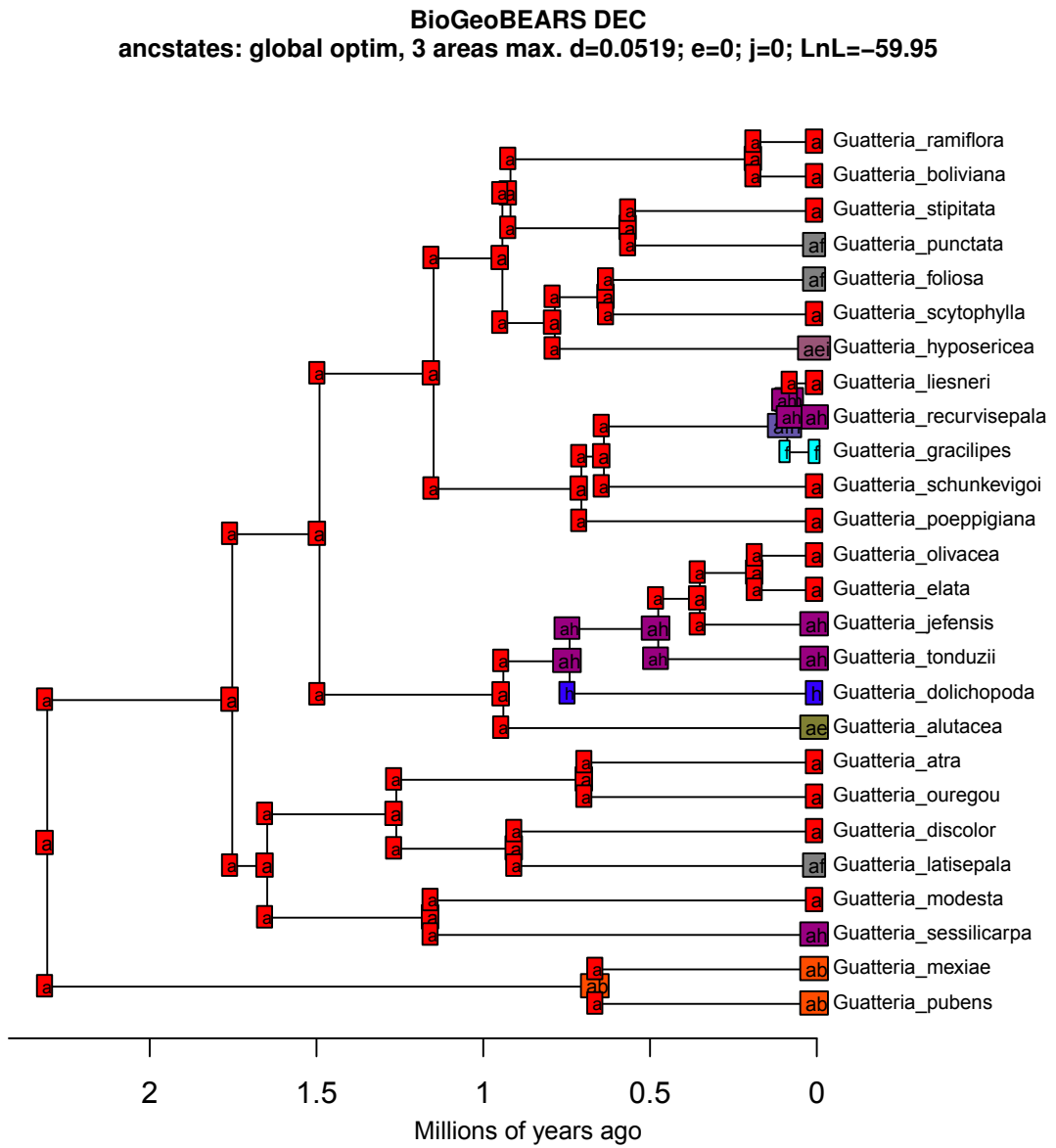


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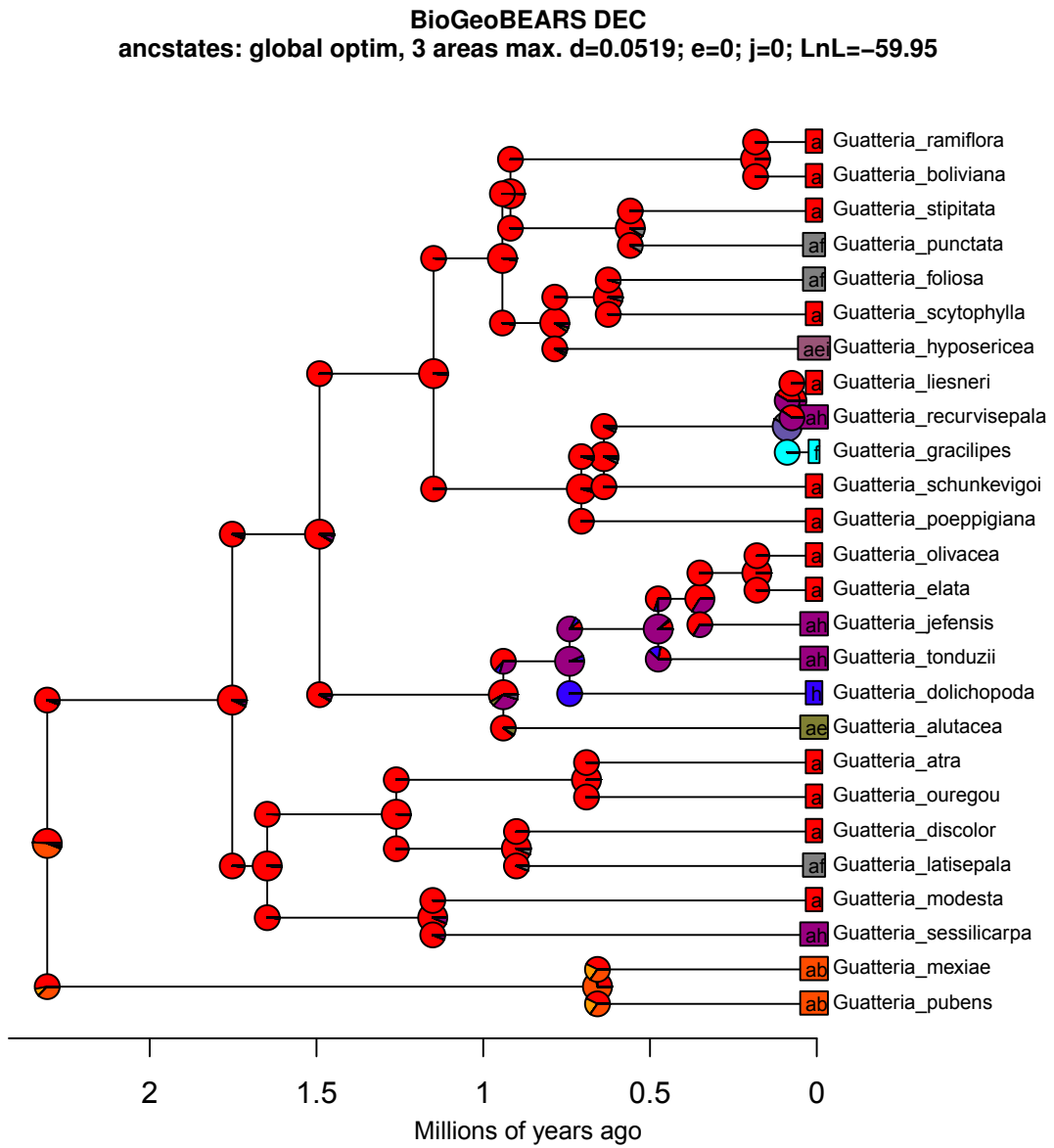


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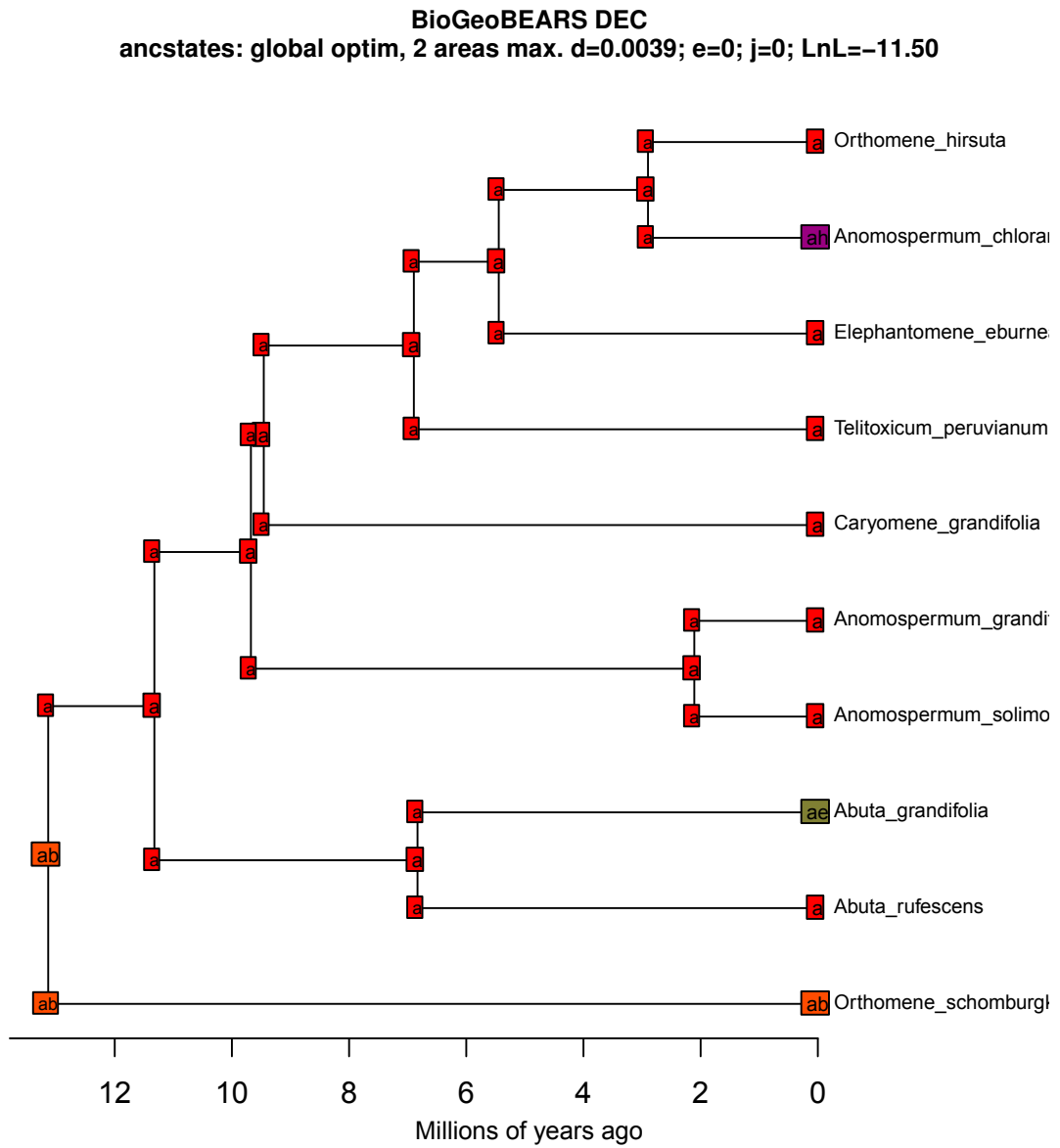


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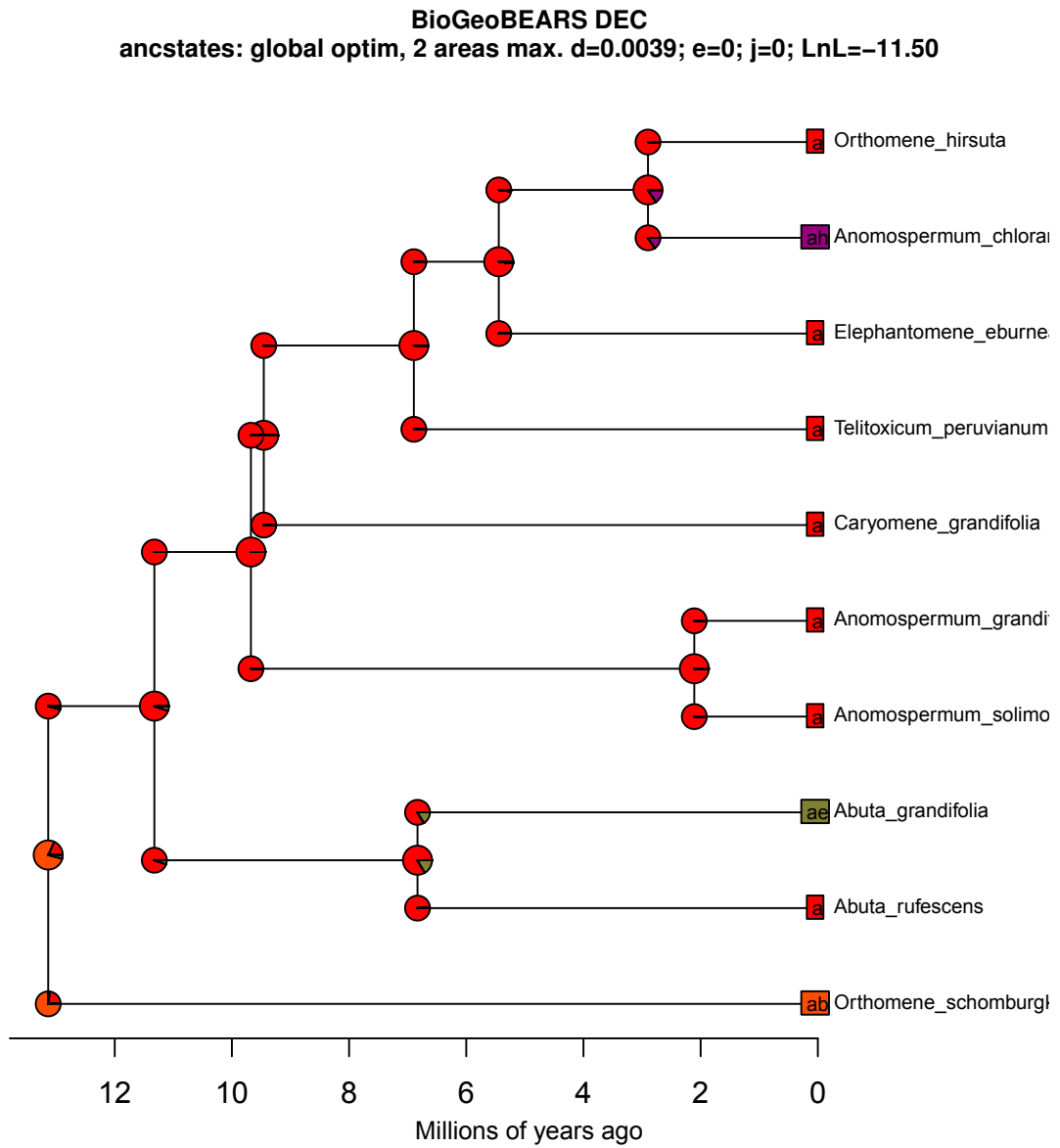


Figure S3: Clades of angiosperms

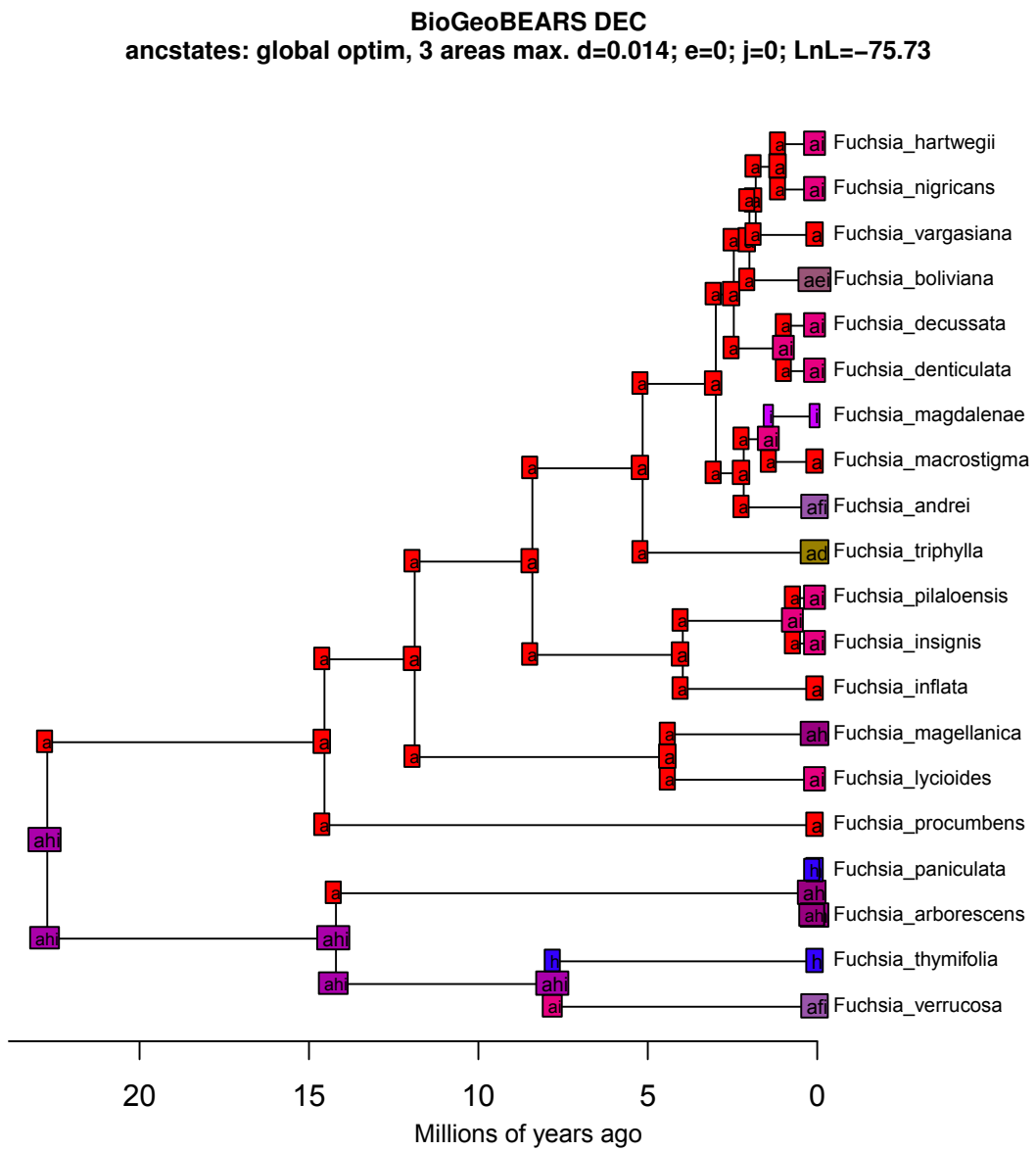


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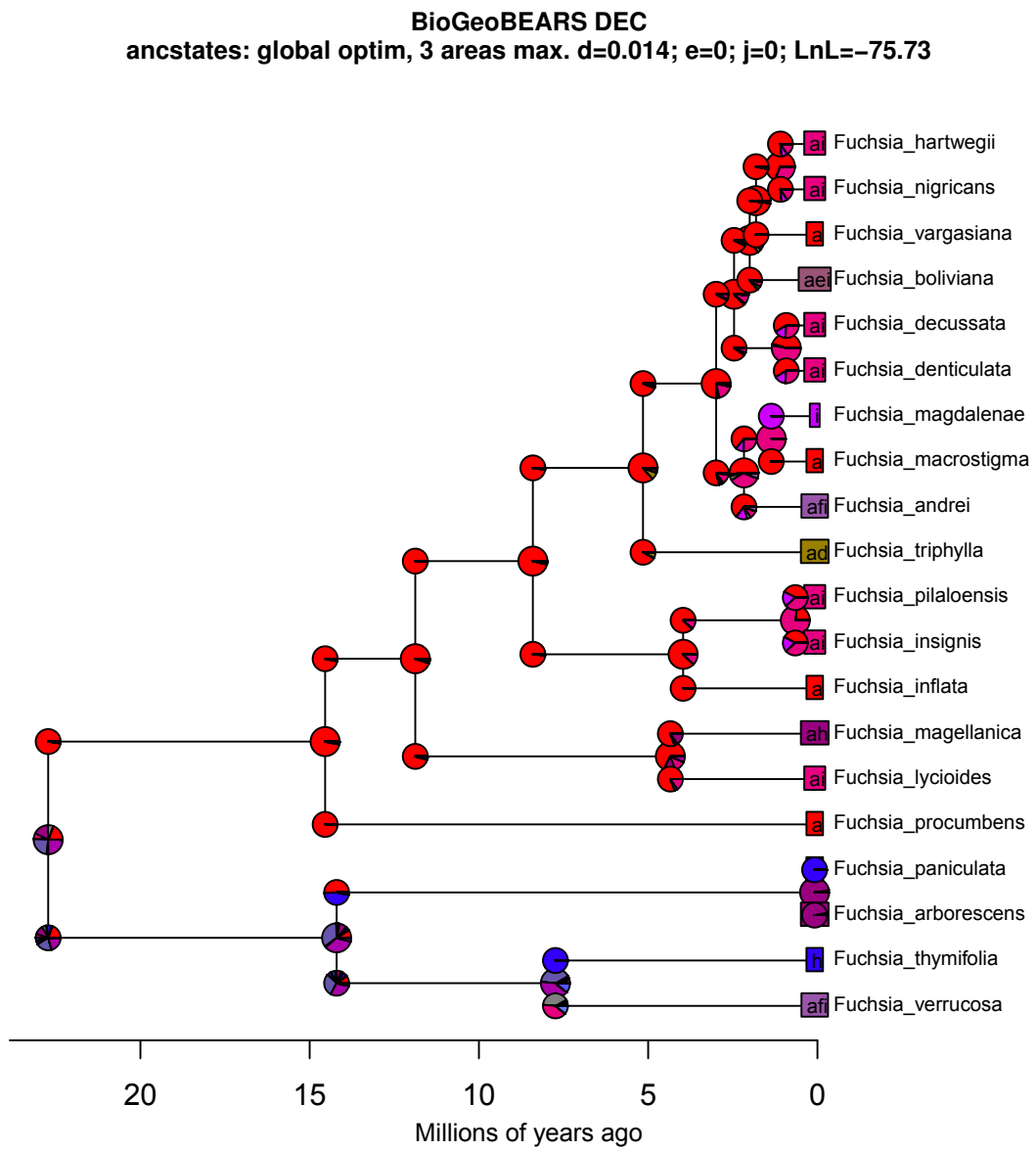


Figure S3: Clades of angiosperms

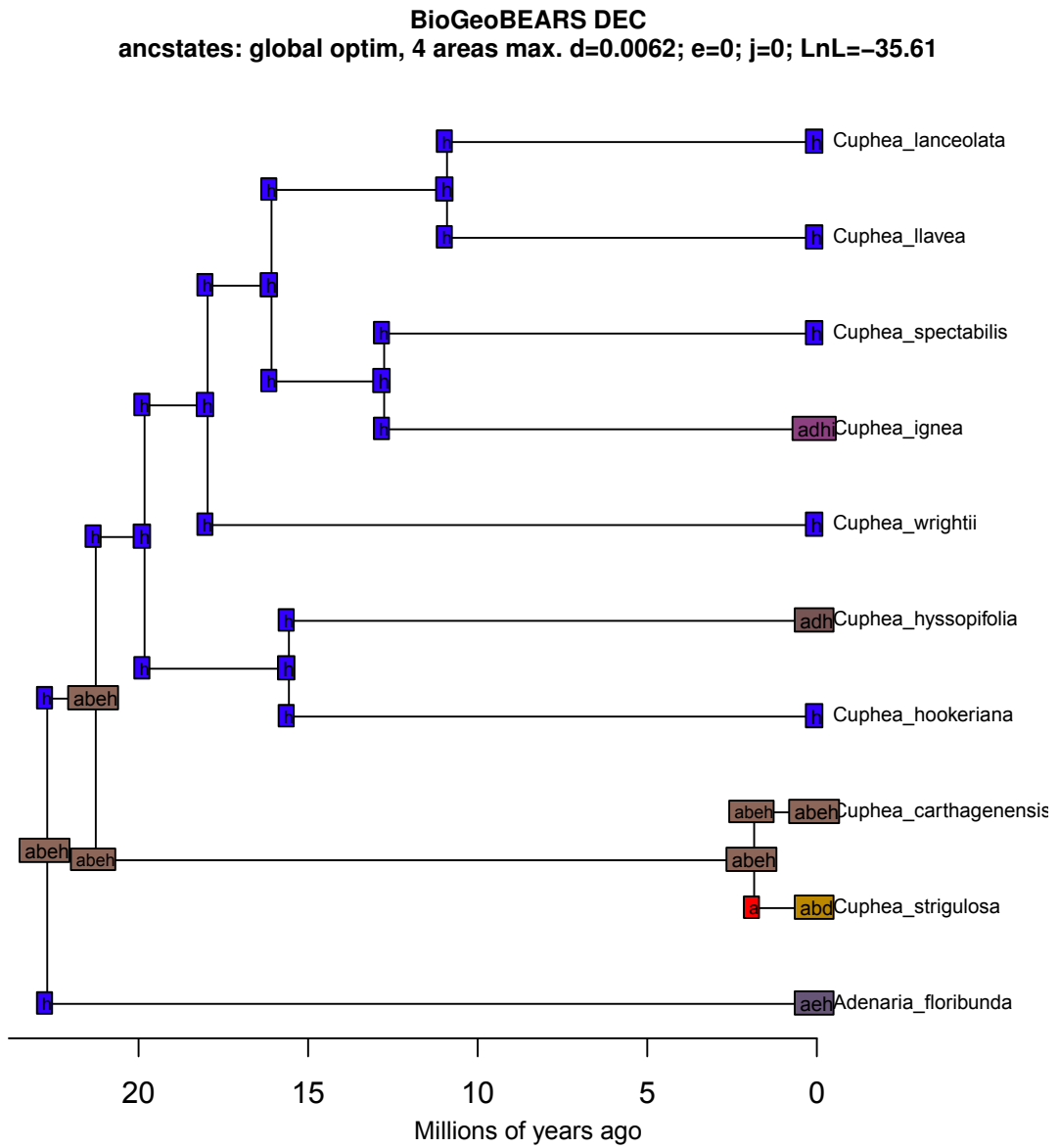


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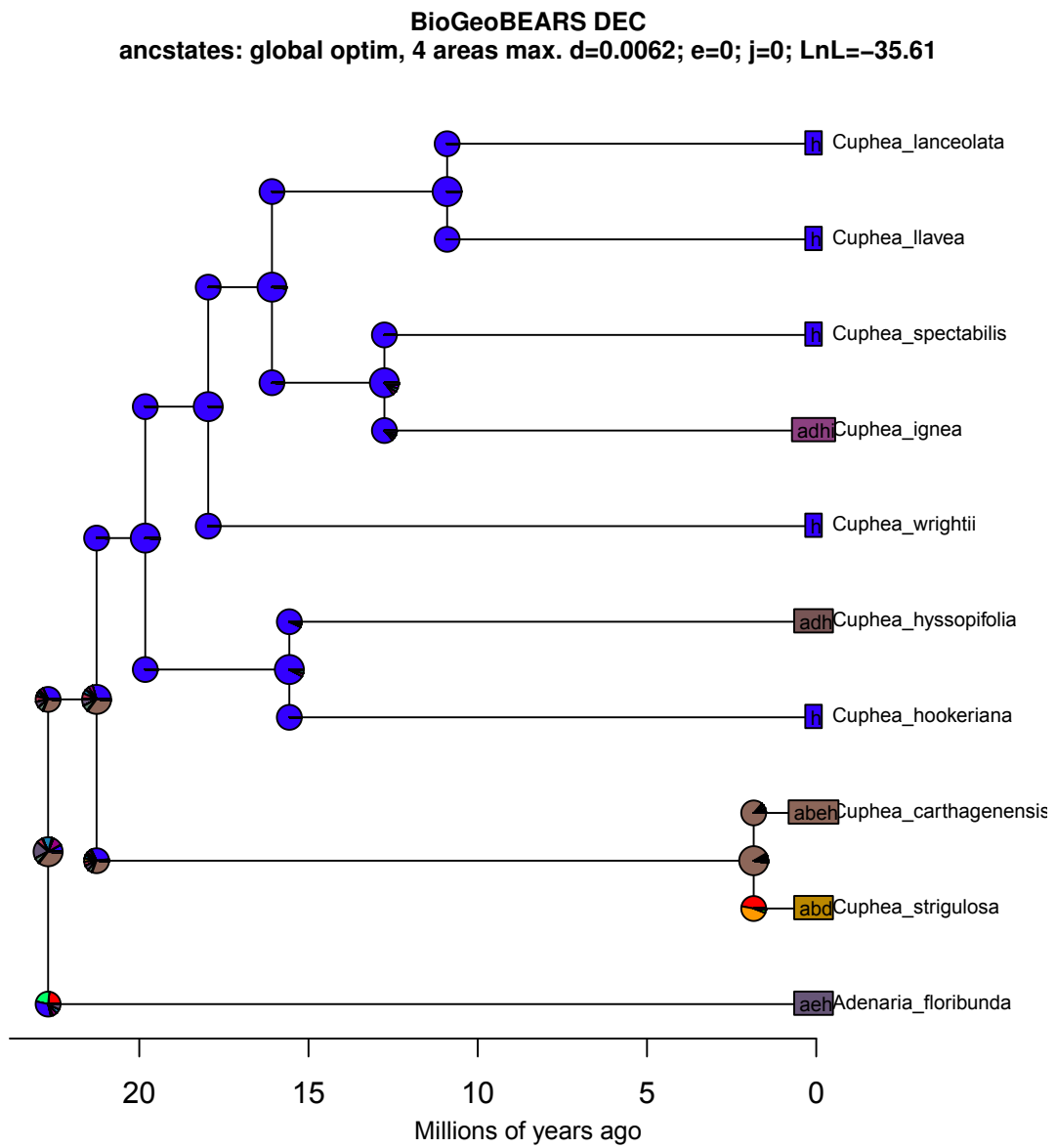


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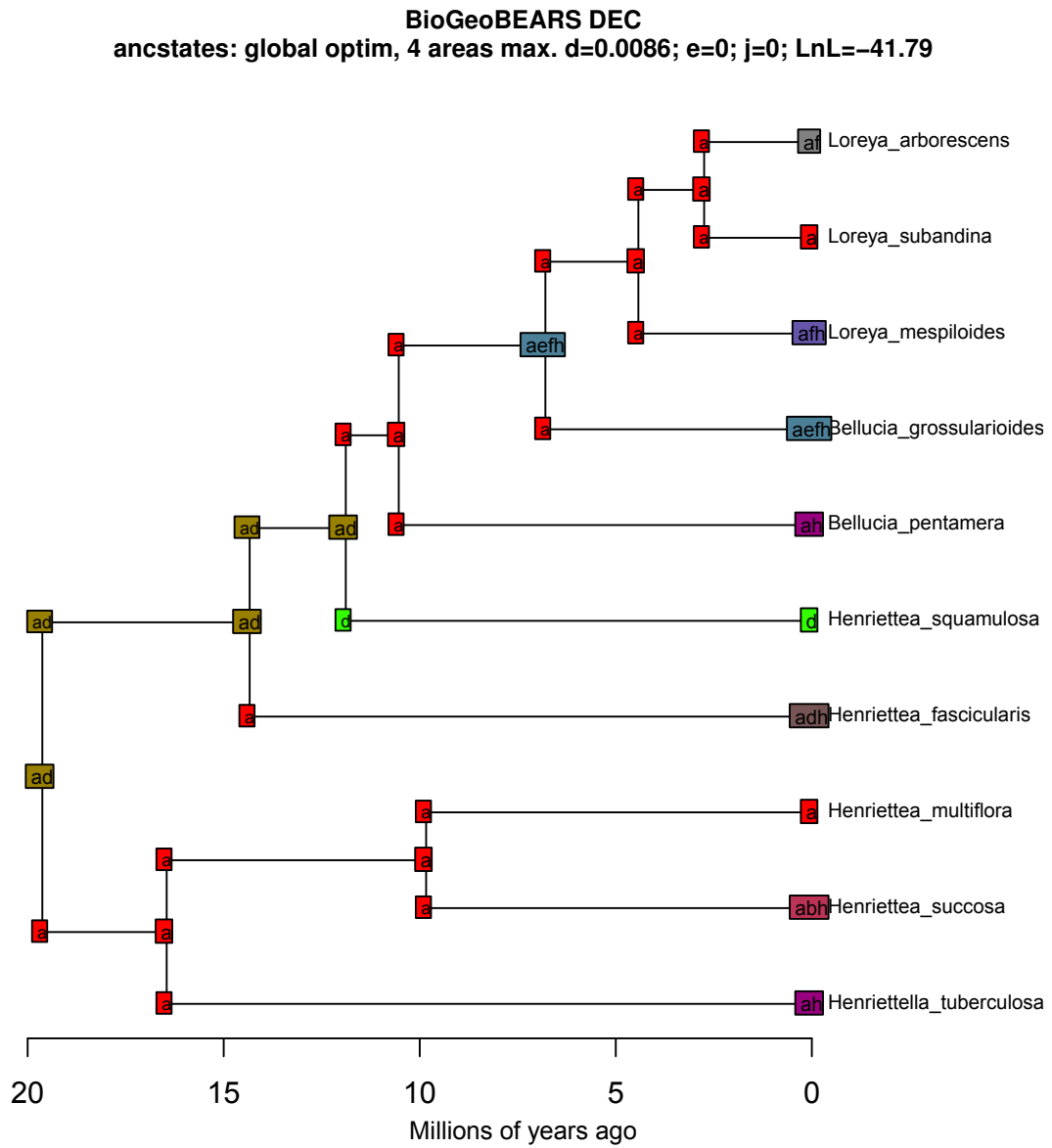


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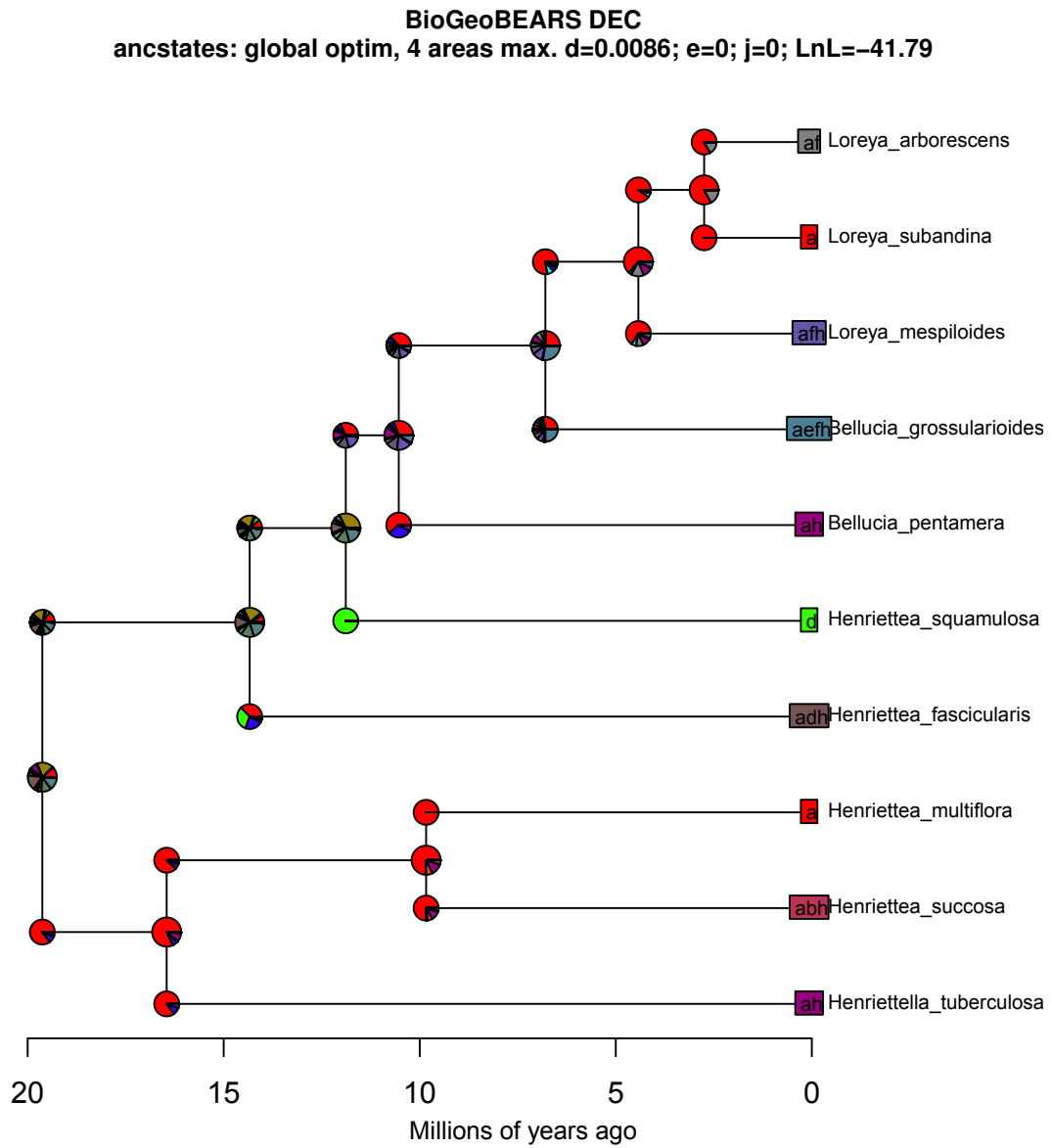


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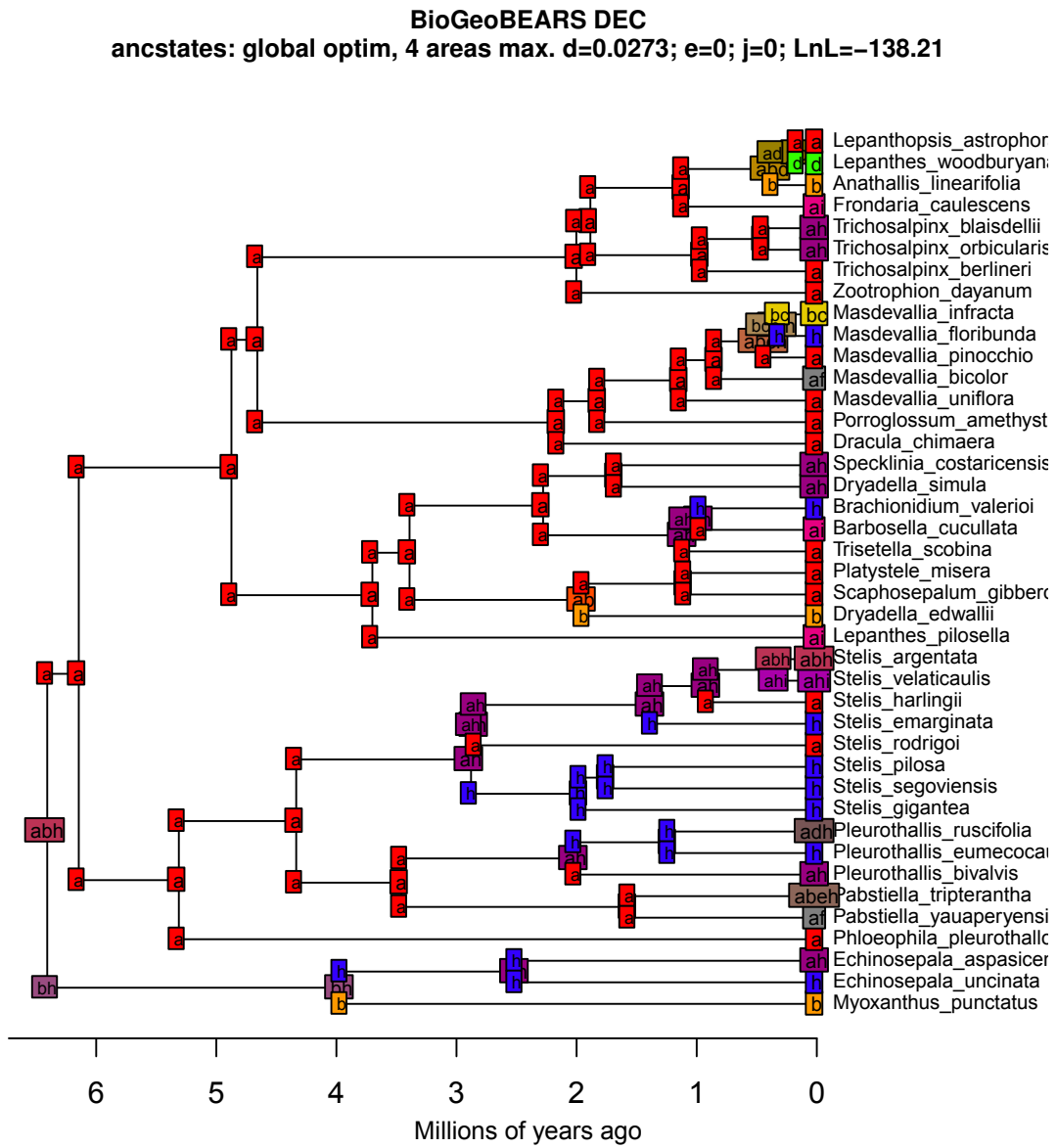


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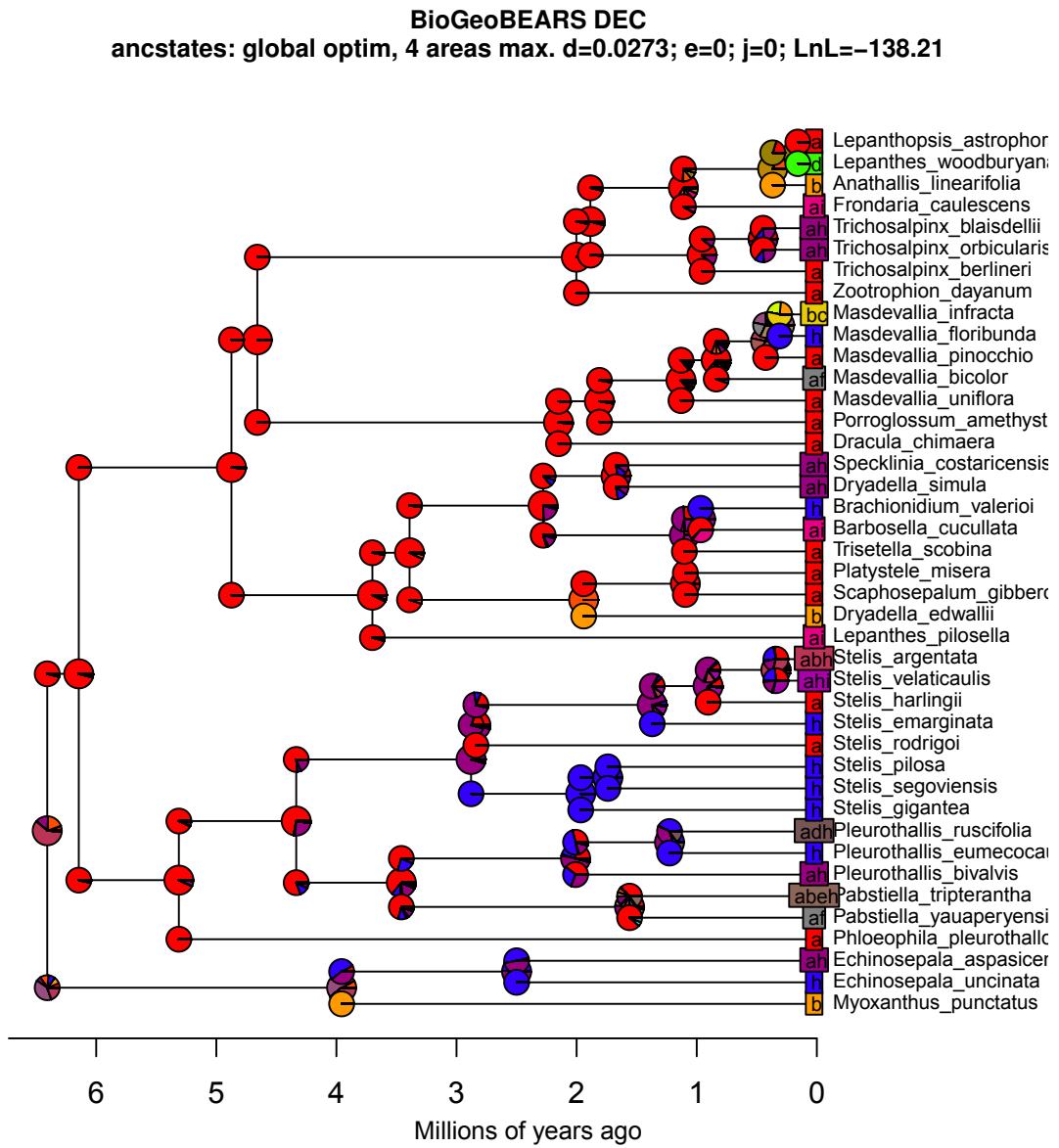


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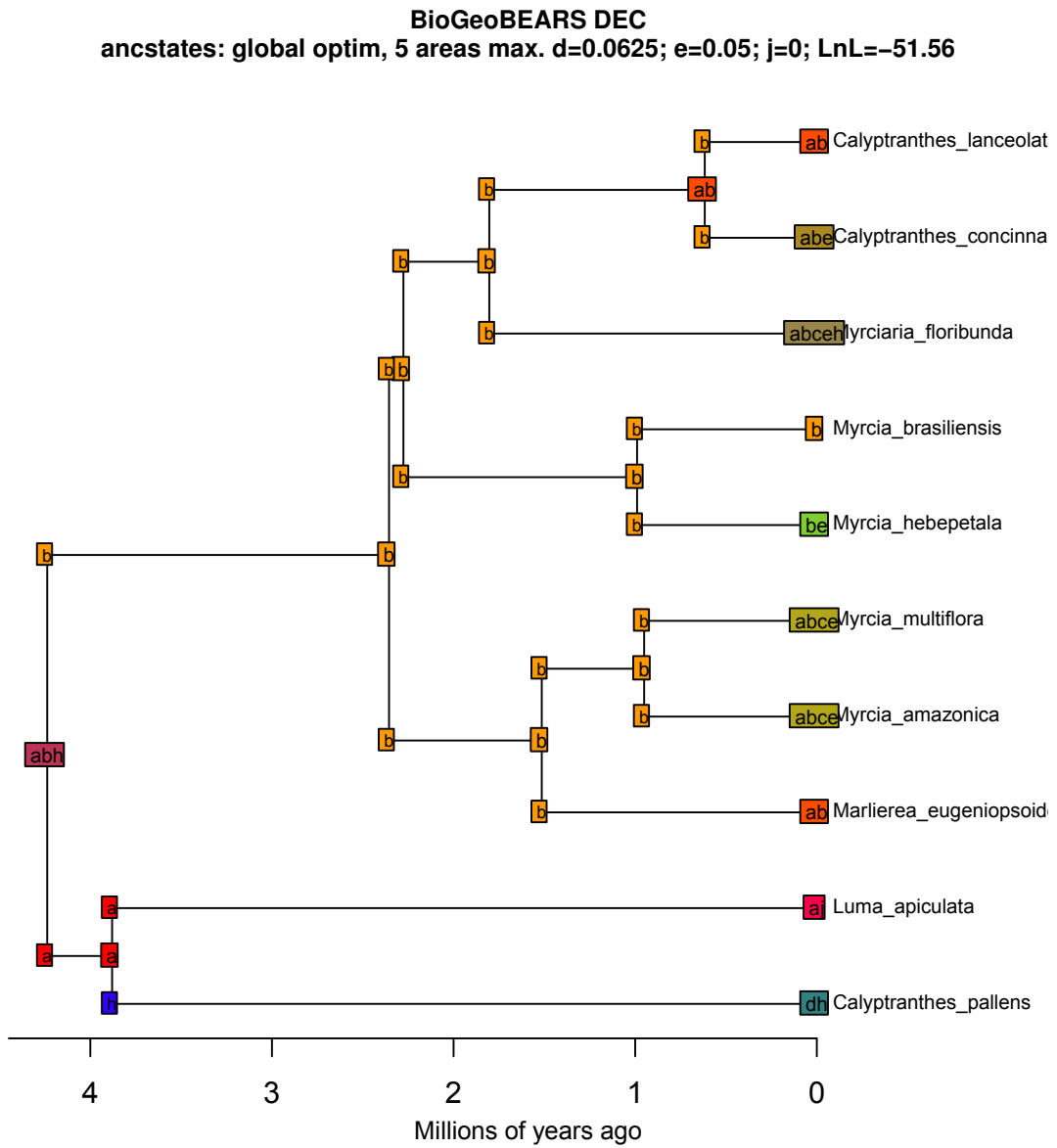


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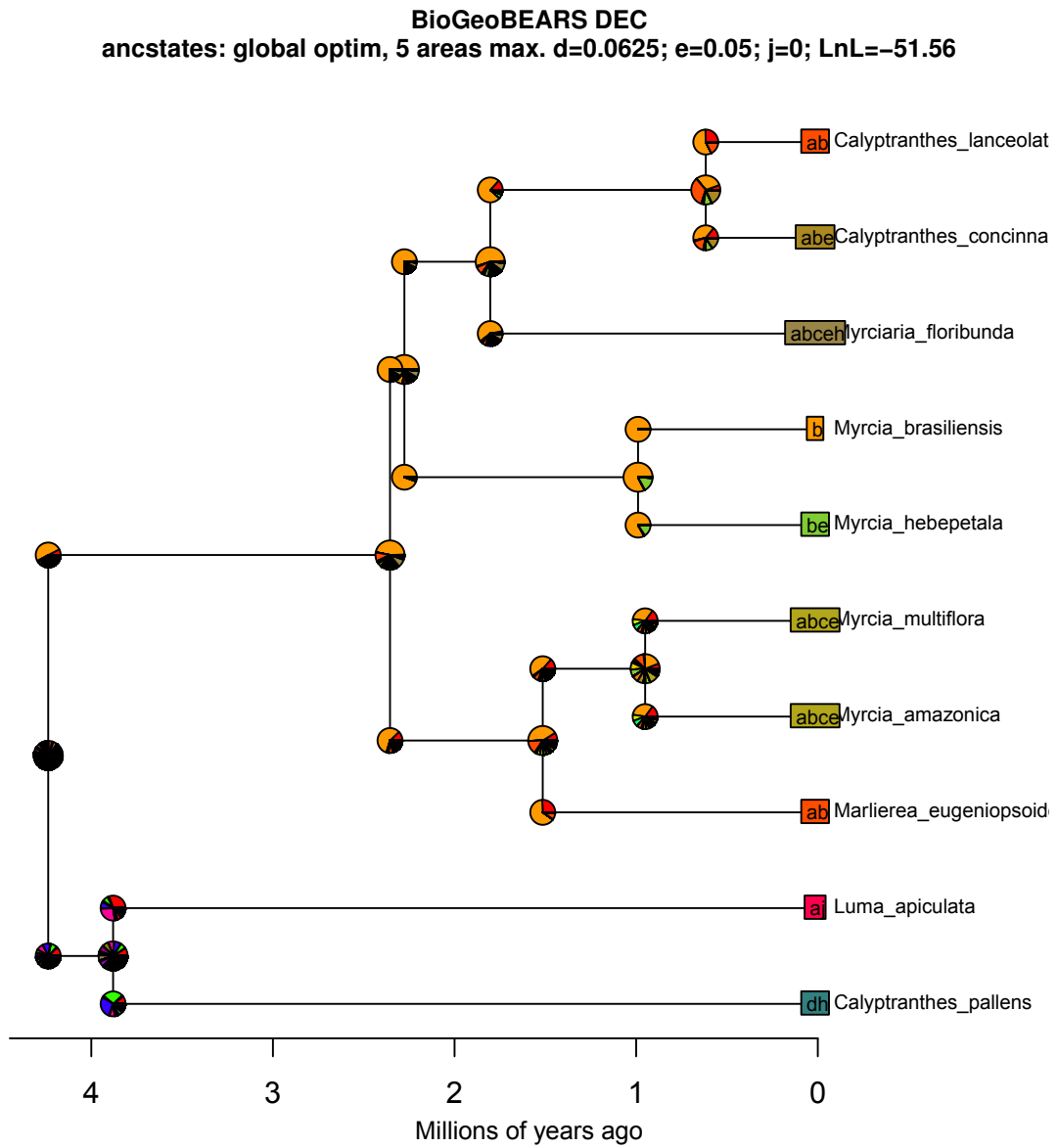


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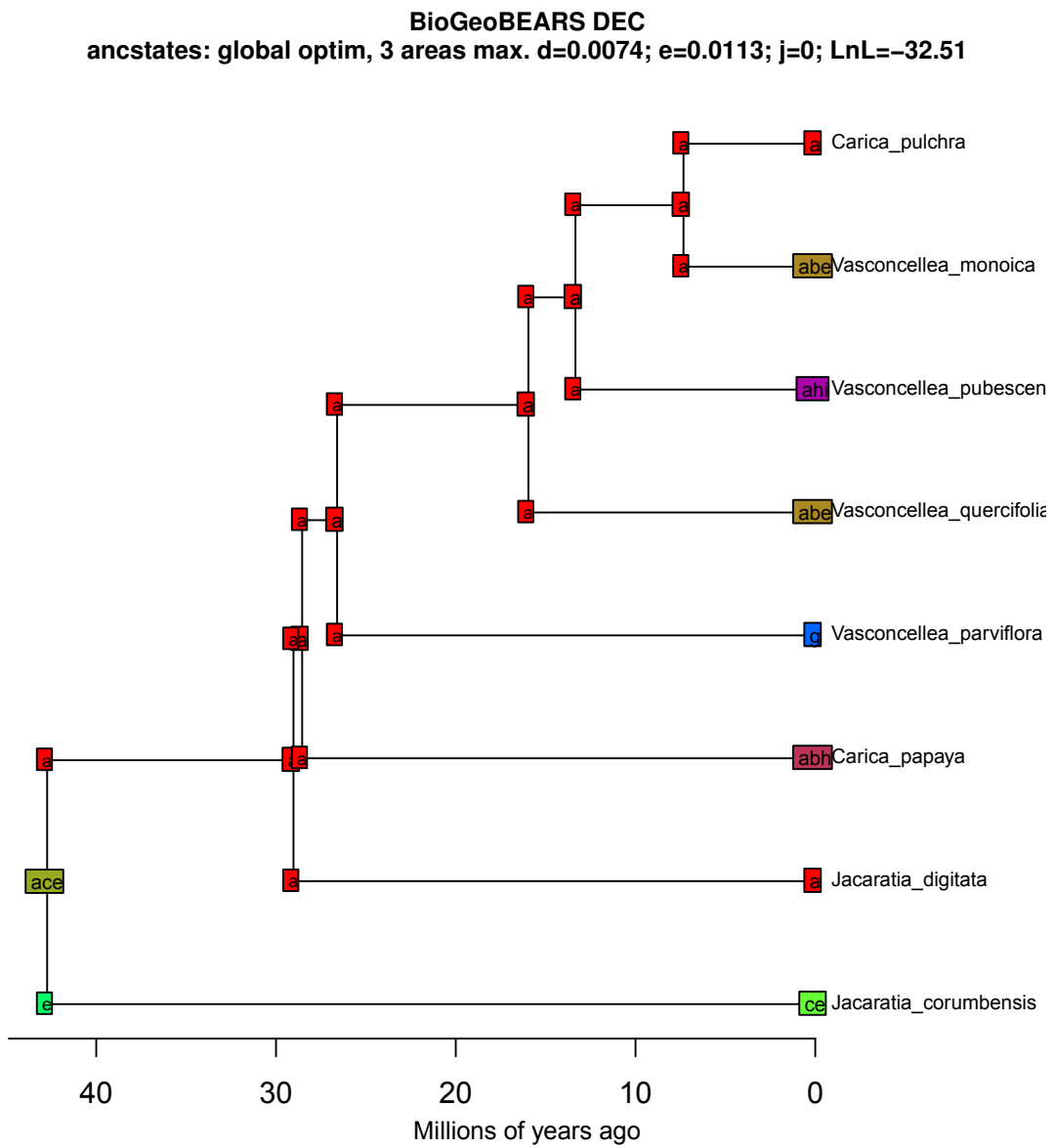


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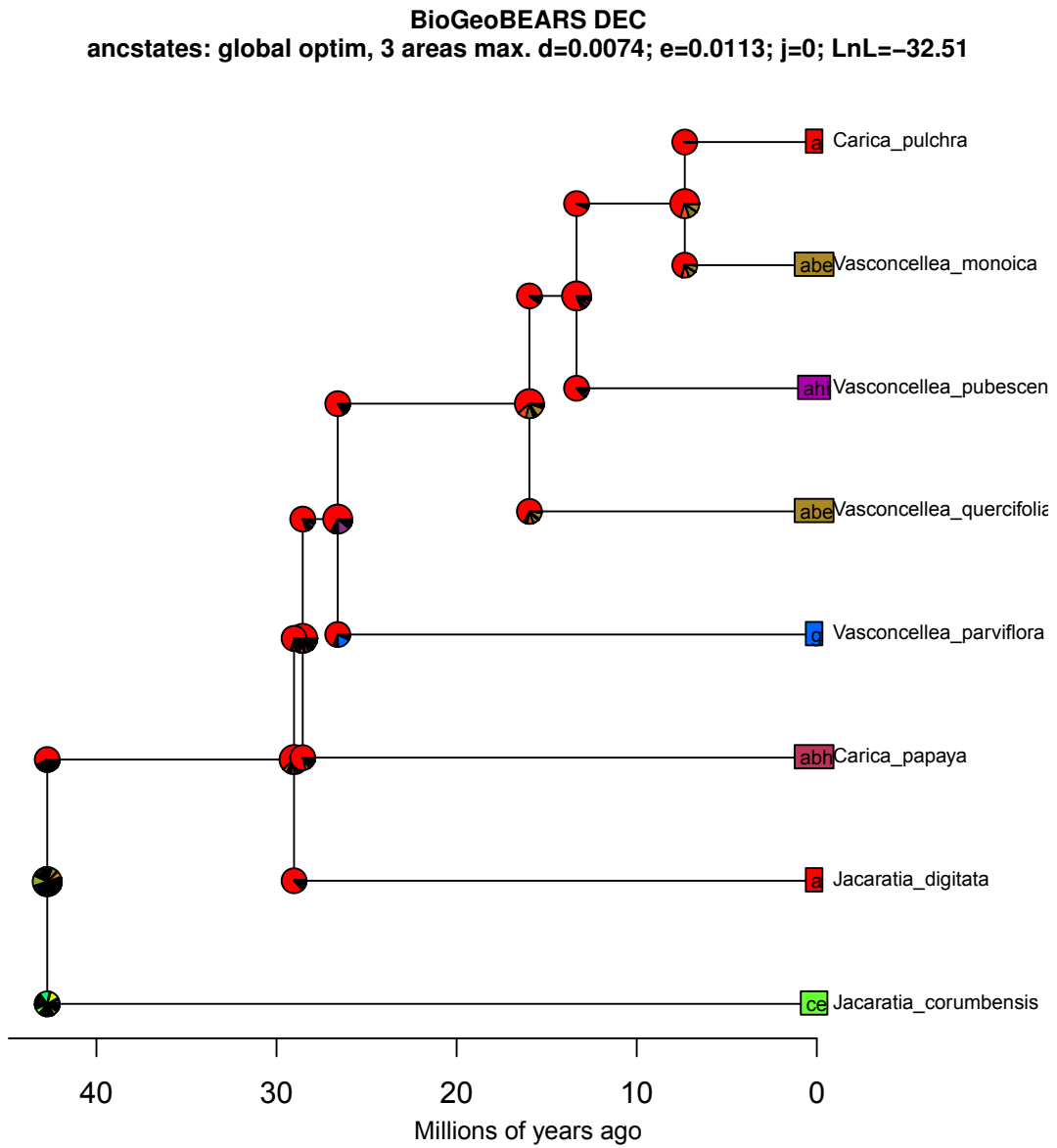


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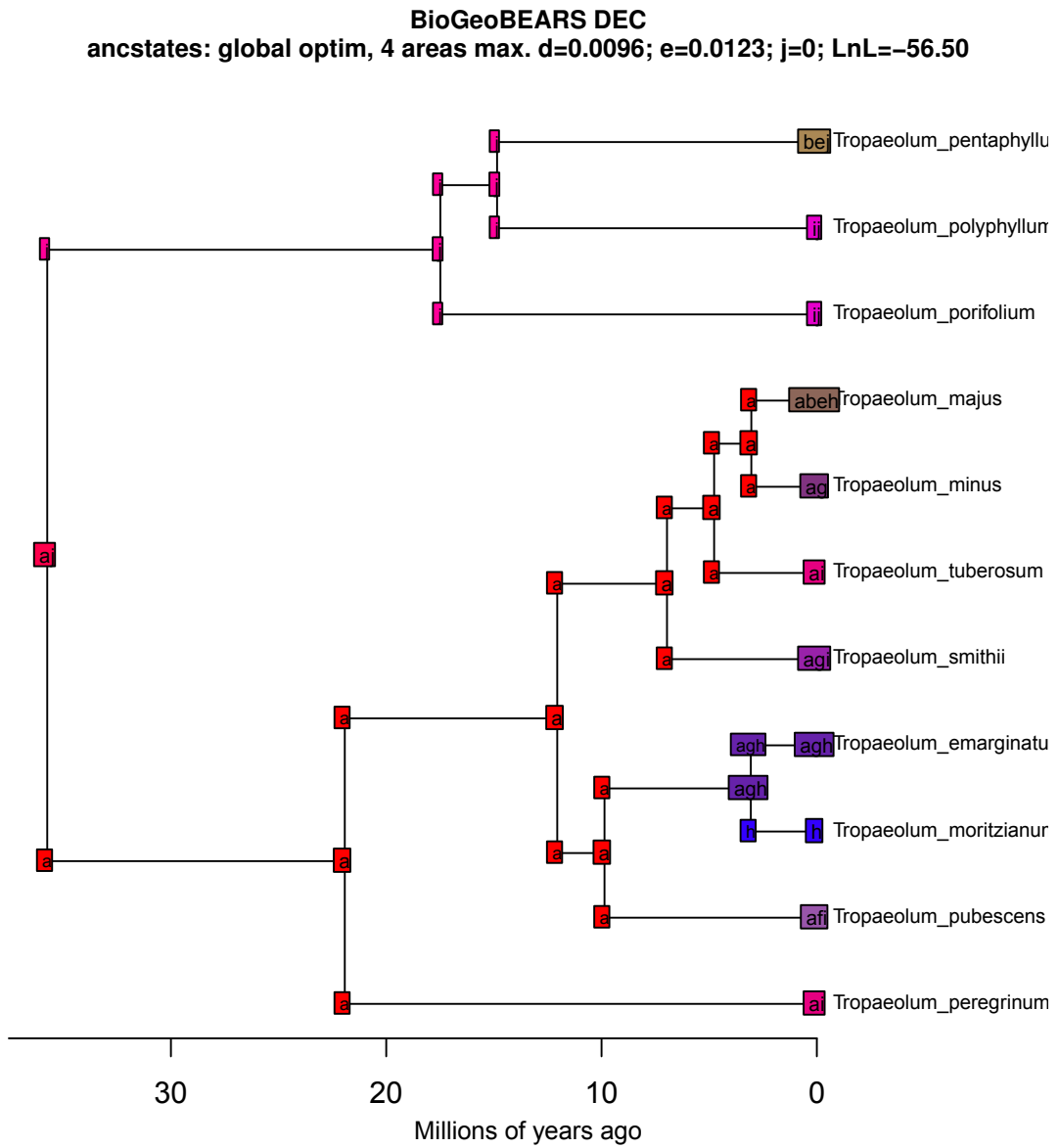


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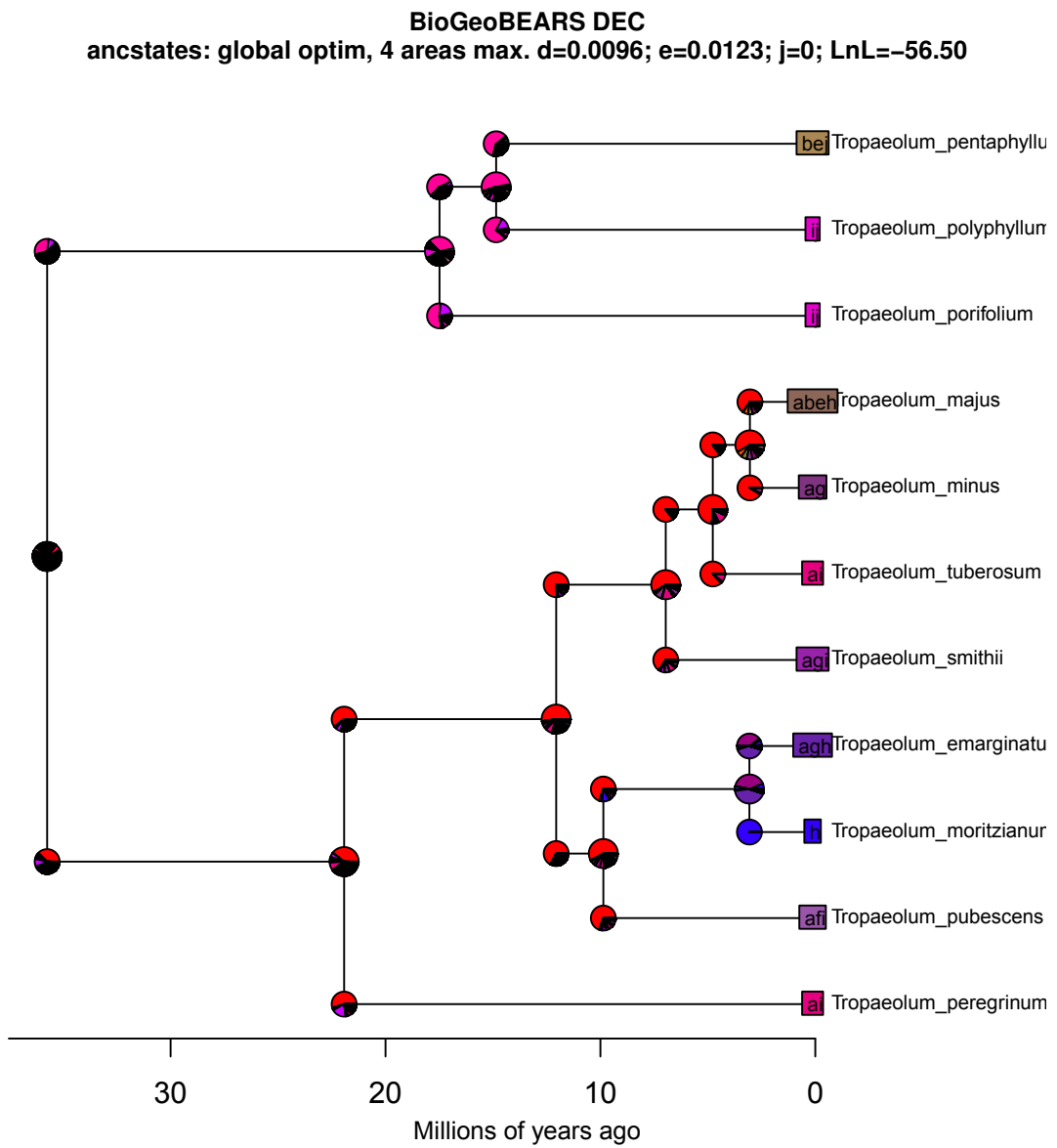


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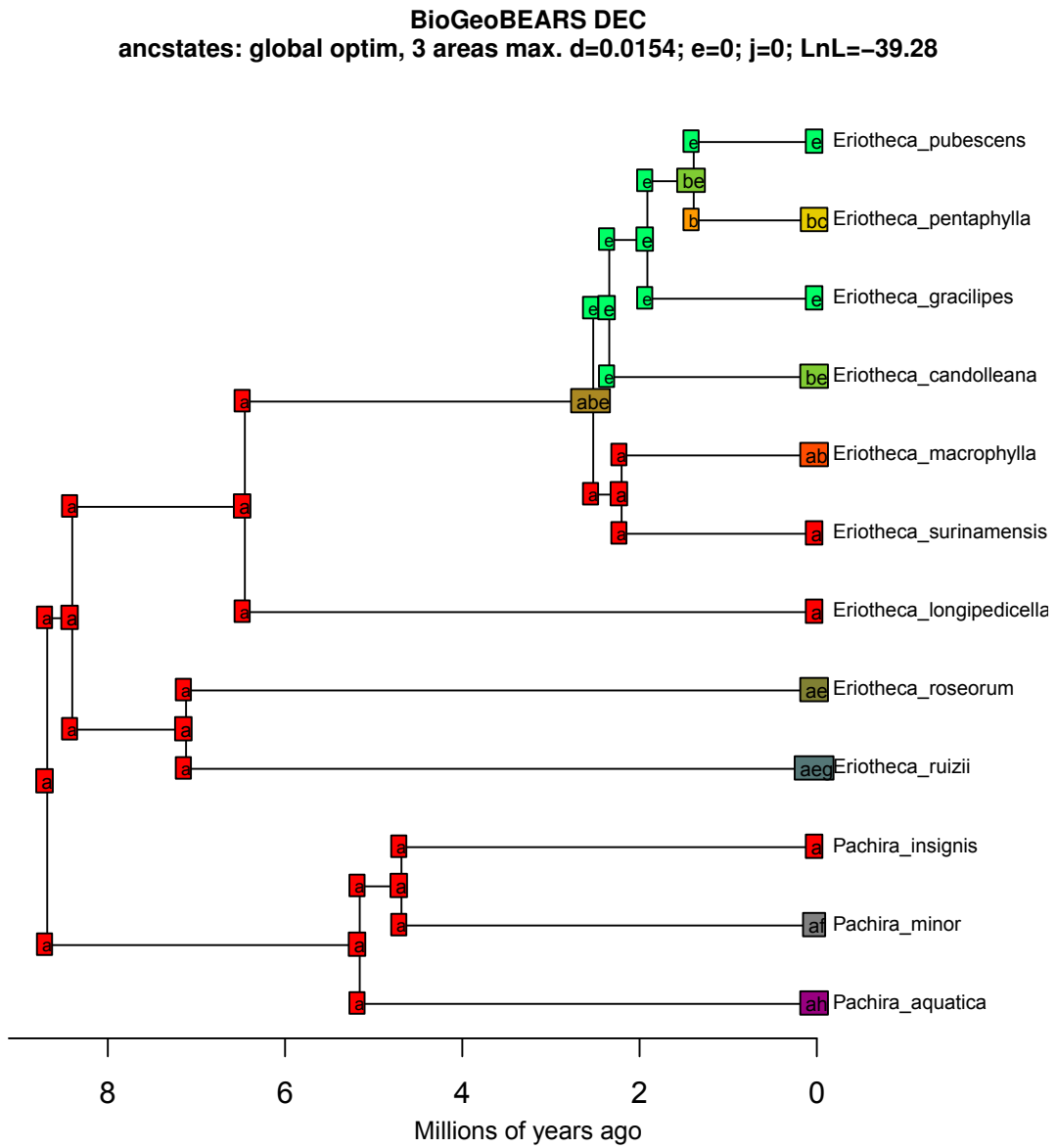


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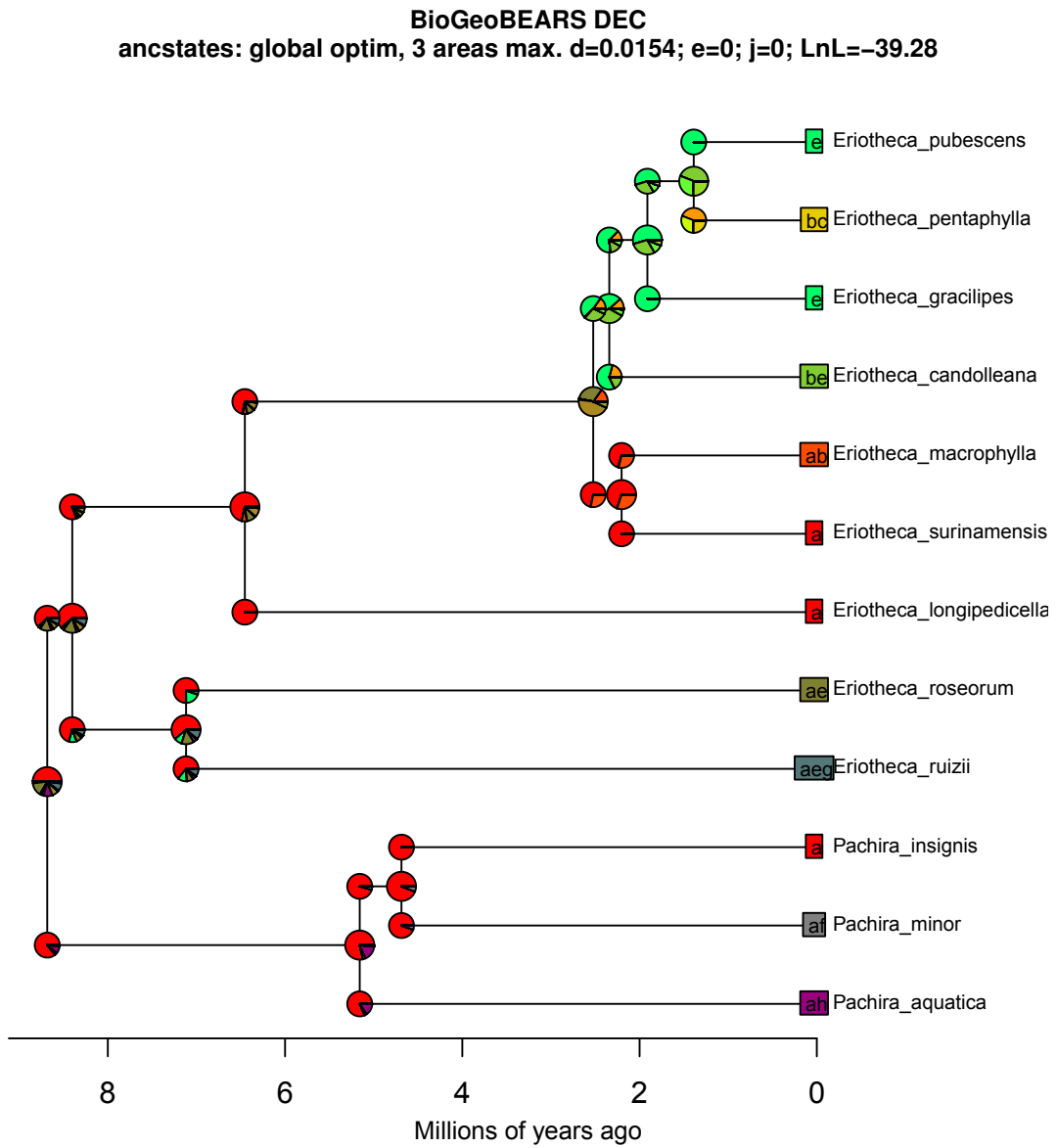


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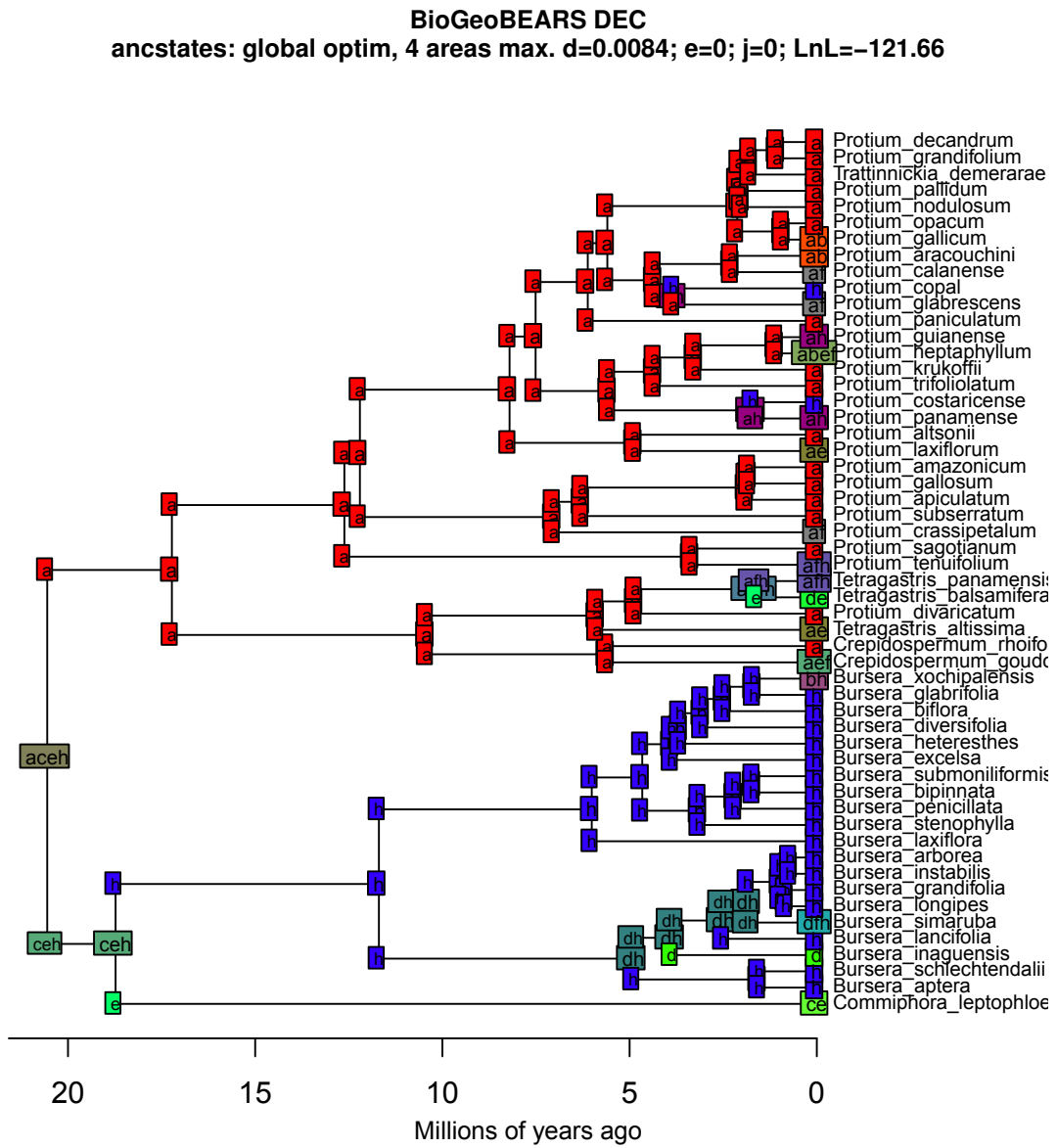


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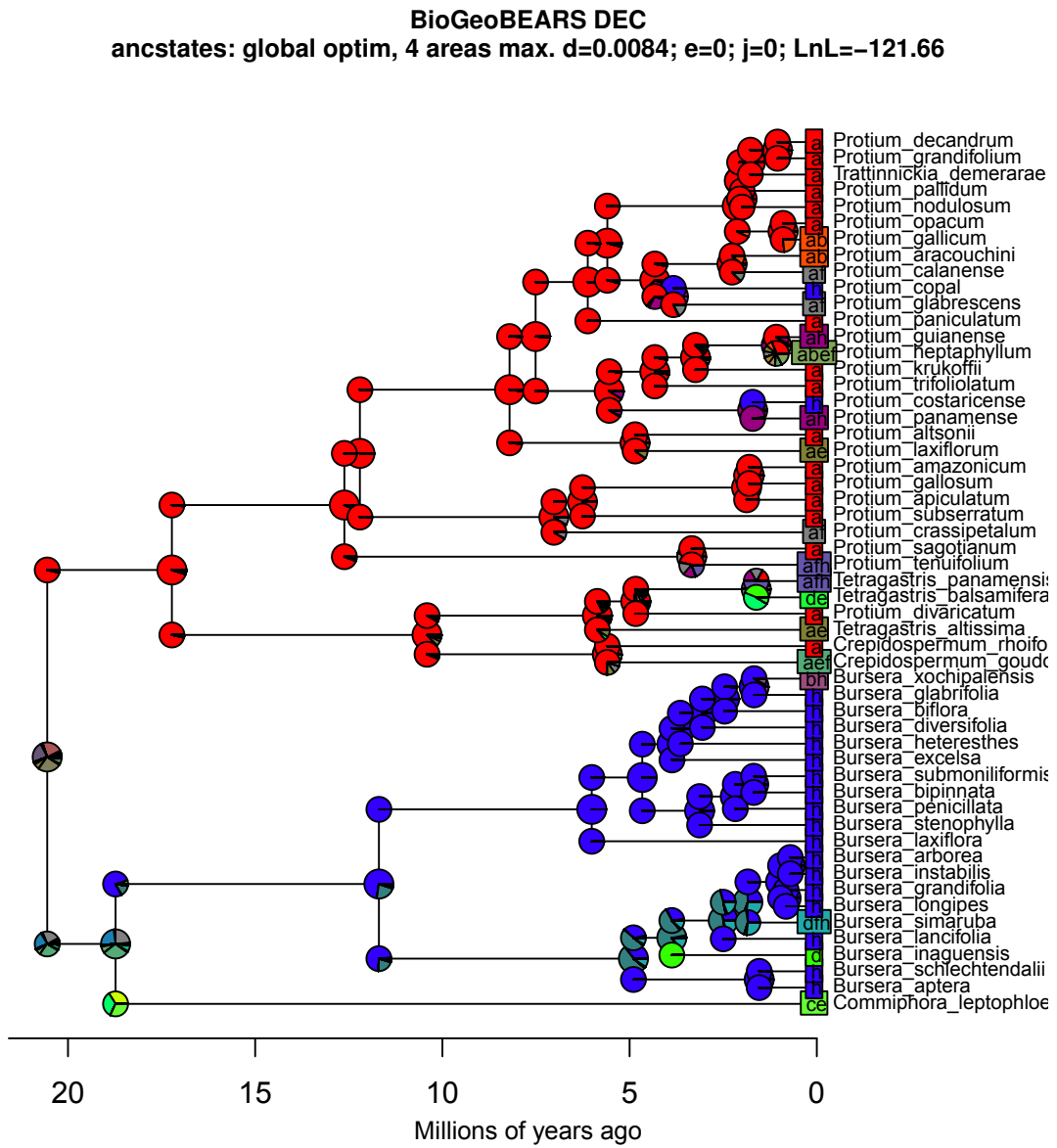


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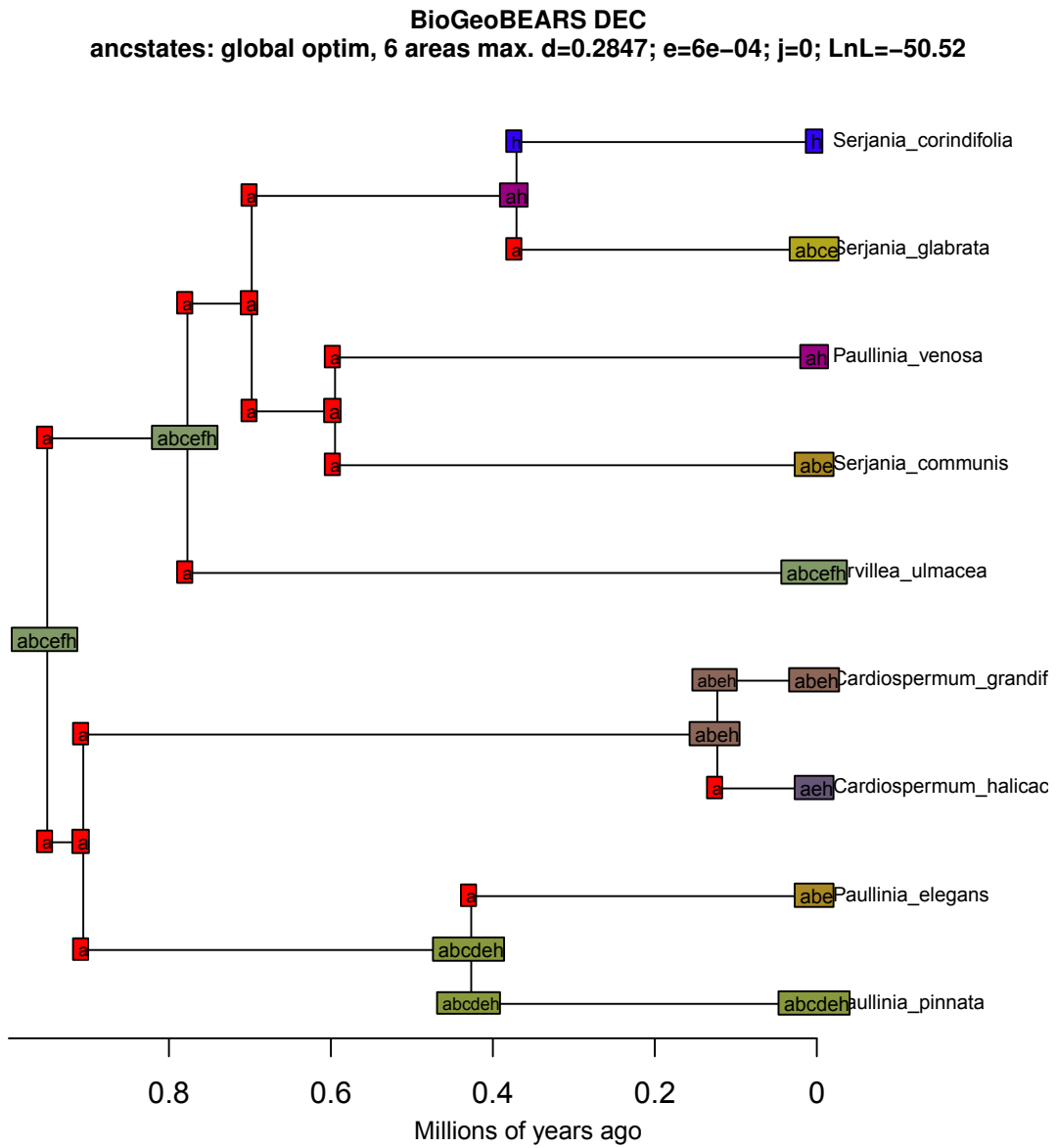


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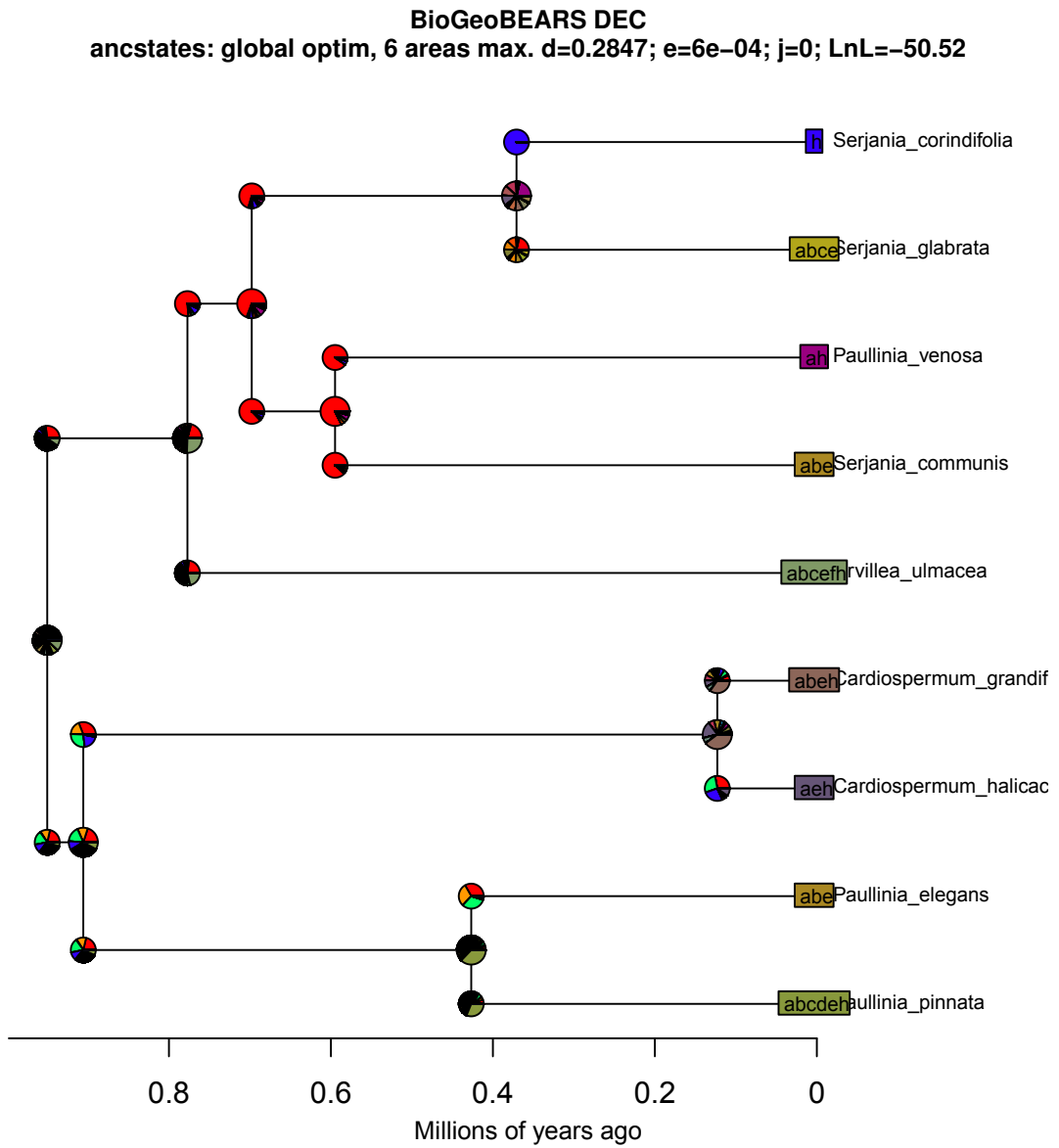


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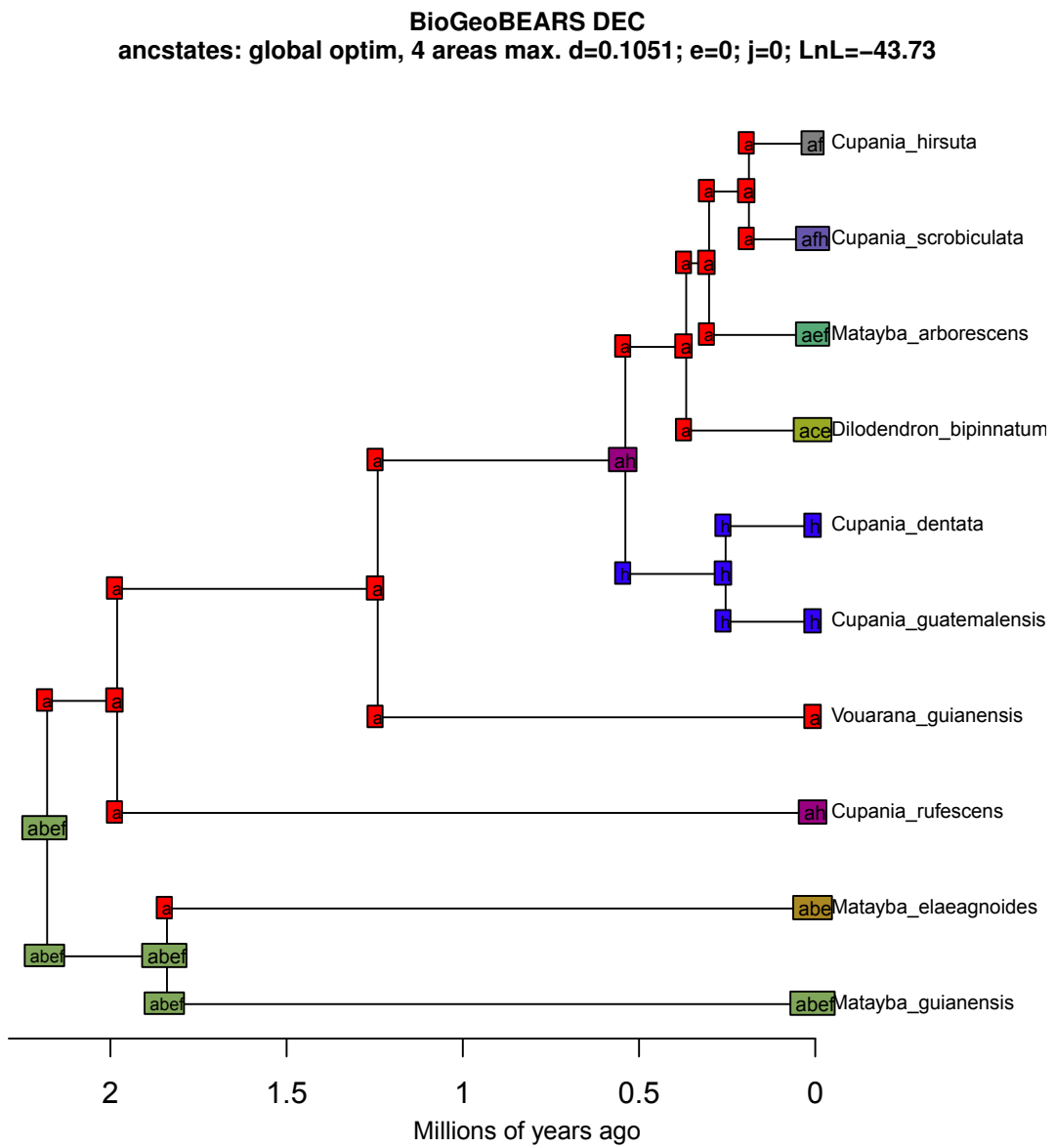


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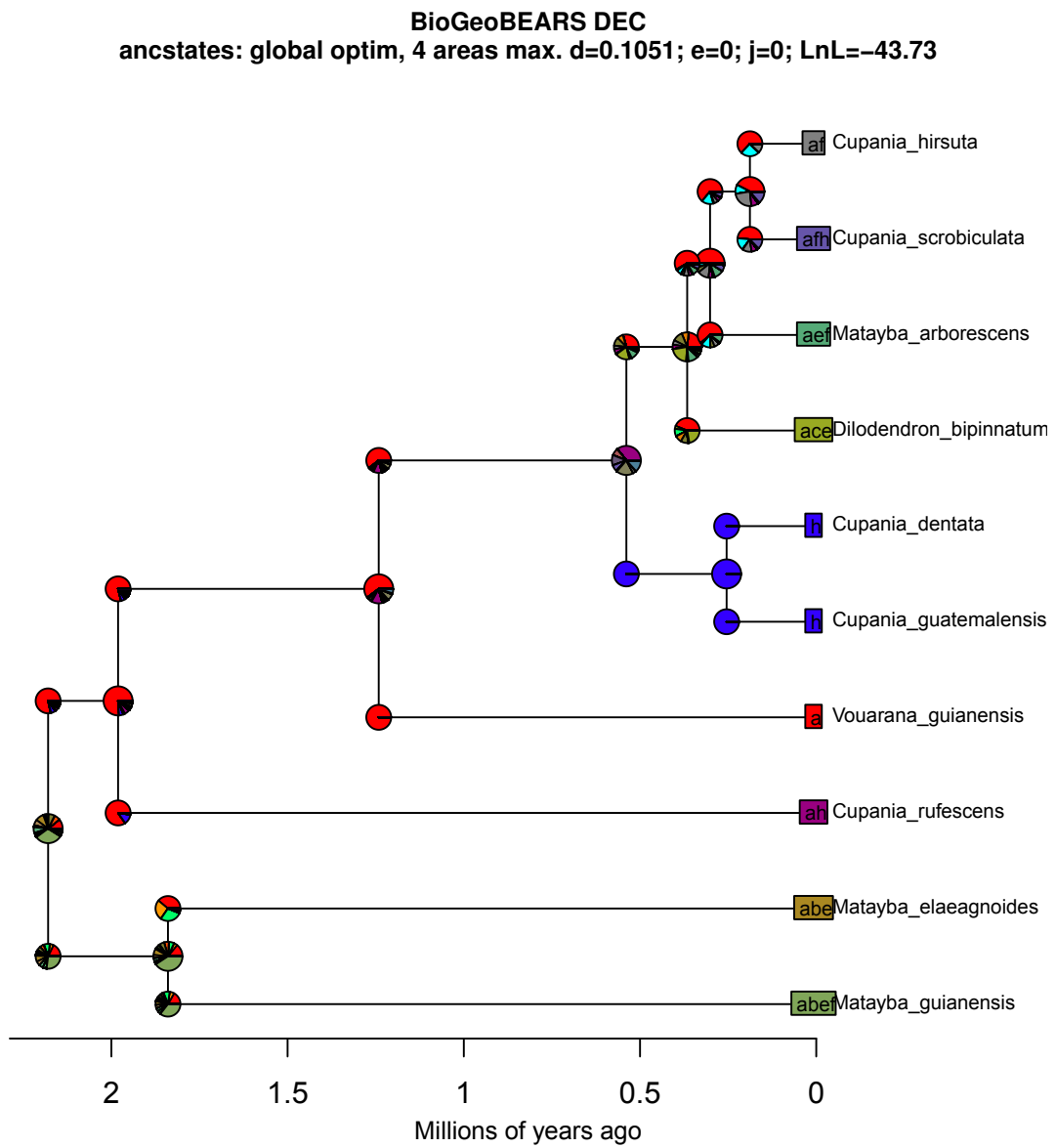


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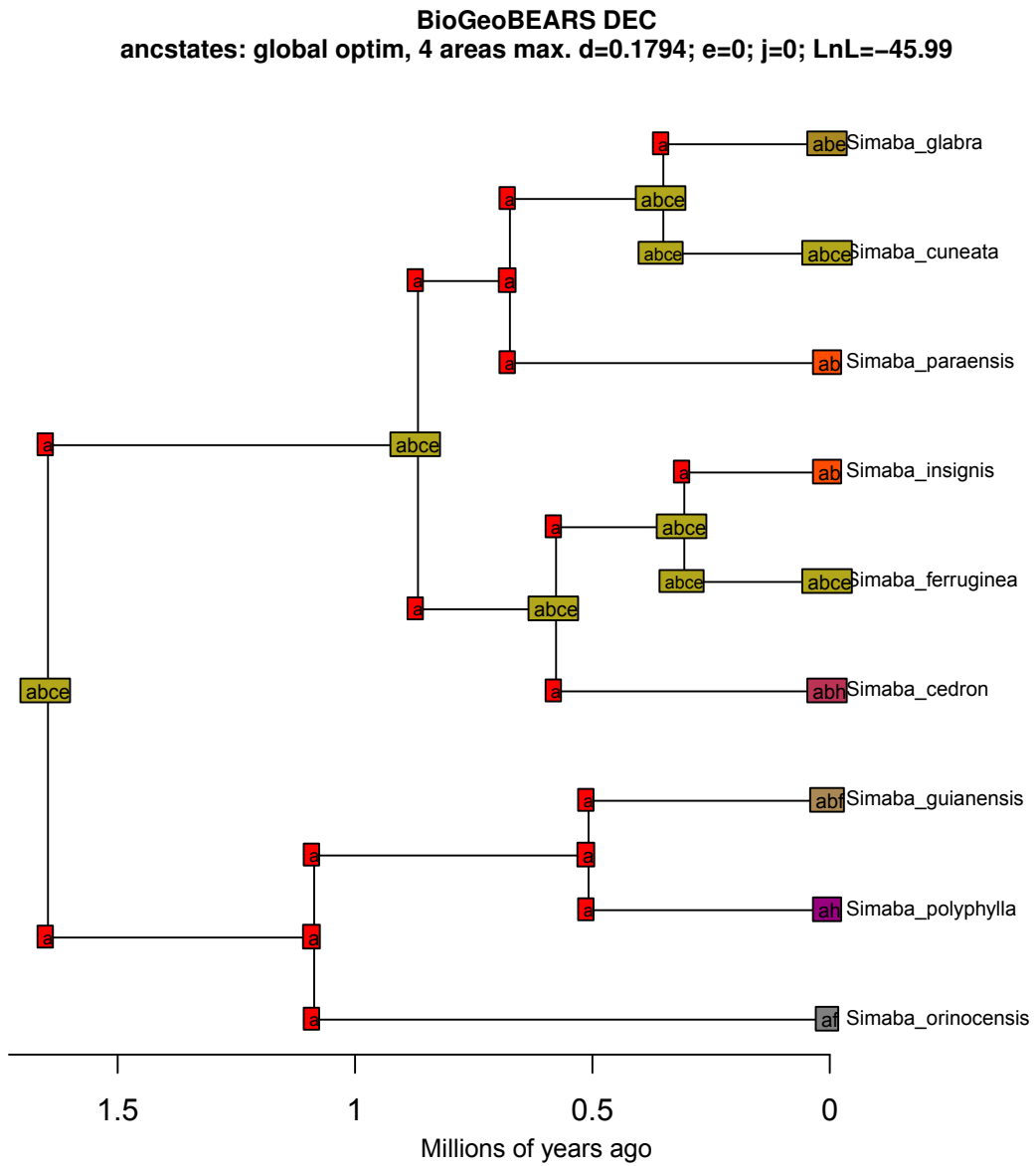


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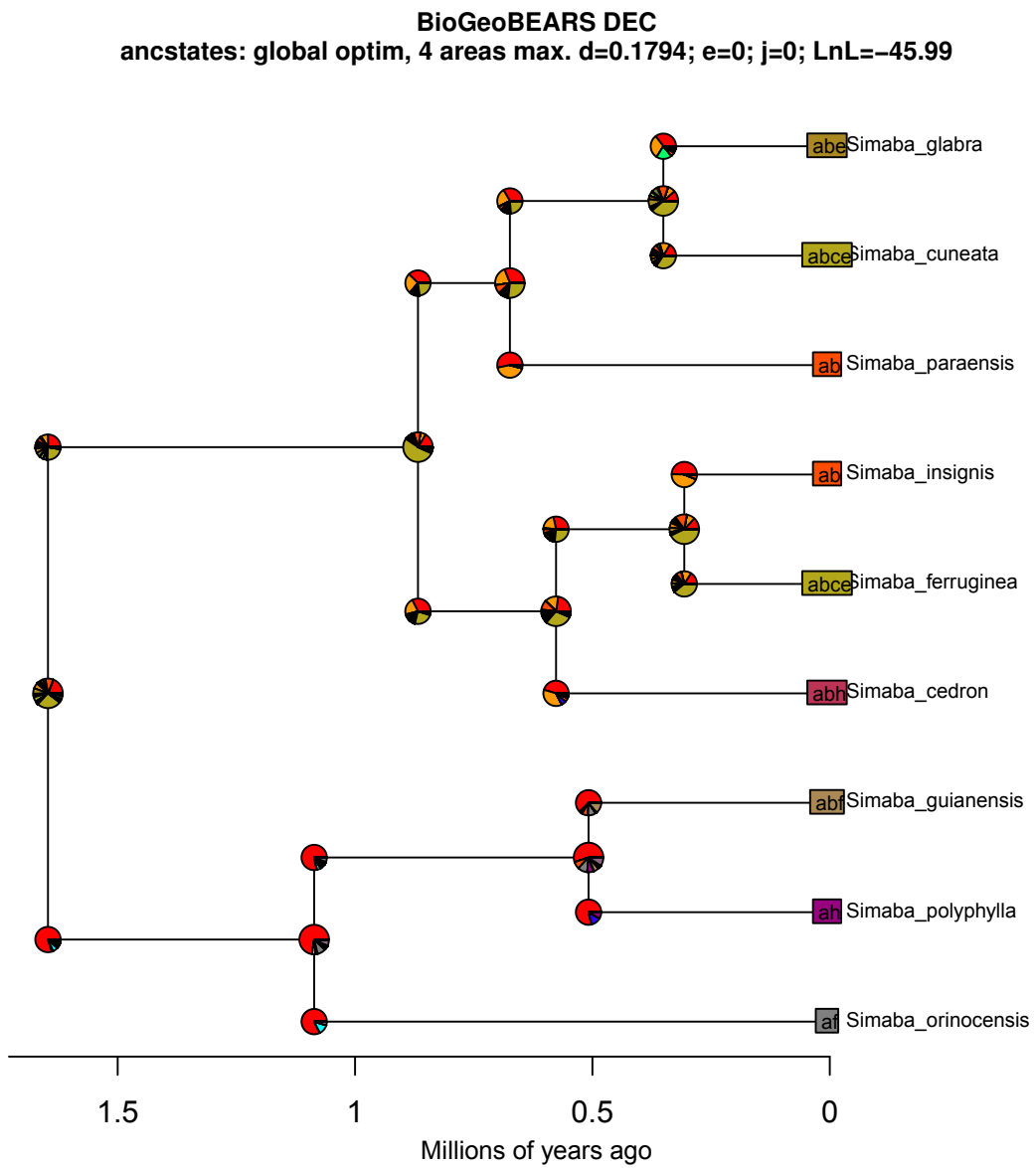


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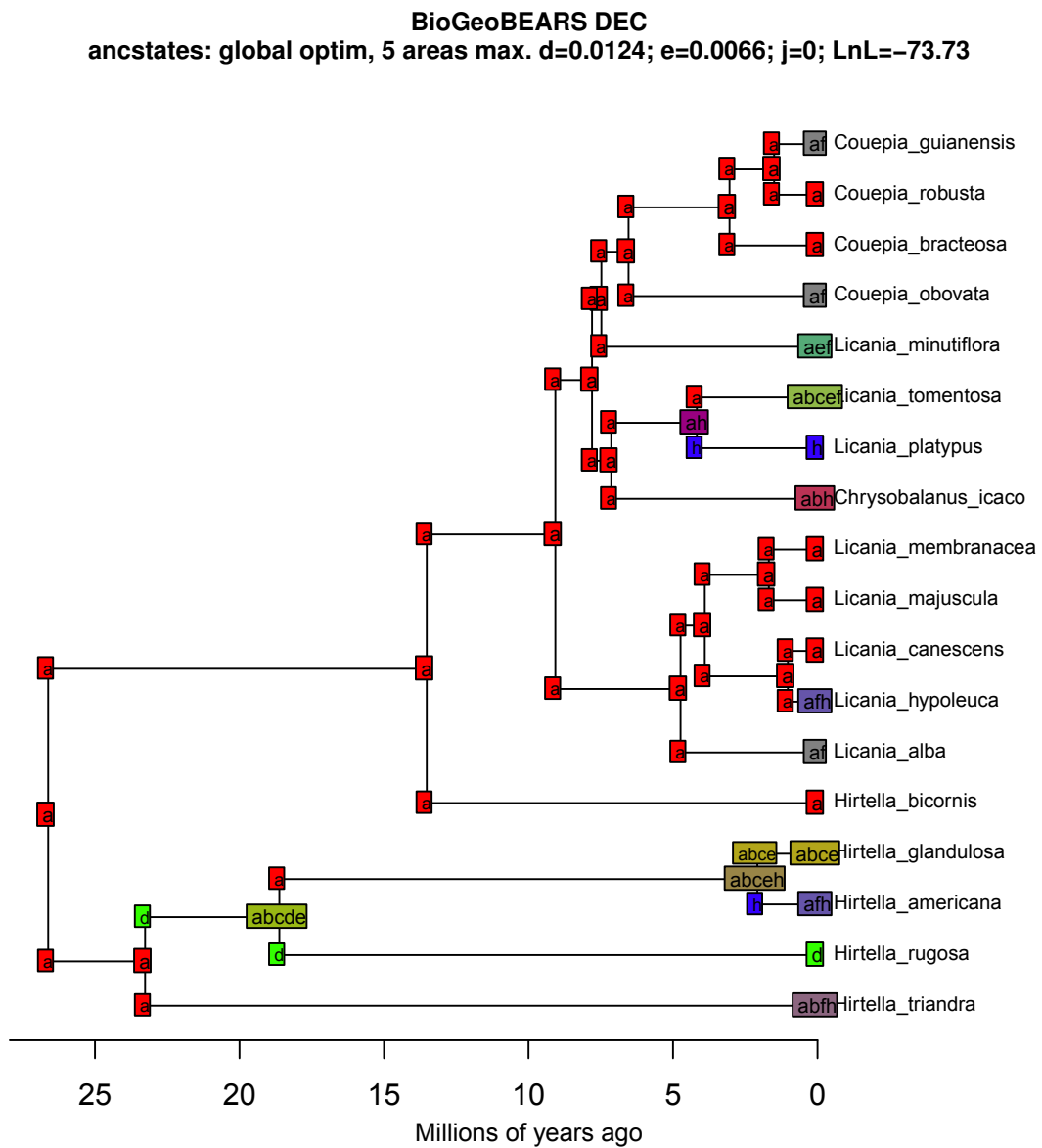


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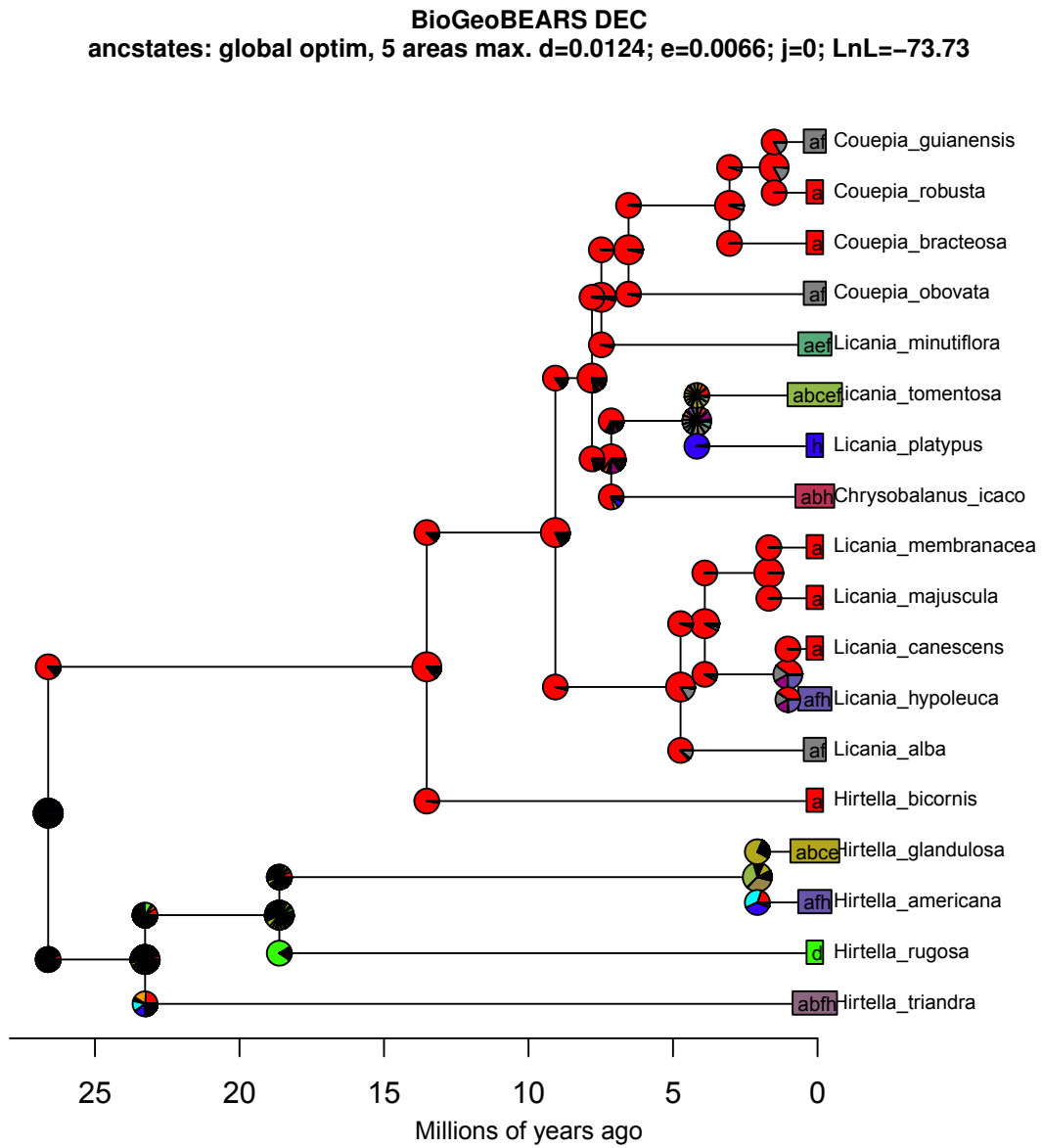


Figure S3: Clades of angiosperms

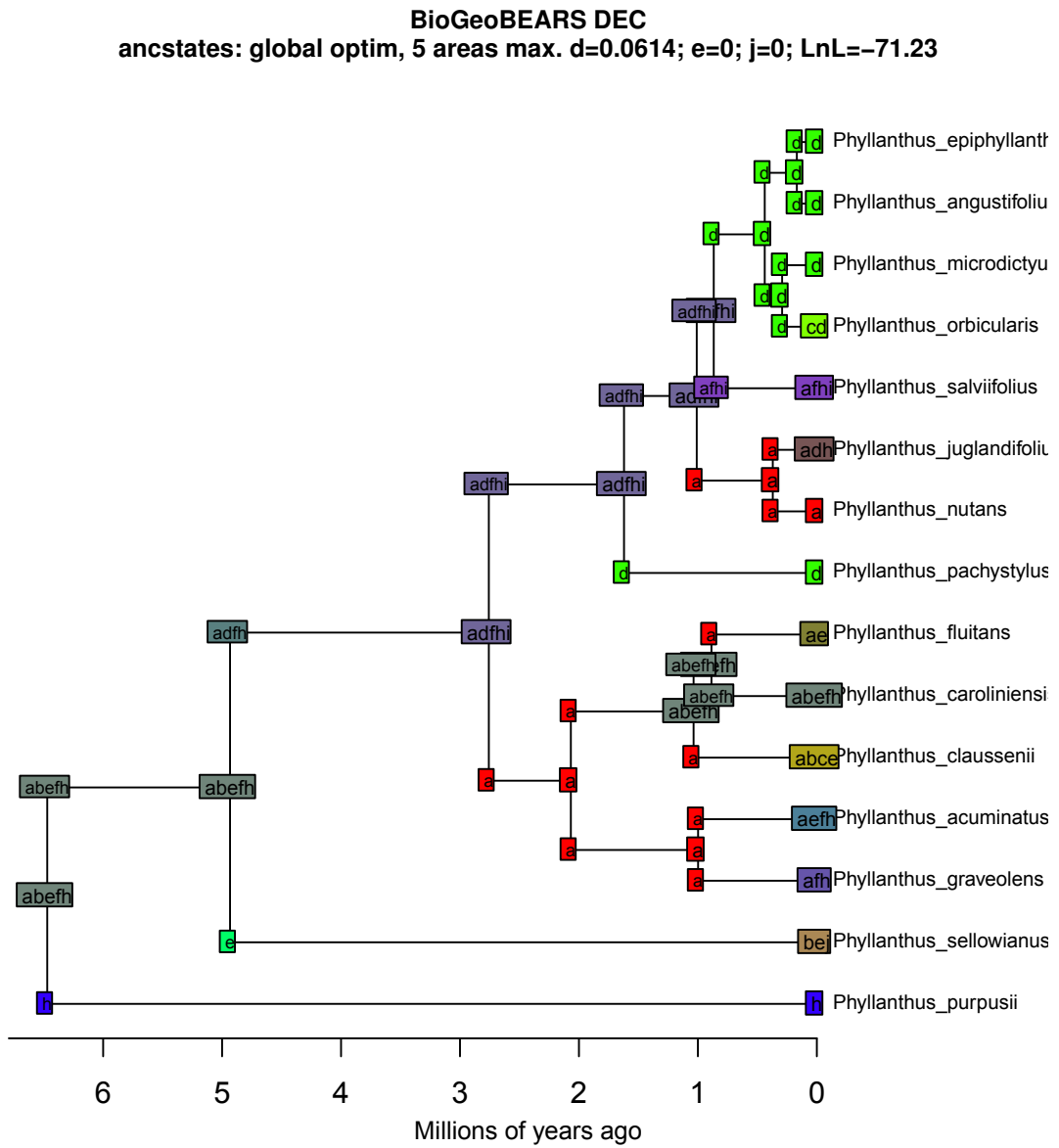


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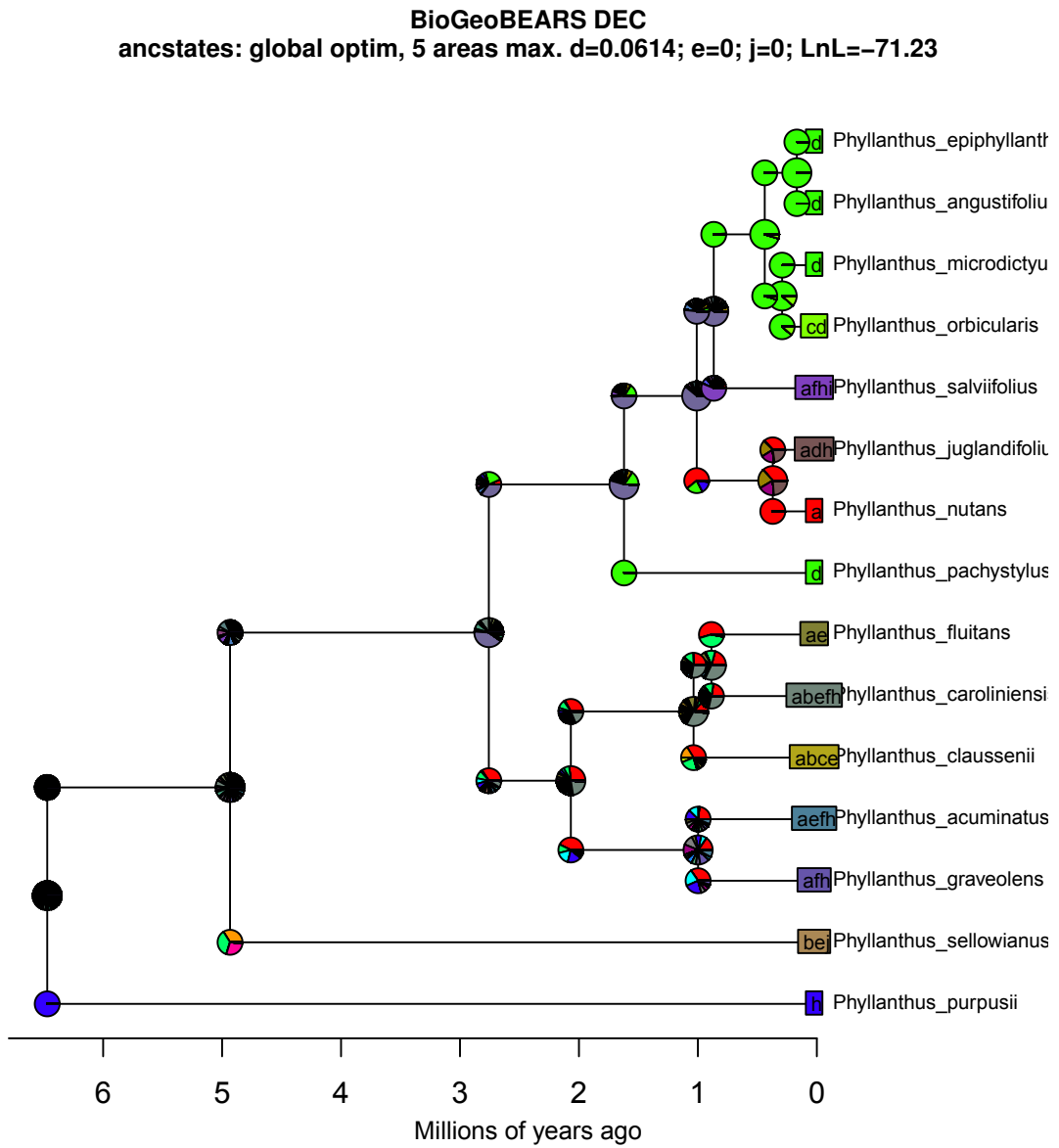


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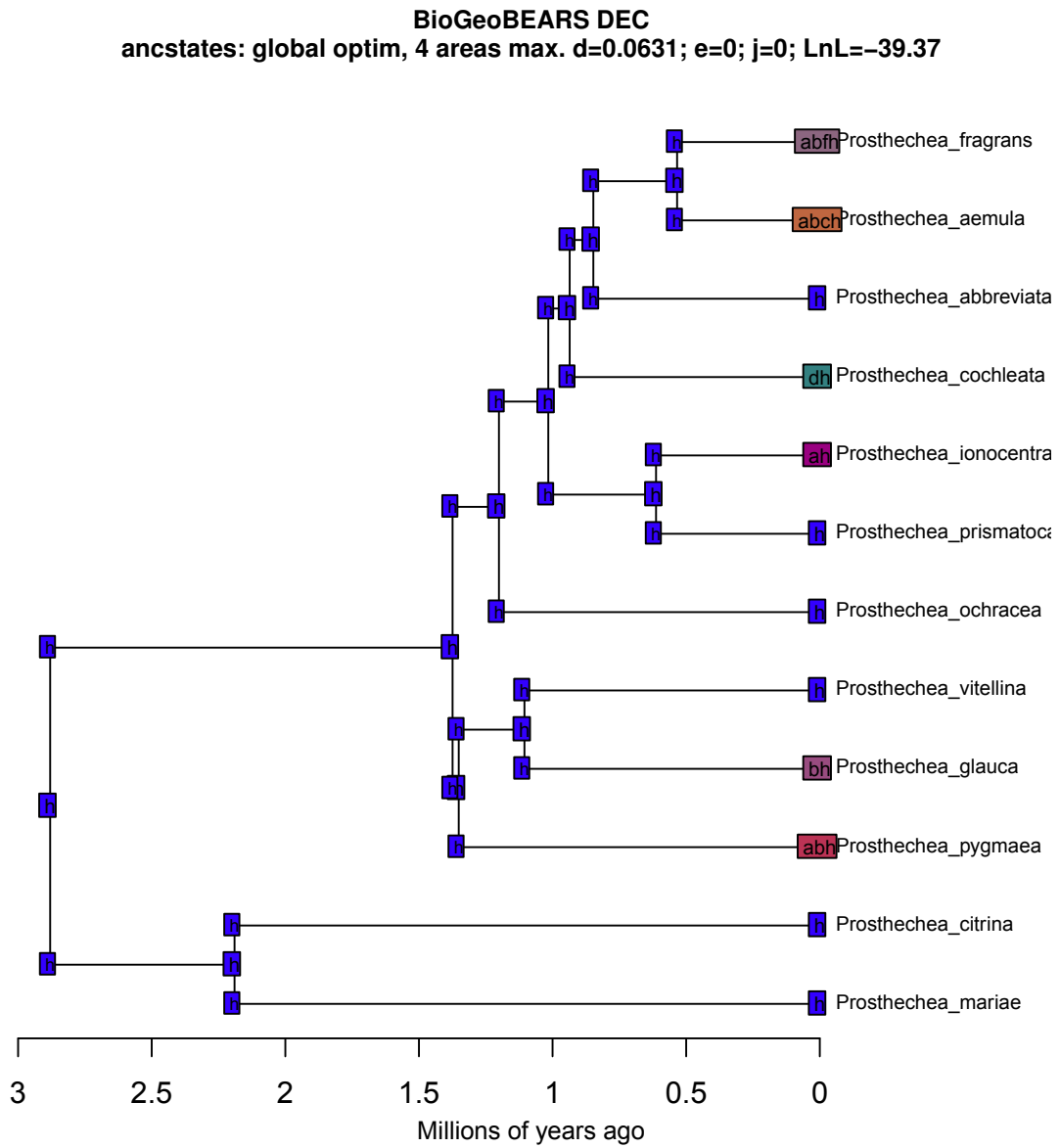


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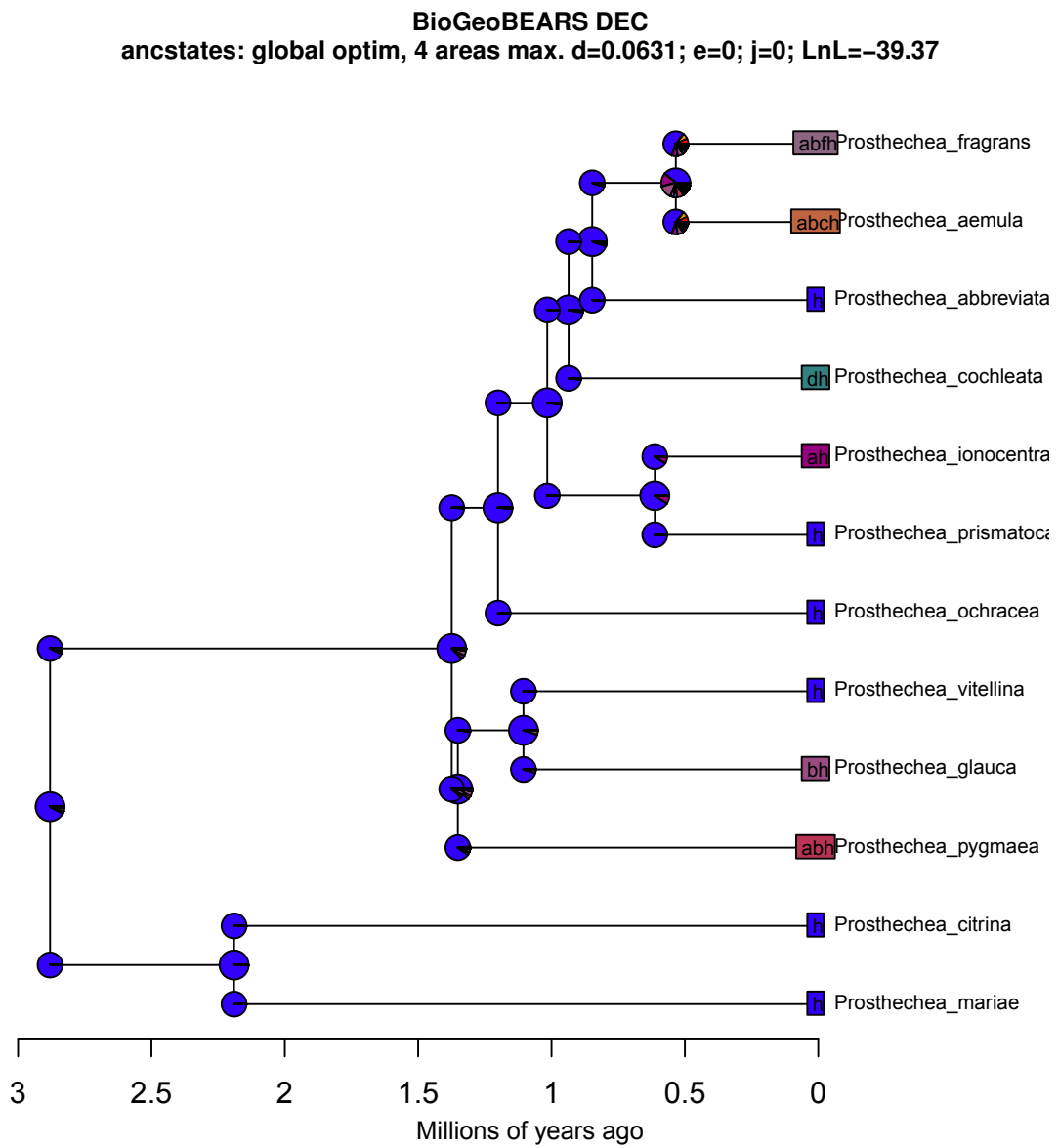


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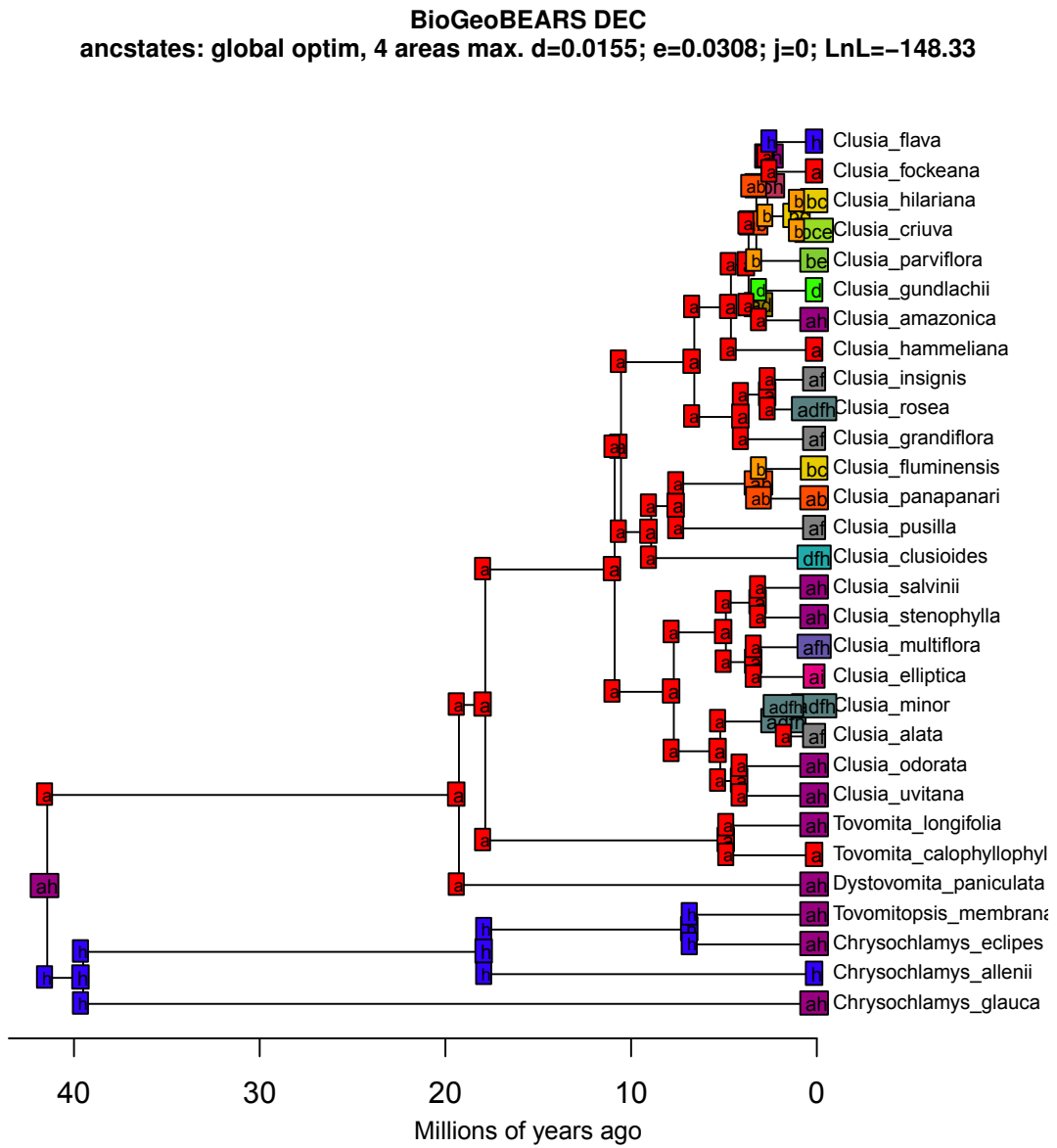


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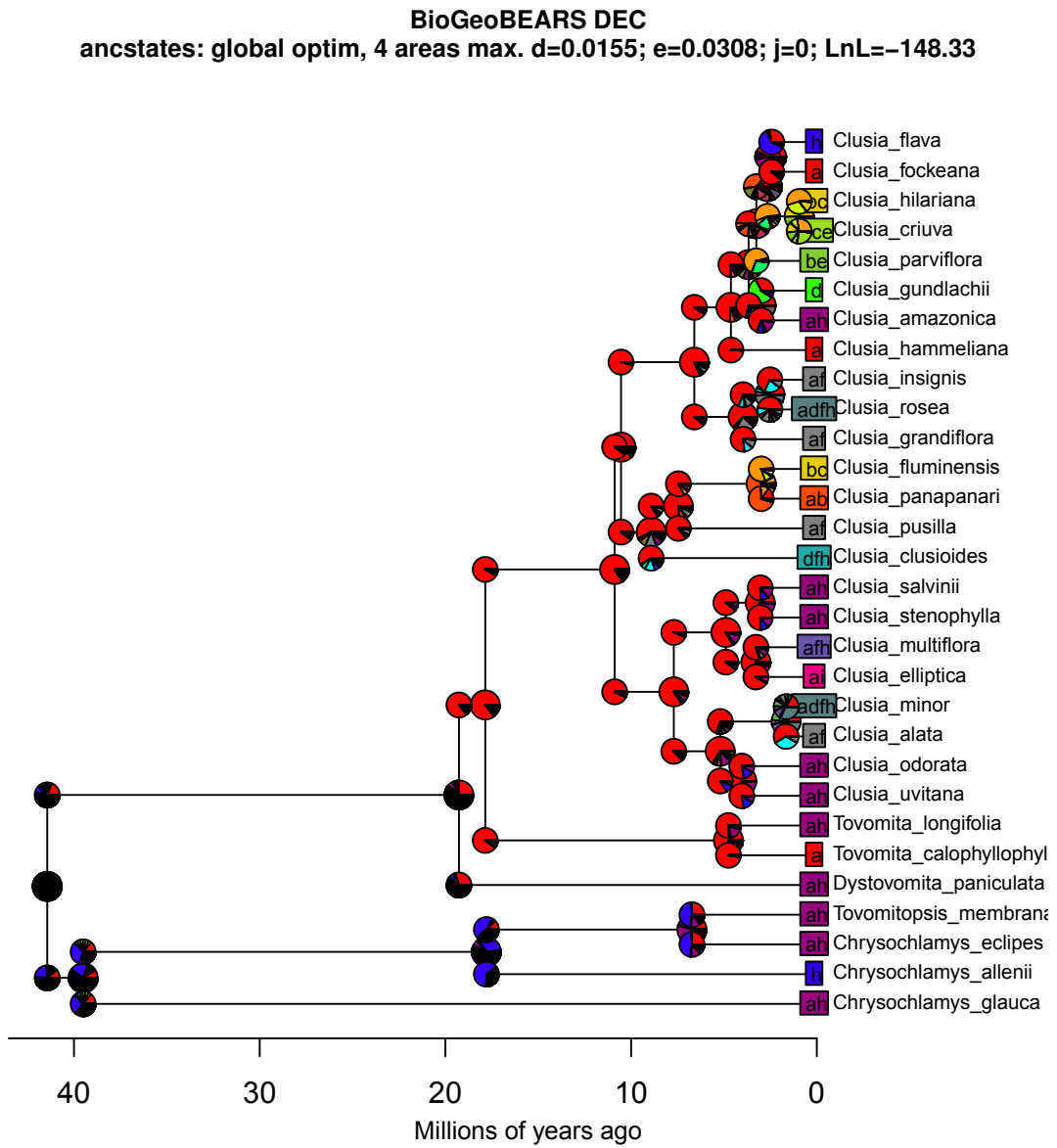


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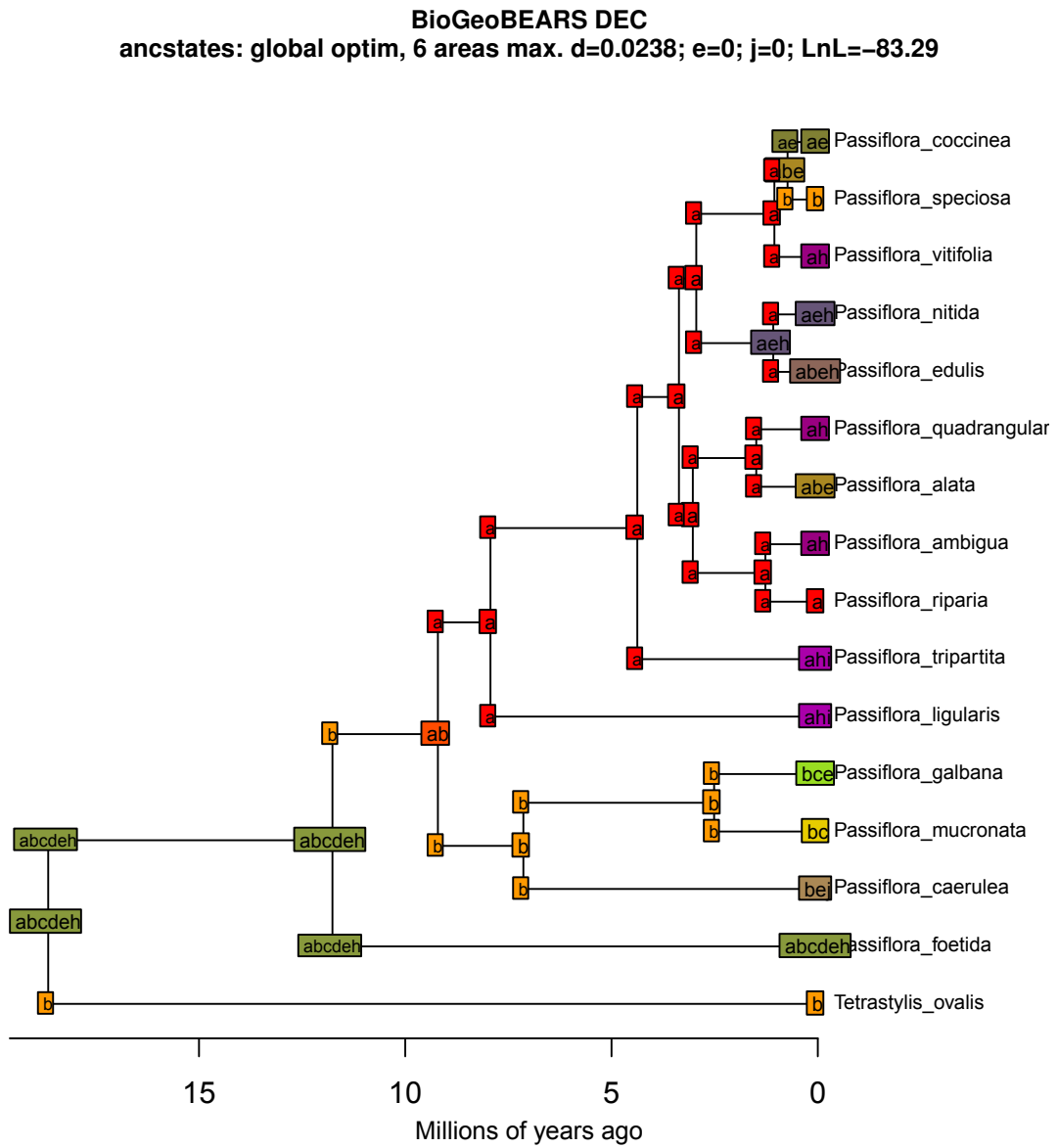


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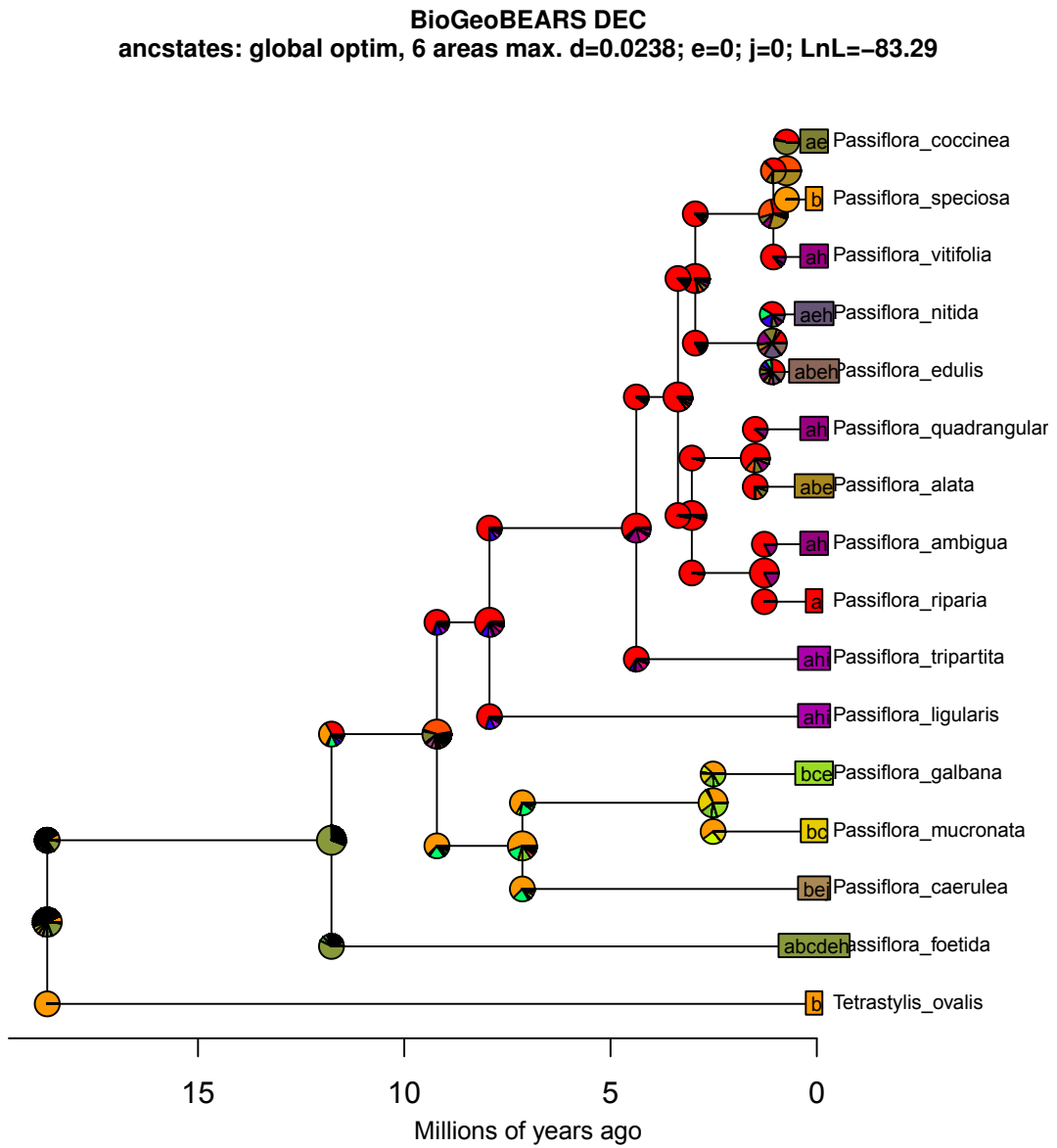


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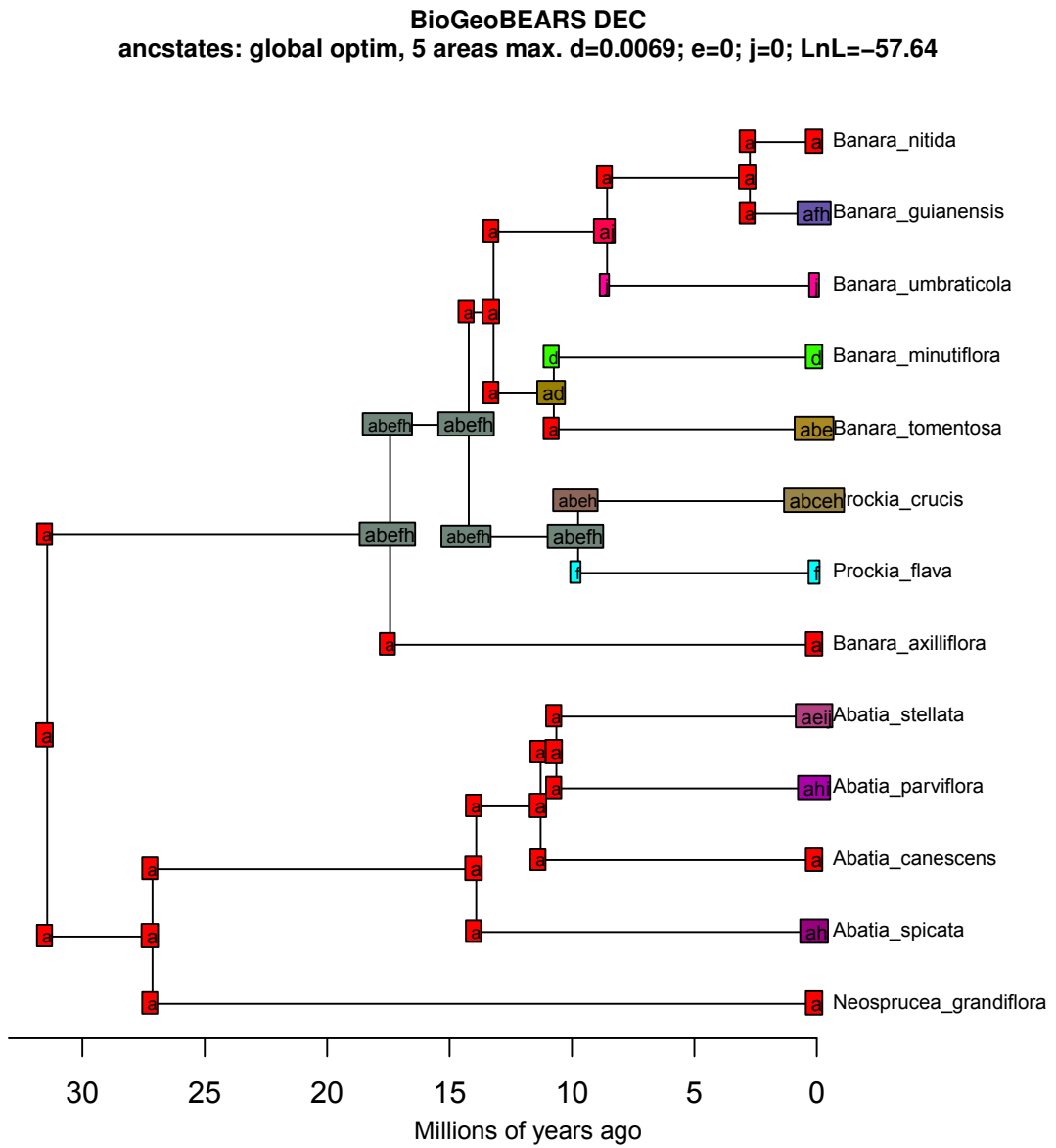


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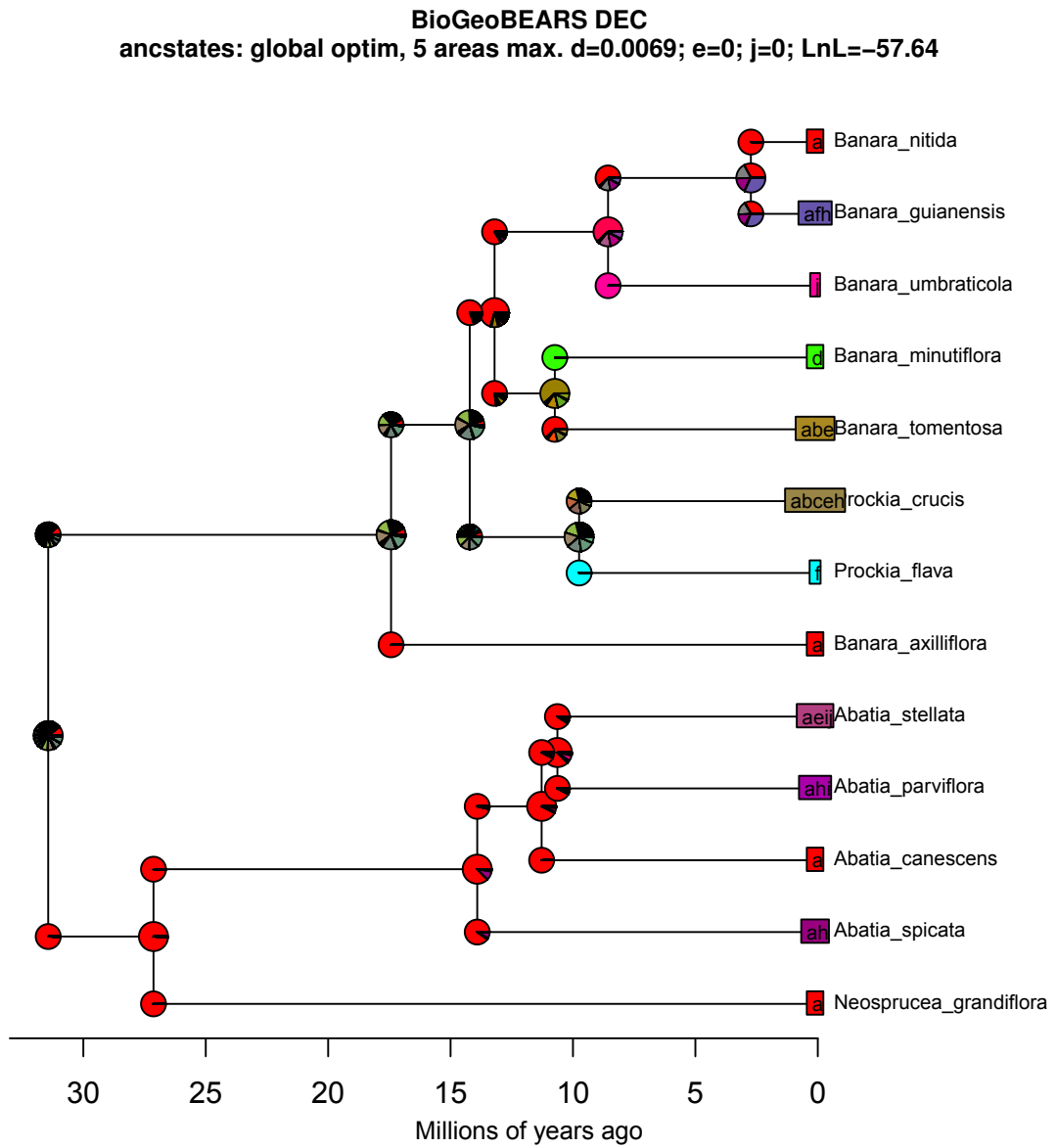


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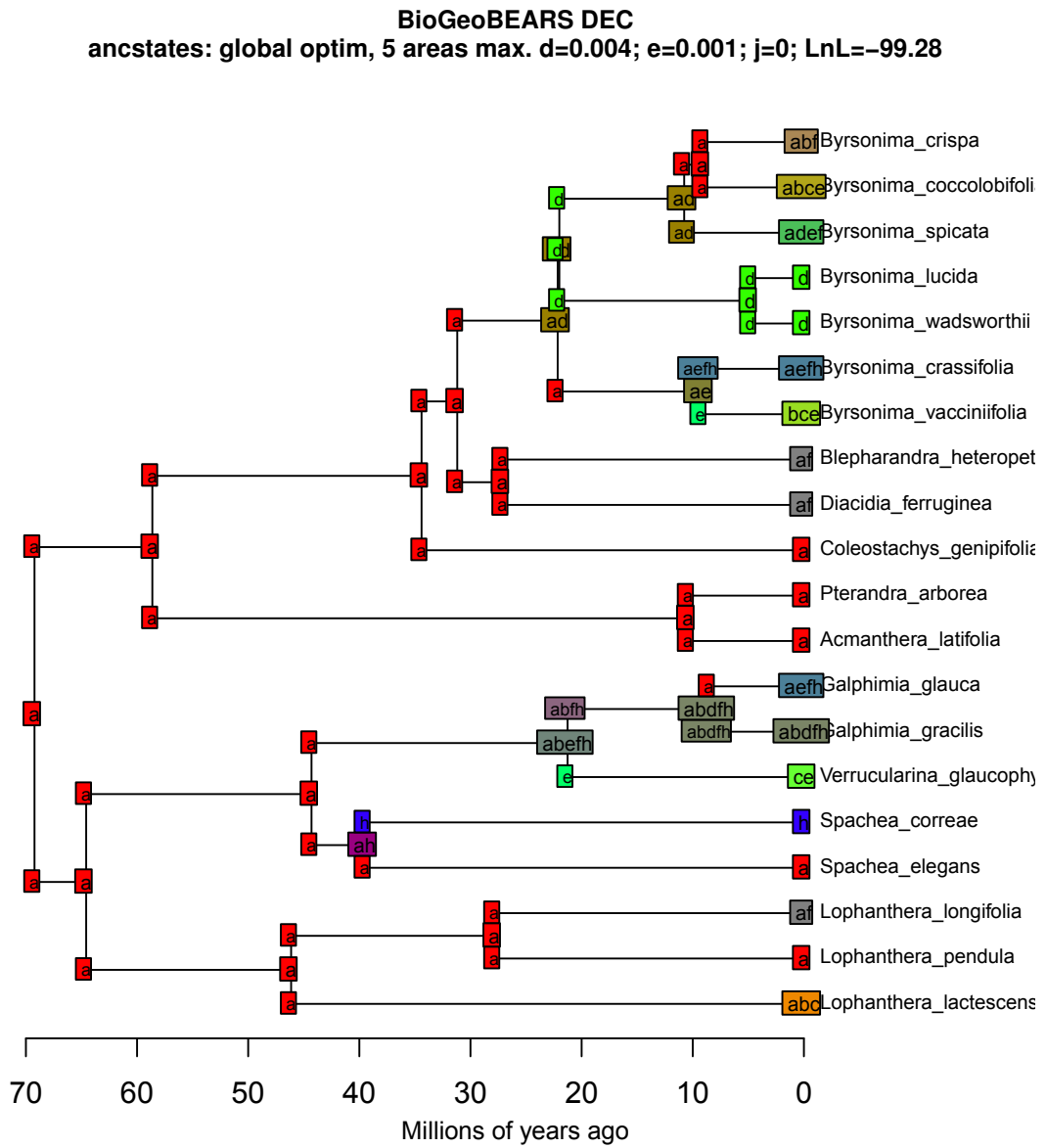


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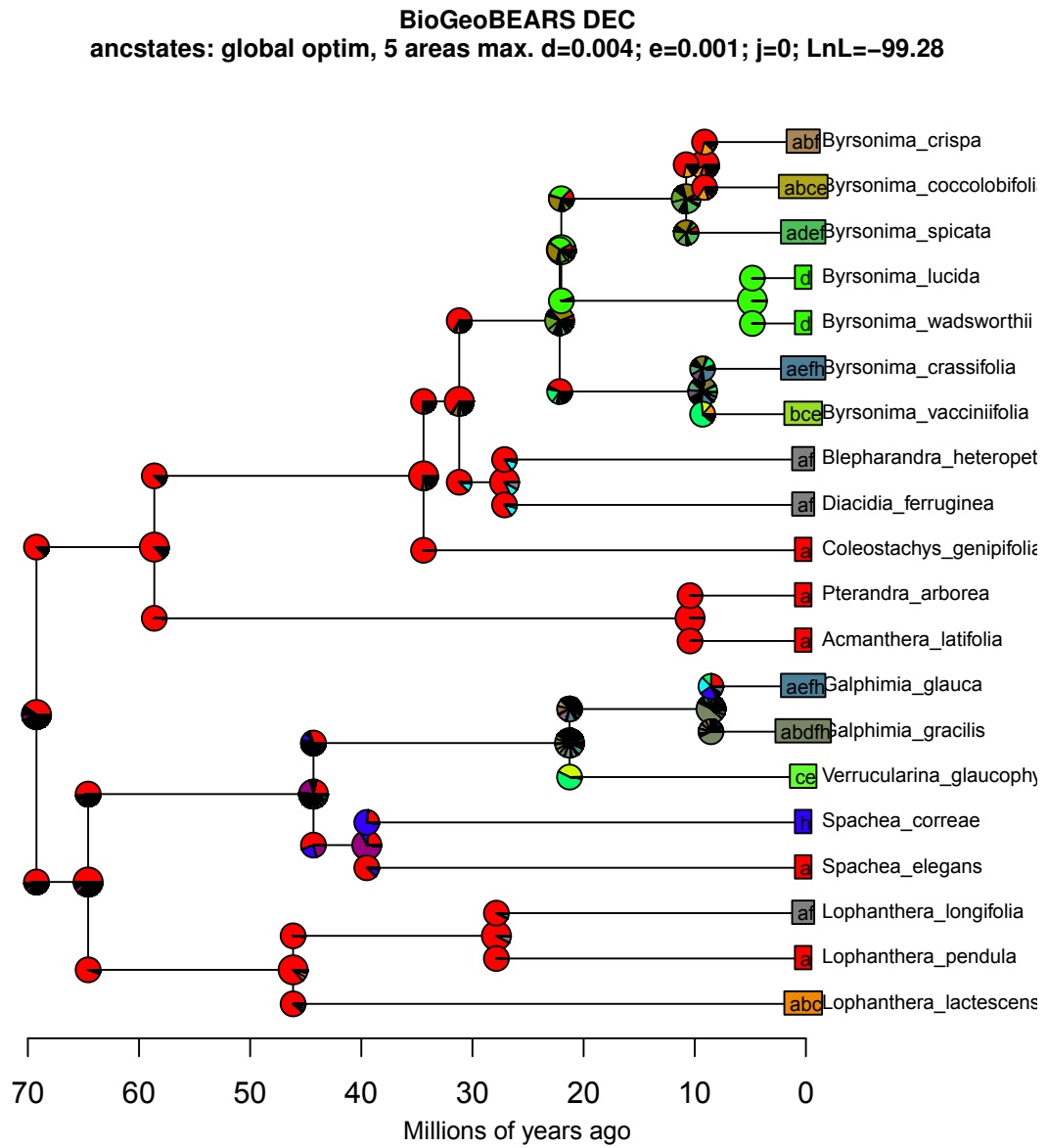


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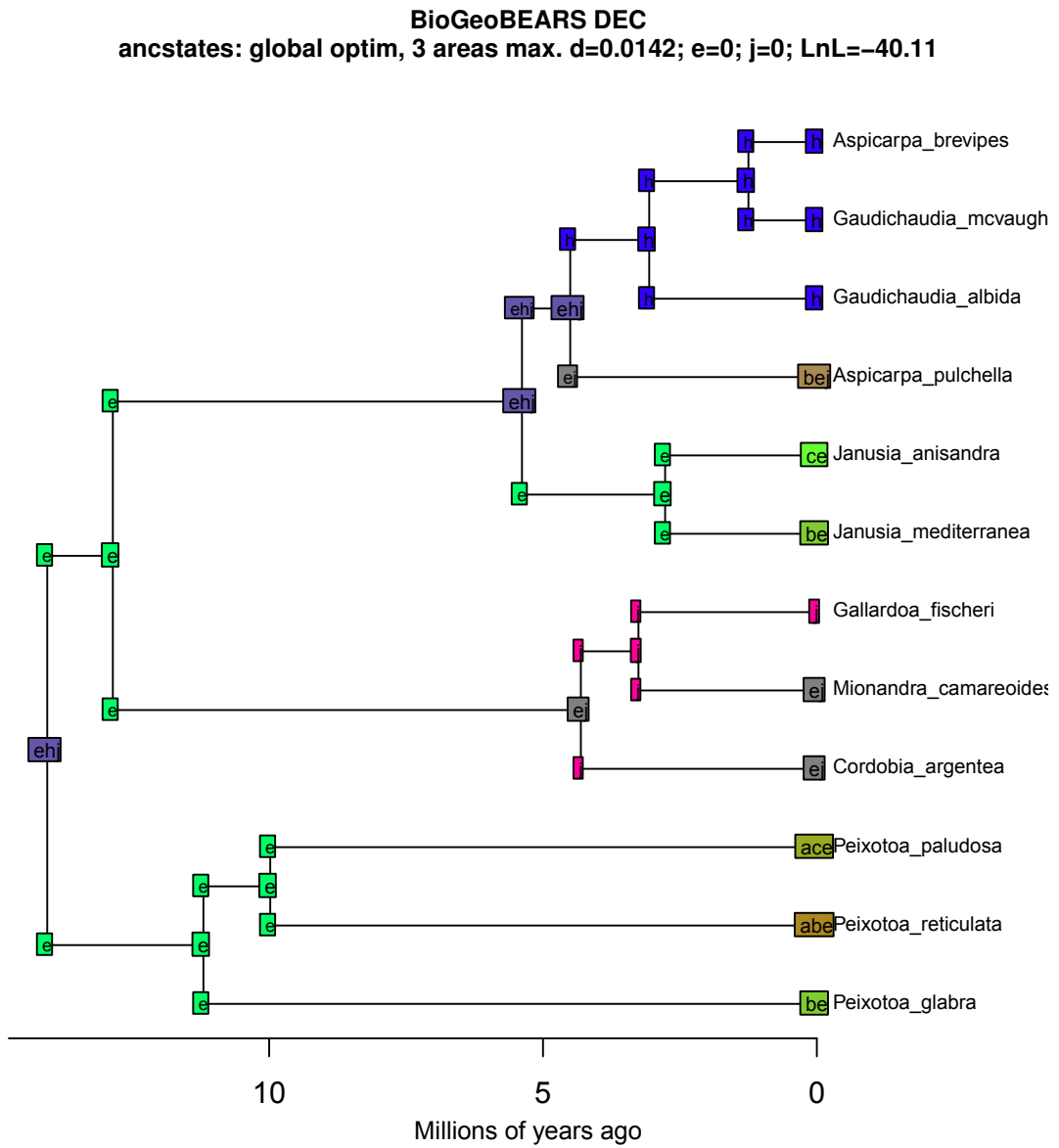


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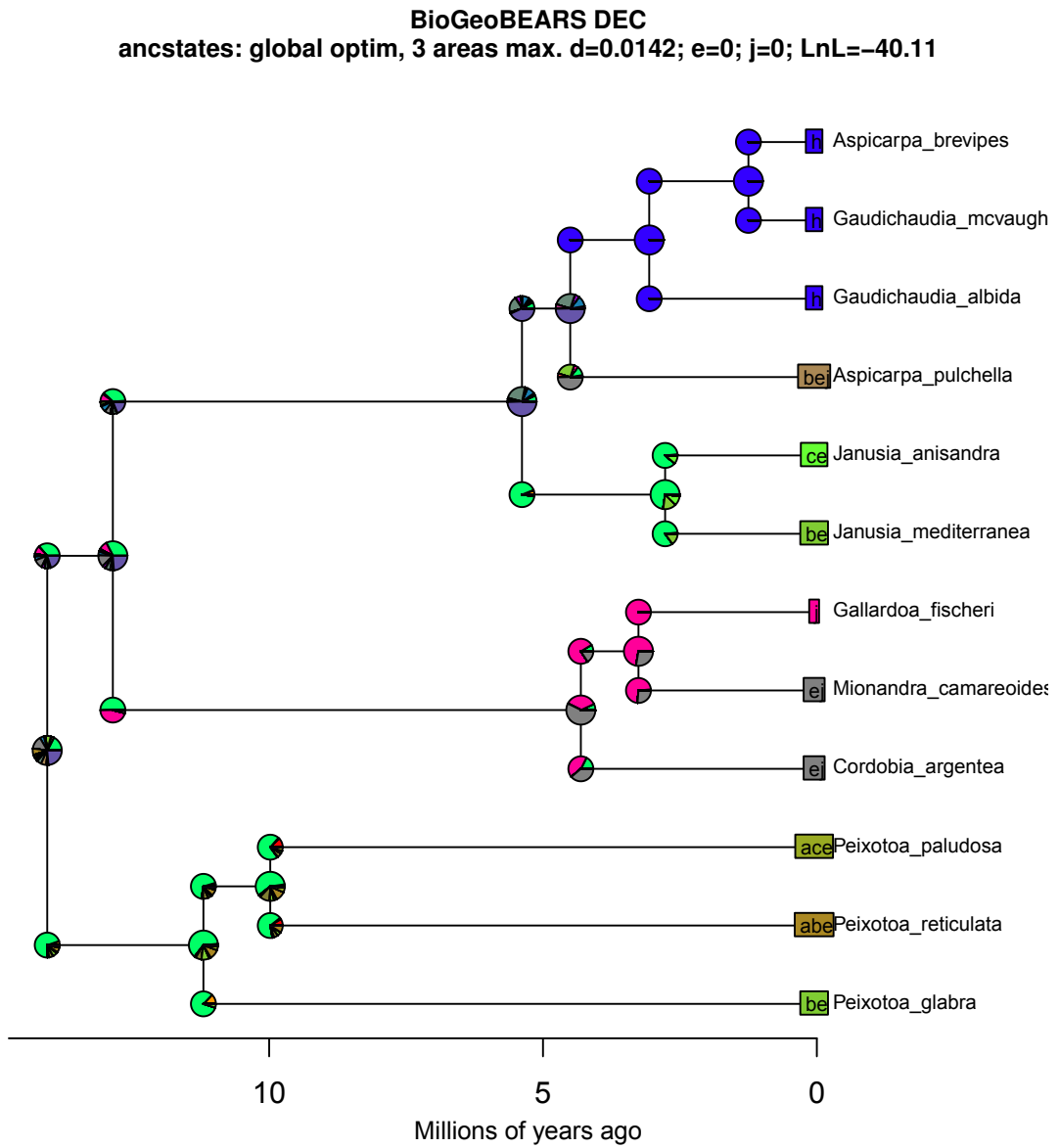


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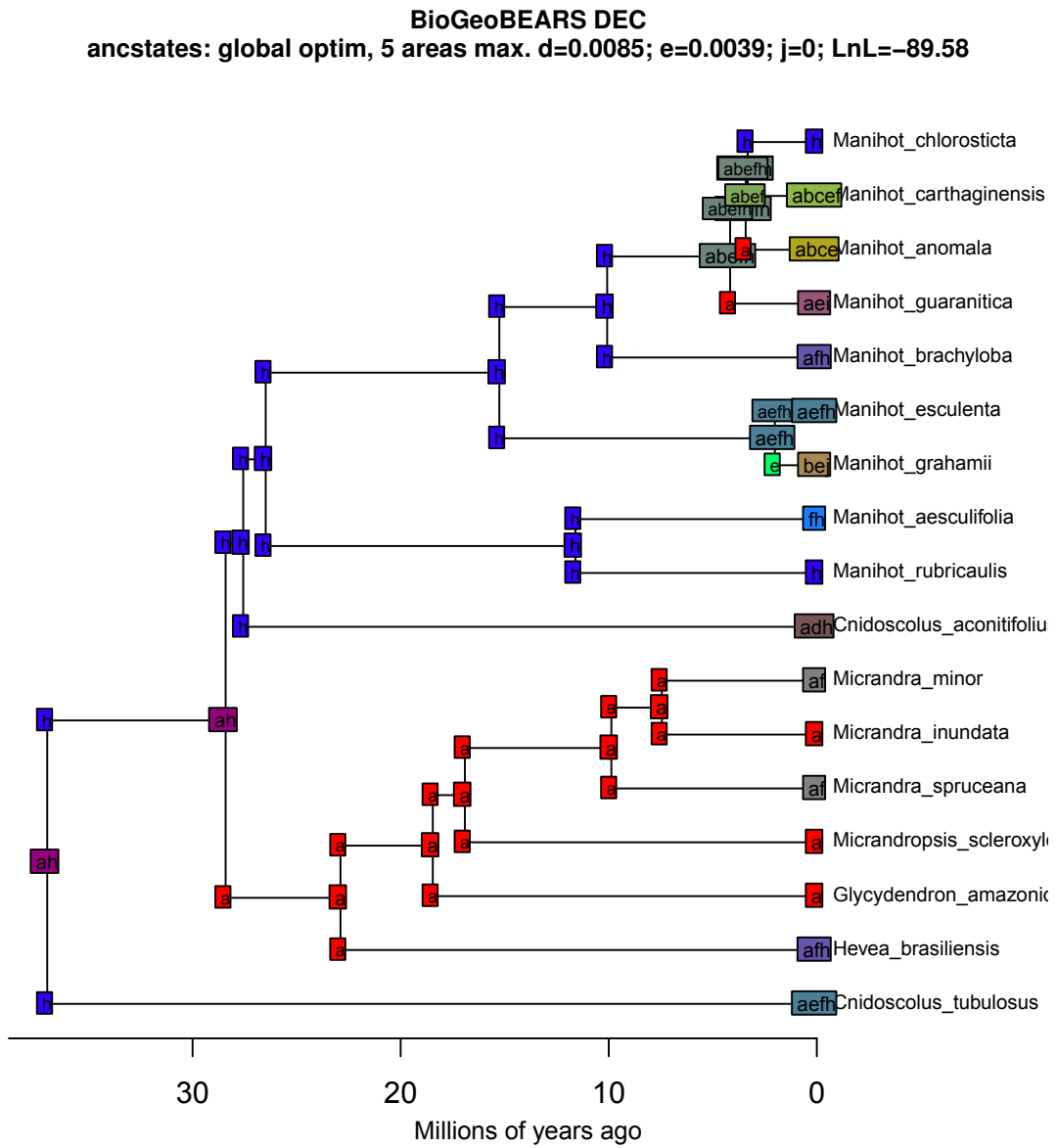


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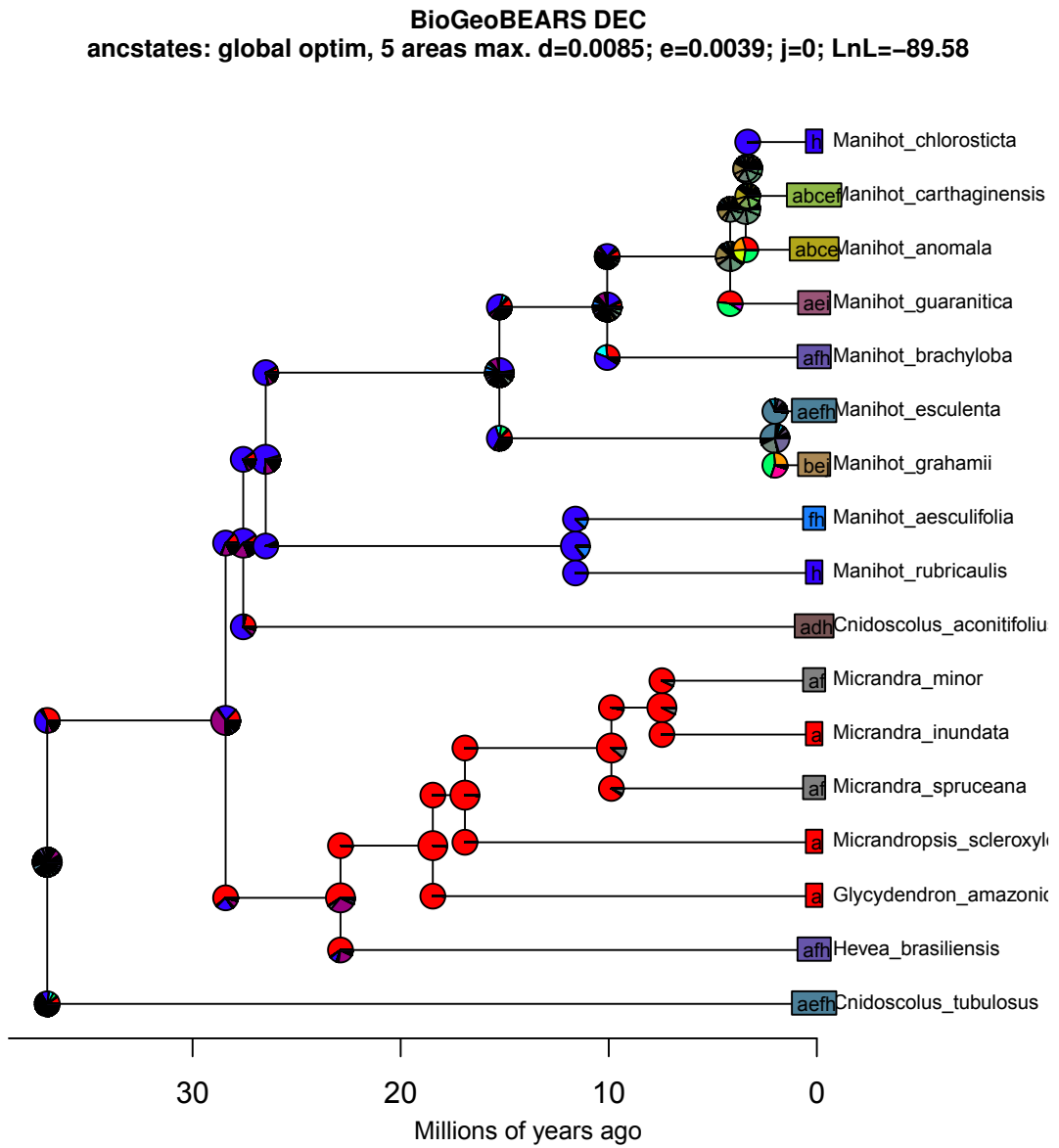


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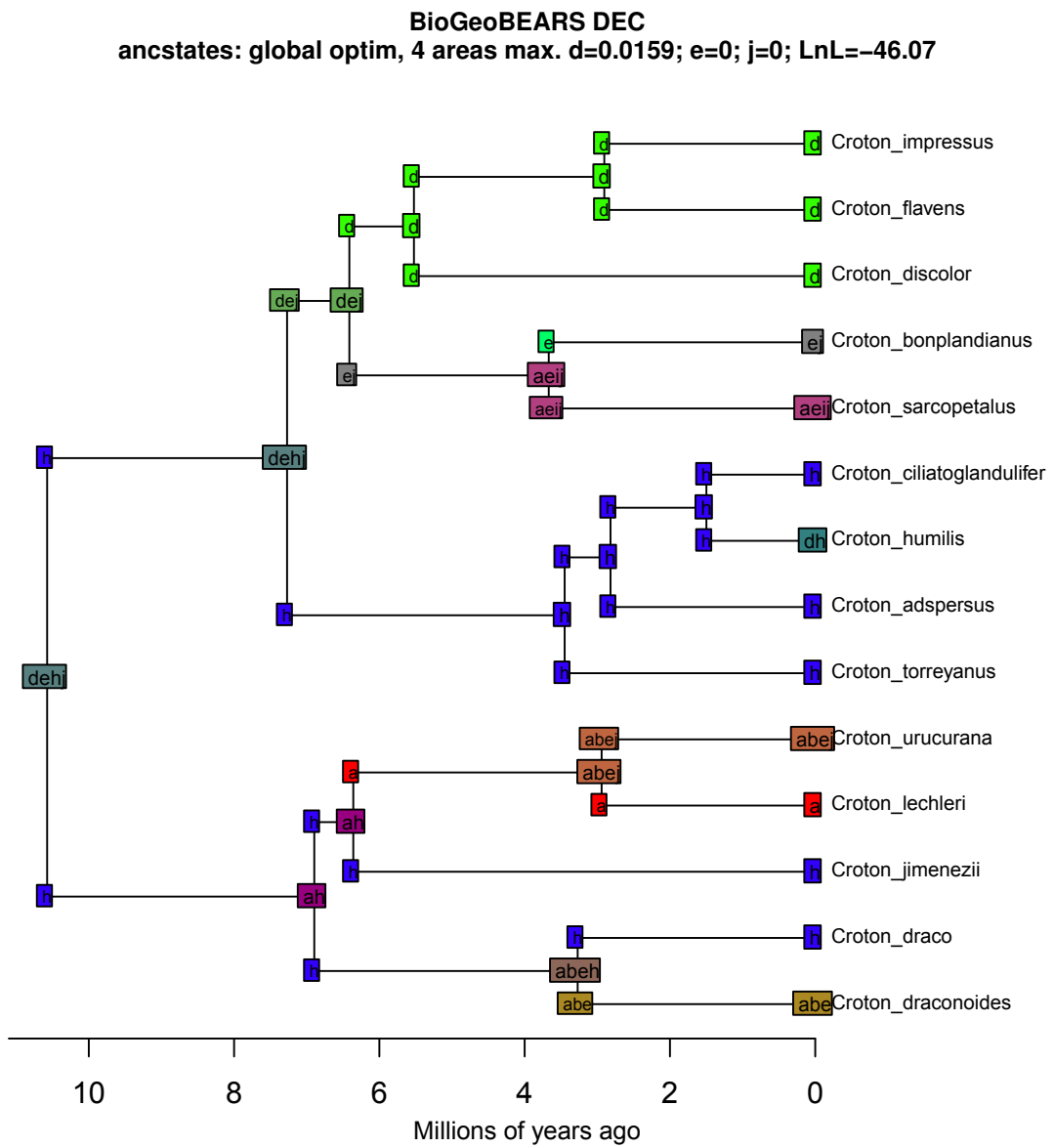


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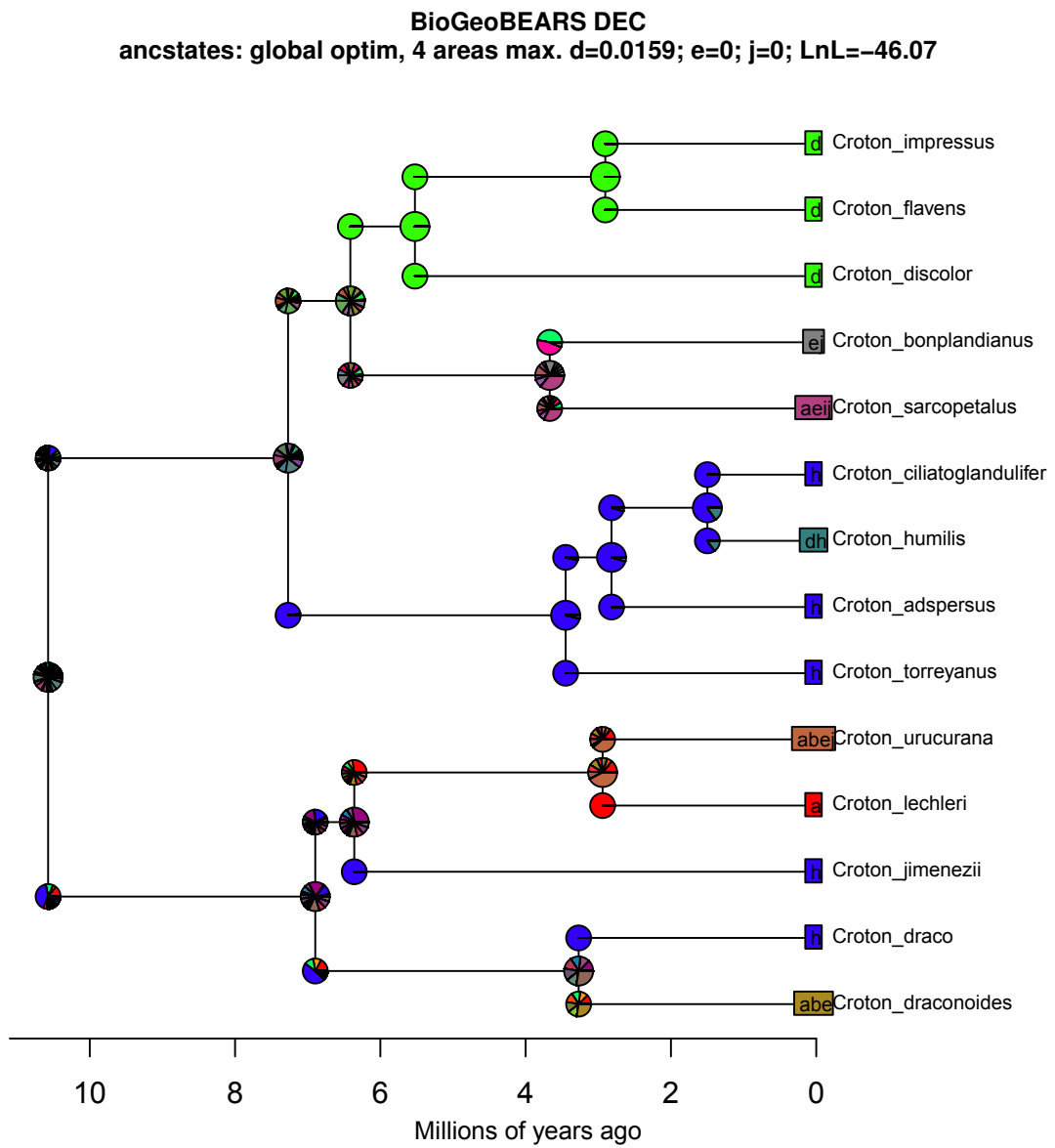


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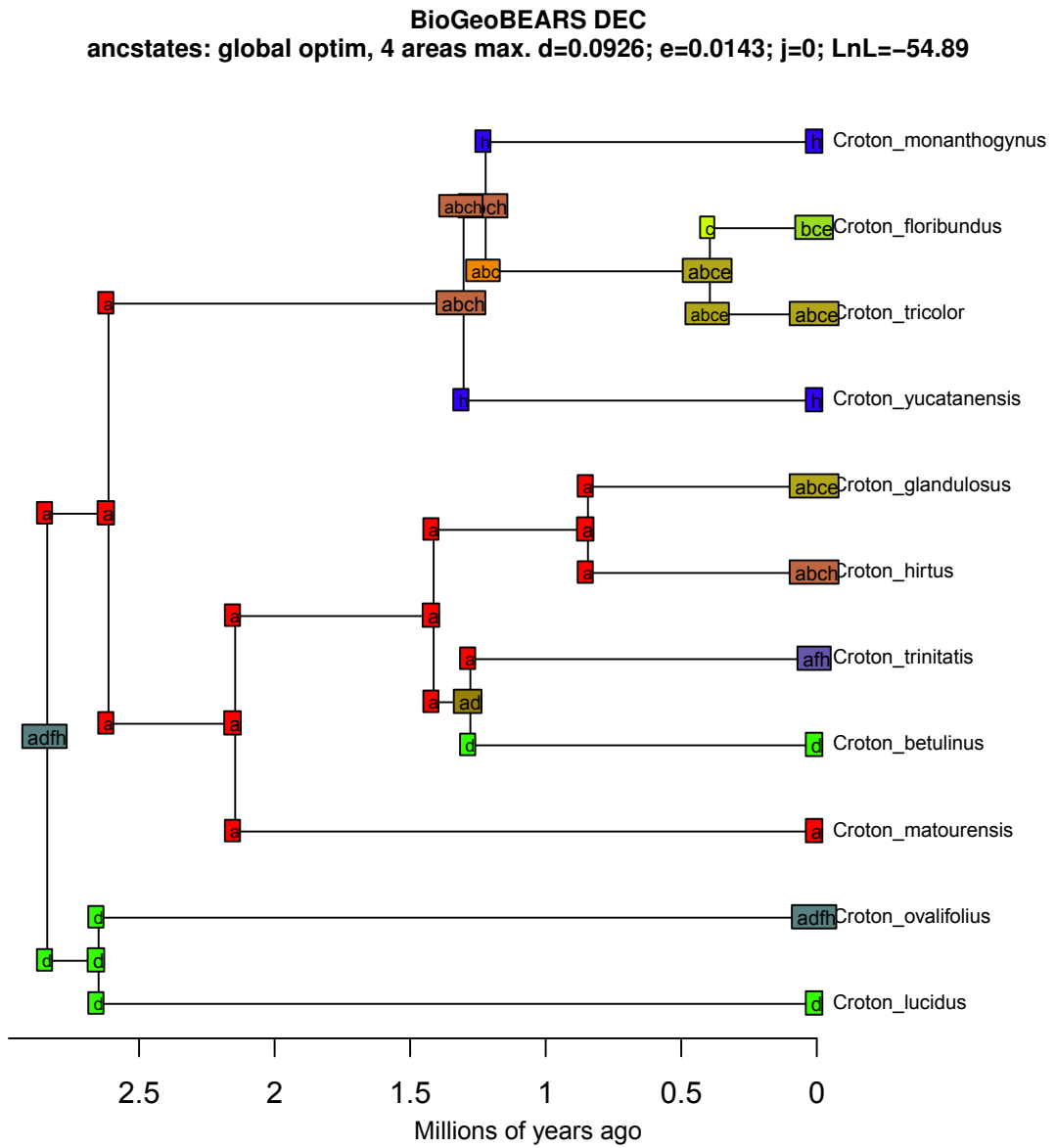


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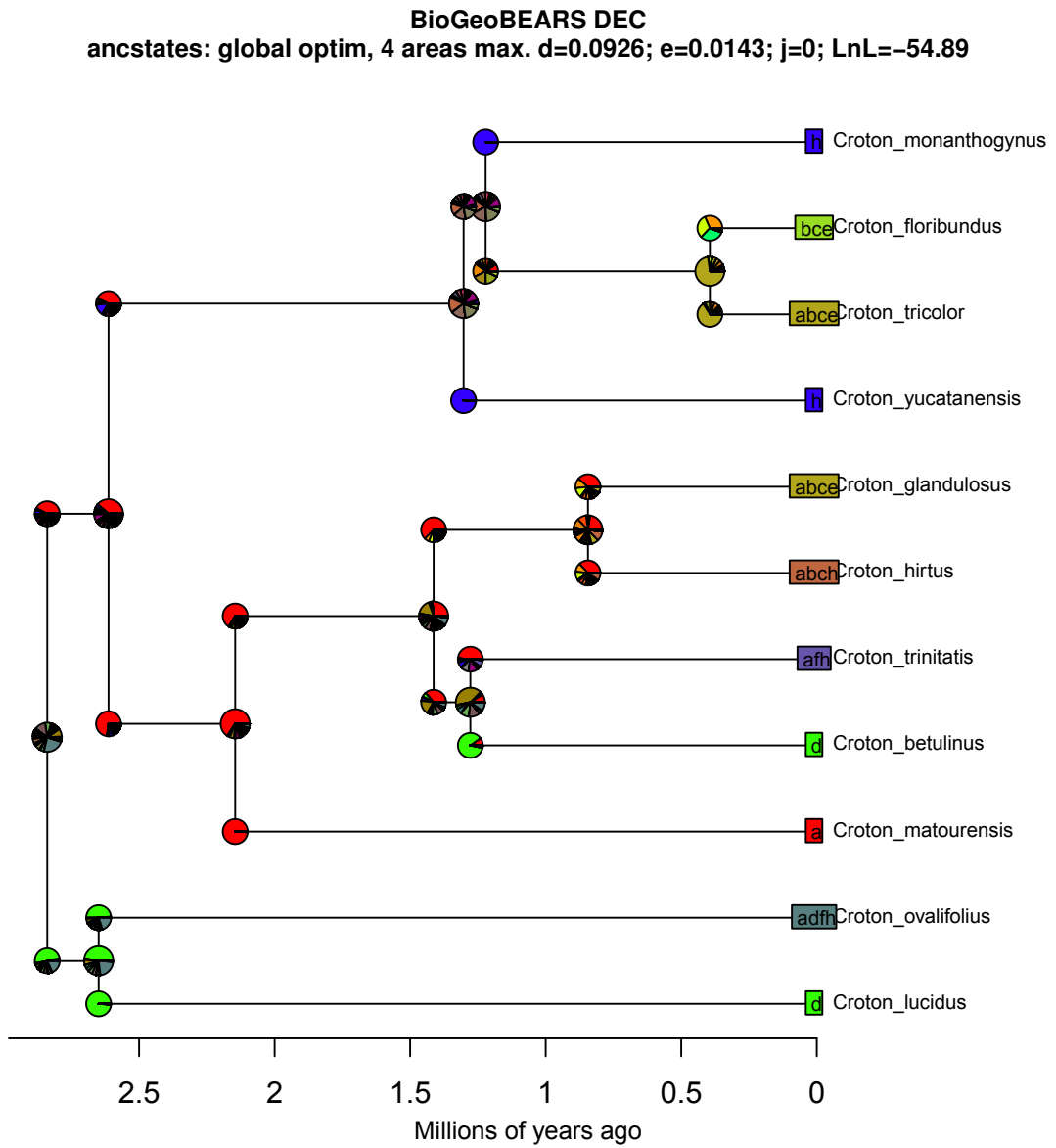


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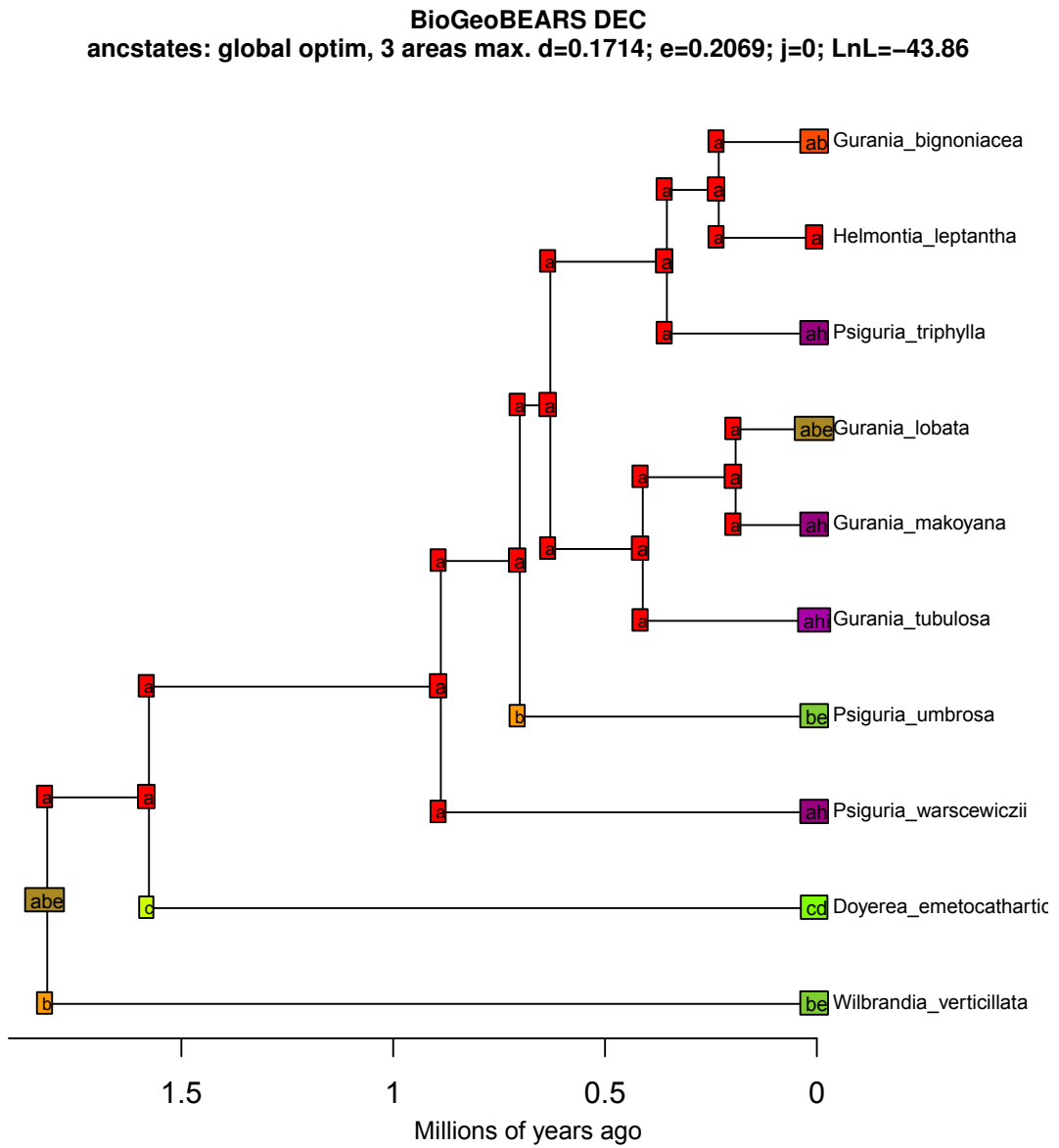


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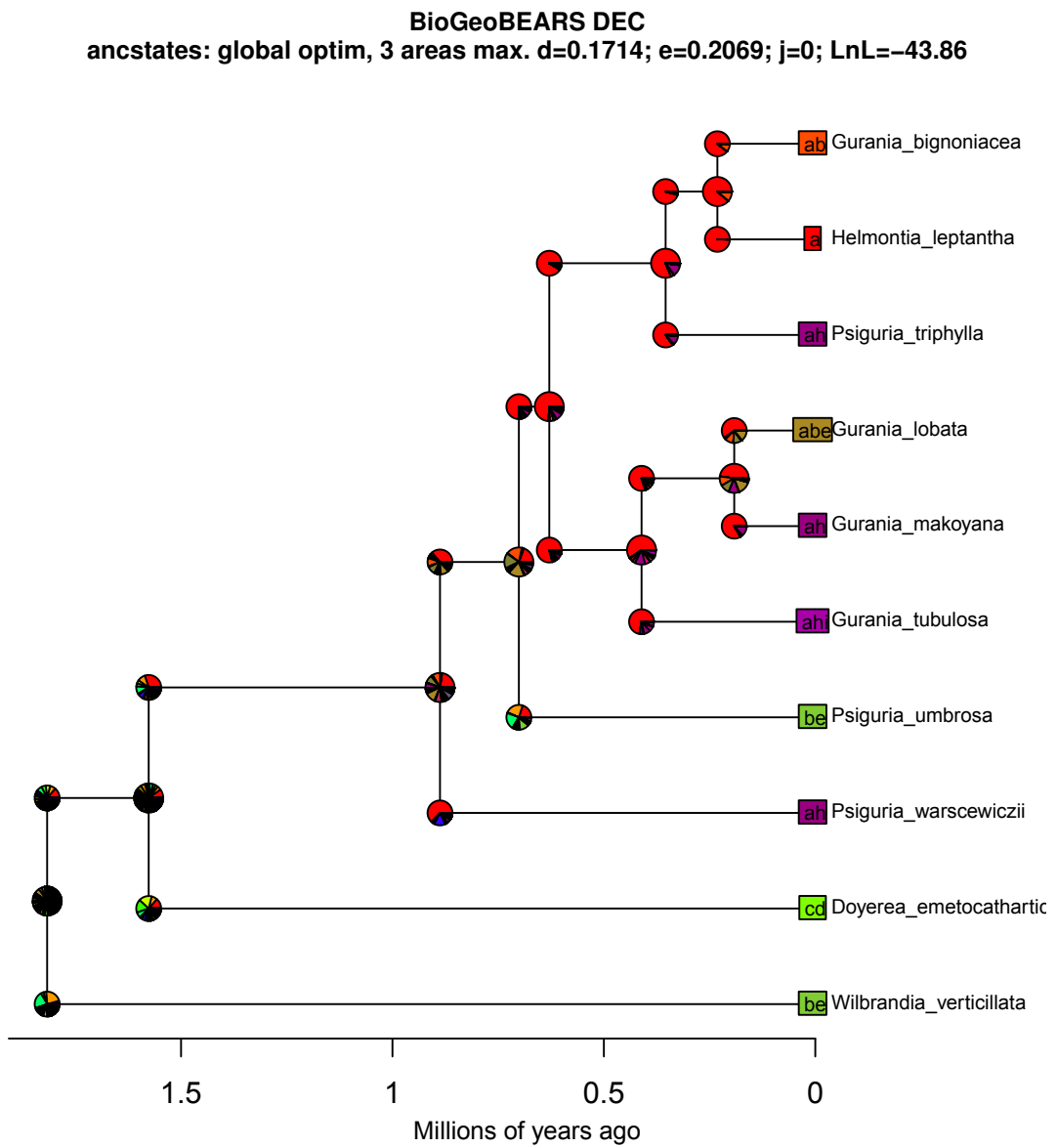


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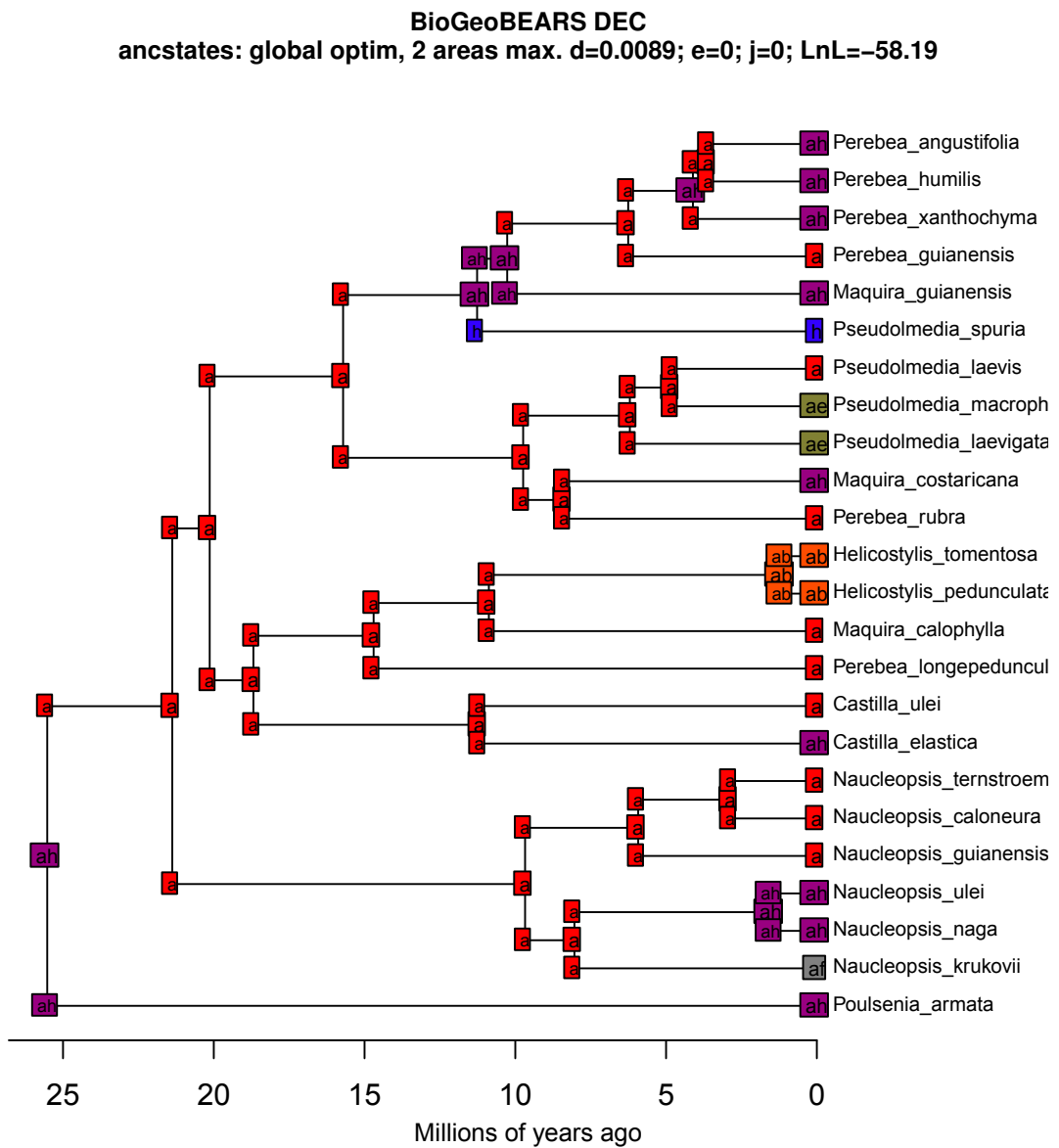


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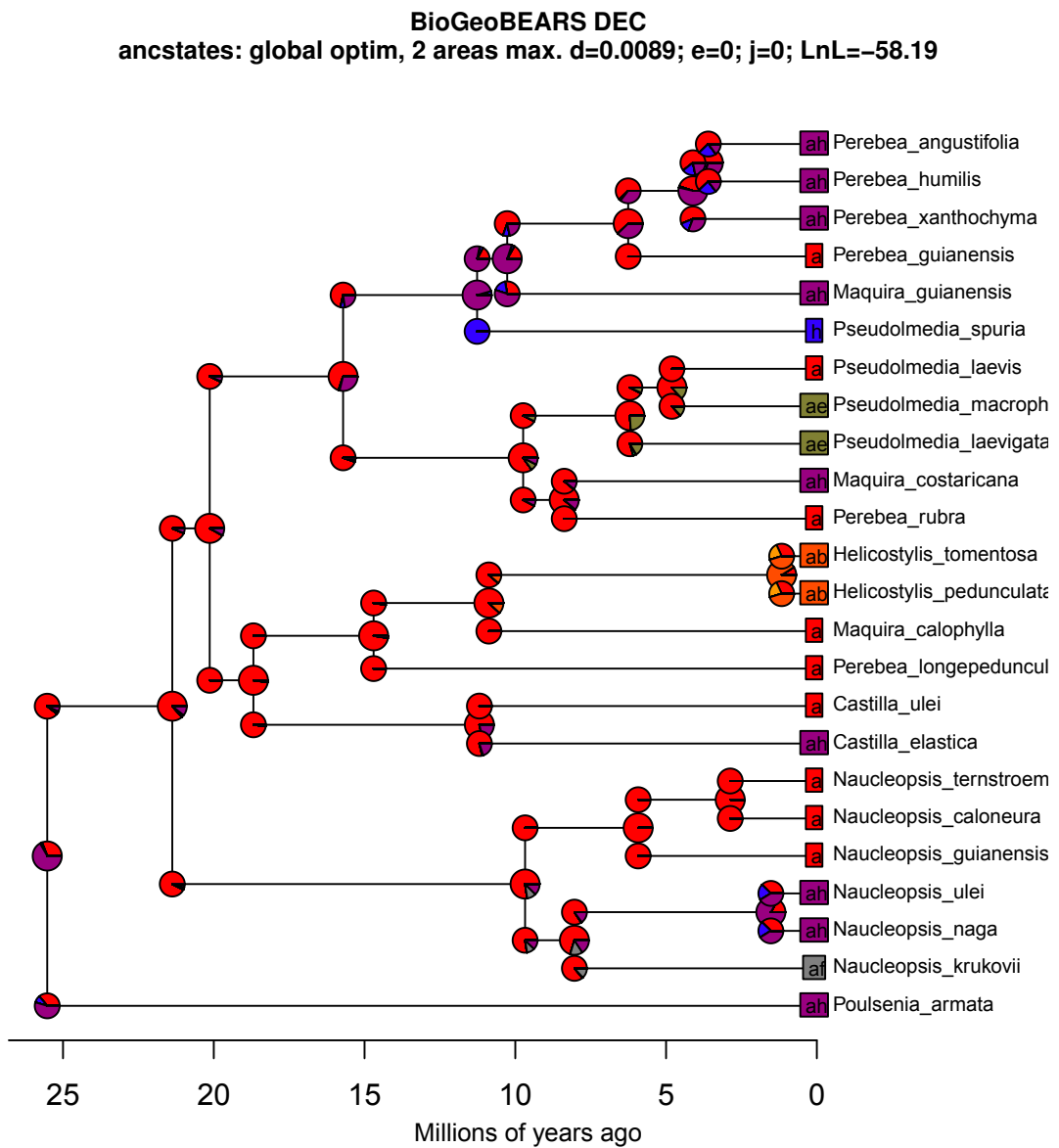


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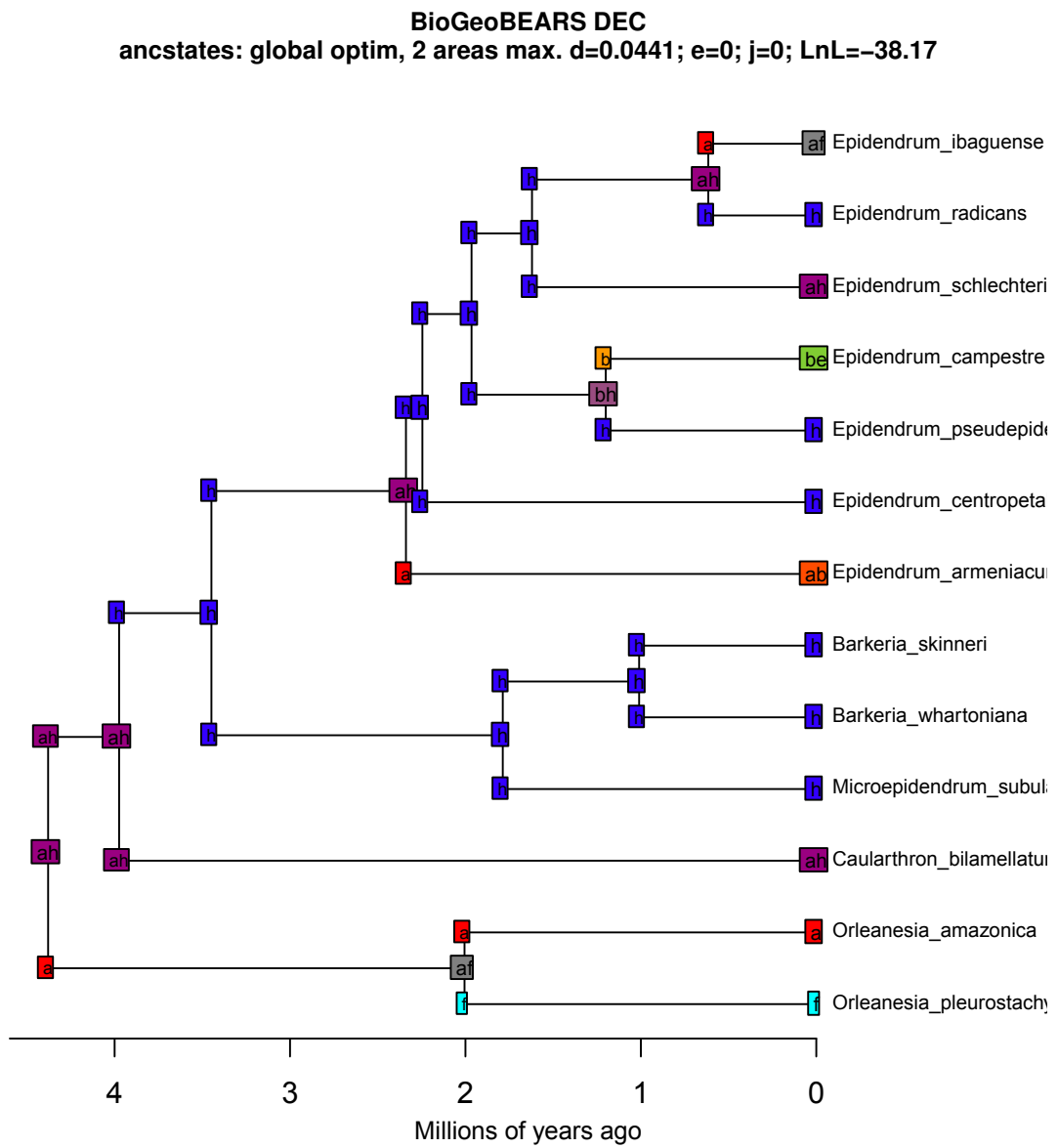


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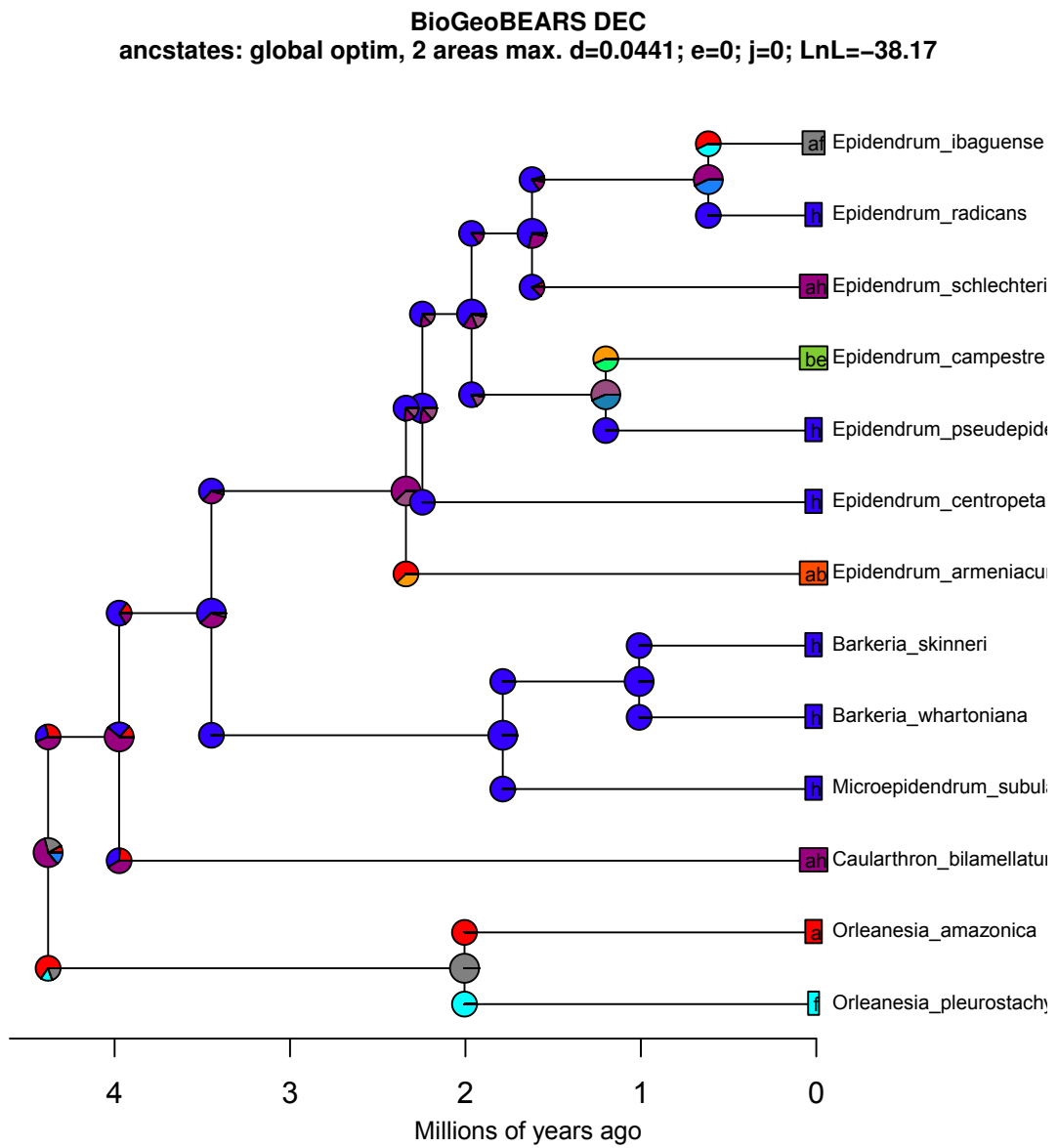


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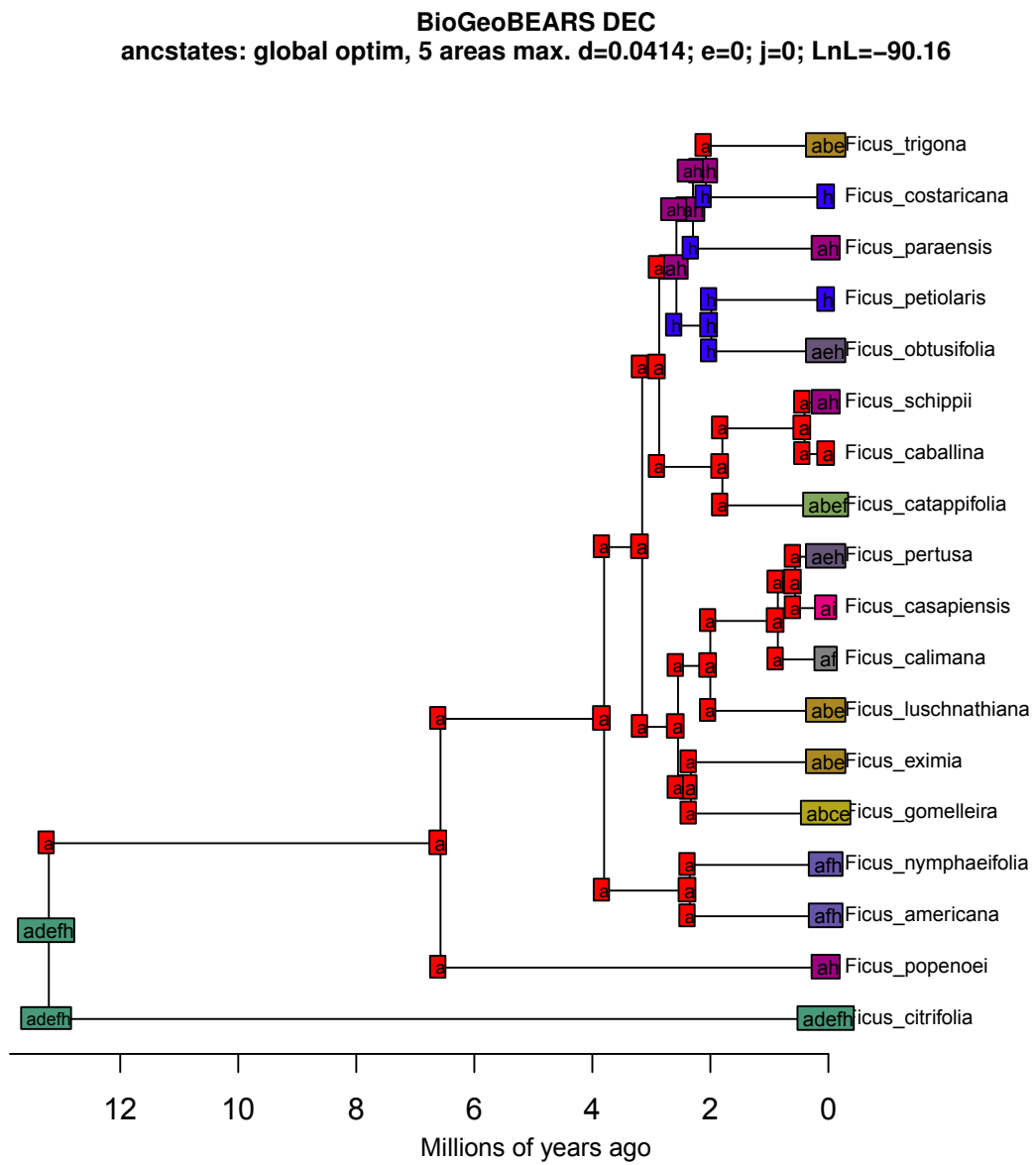


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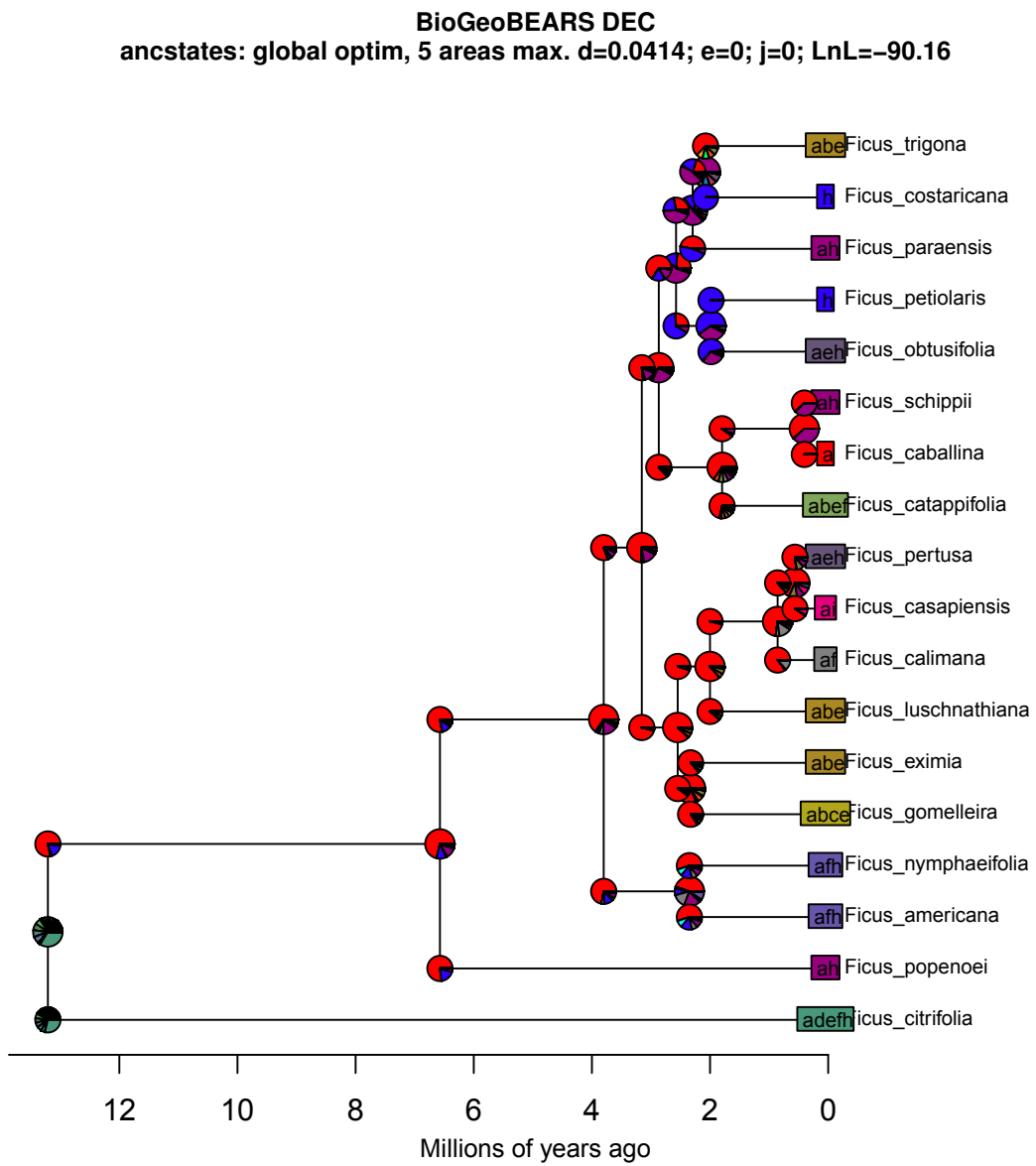


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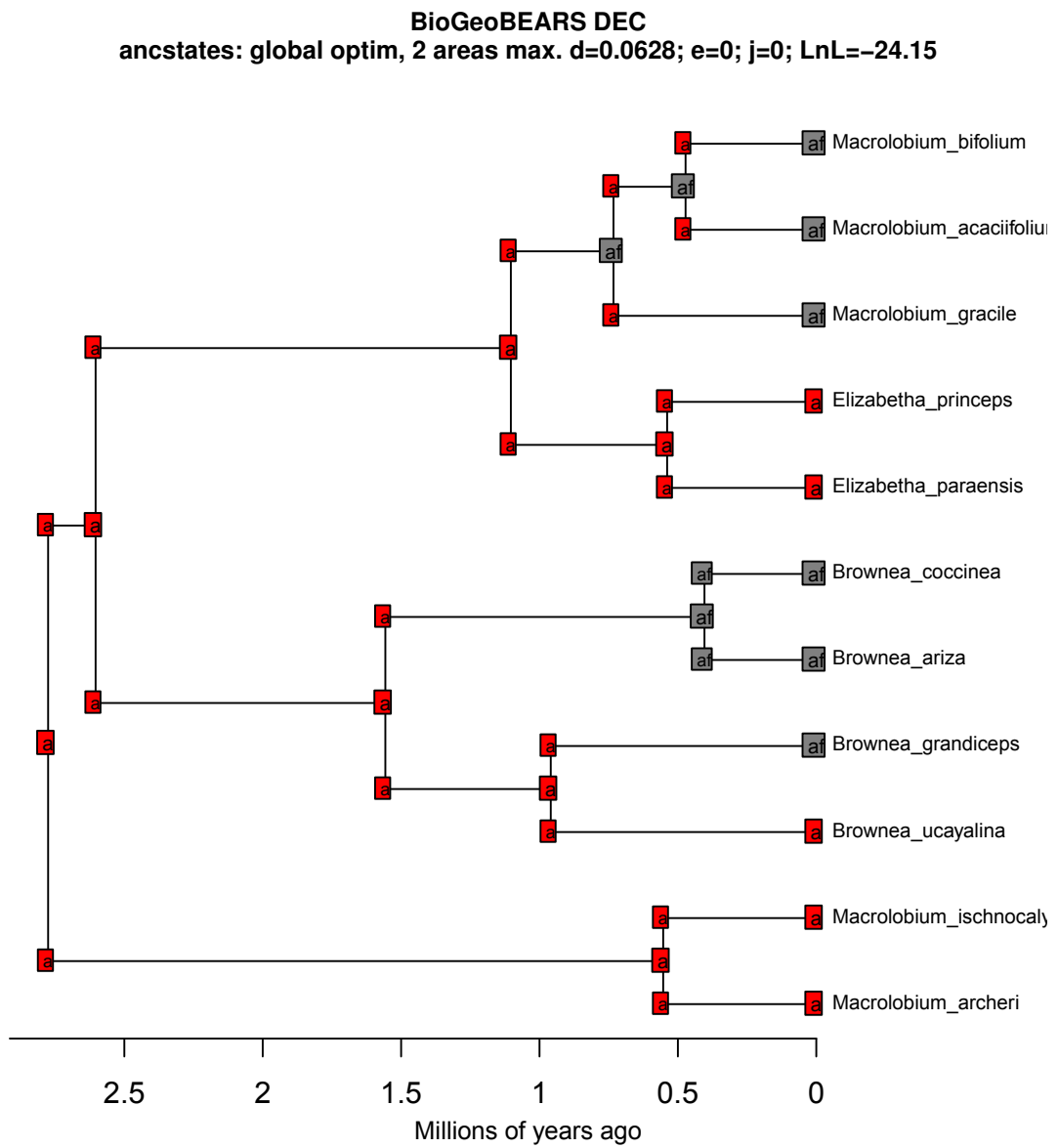


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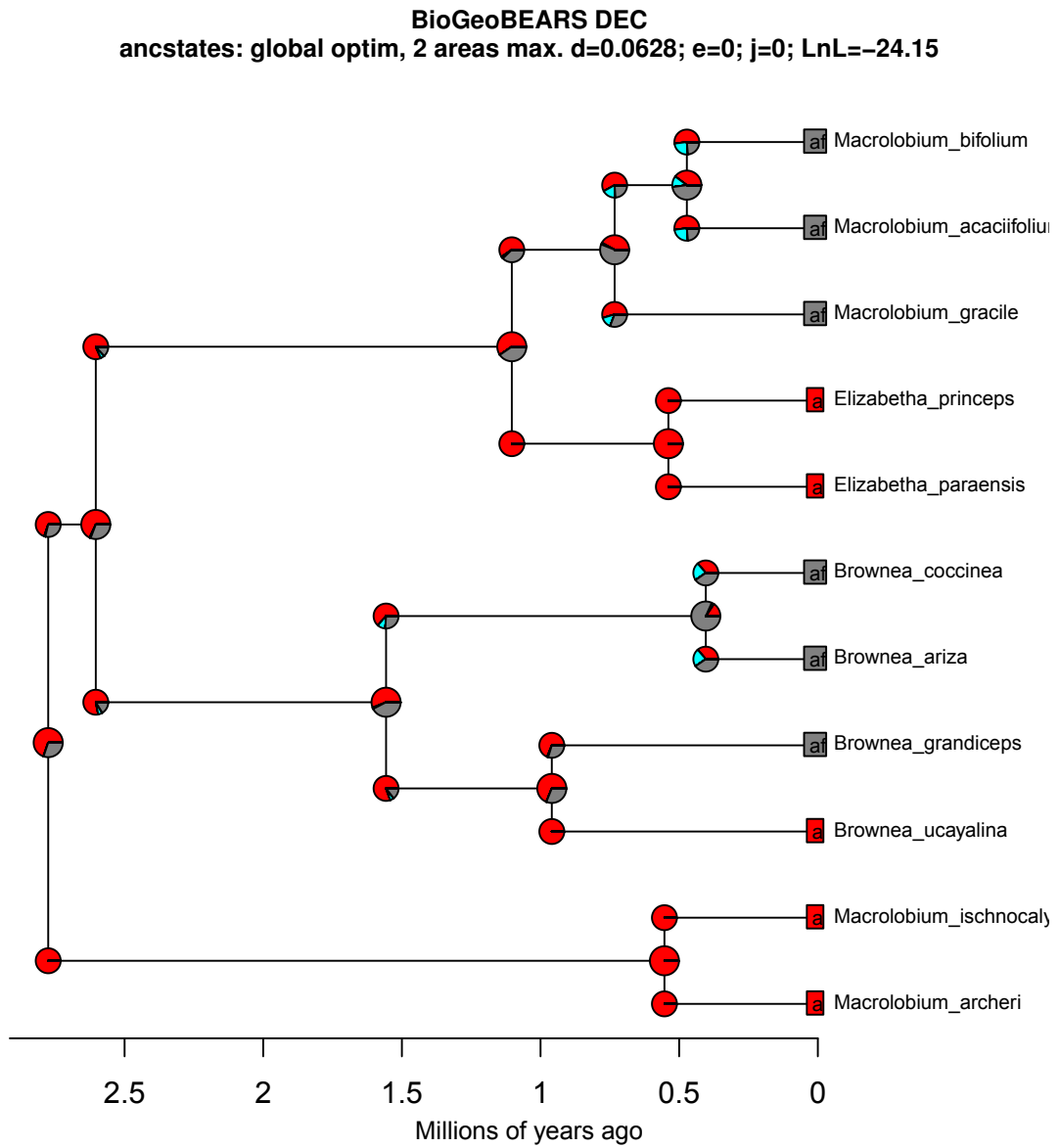


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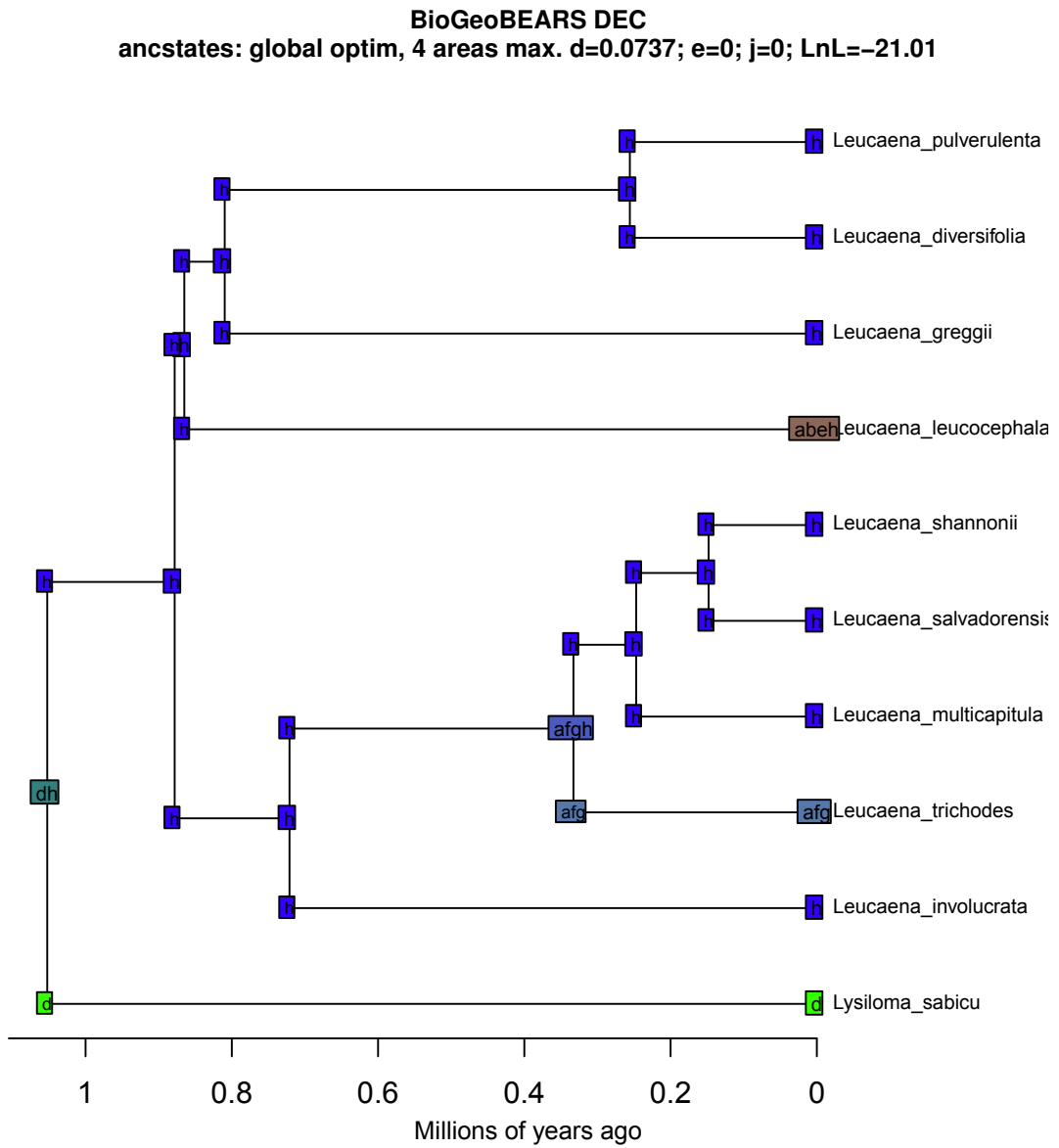


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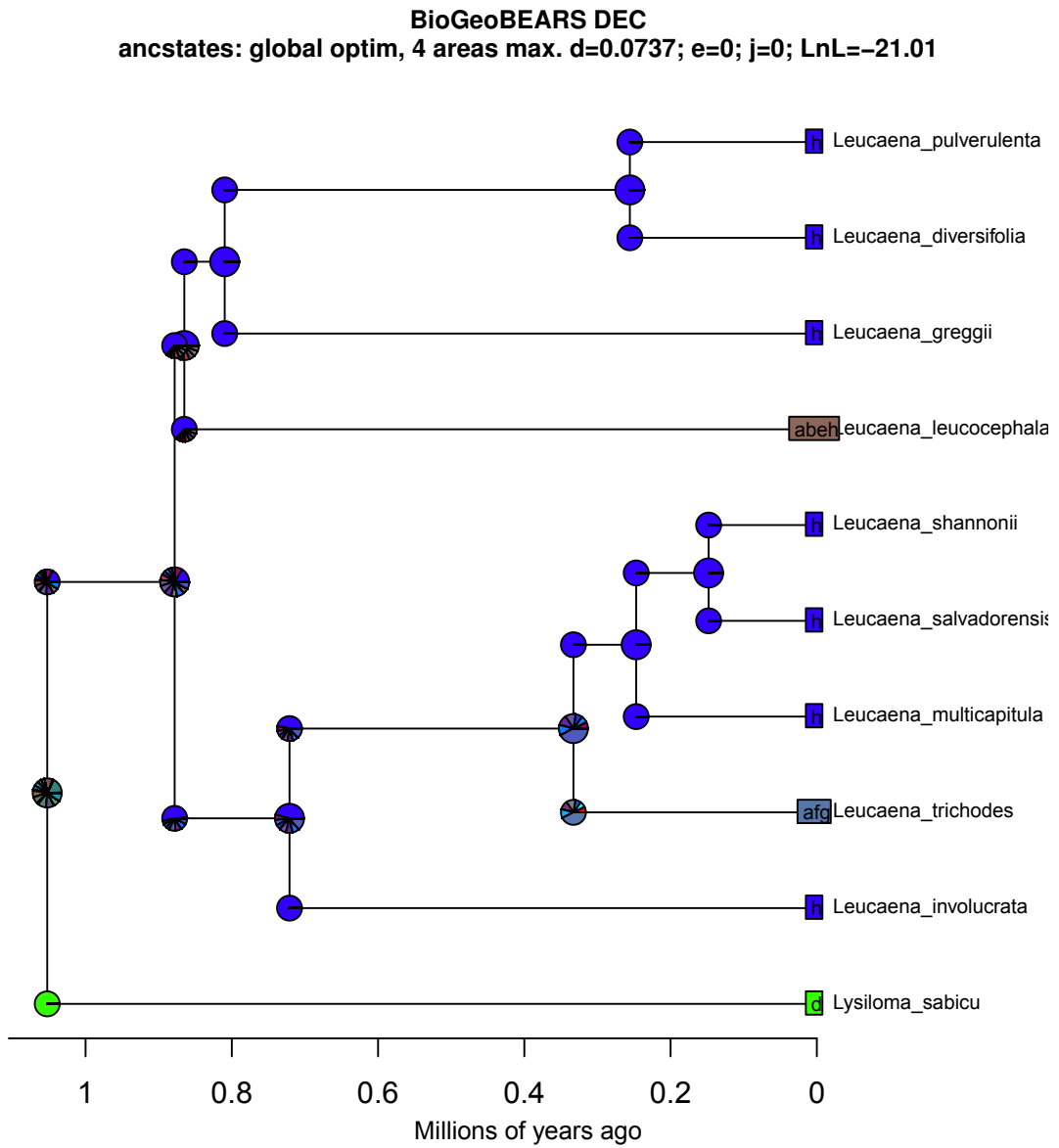


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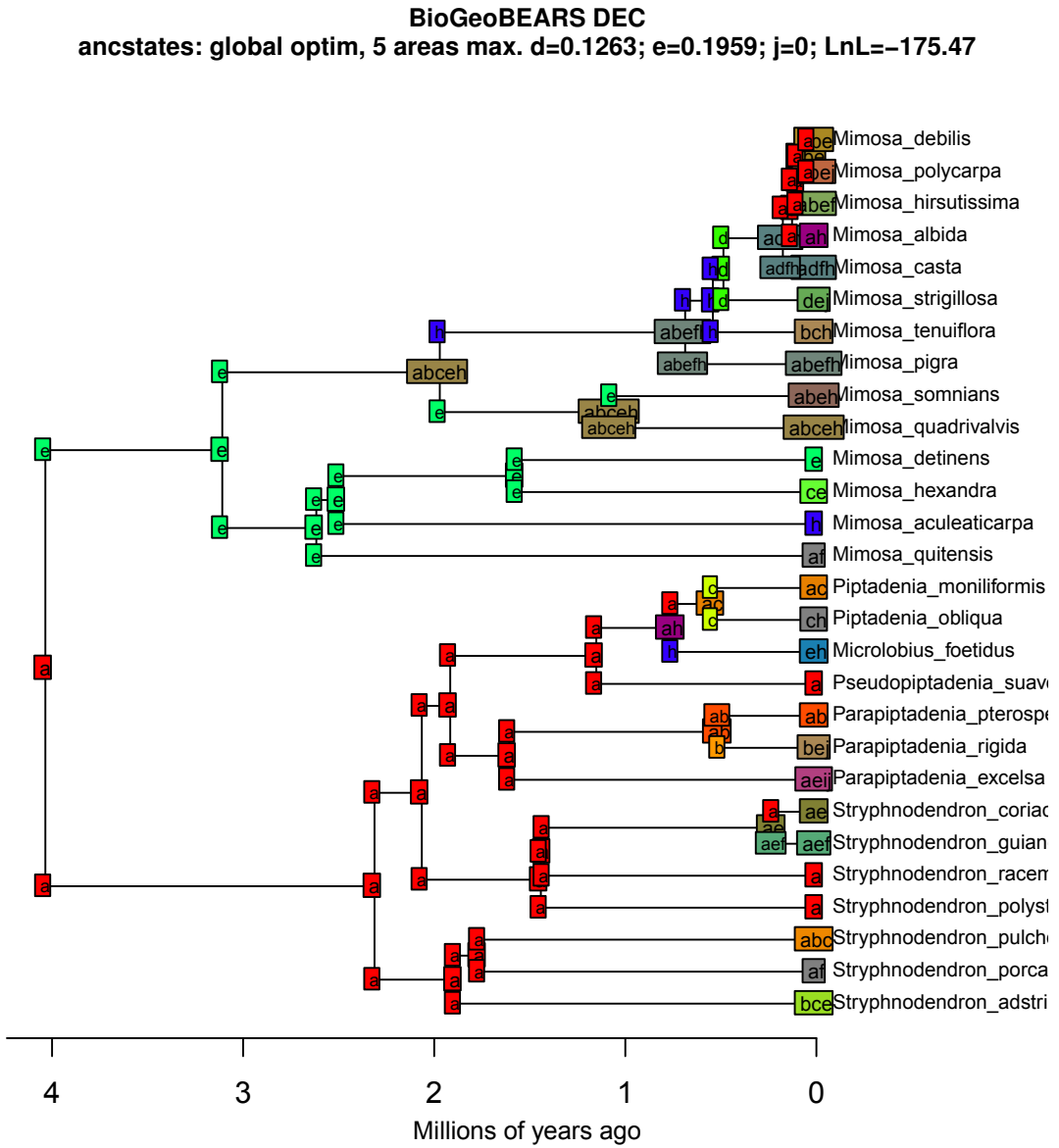


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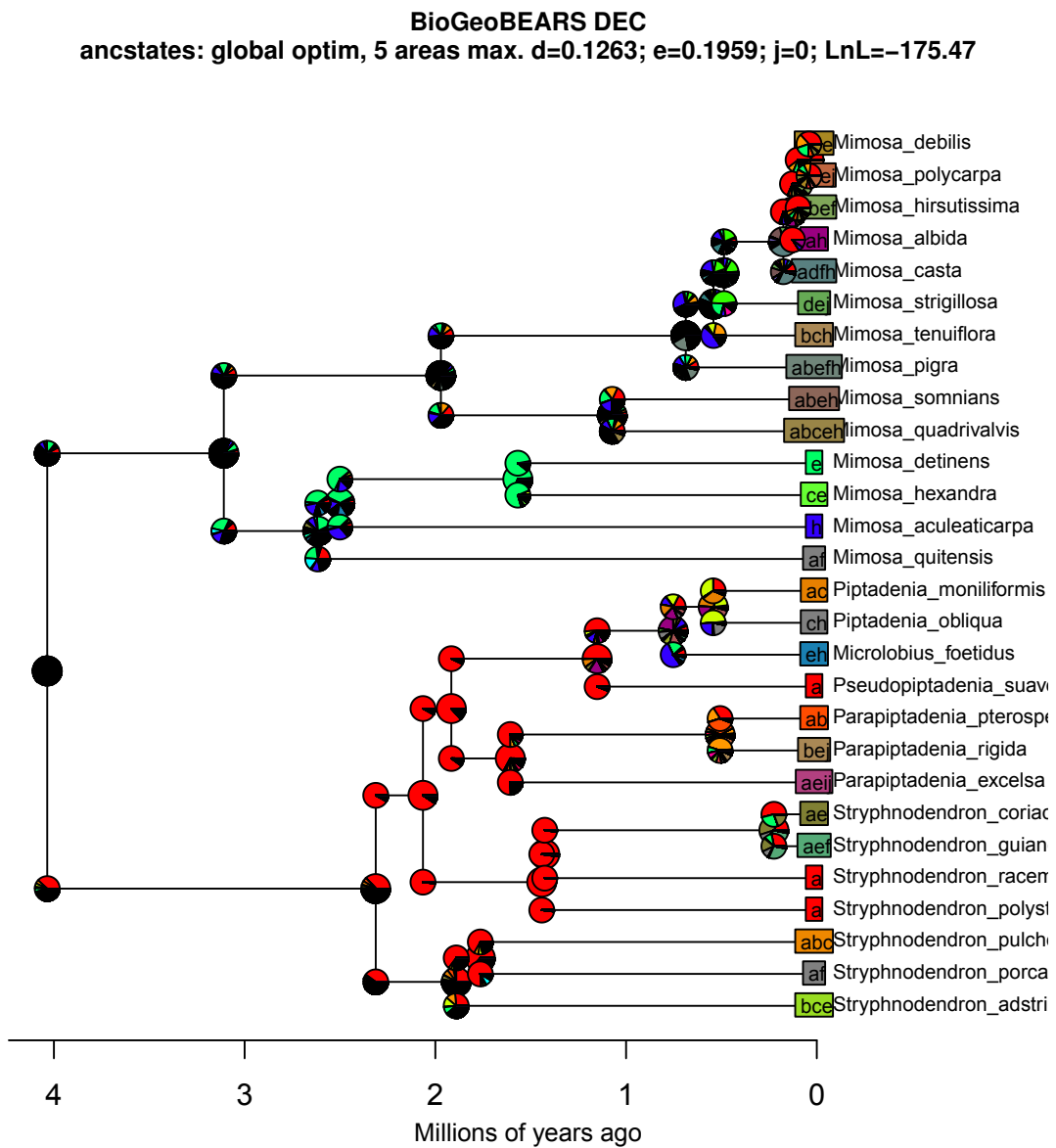


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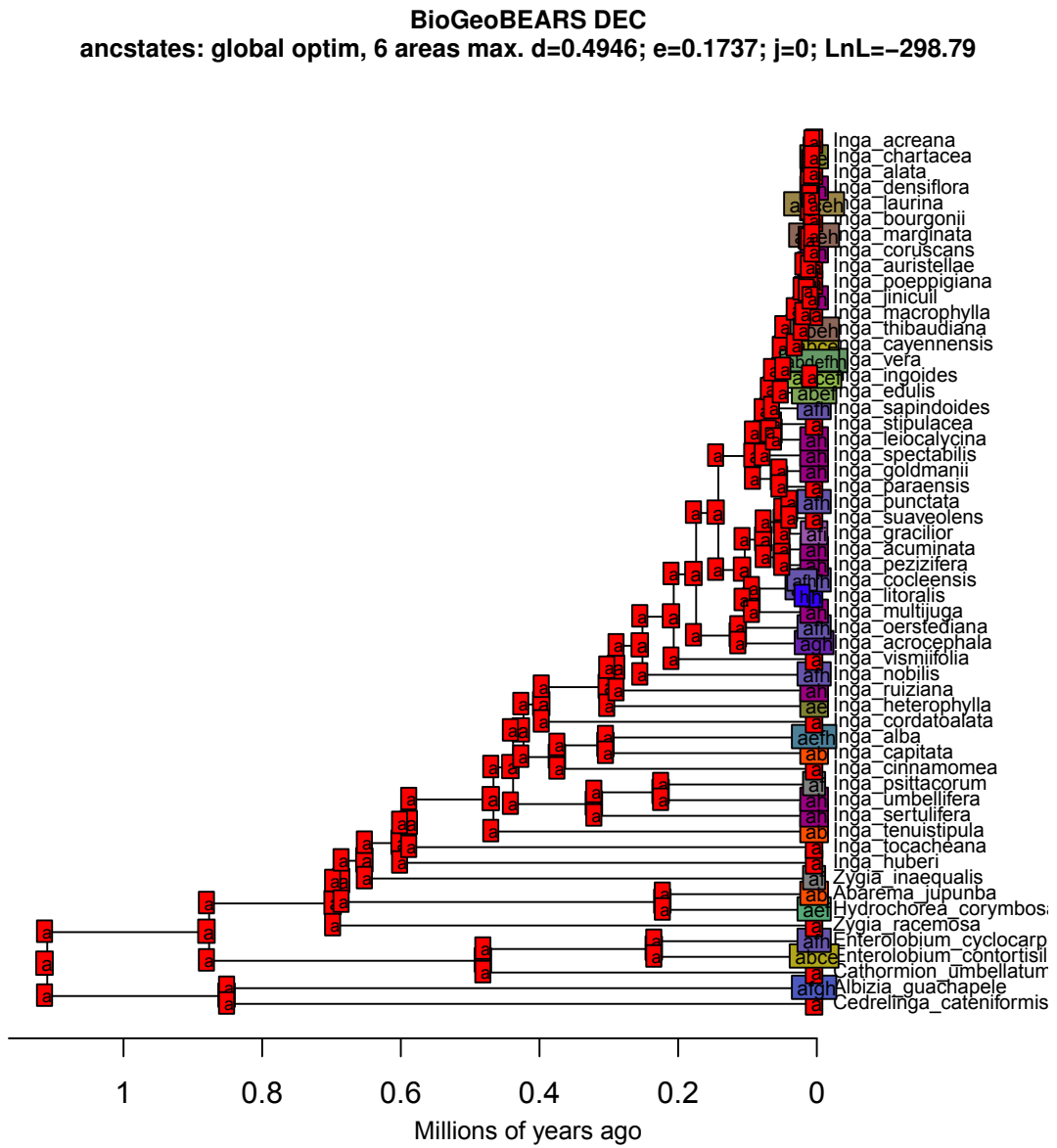


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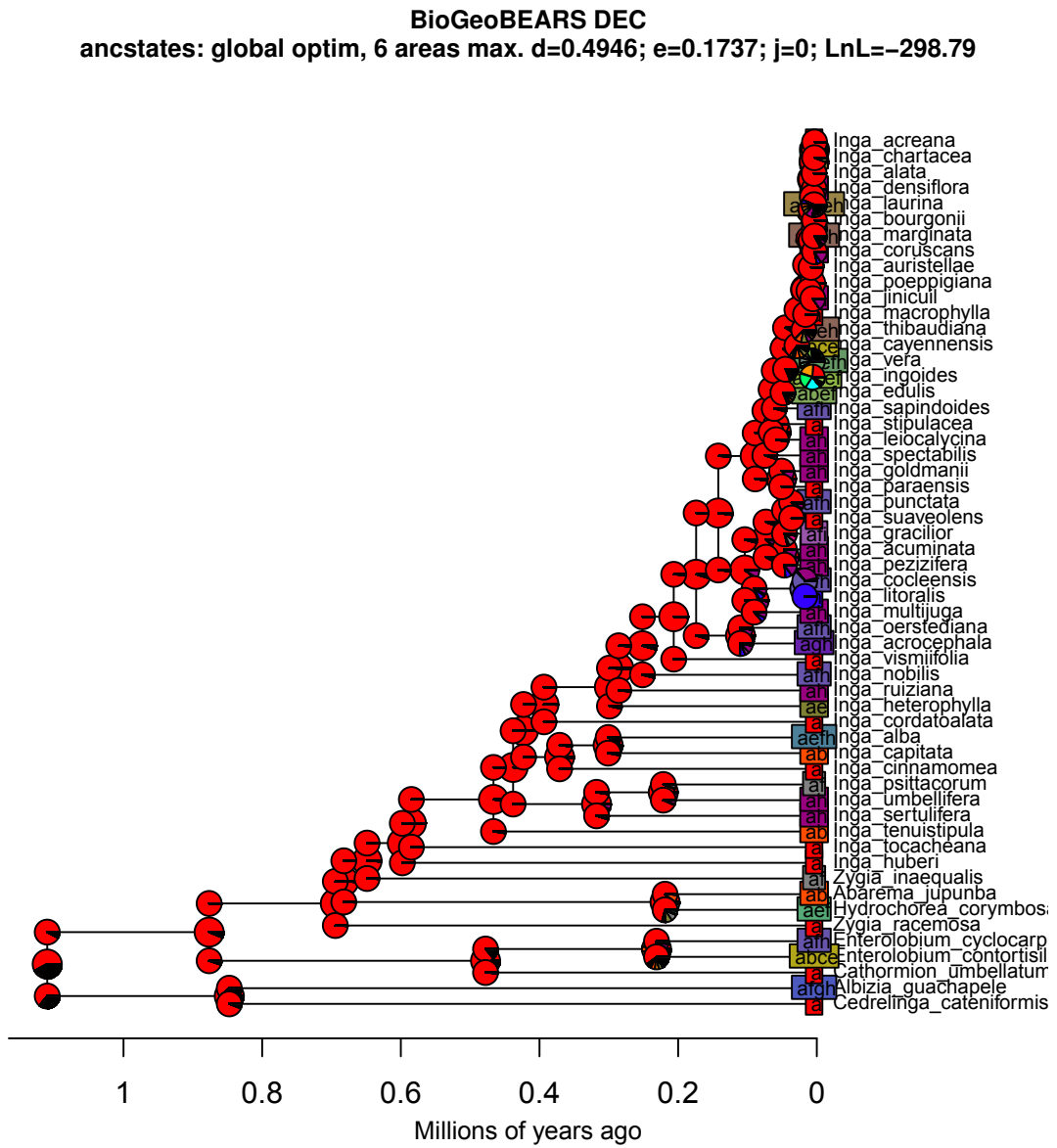


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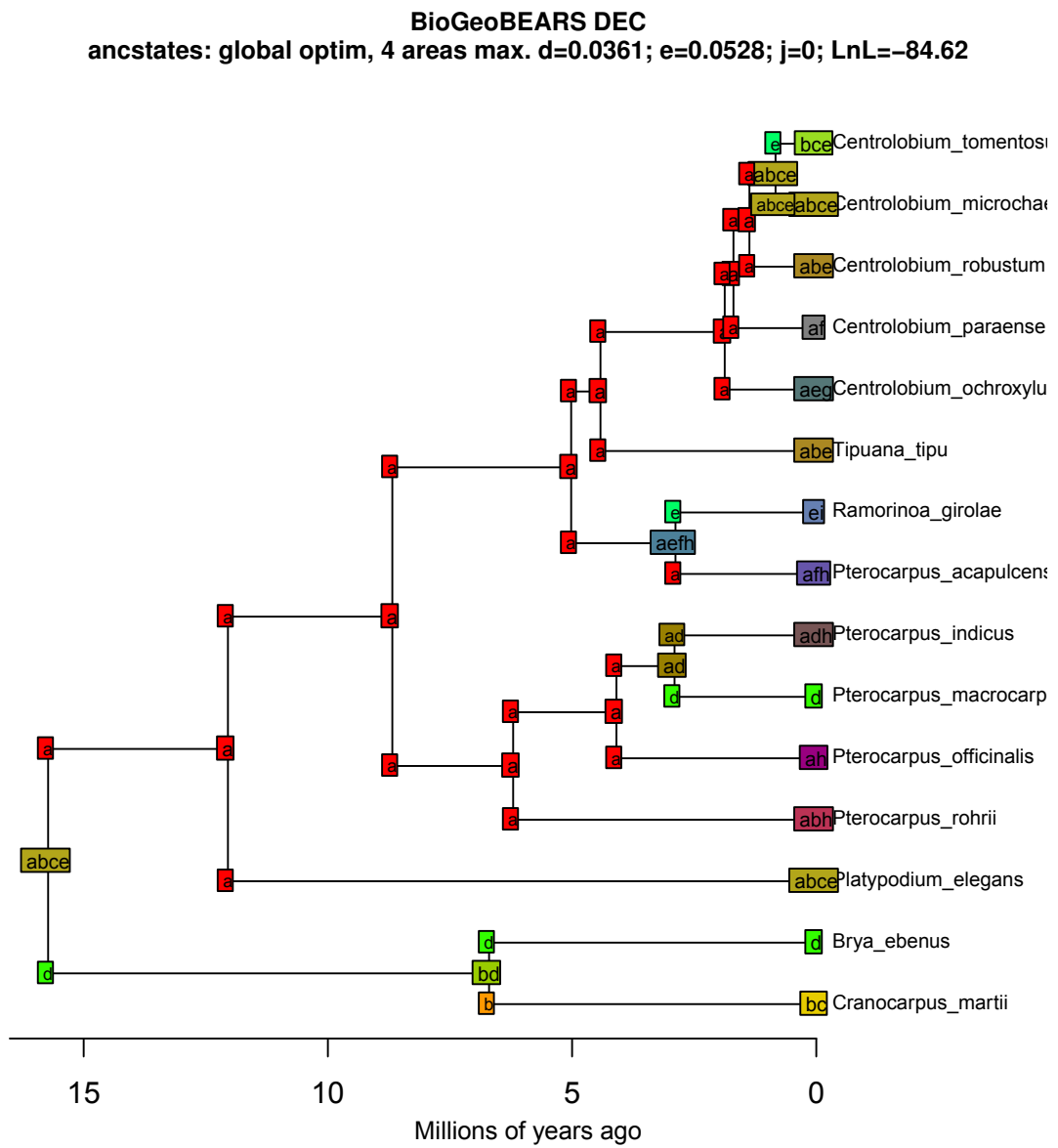


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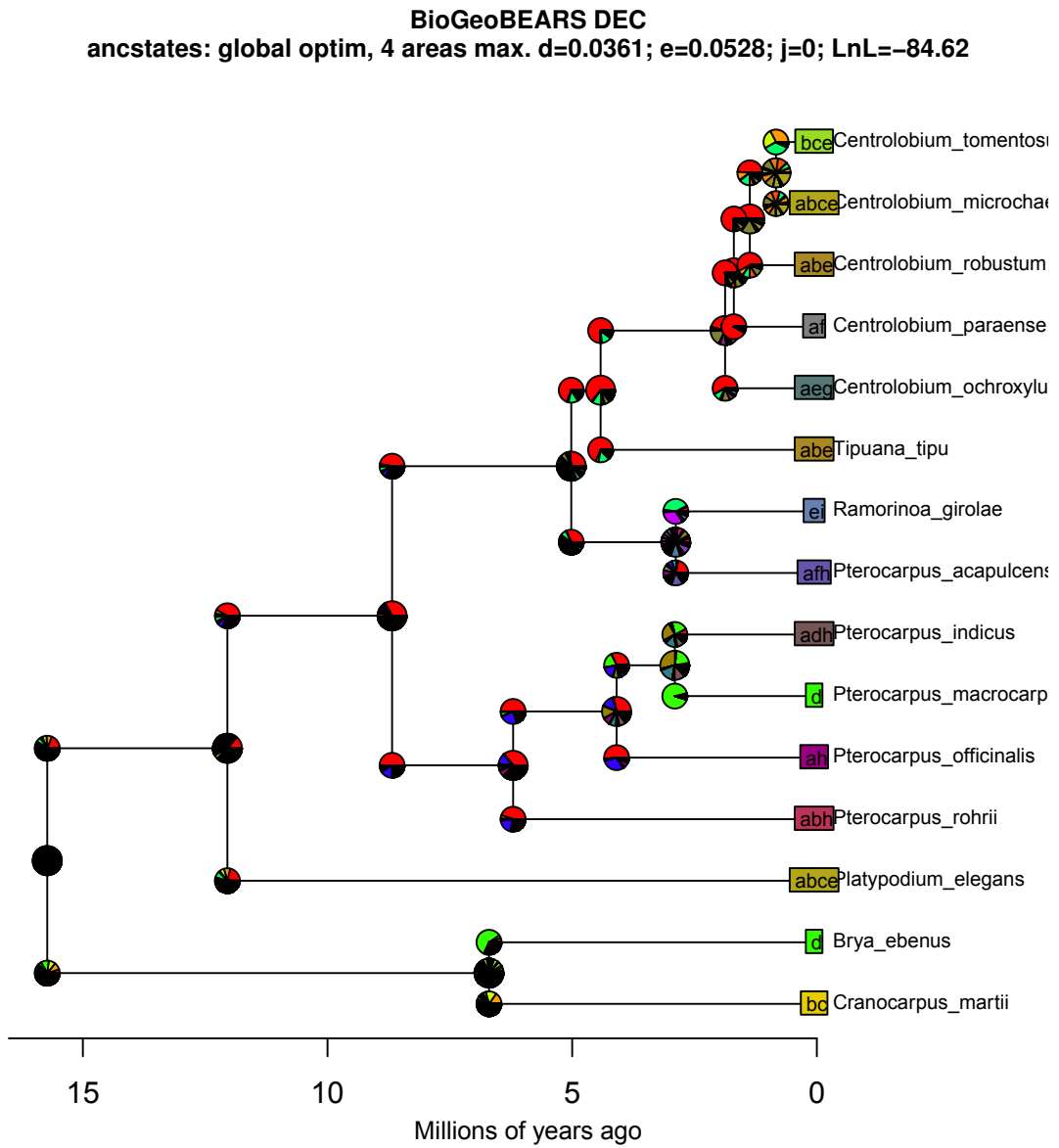


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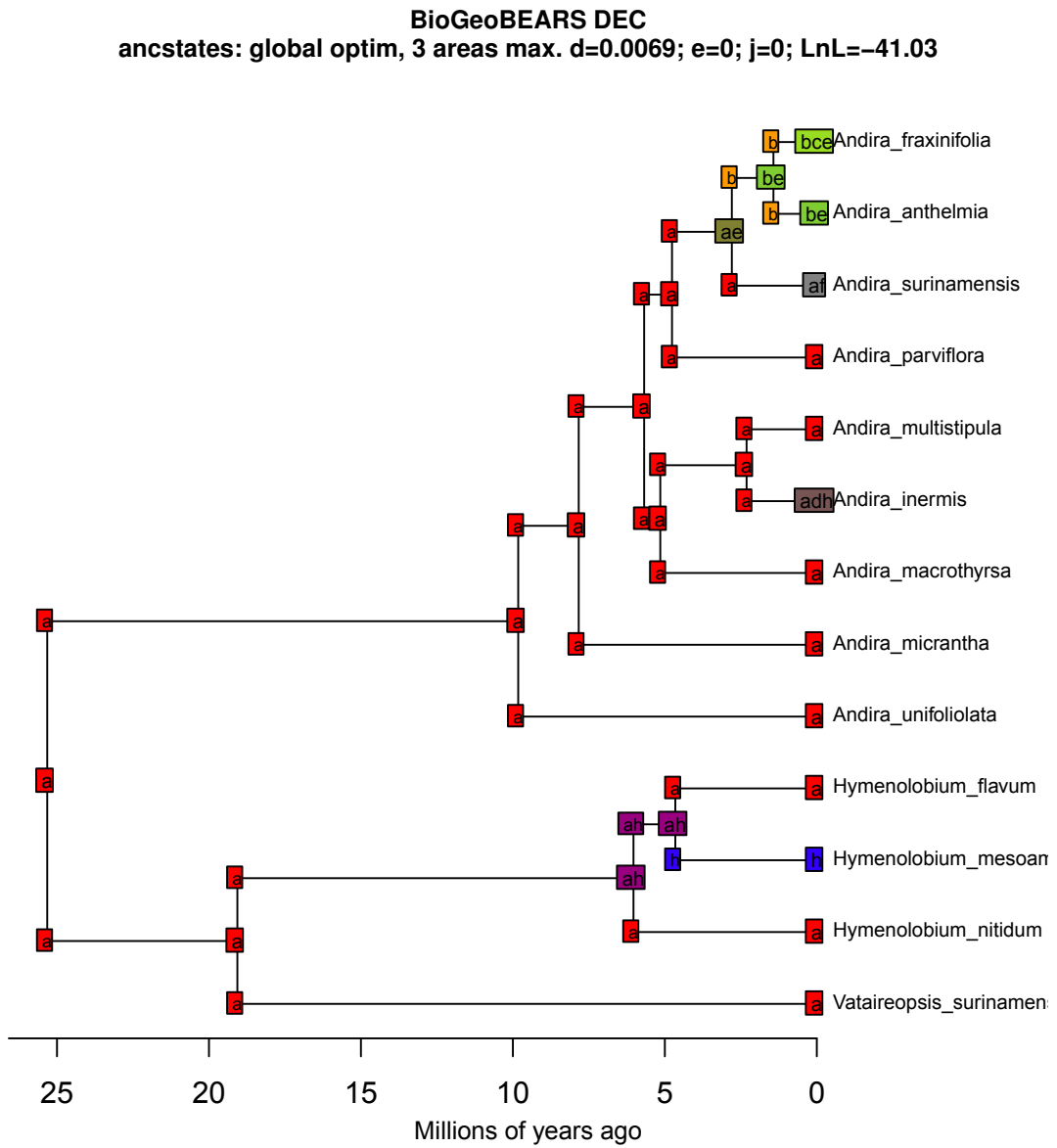


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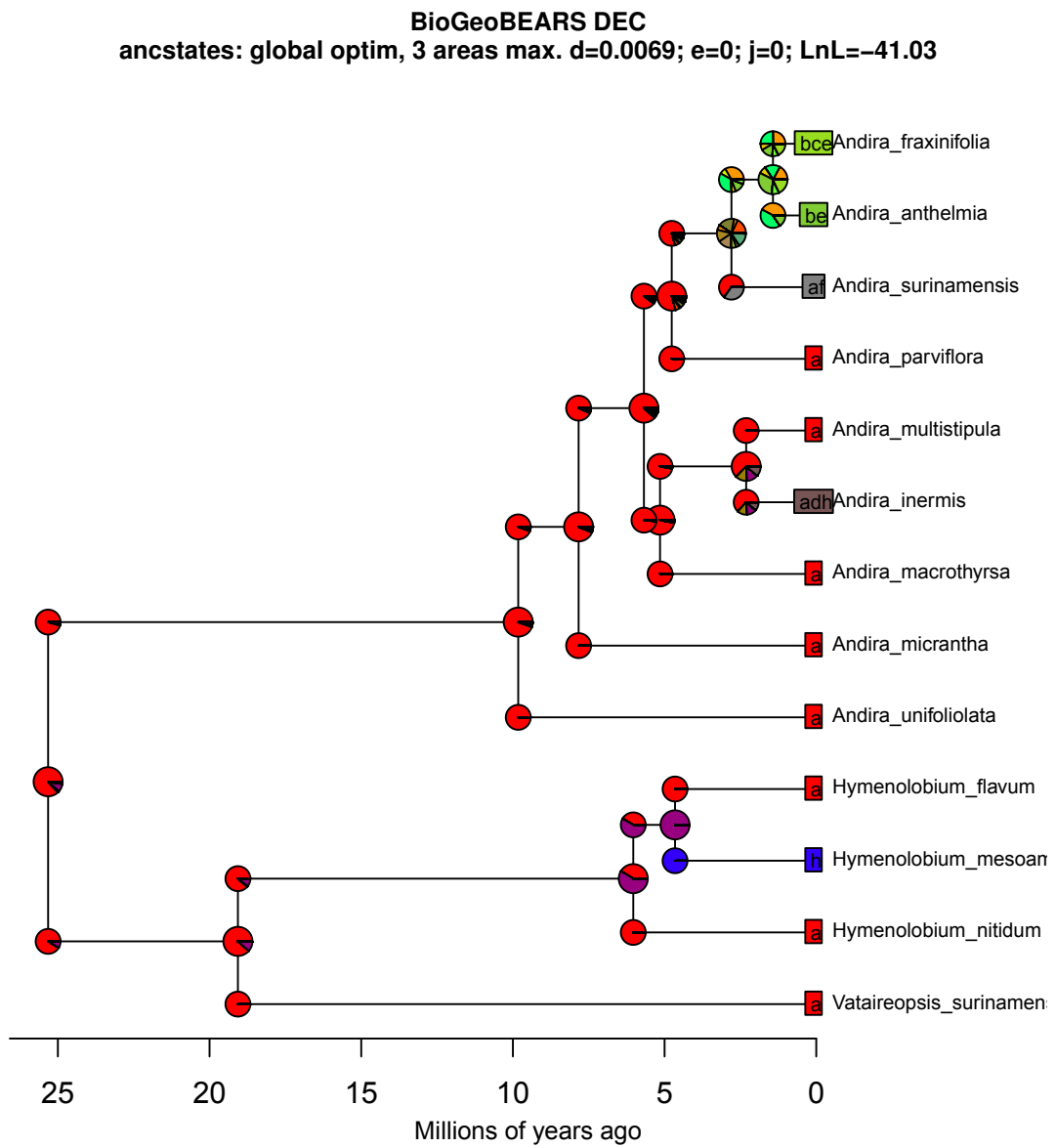


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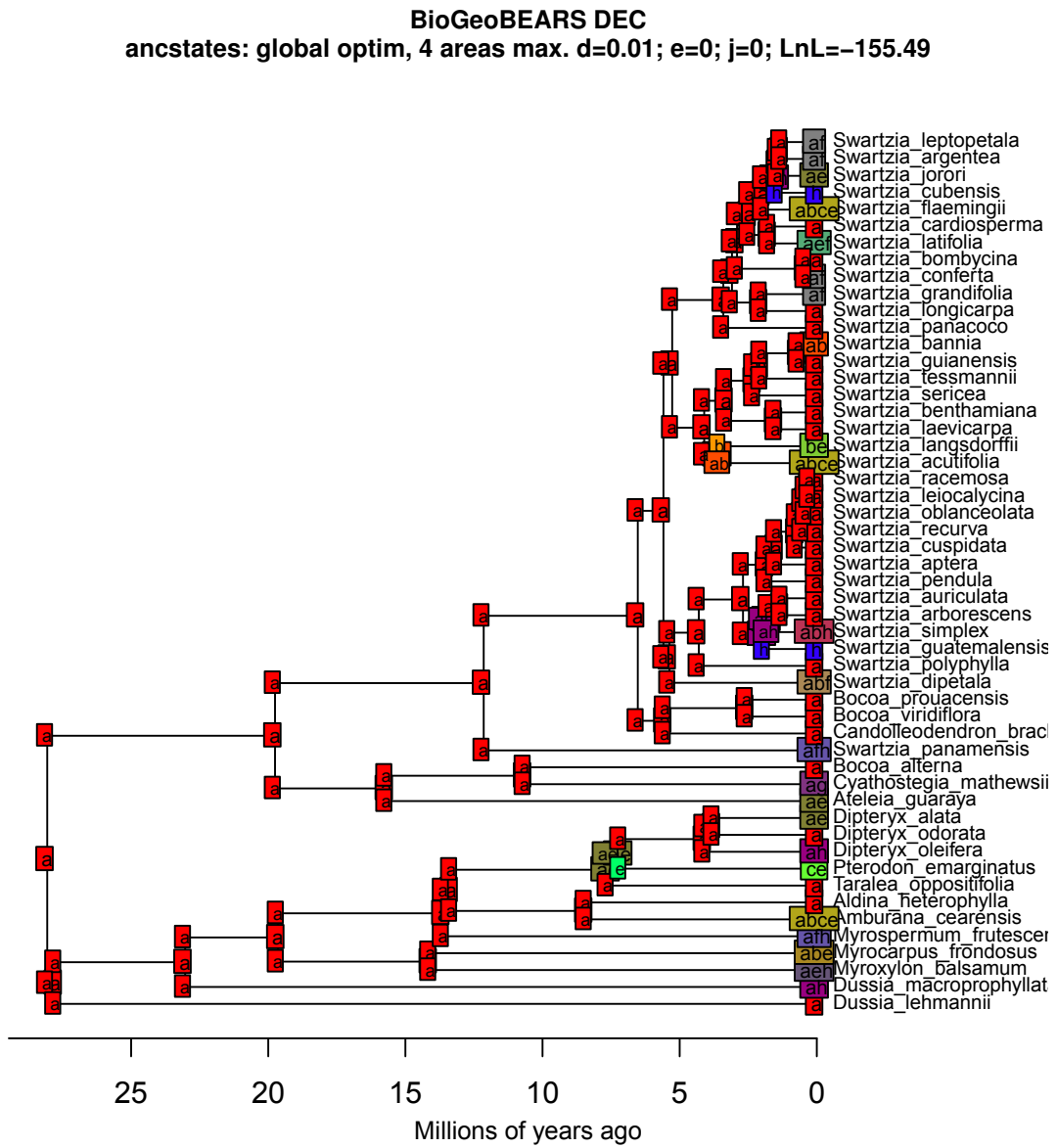


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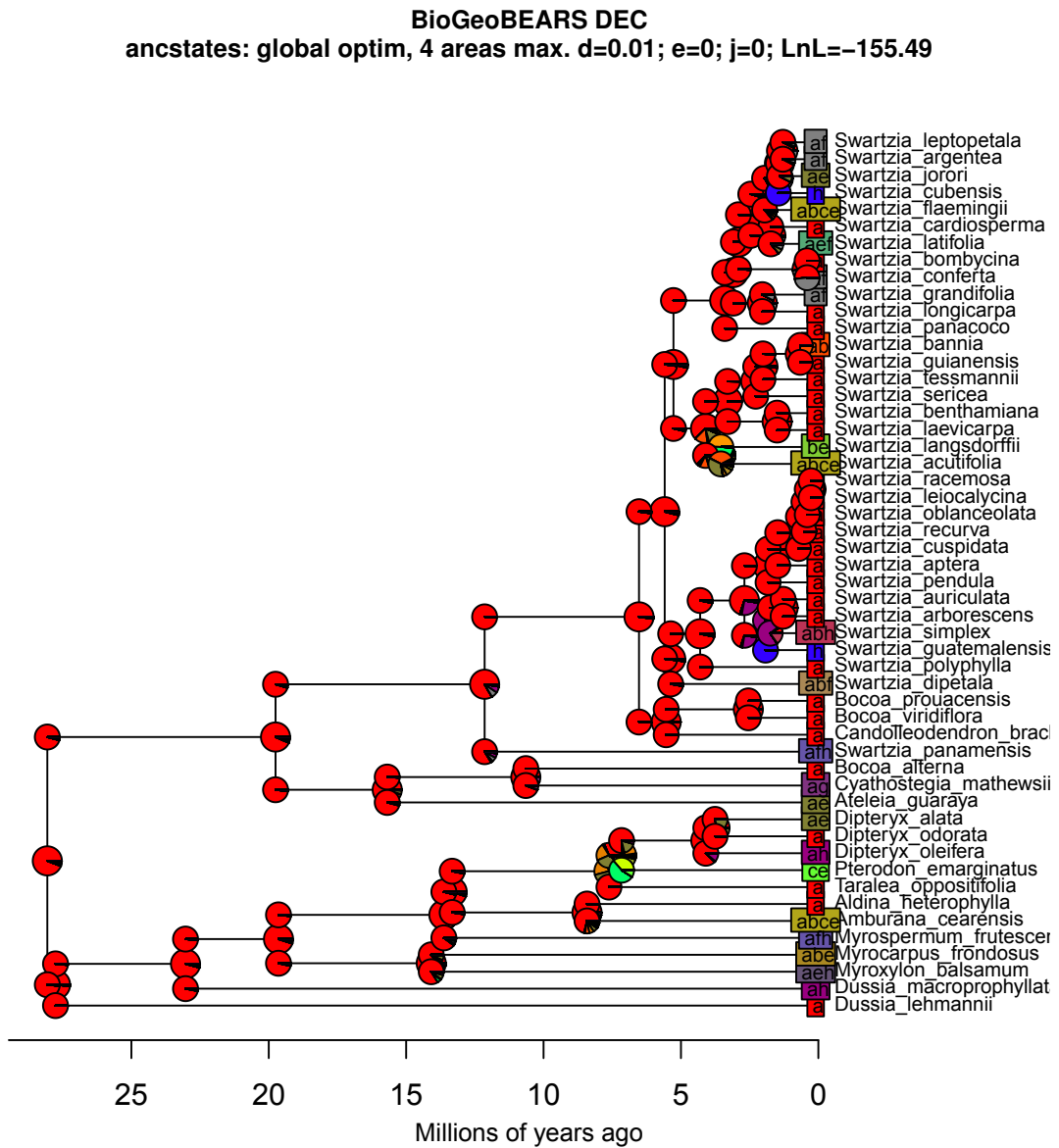


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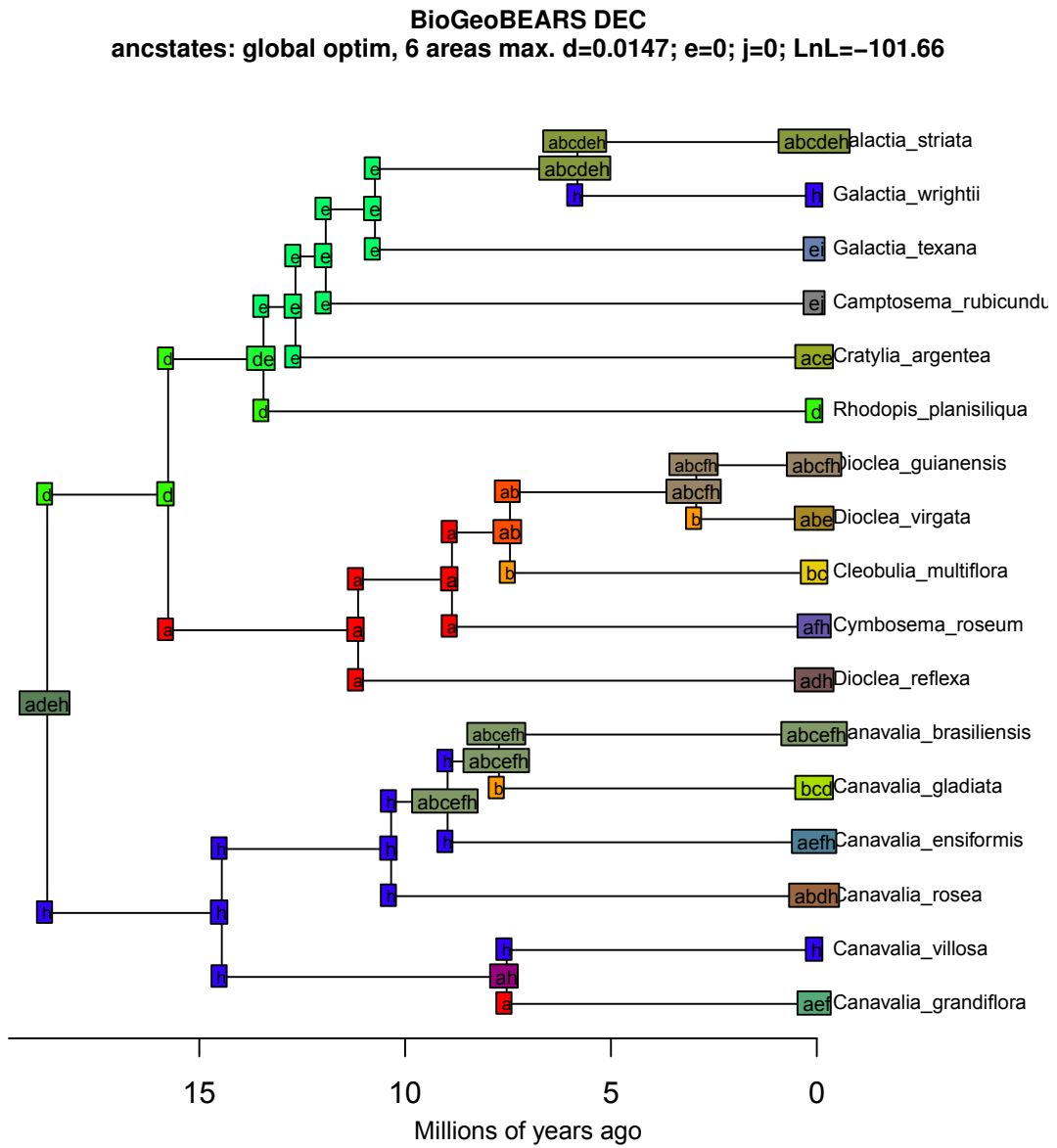


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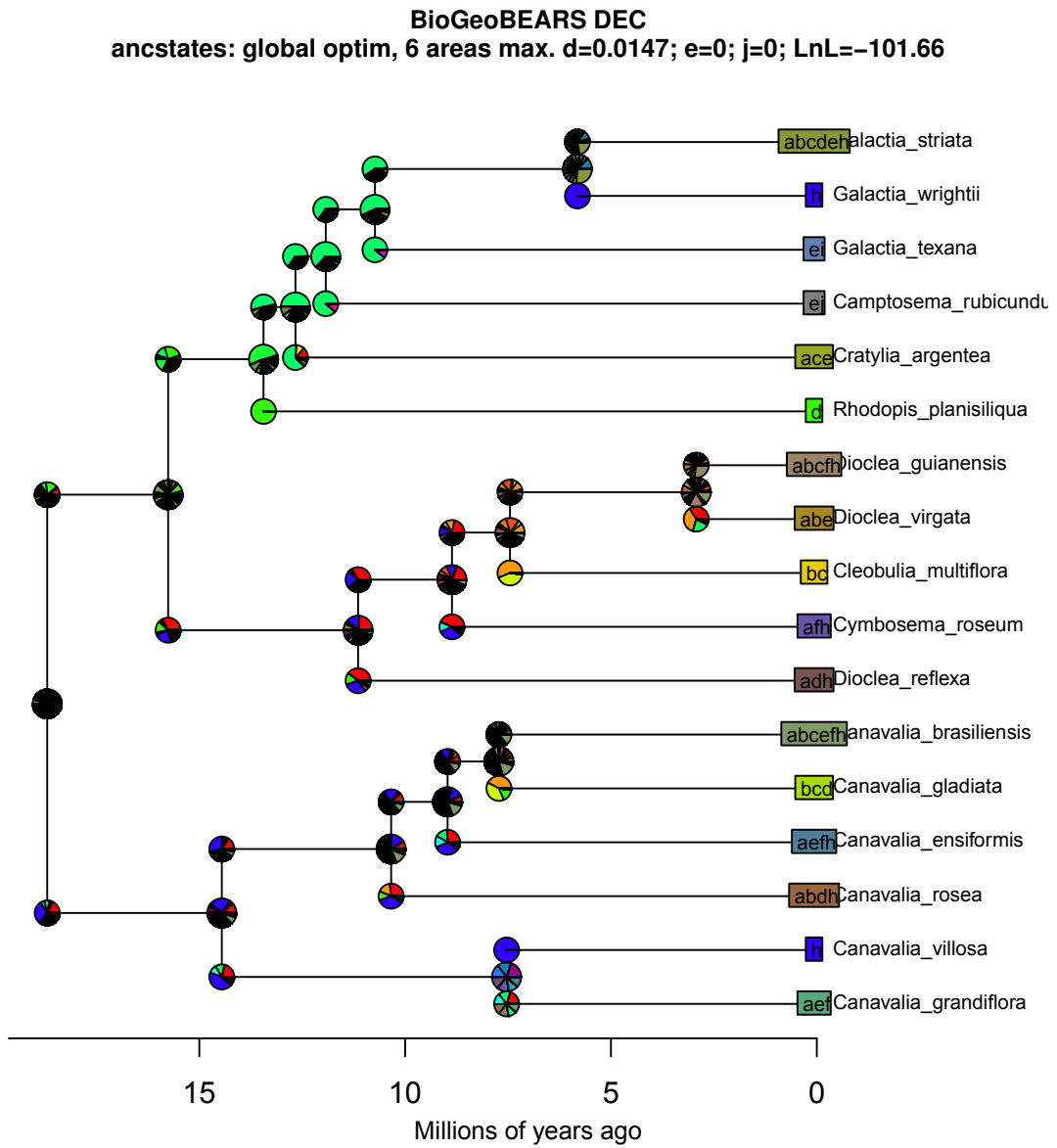


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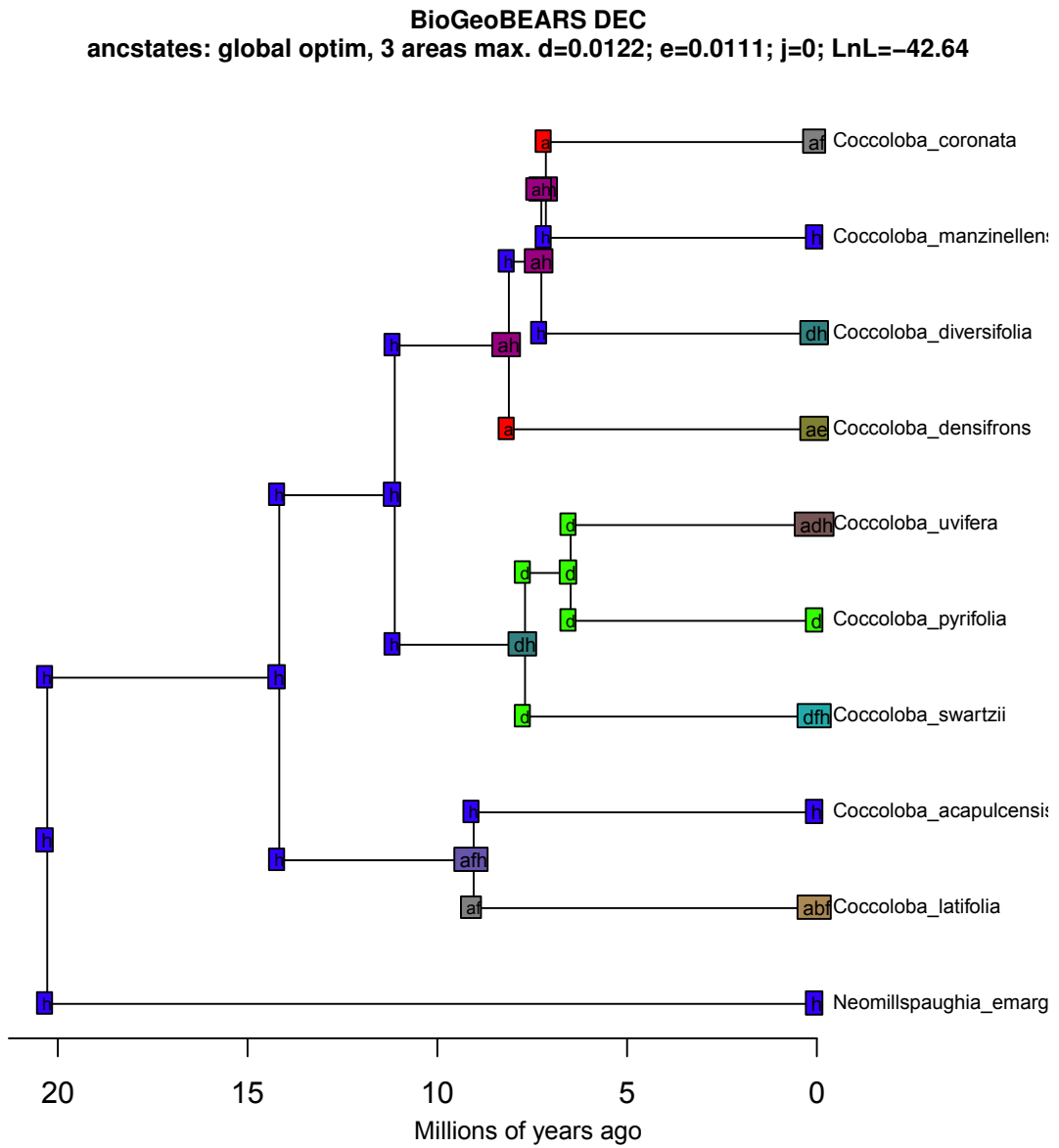


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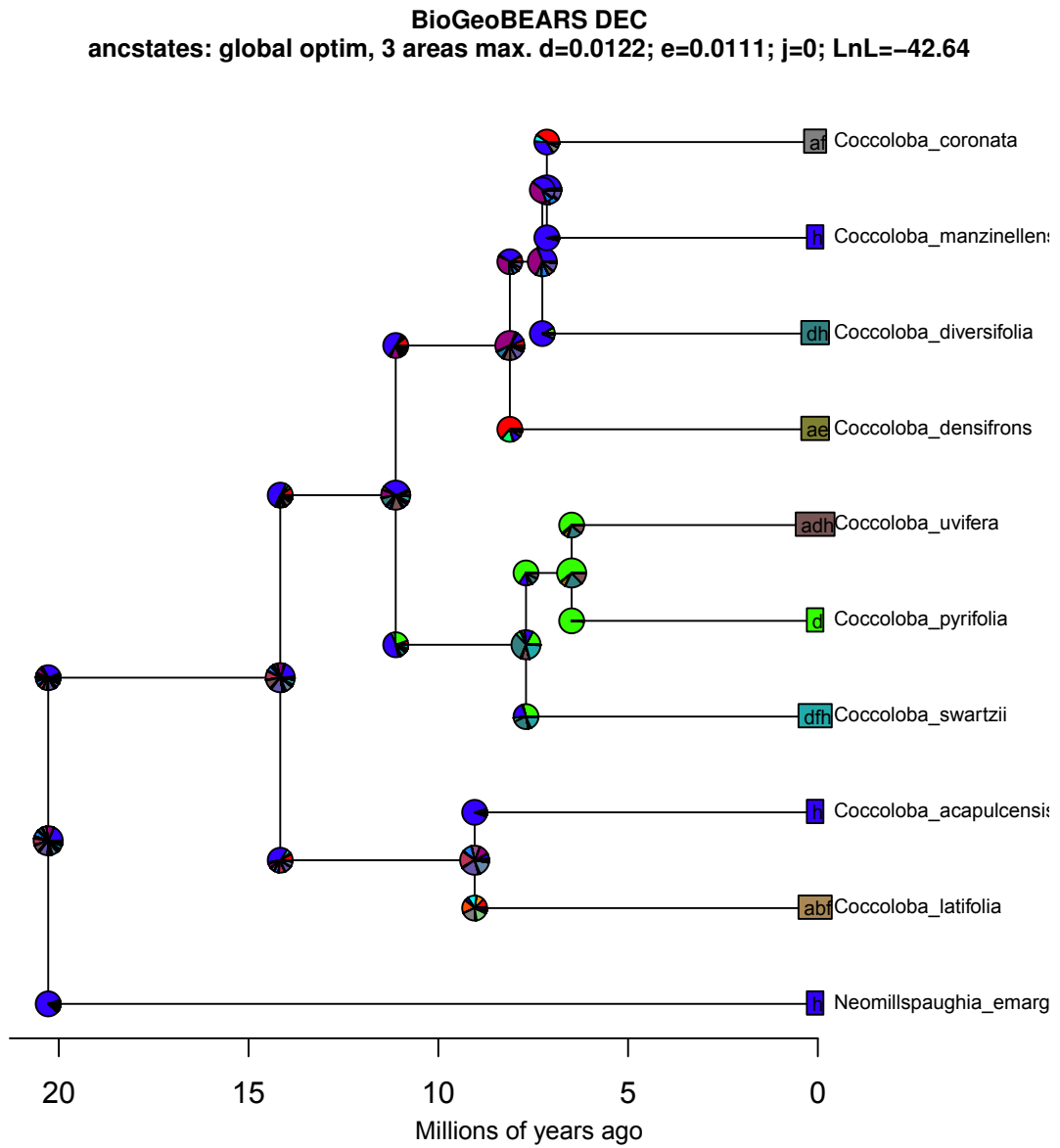


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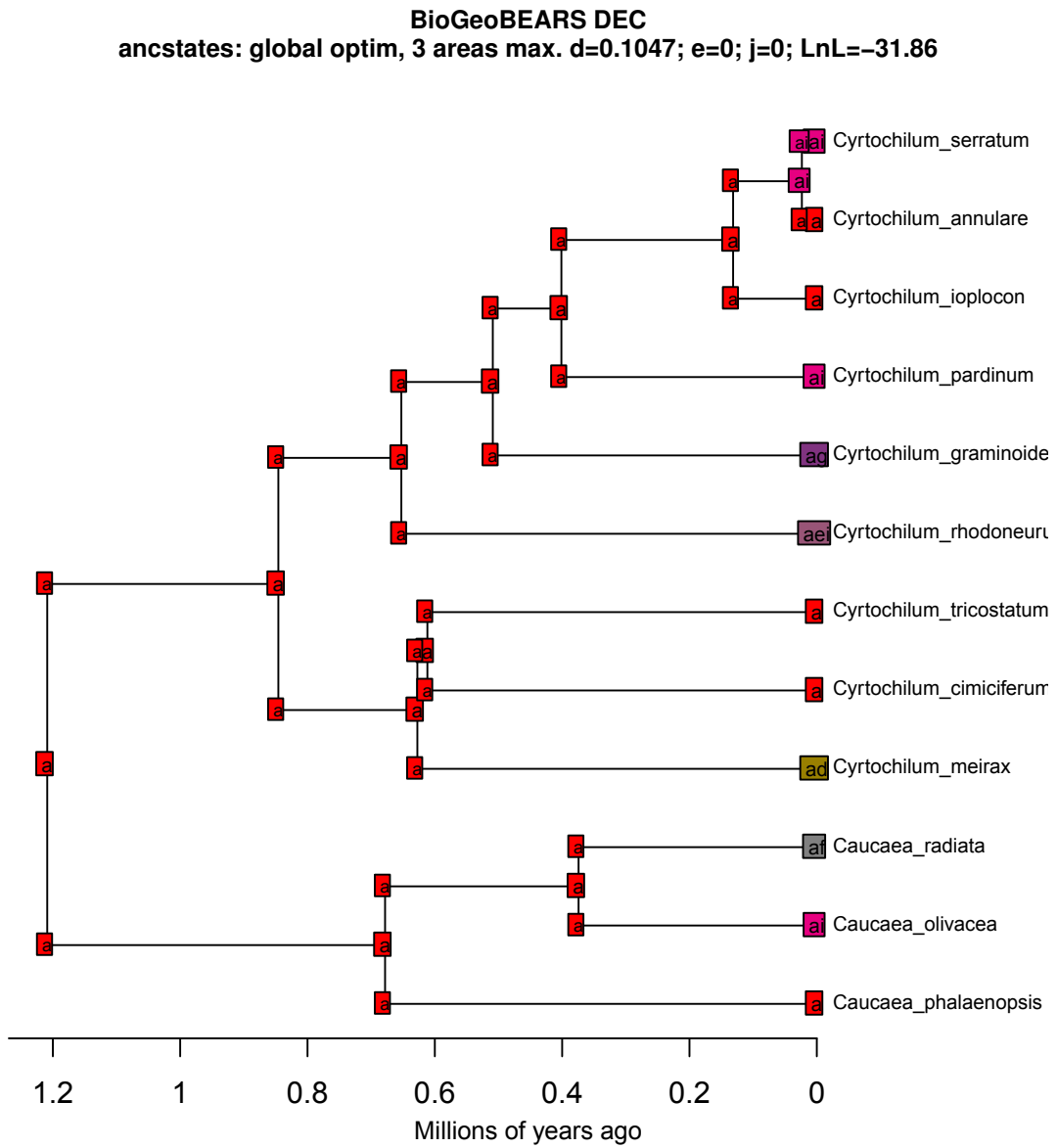


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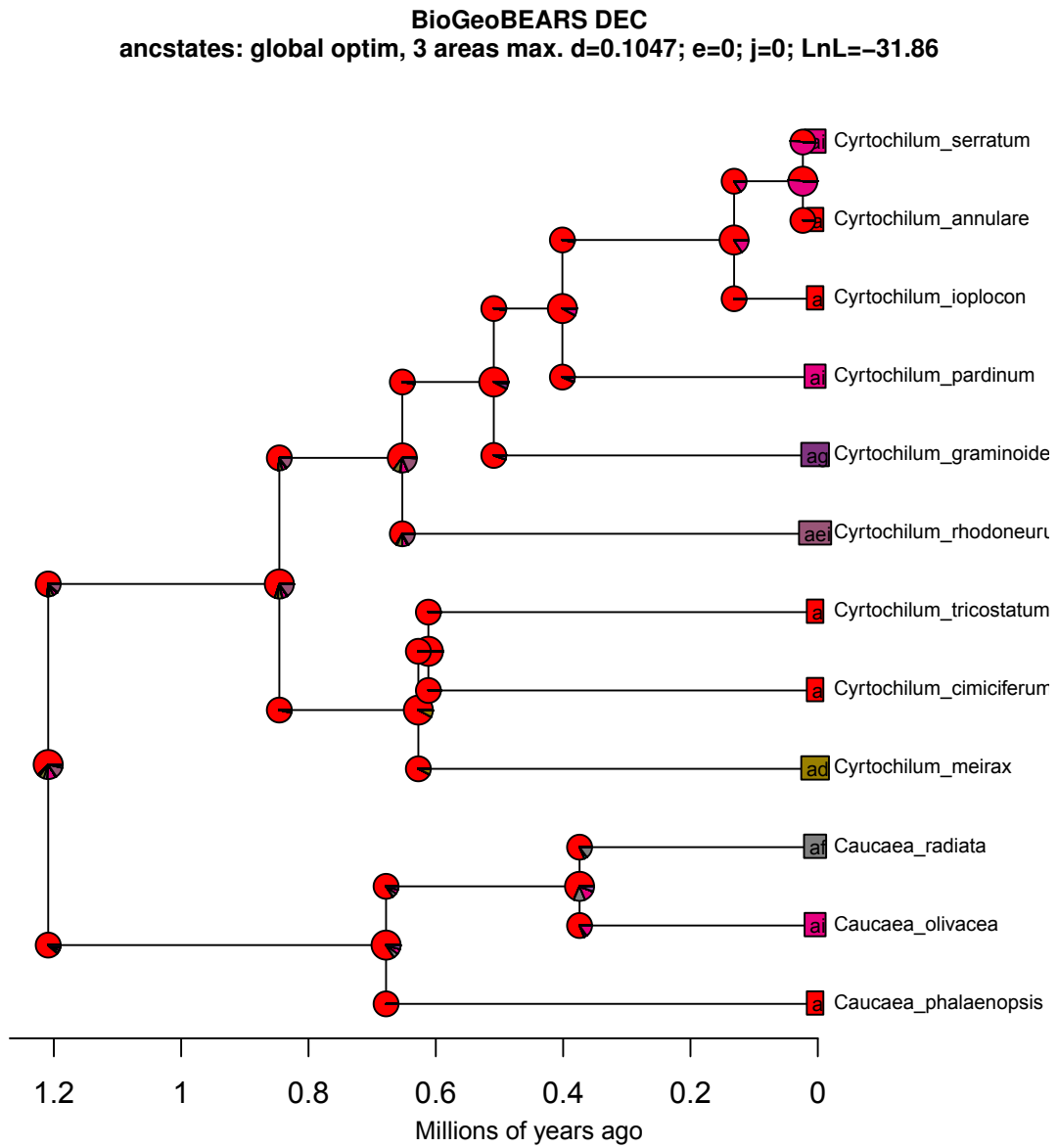


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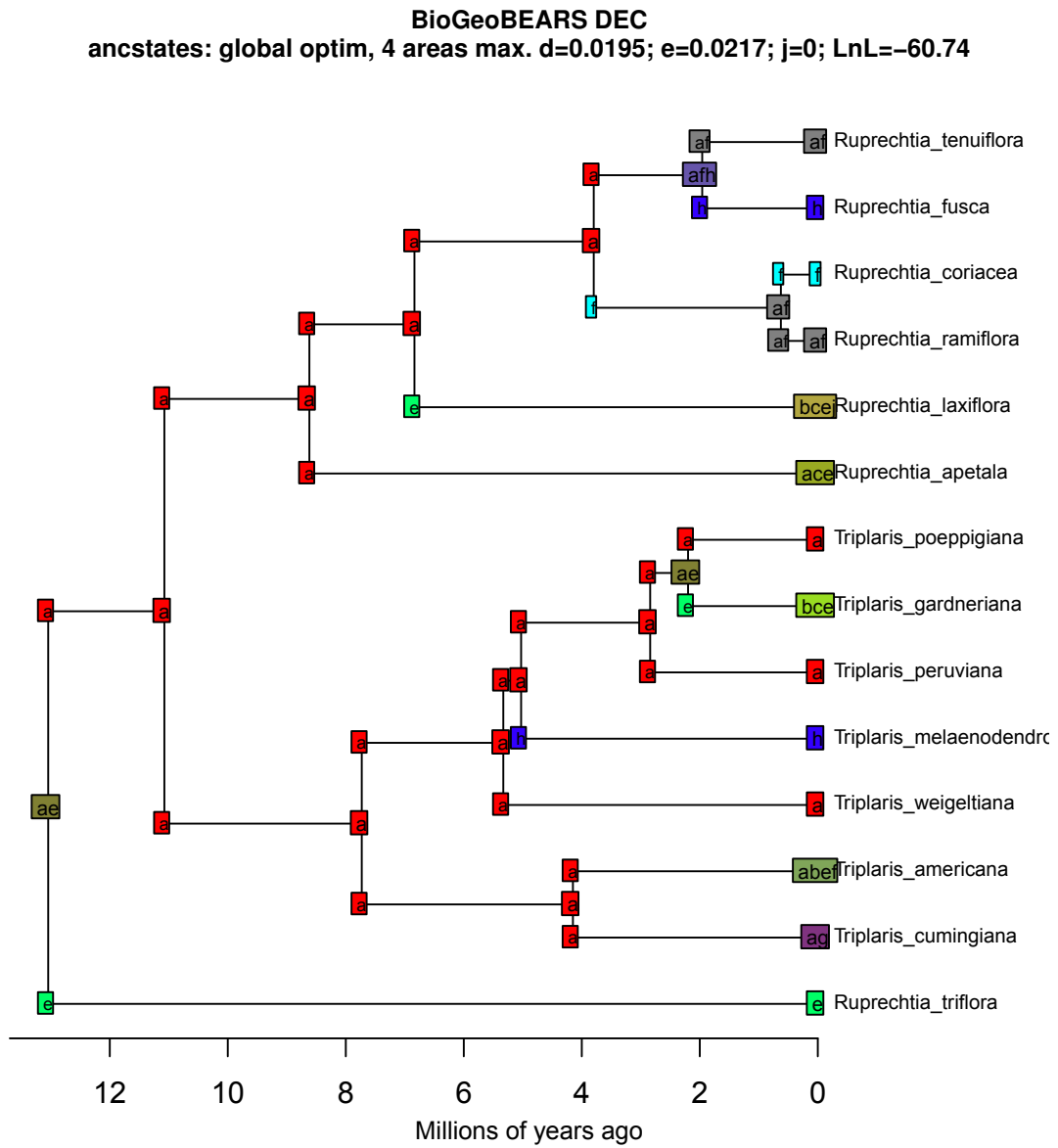


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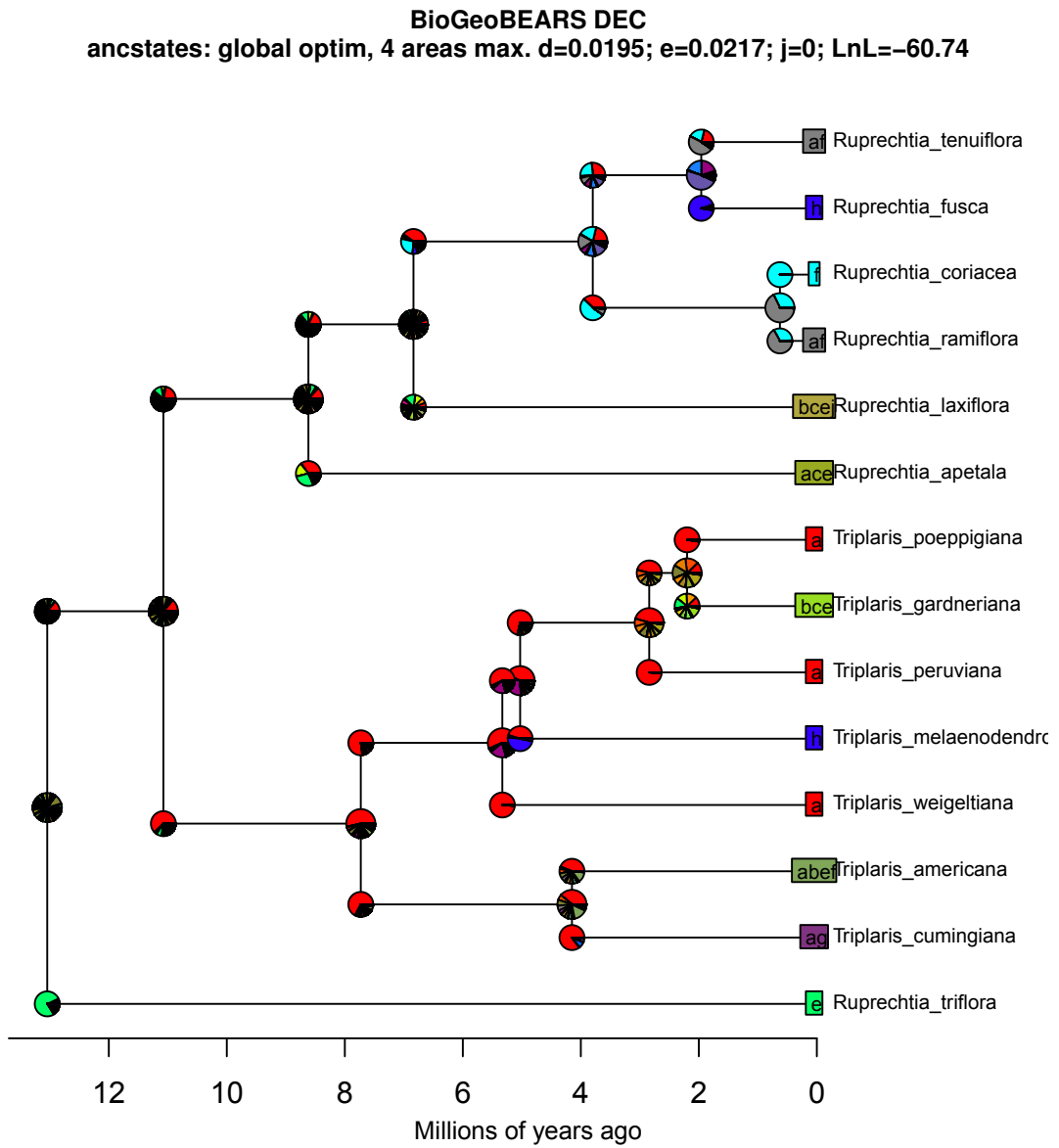


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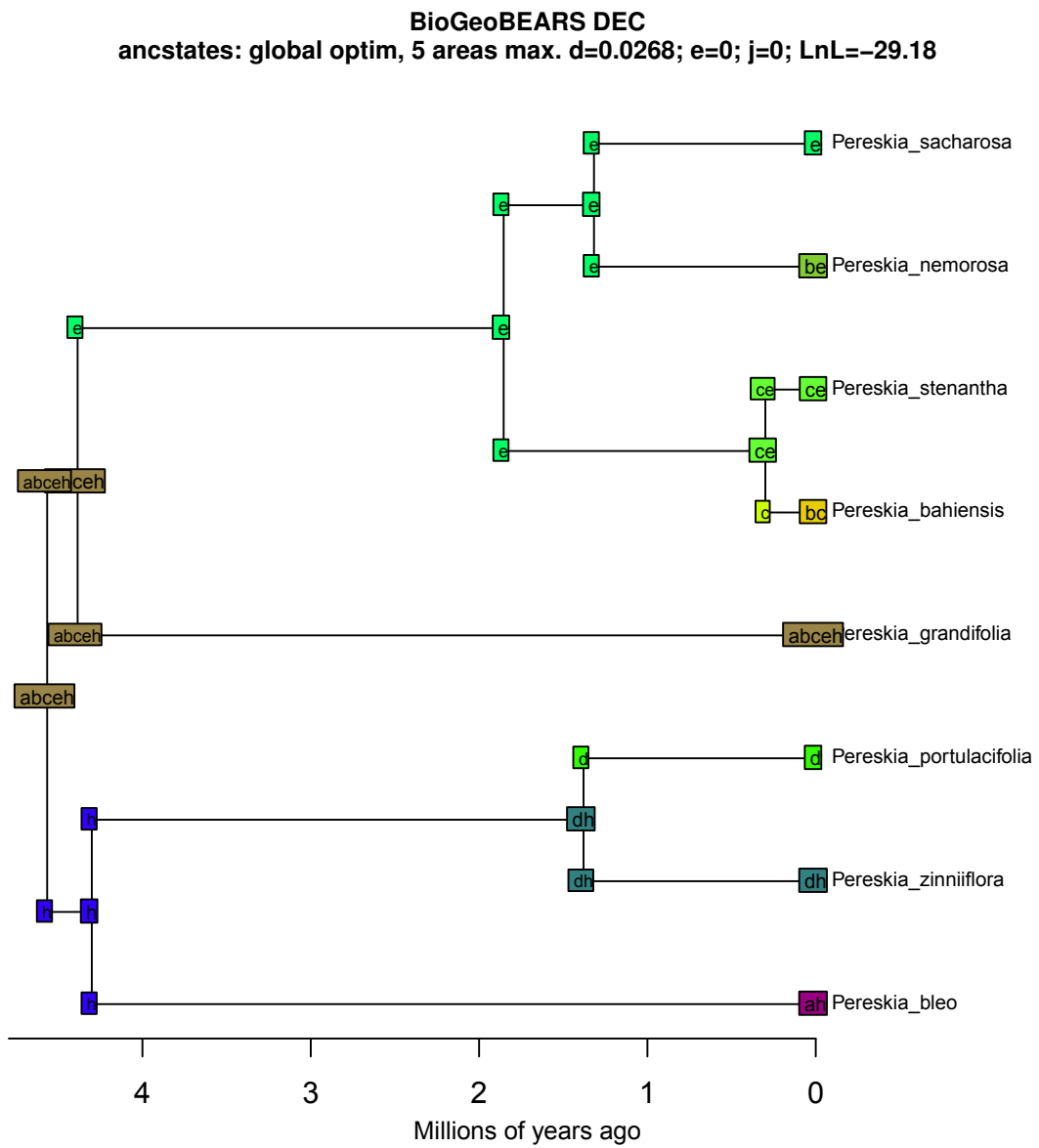


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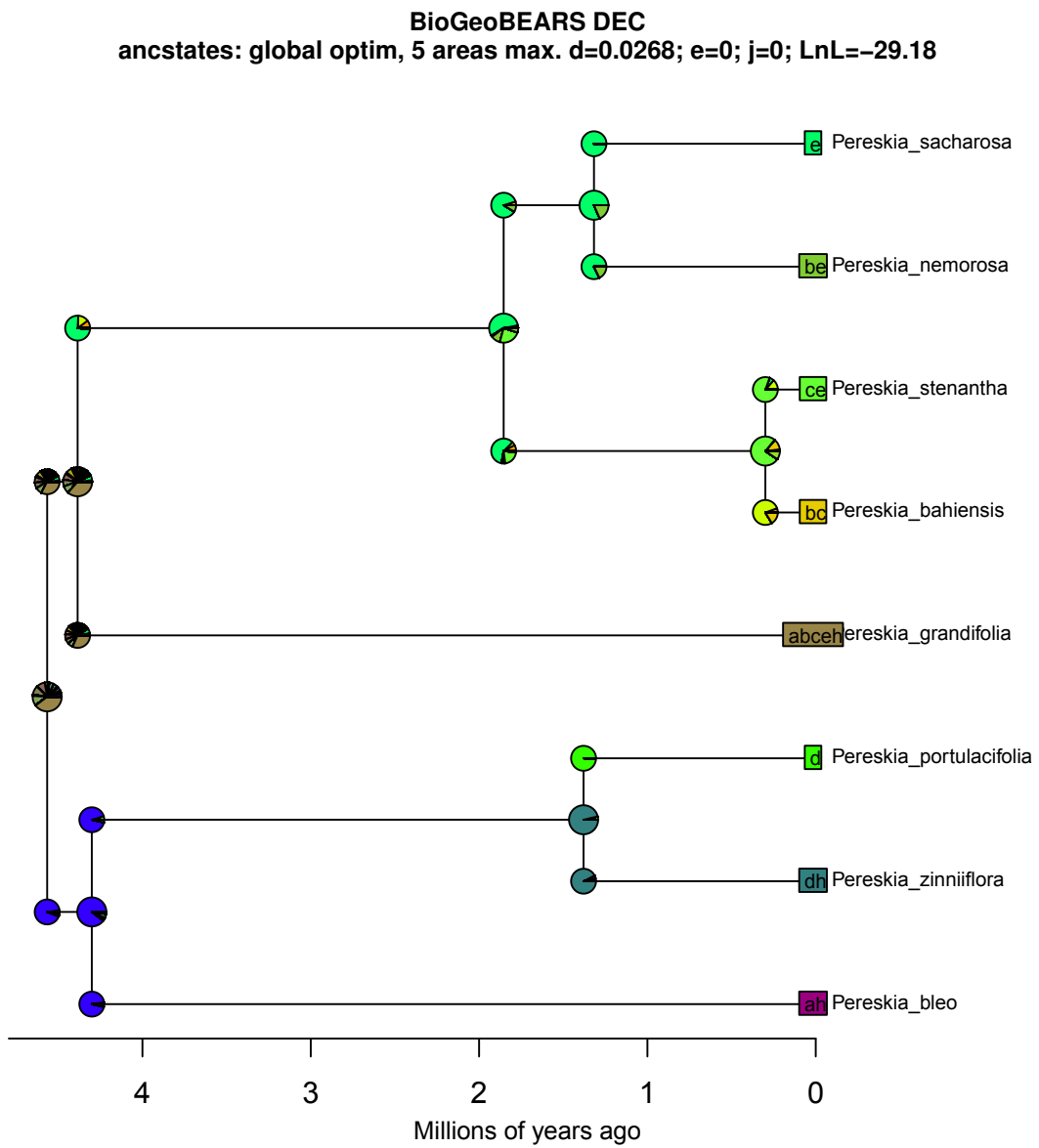


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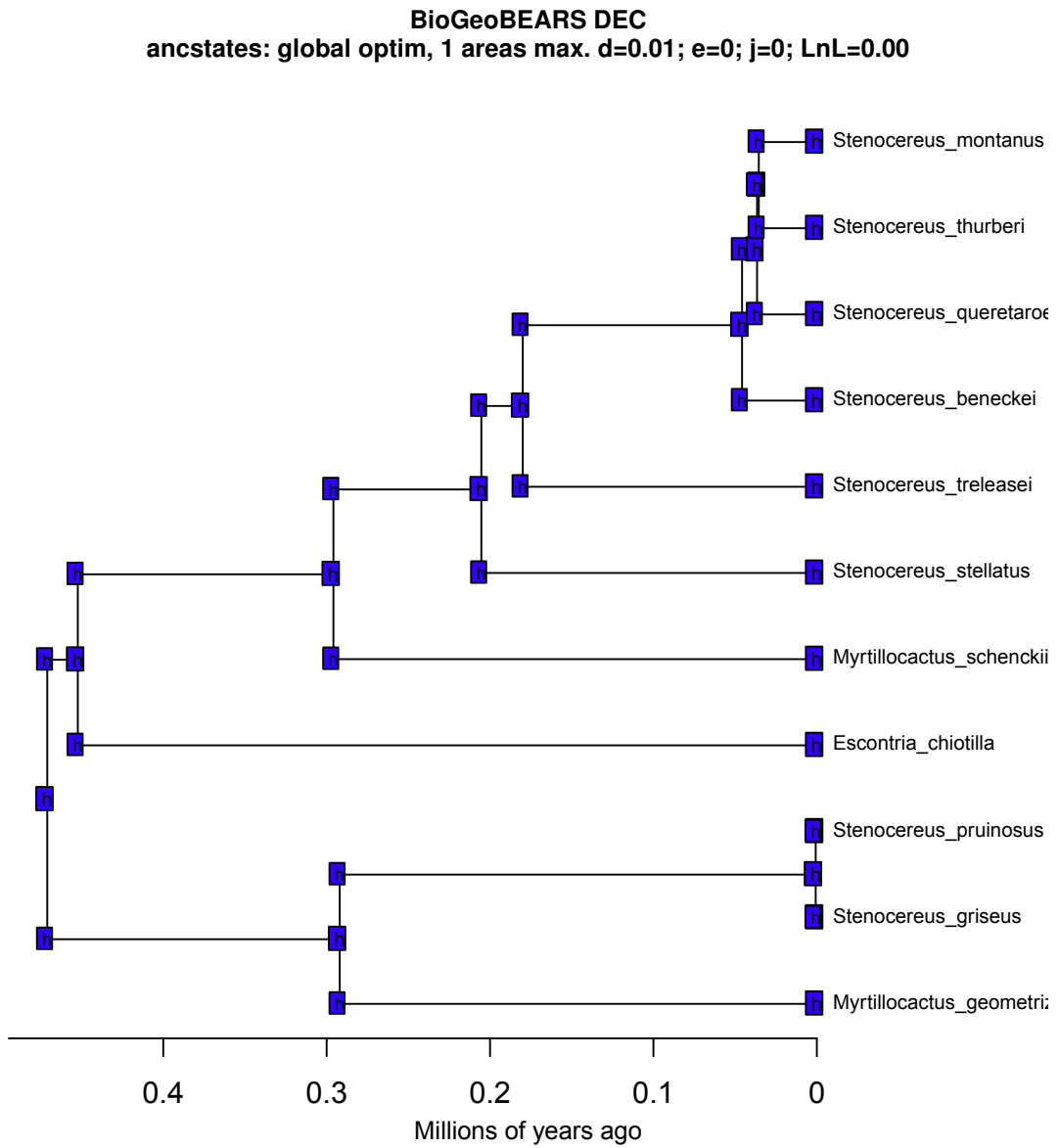


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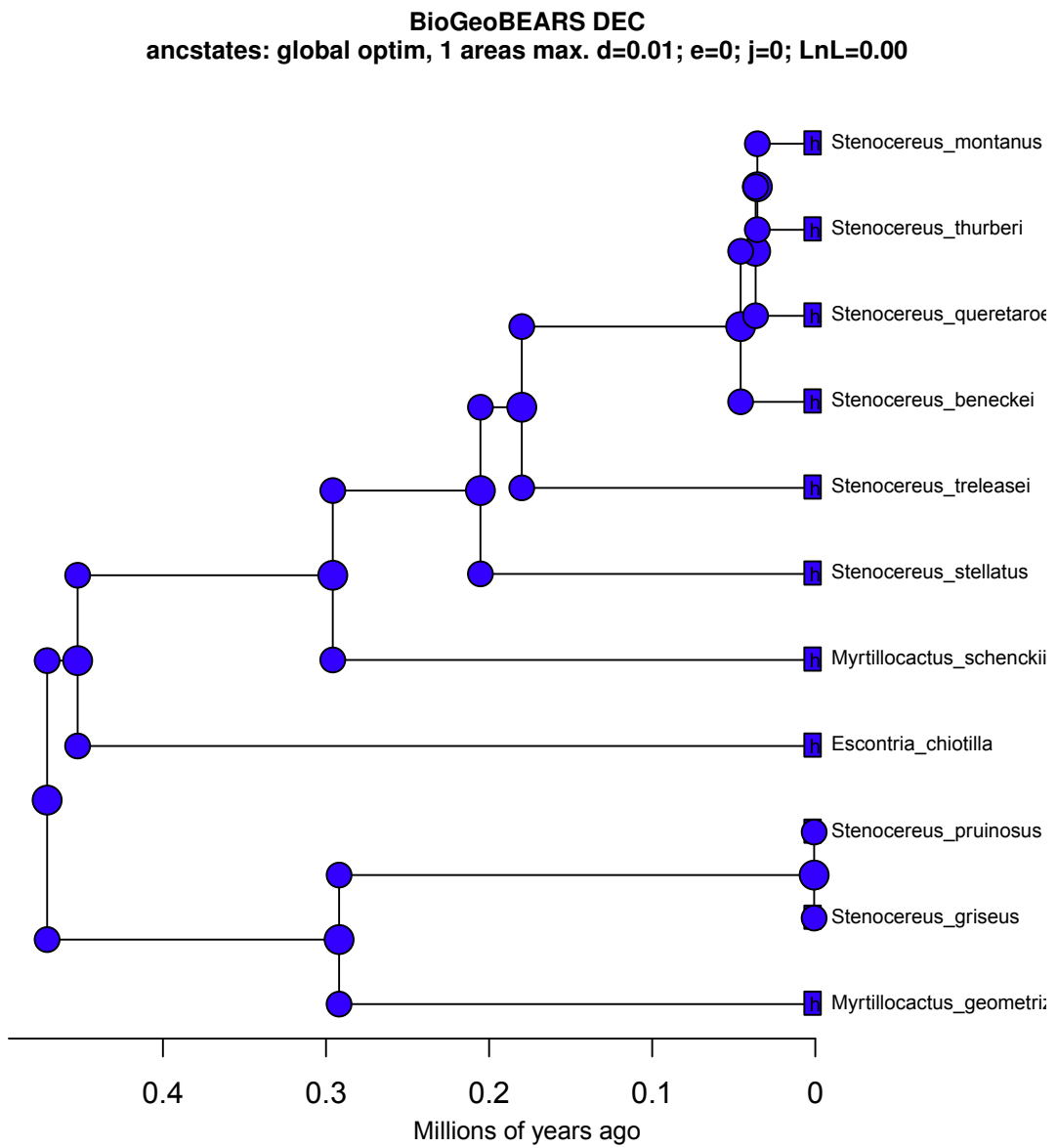


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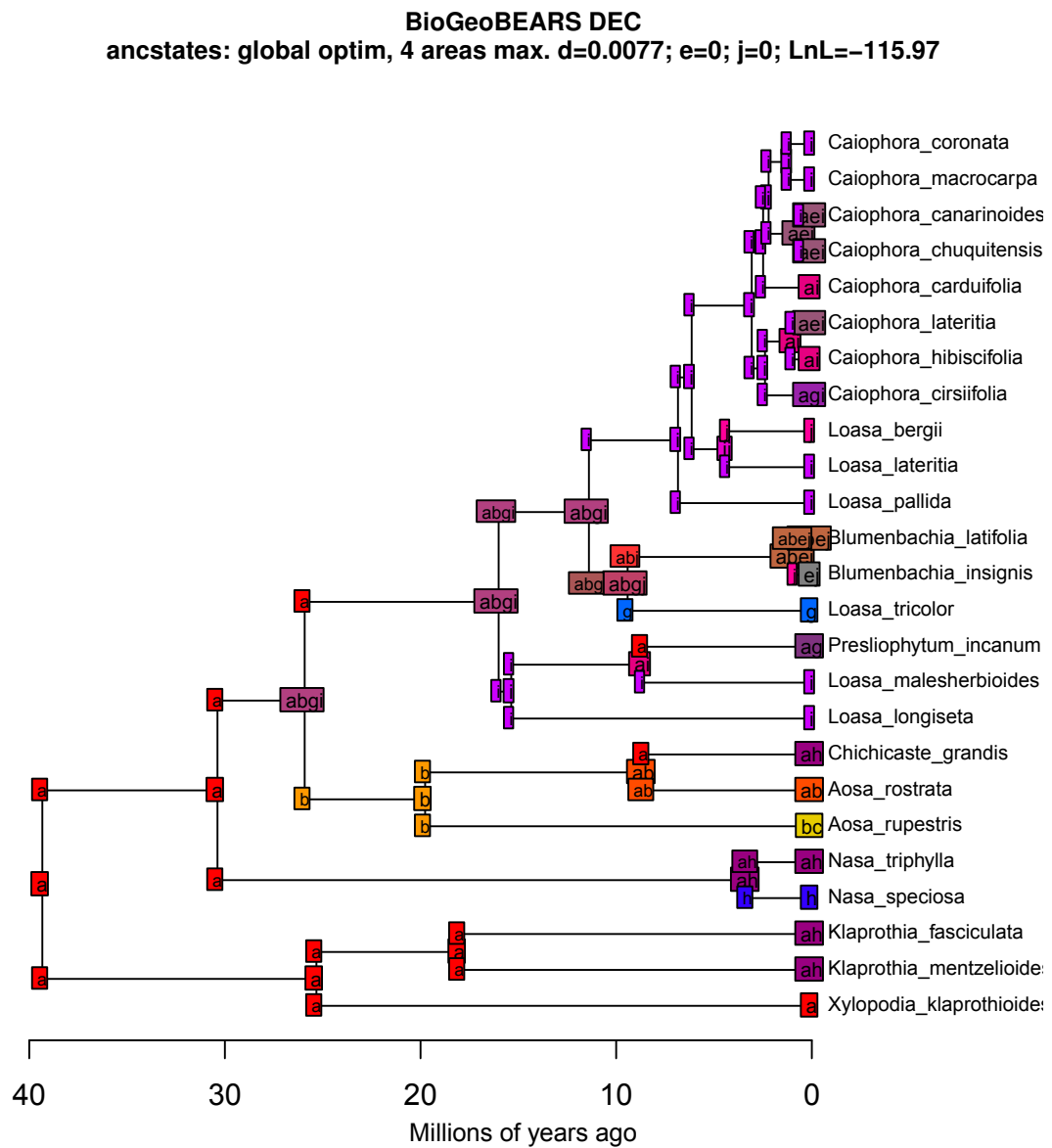


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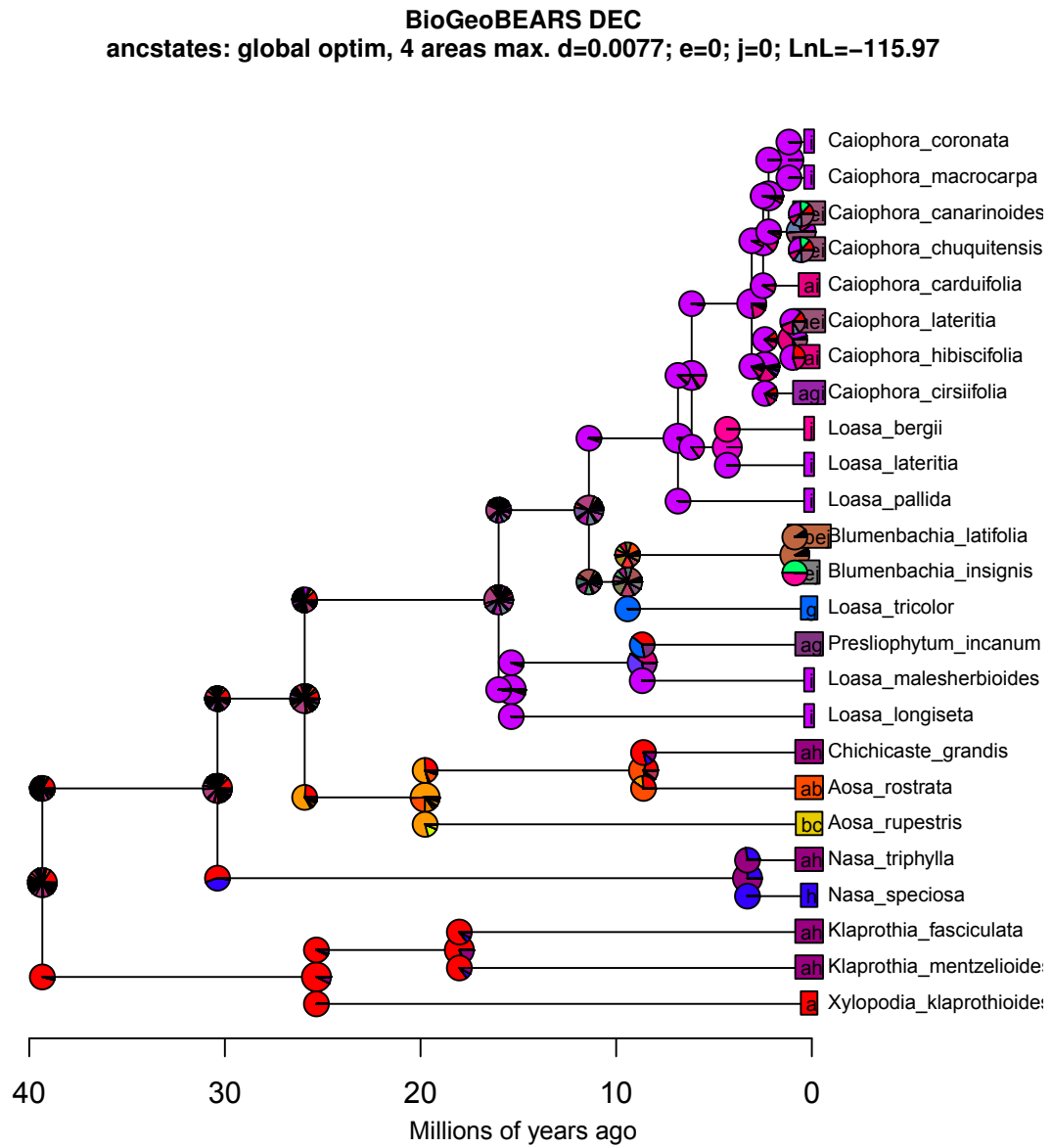


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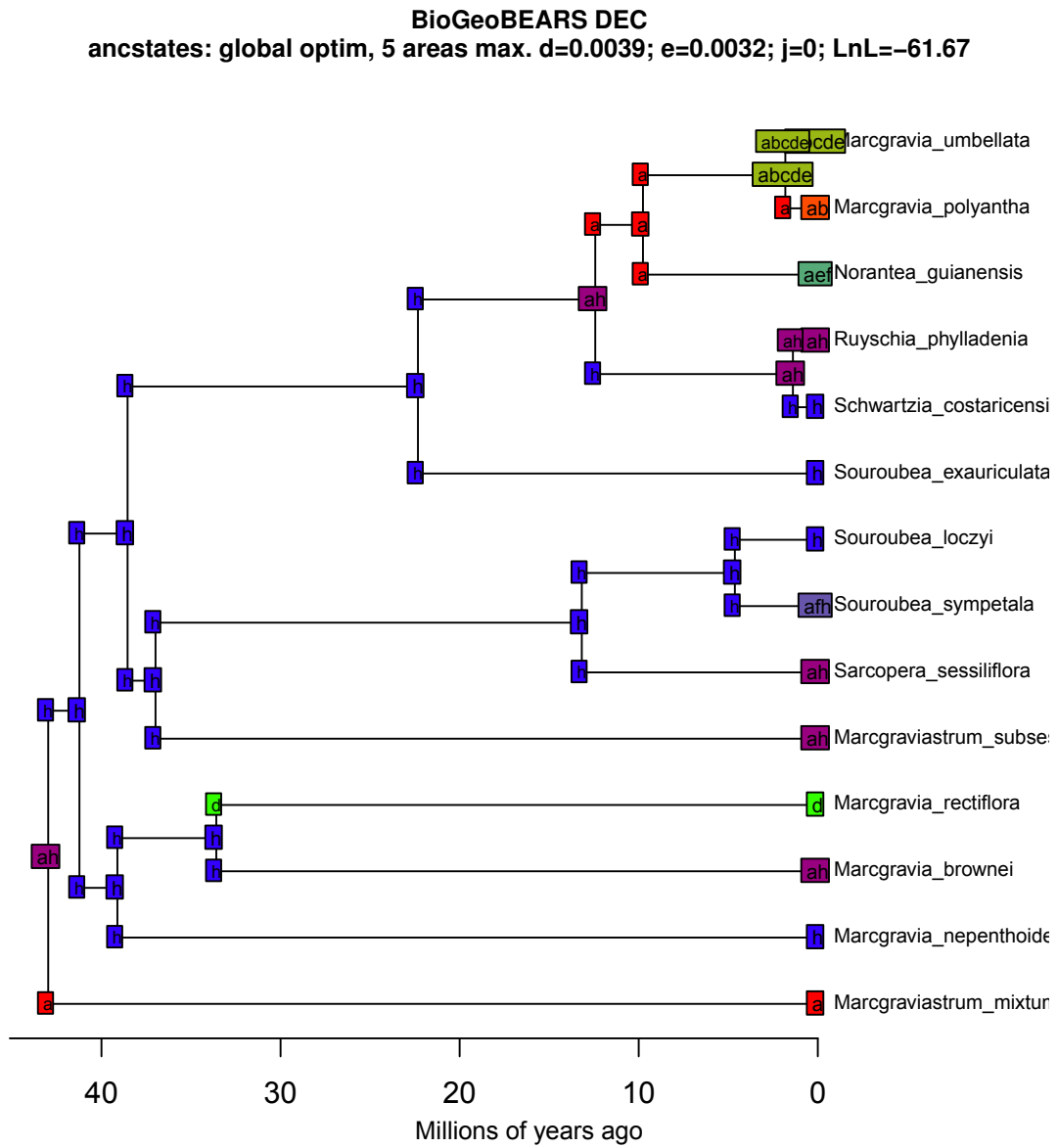


Figure S3: Clades of angiosperms

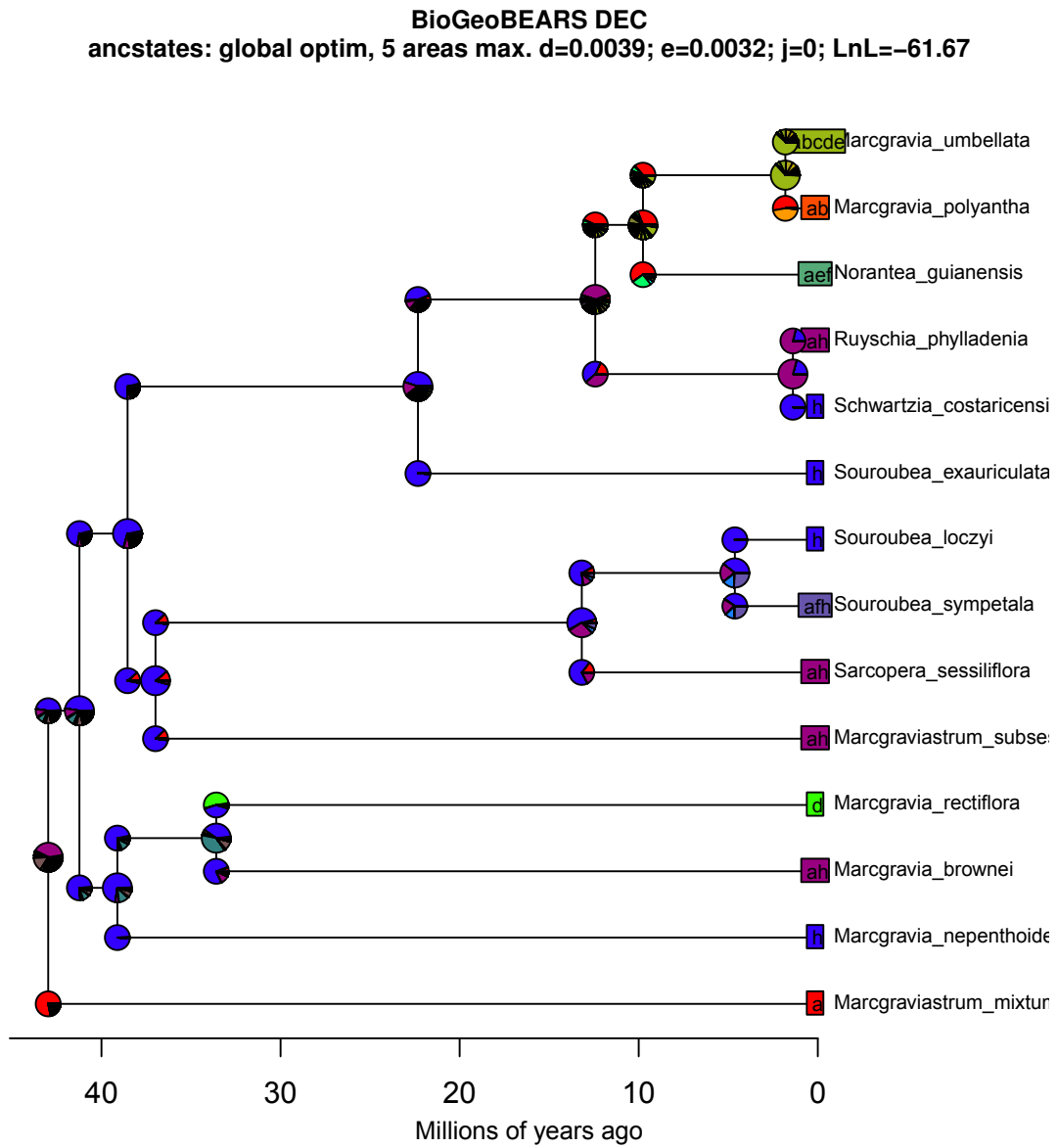


Figure S3: Clades of angiosperms

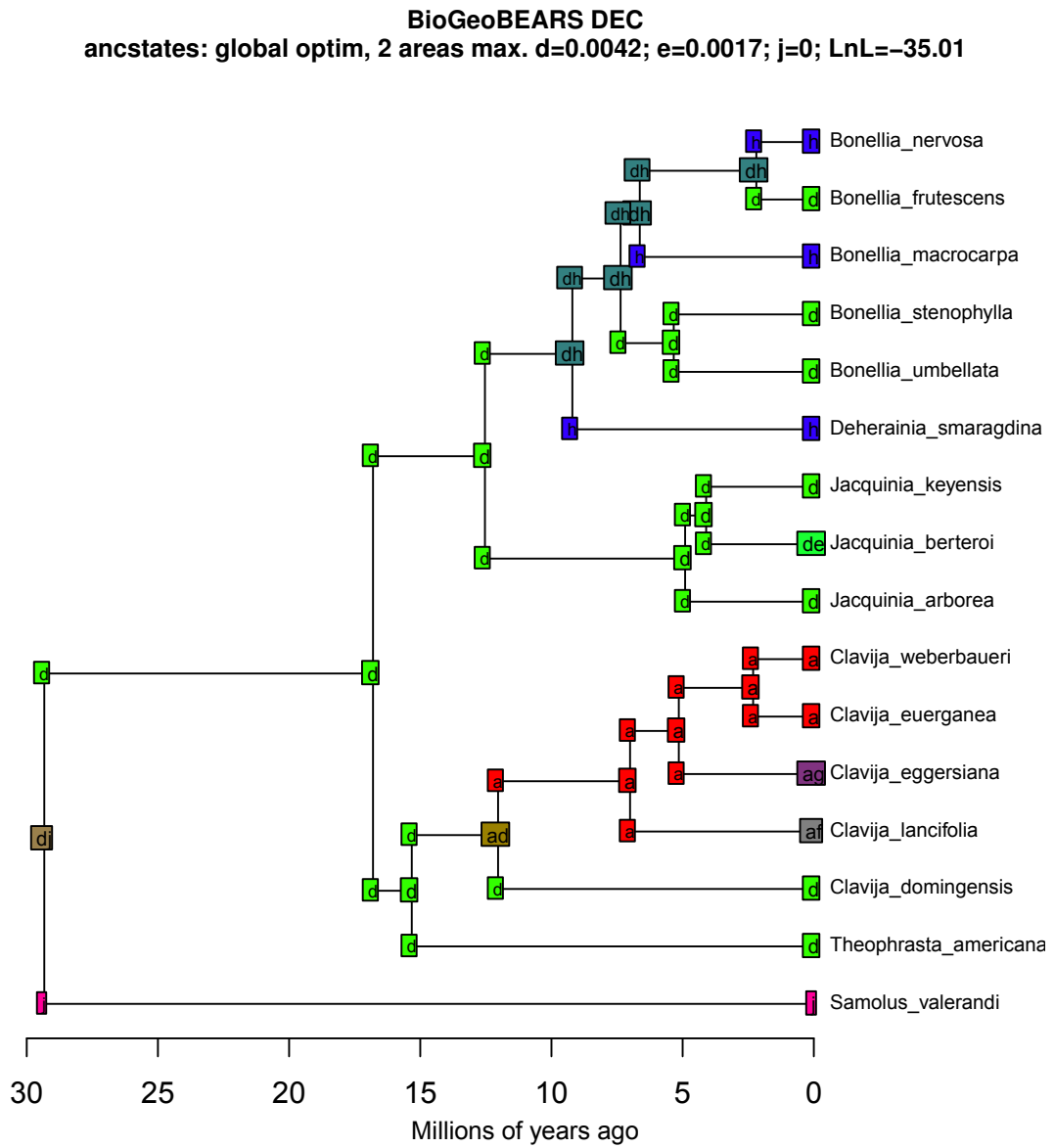


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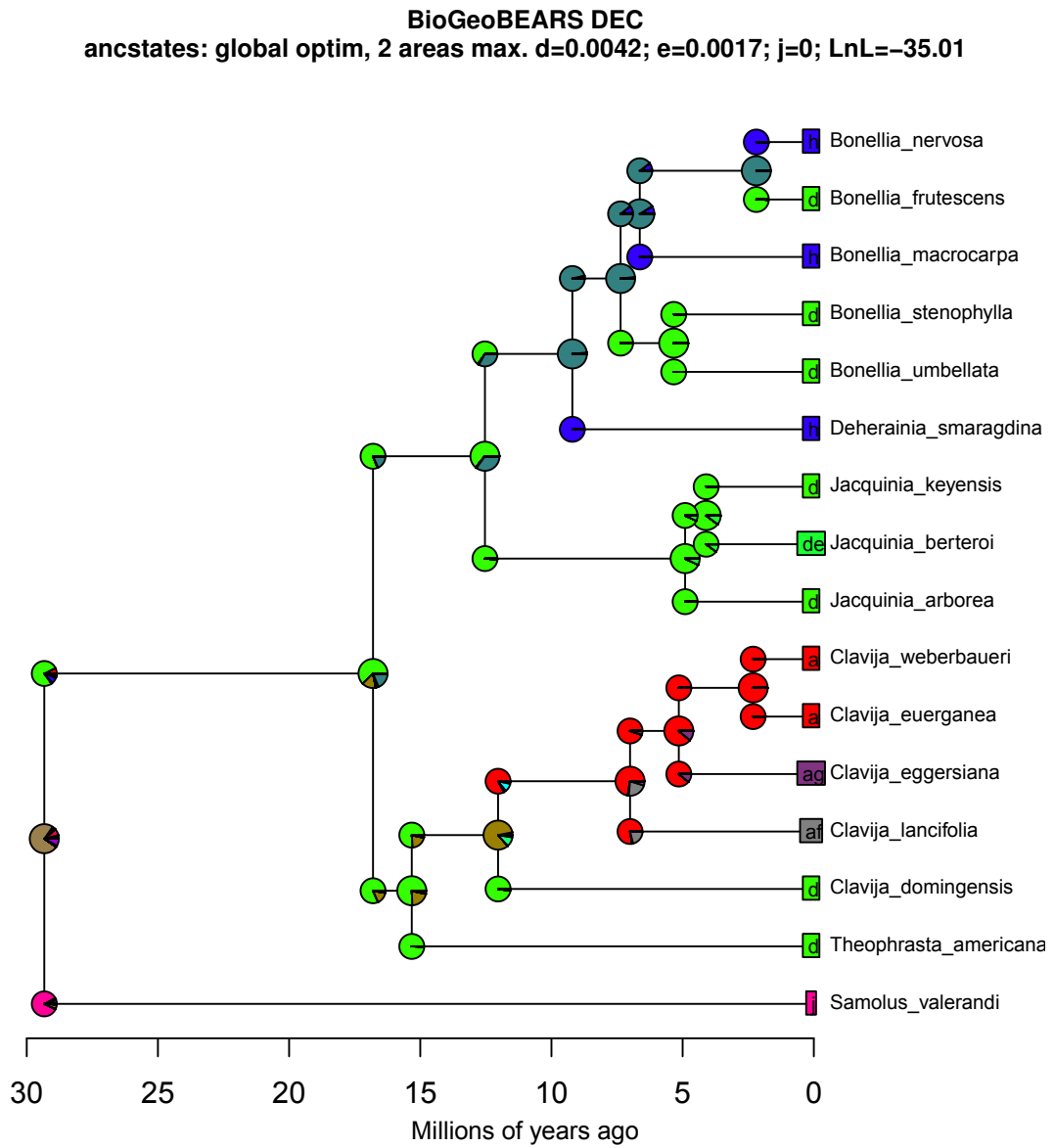


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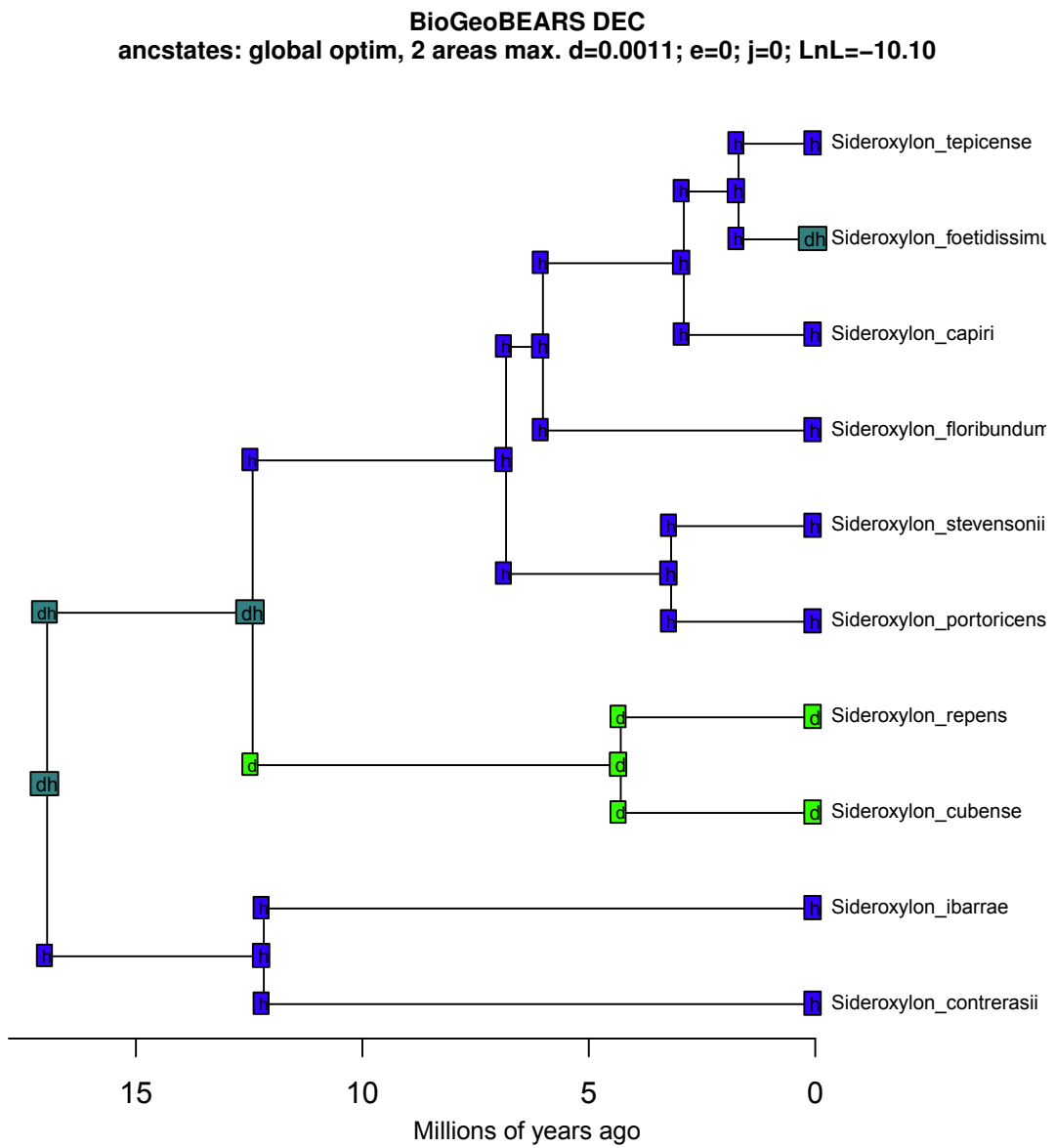


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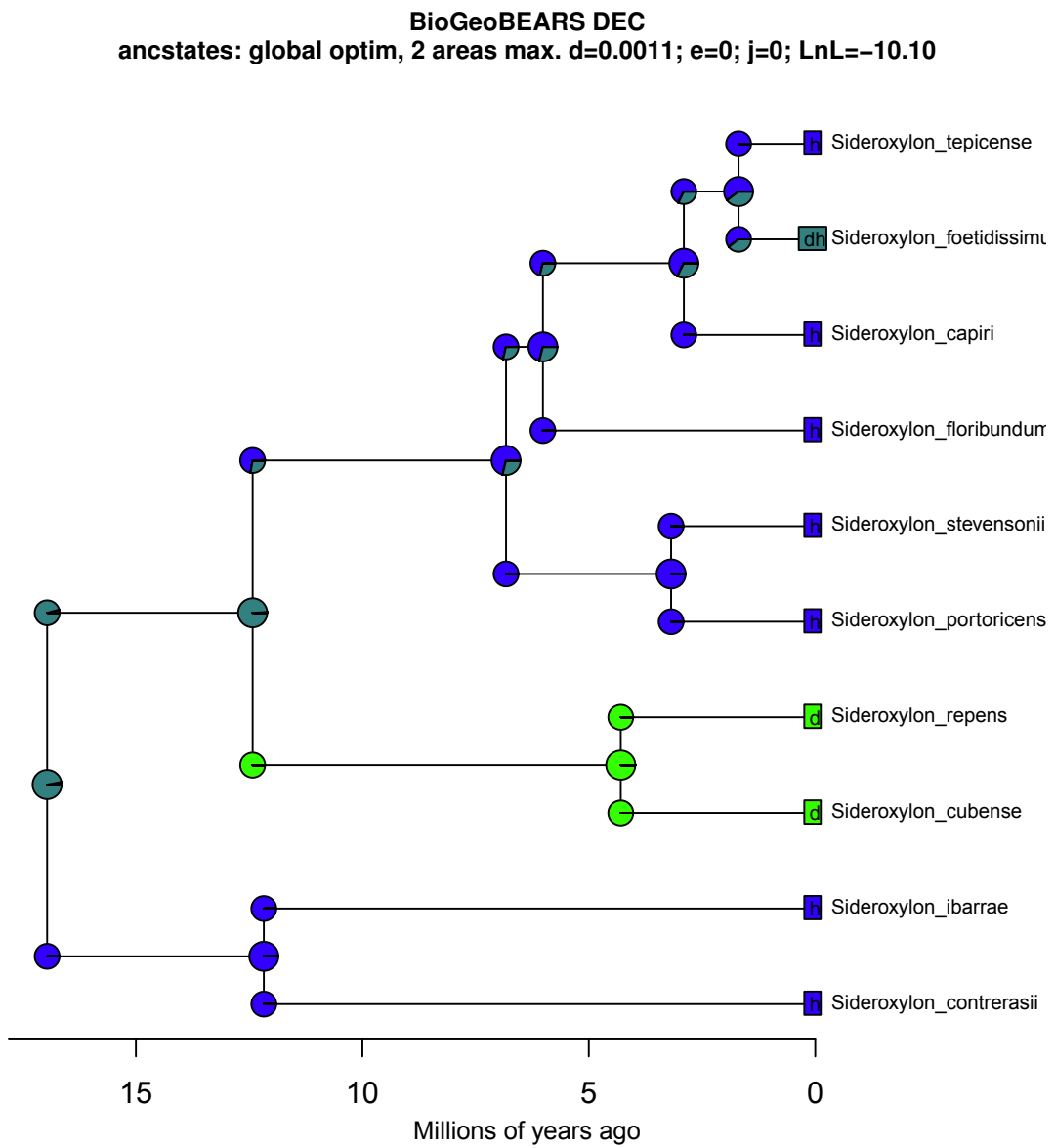


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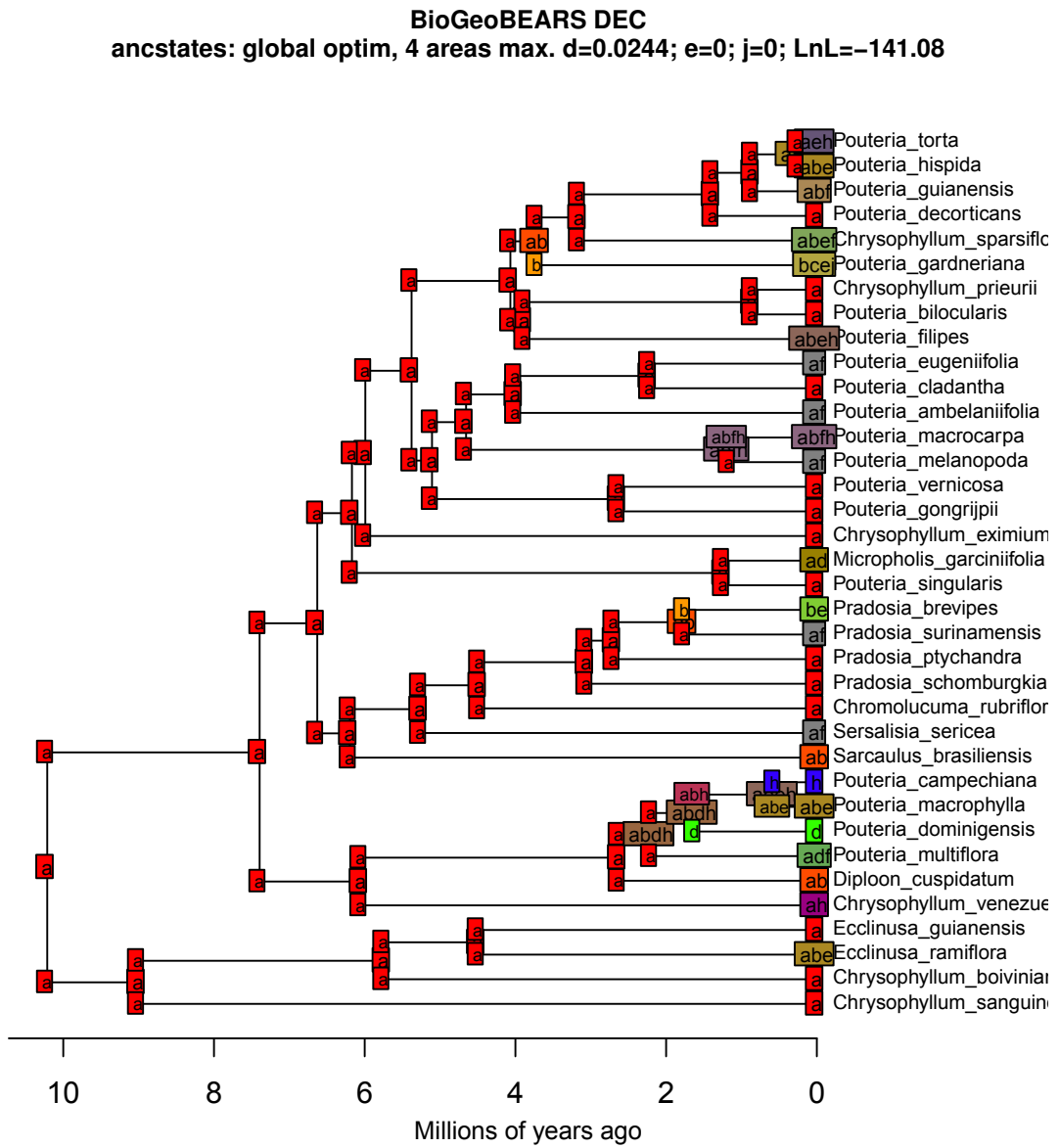


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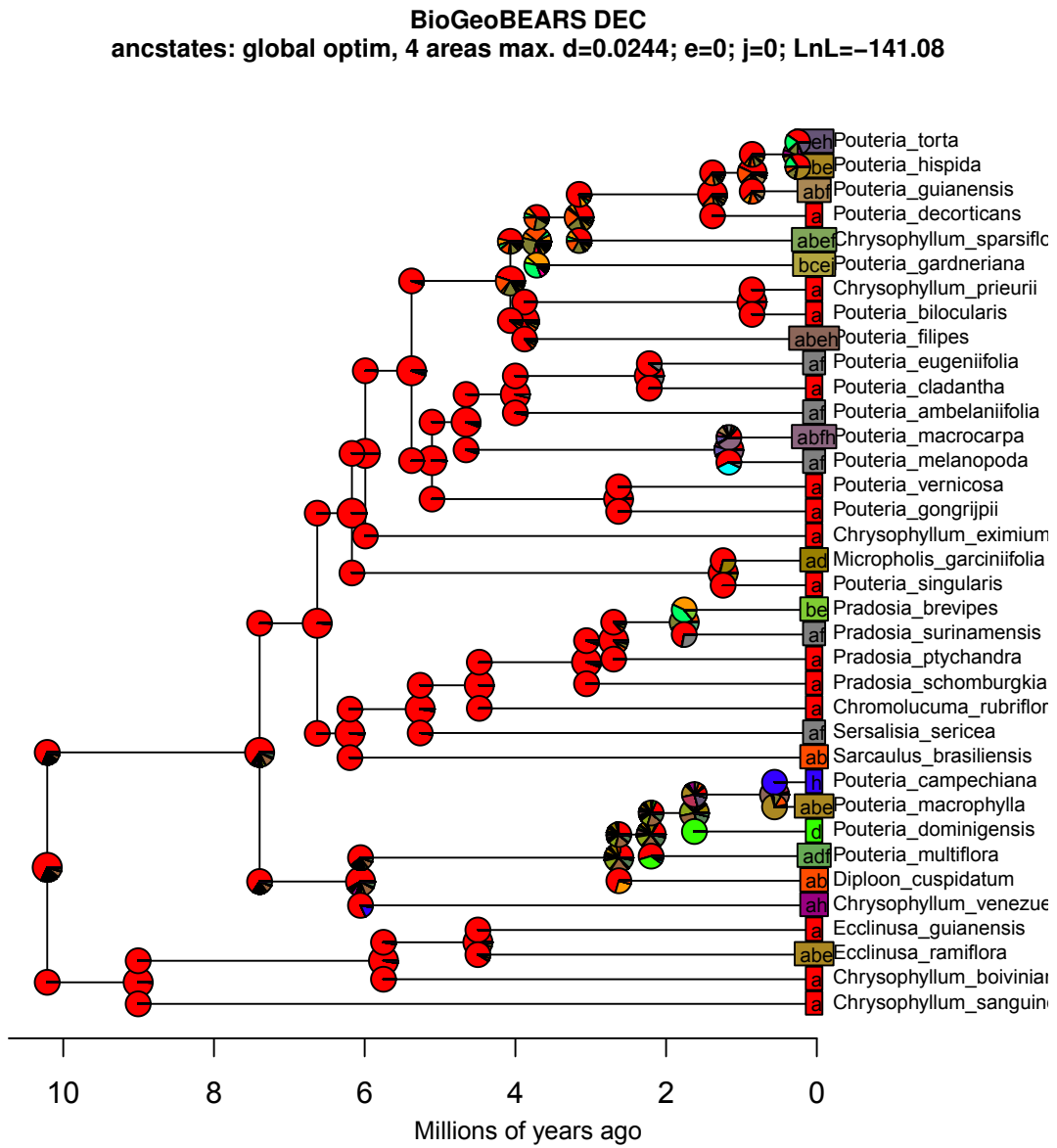


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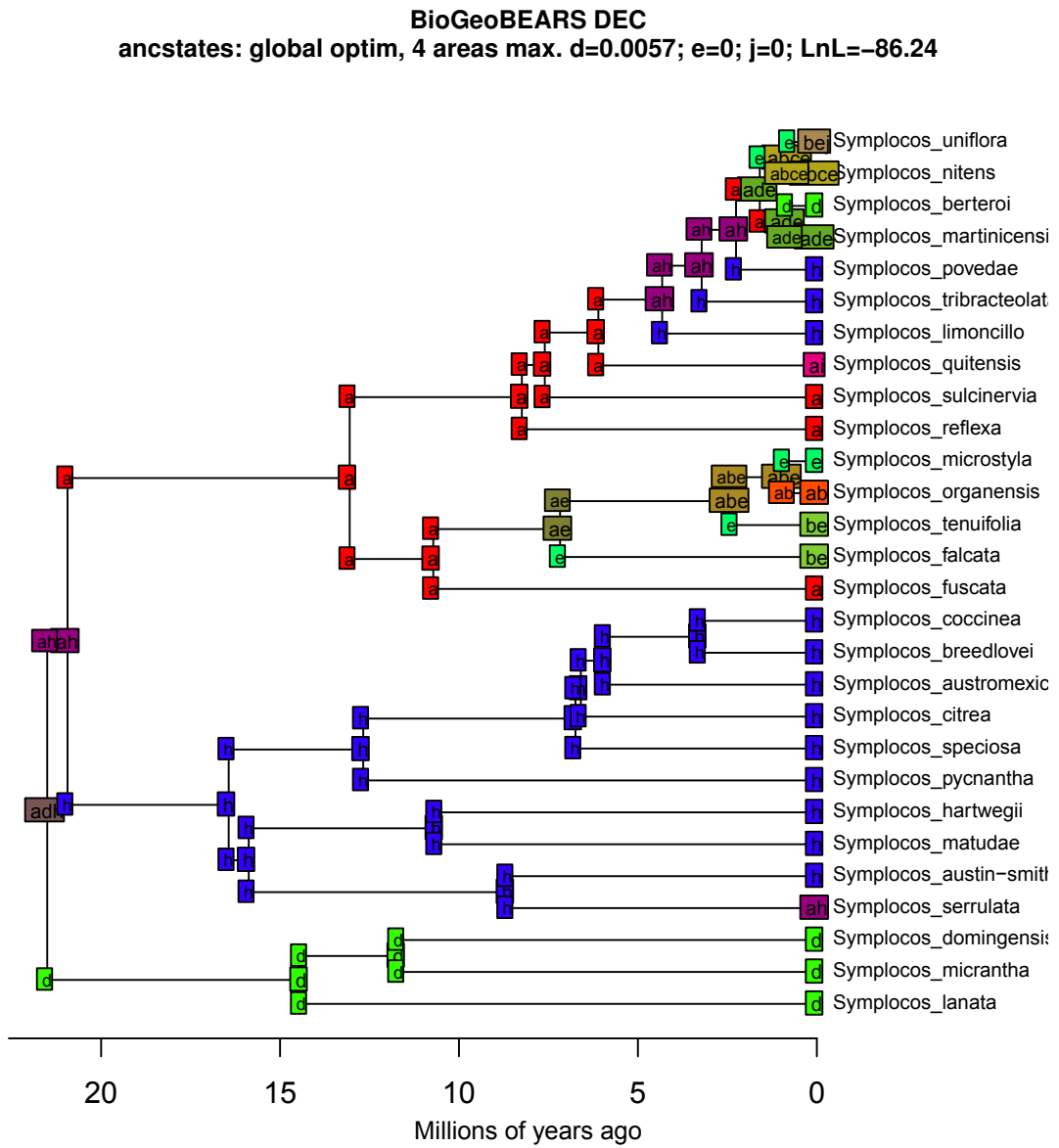


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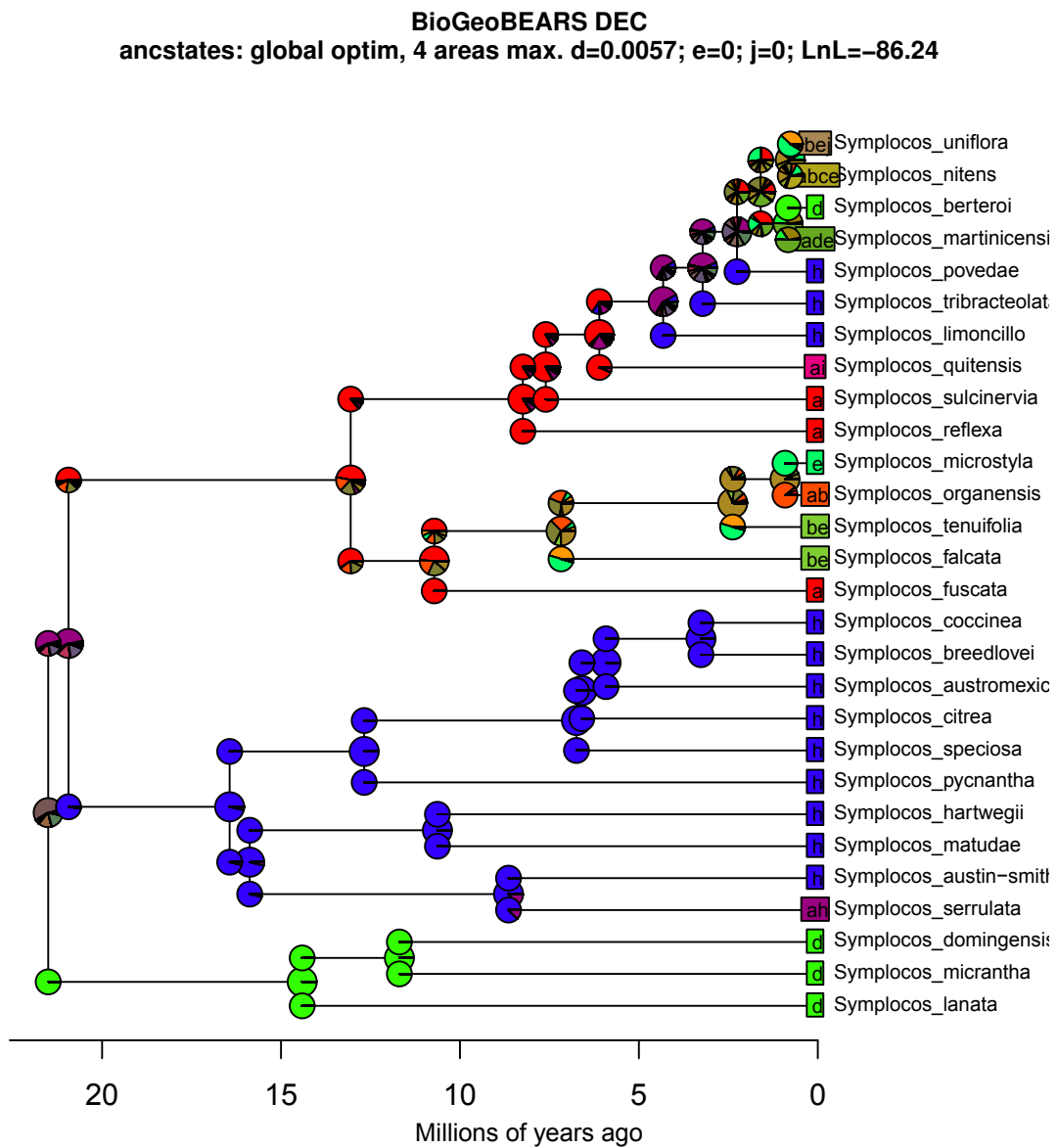


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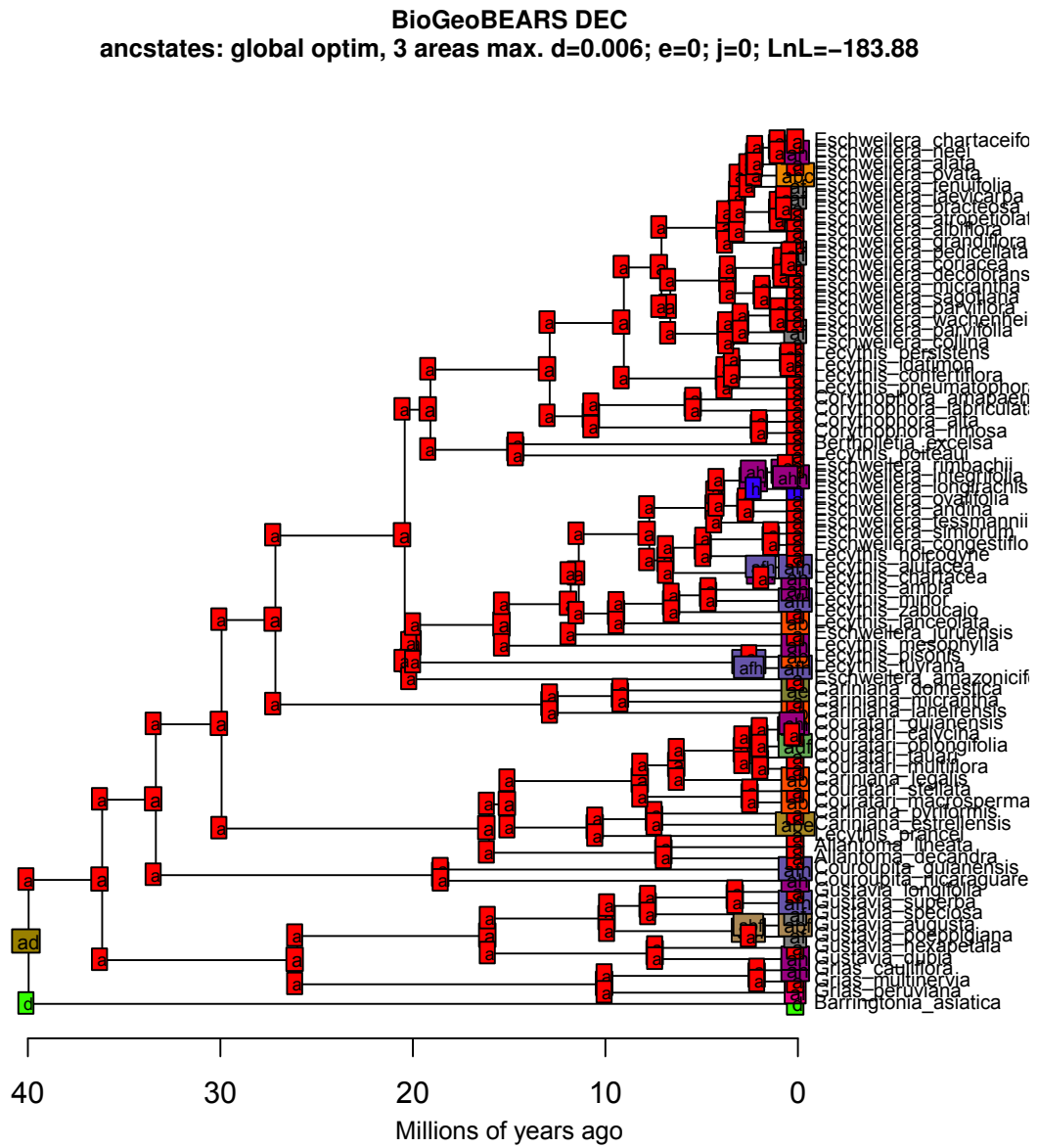


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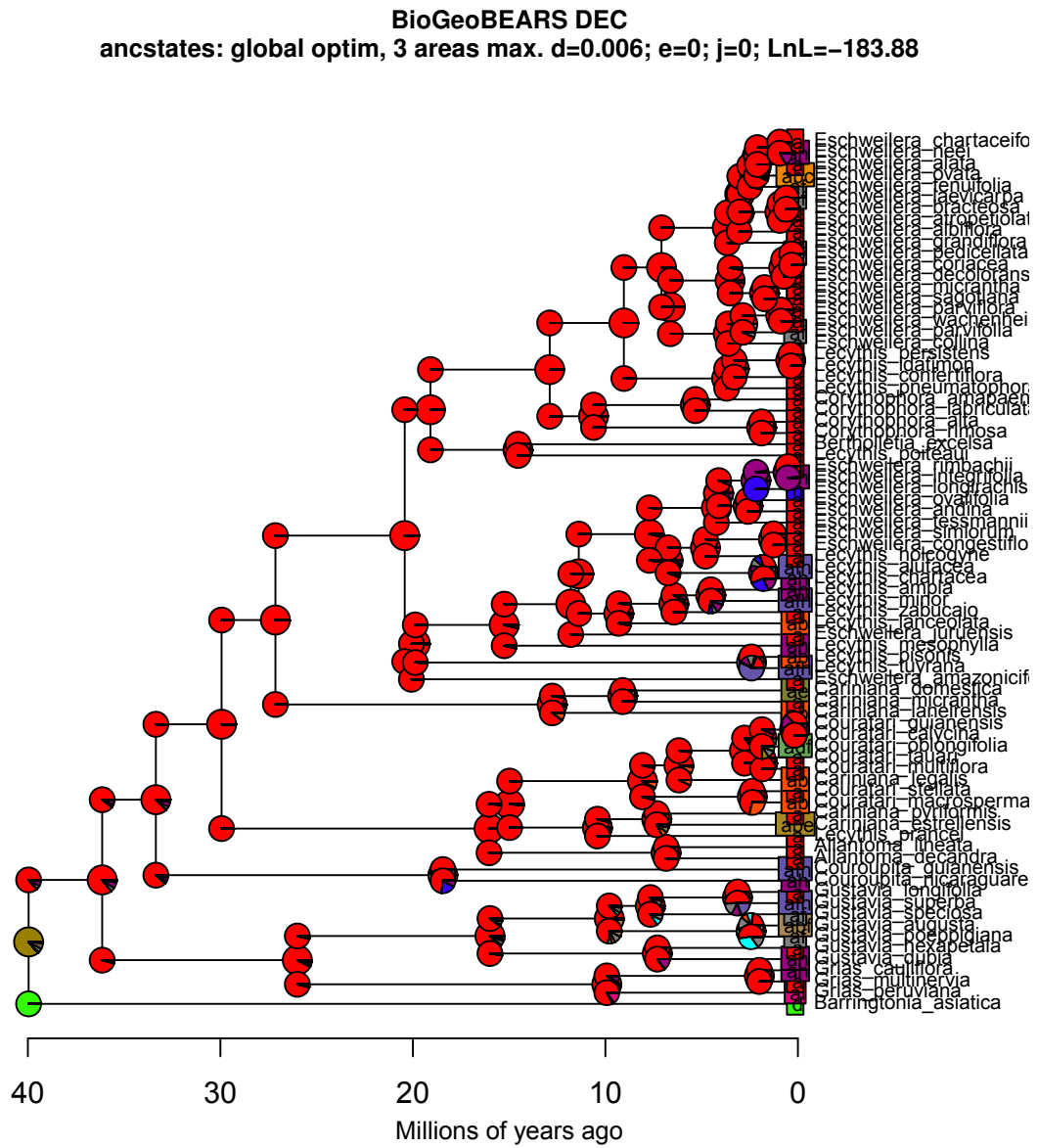


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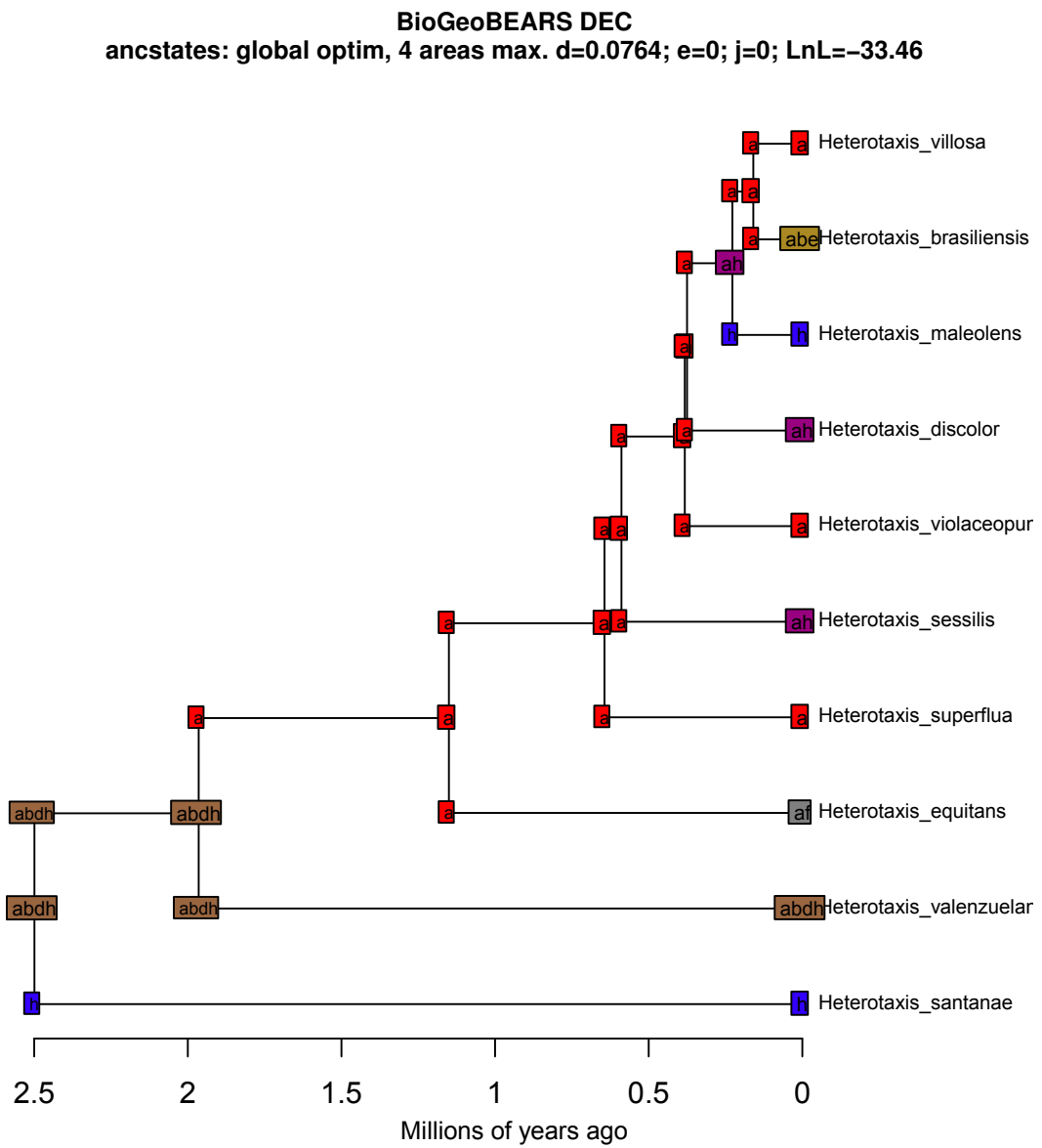


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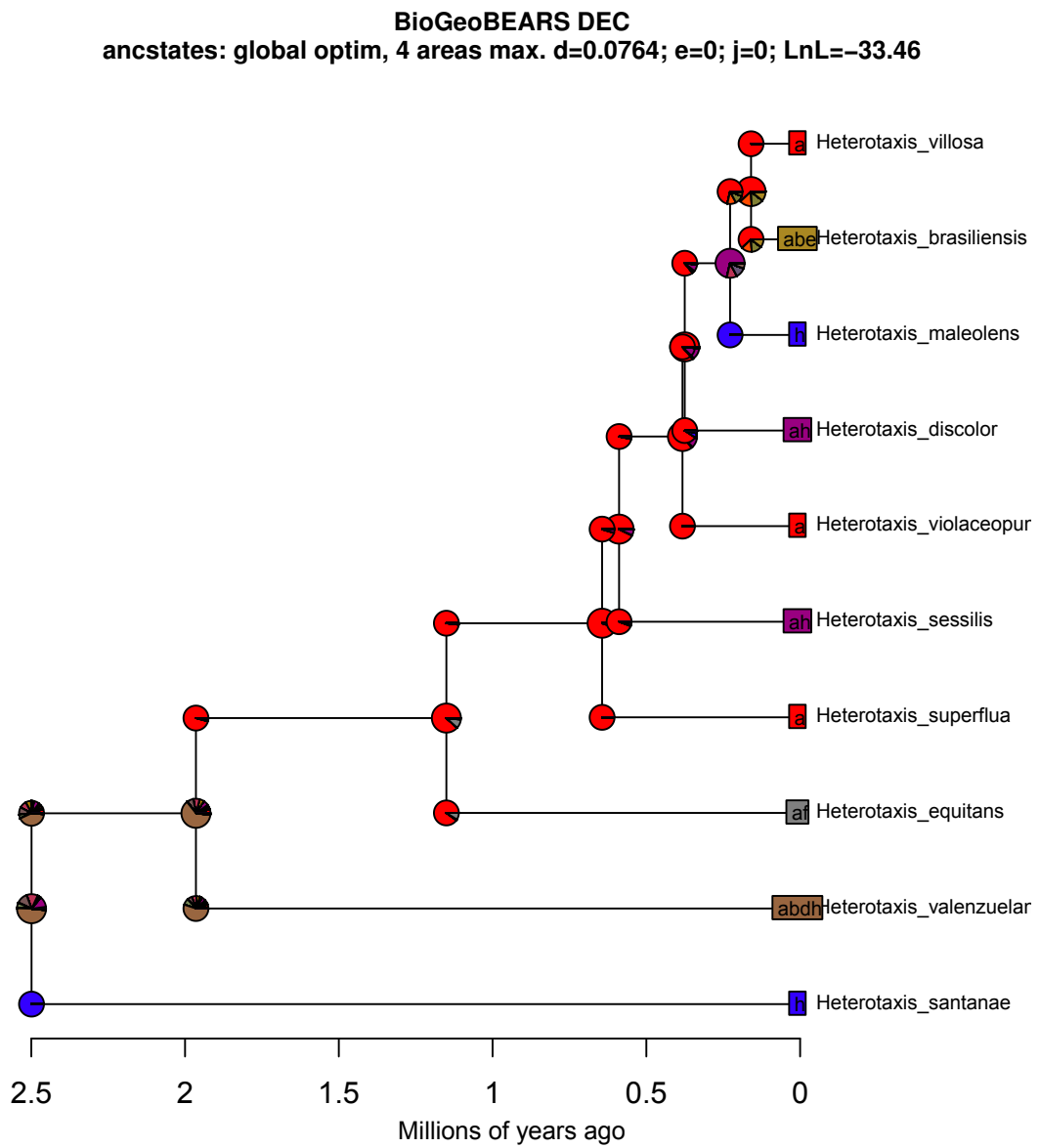


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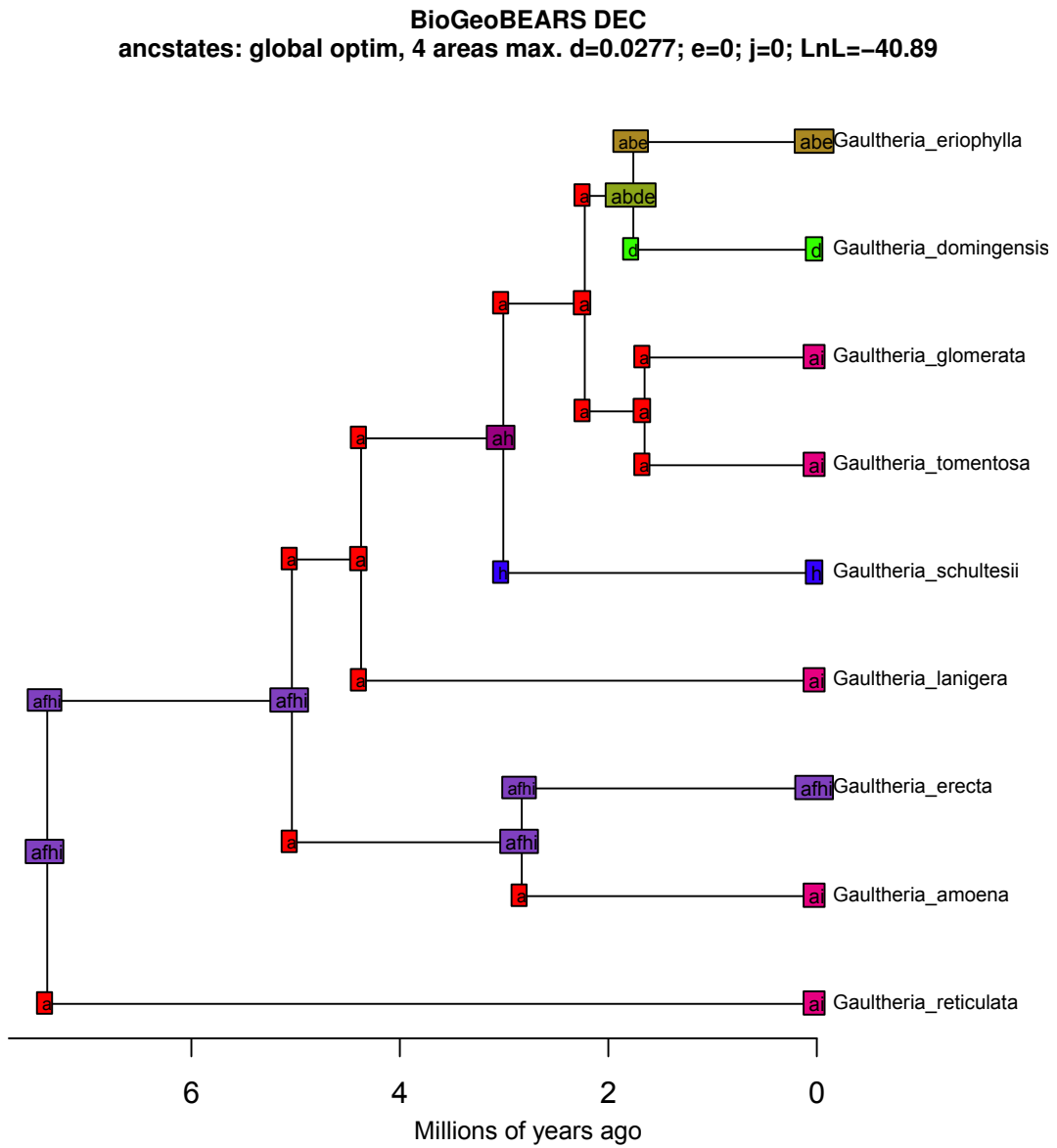


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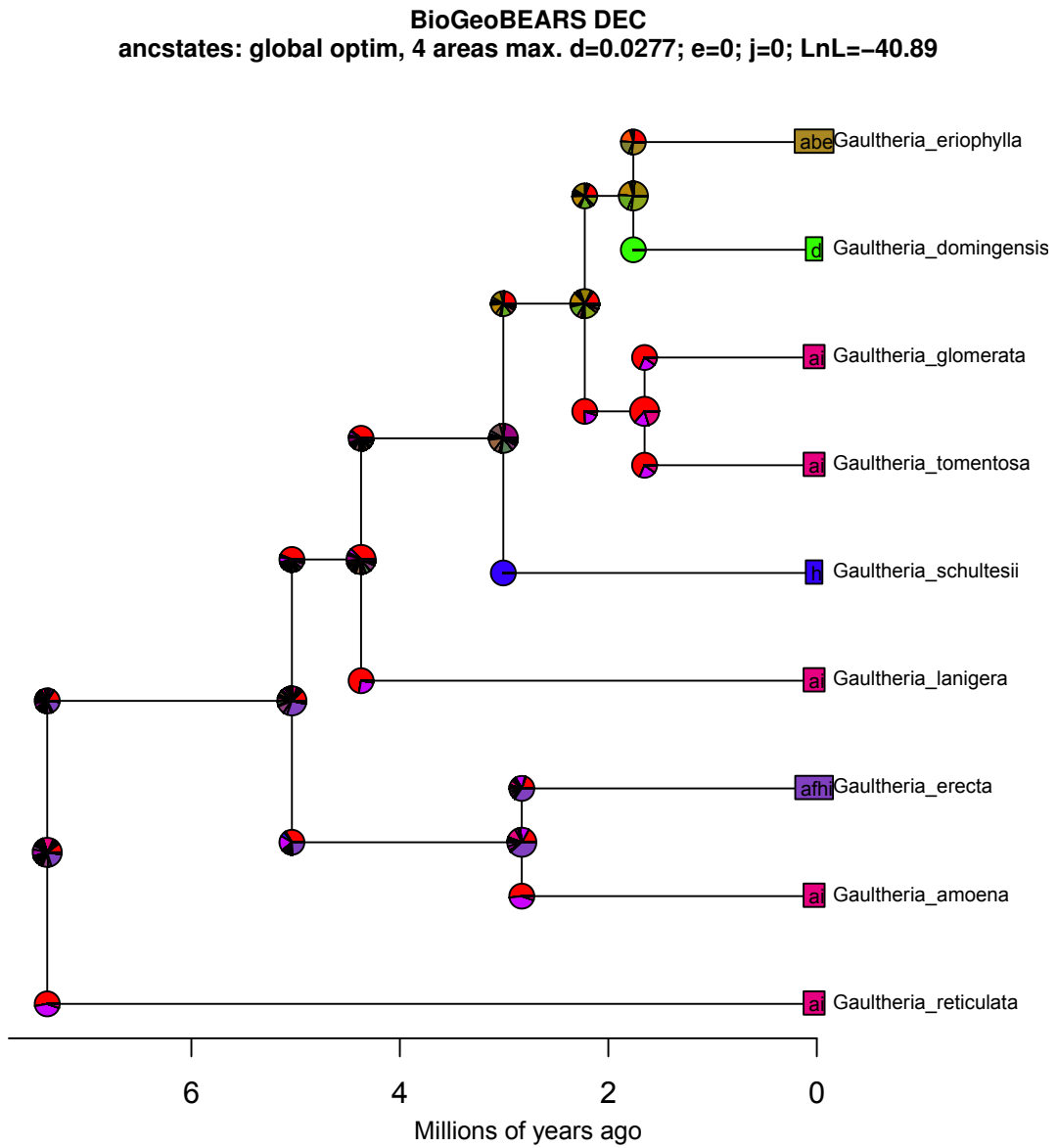


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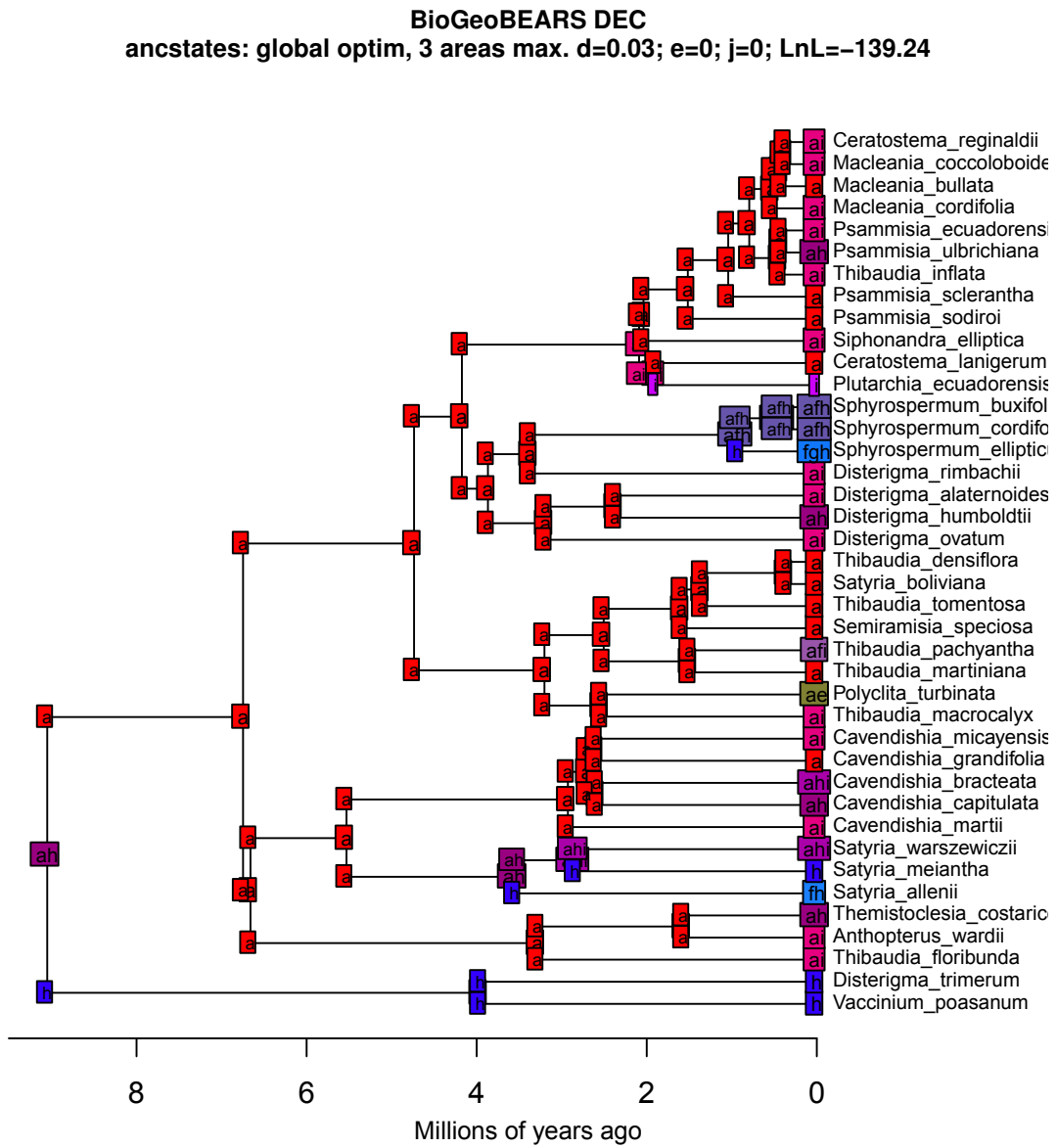


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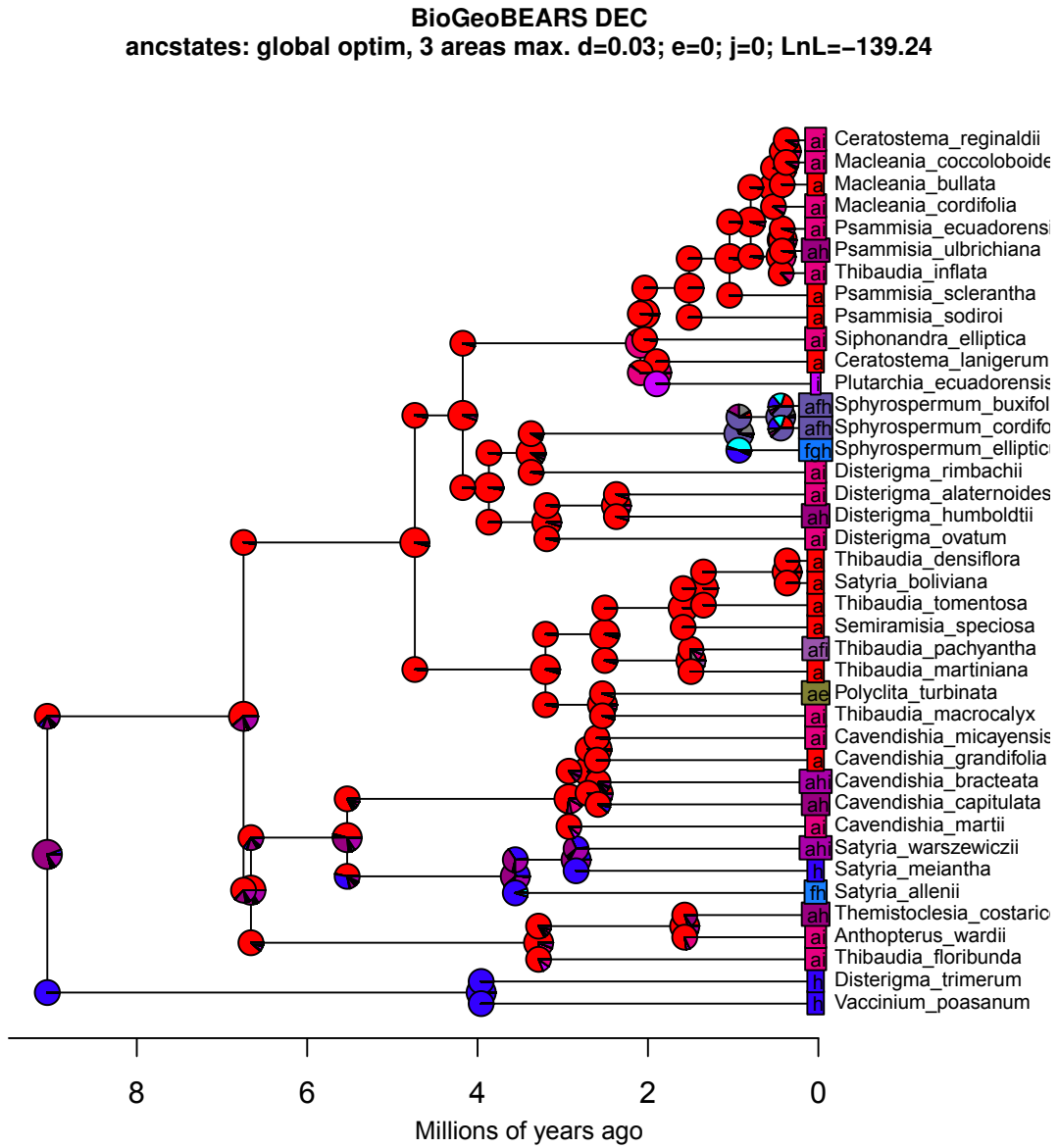


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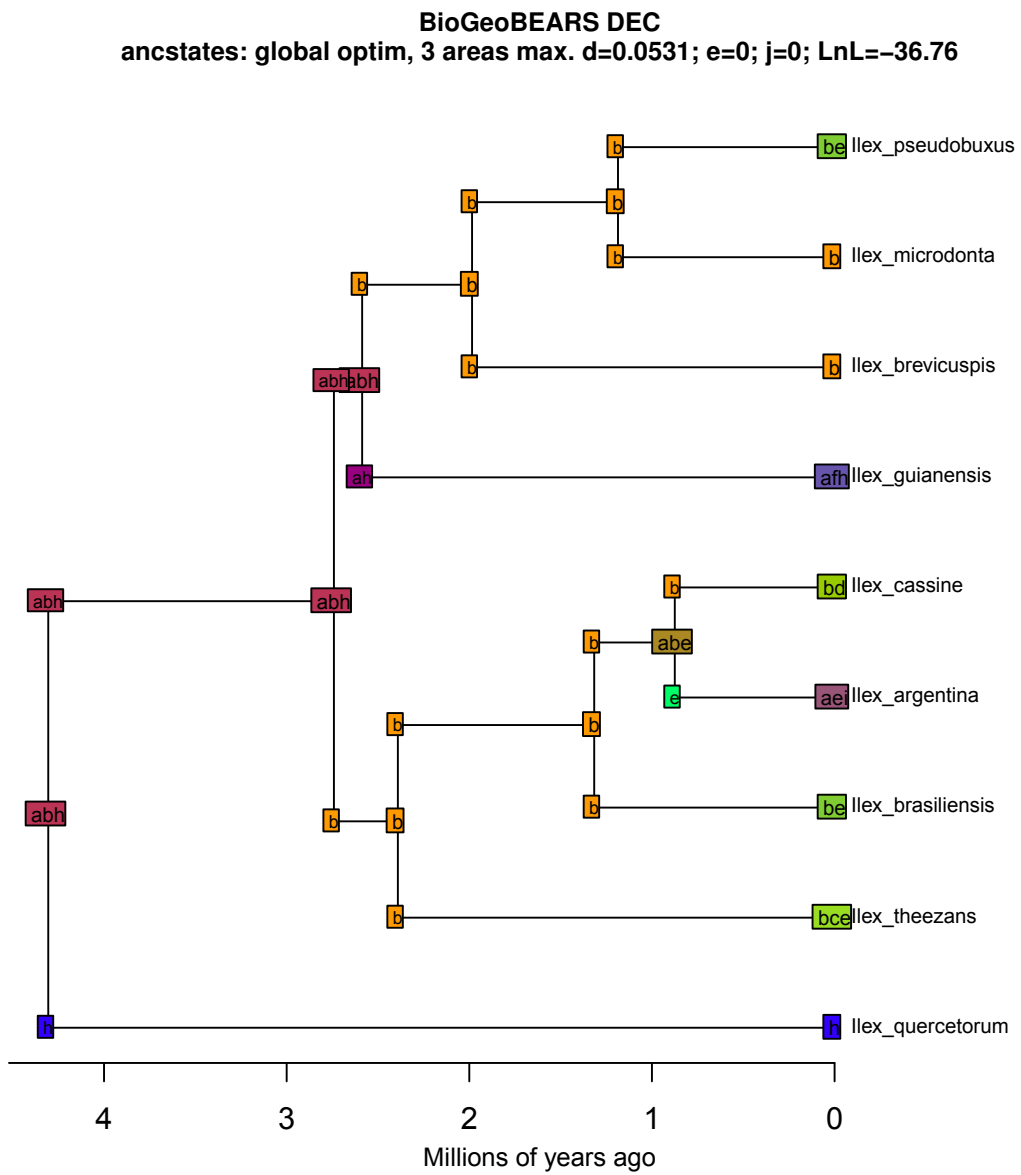


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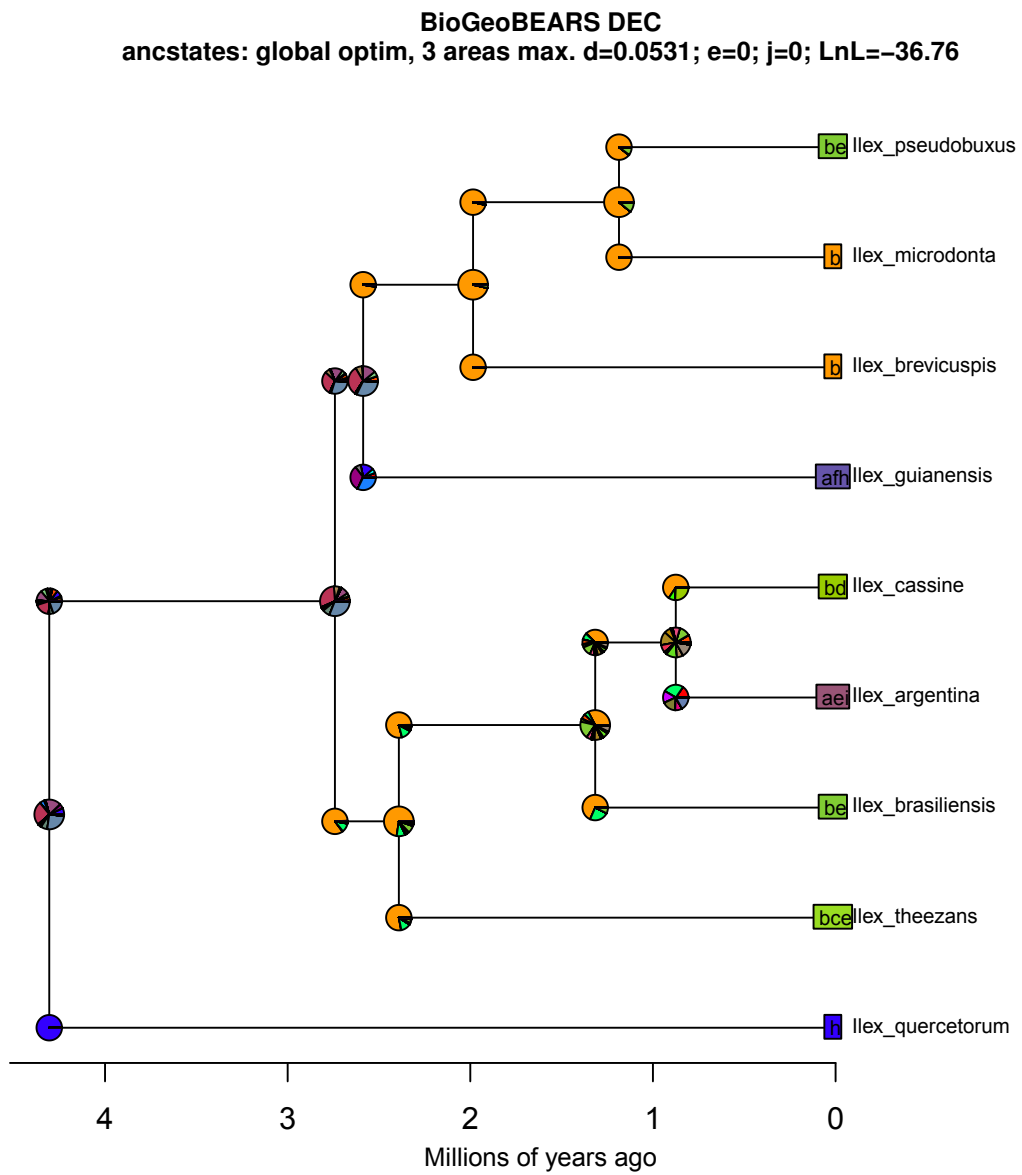


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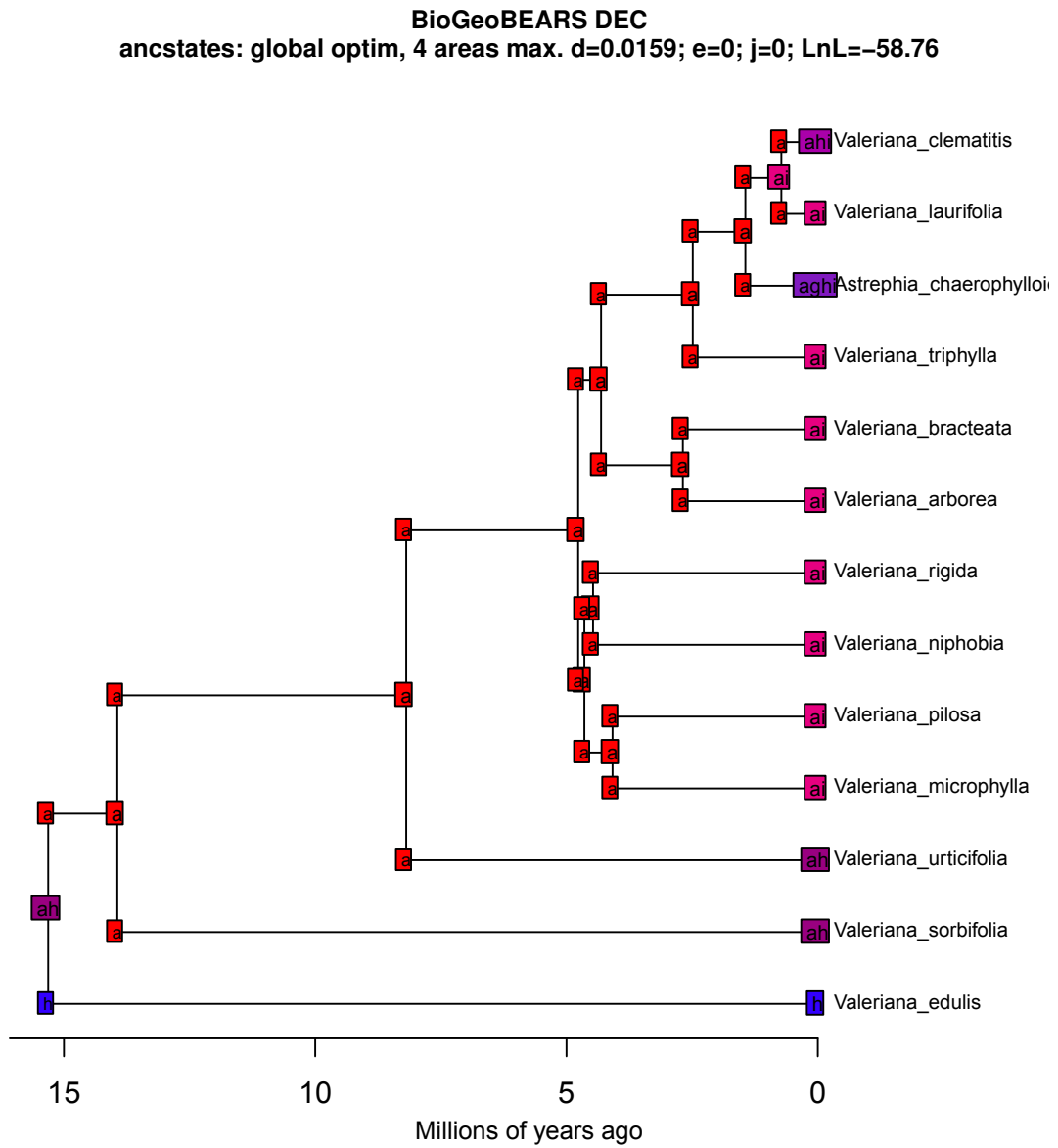


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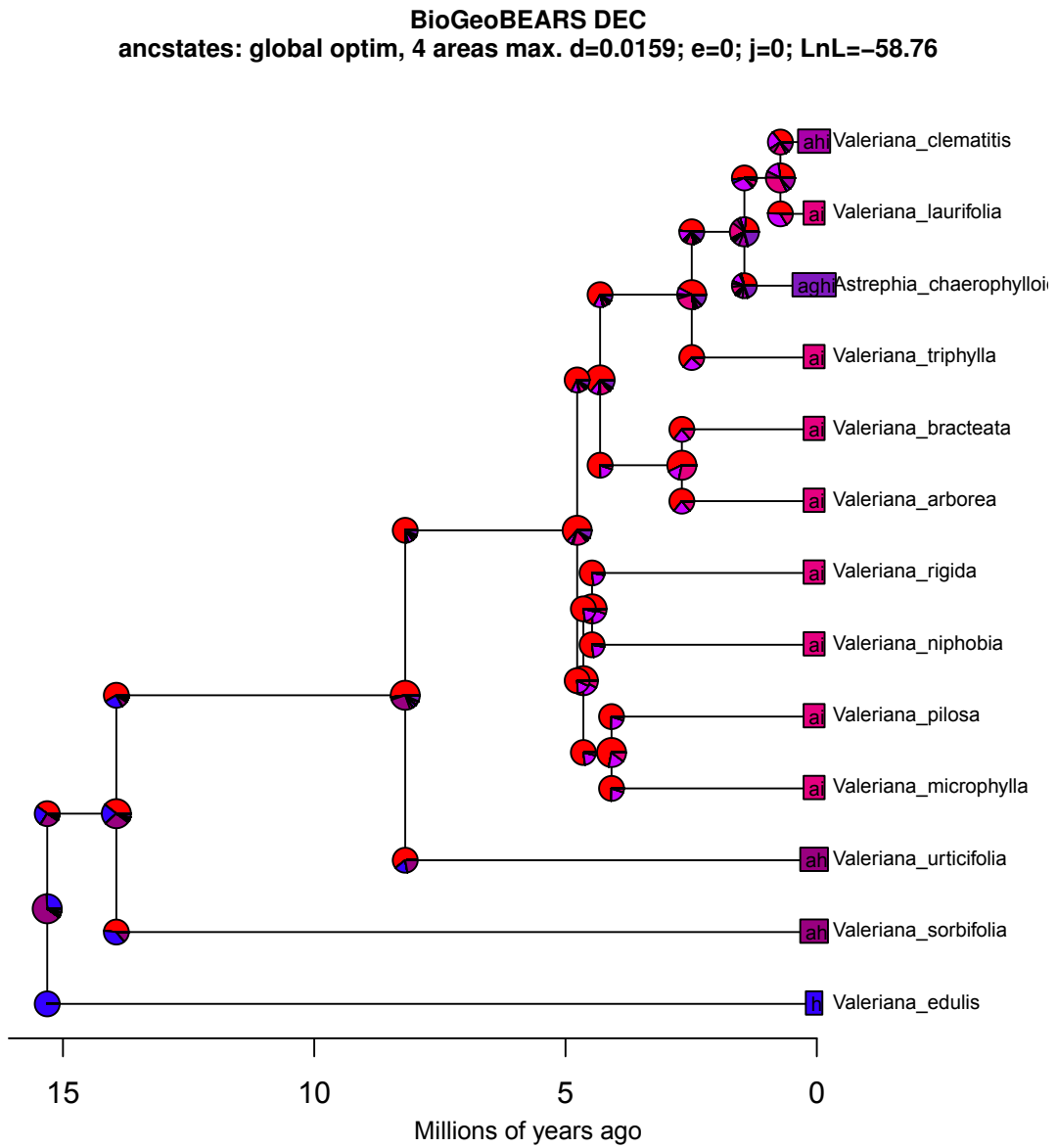


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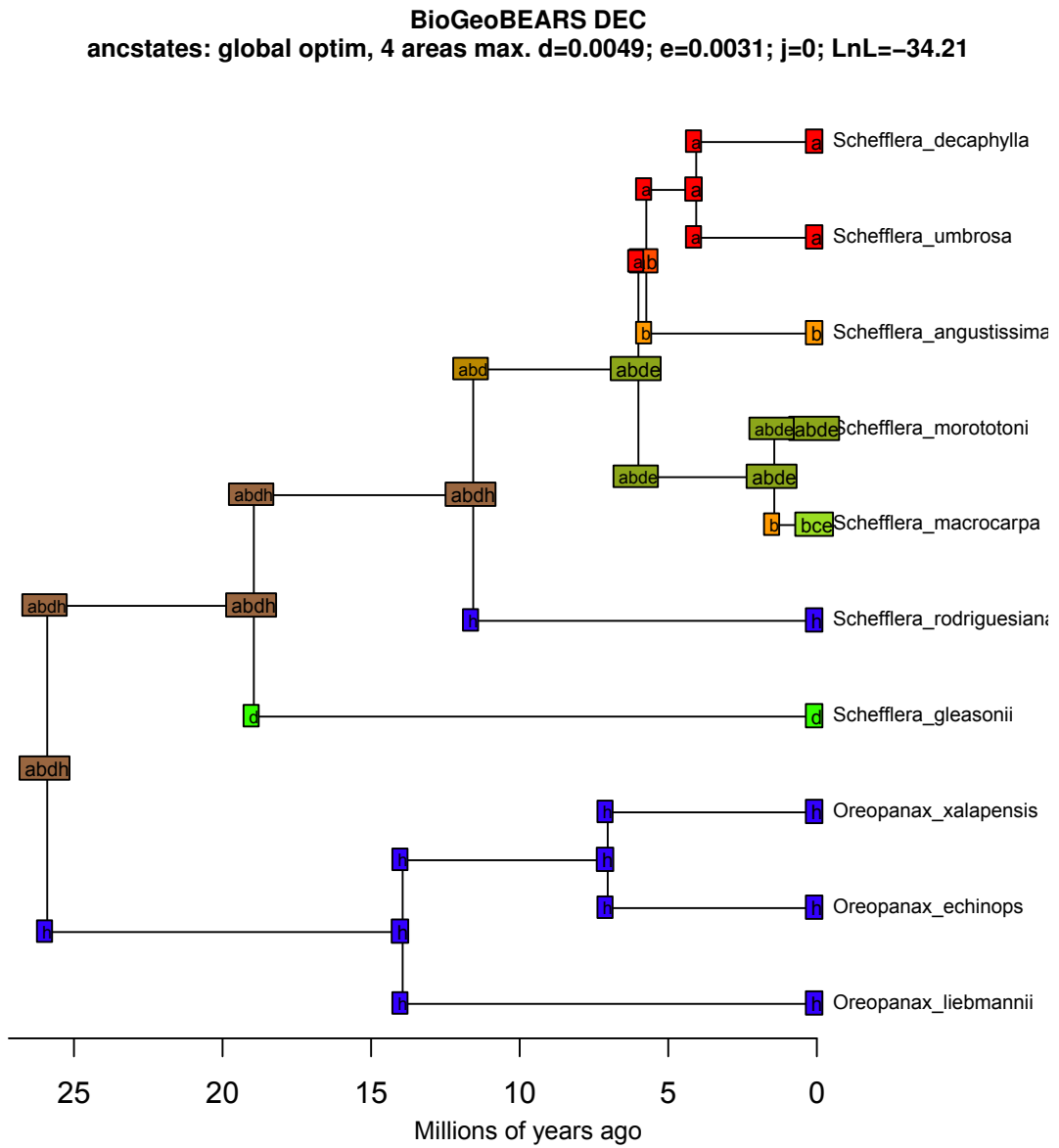


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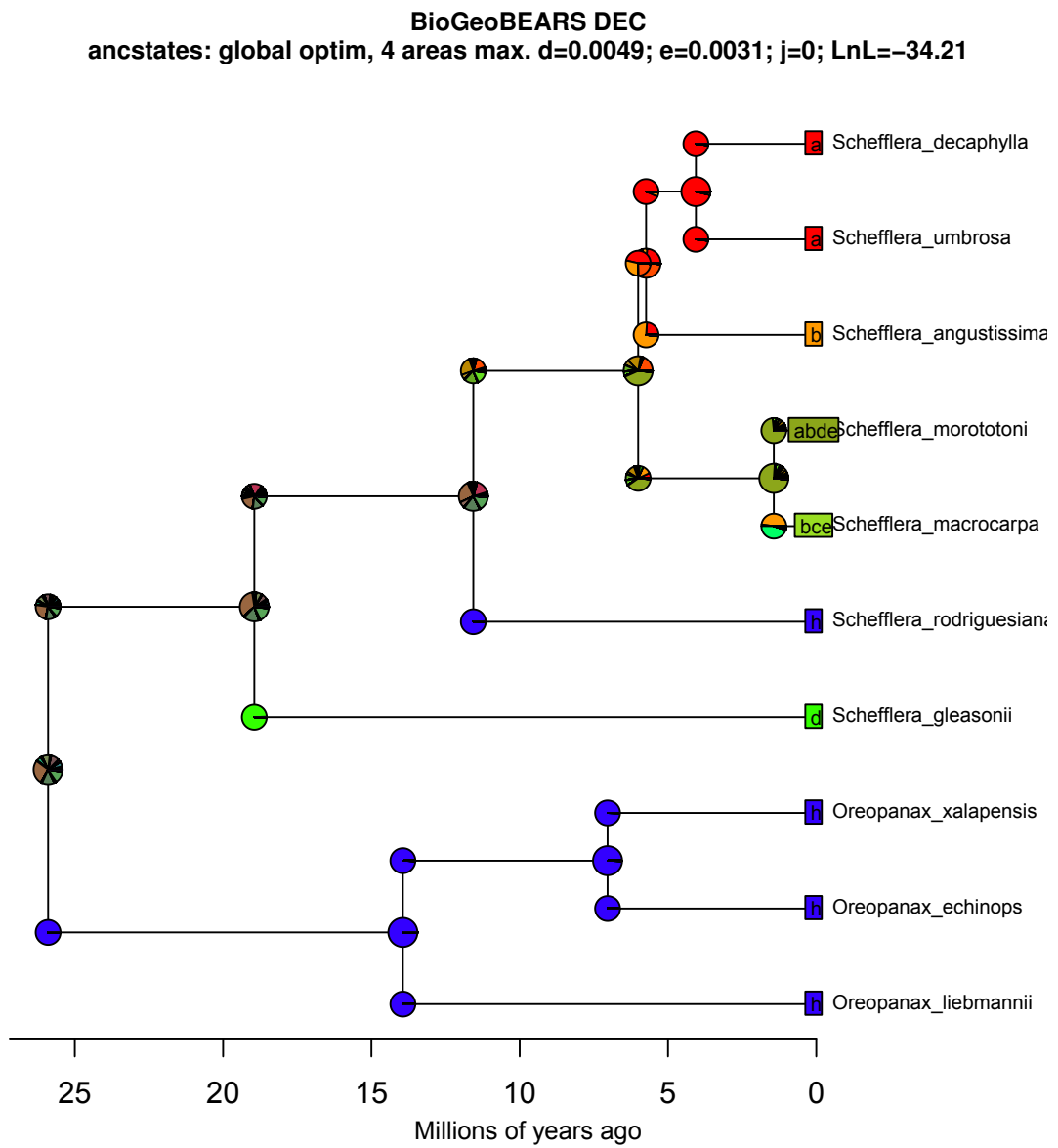


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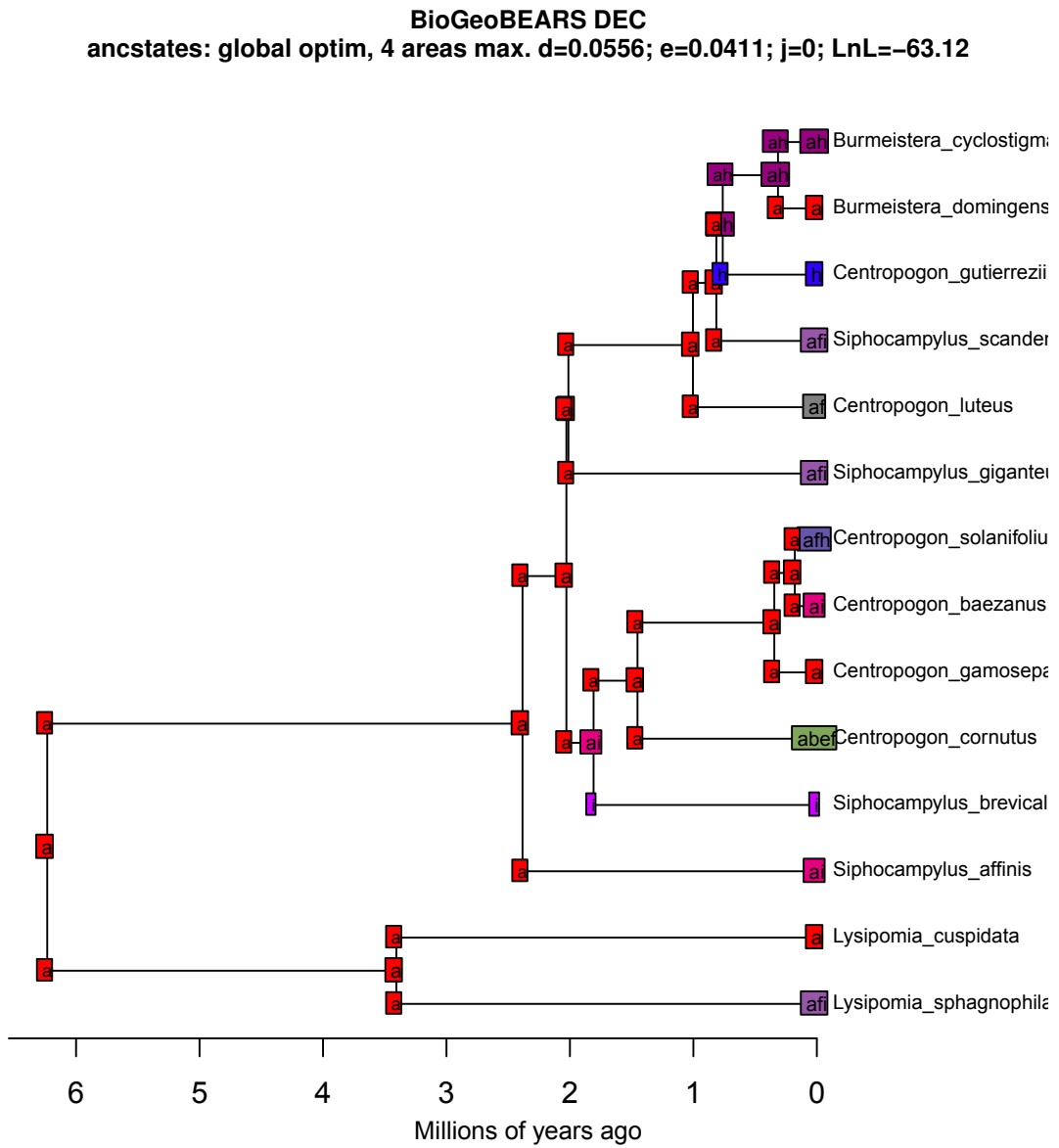


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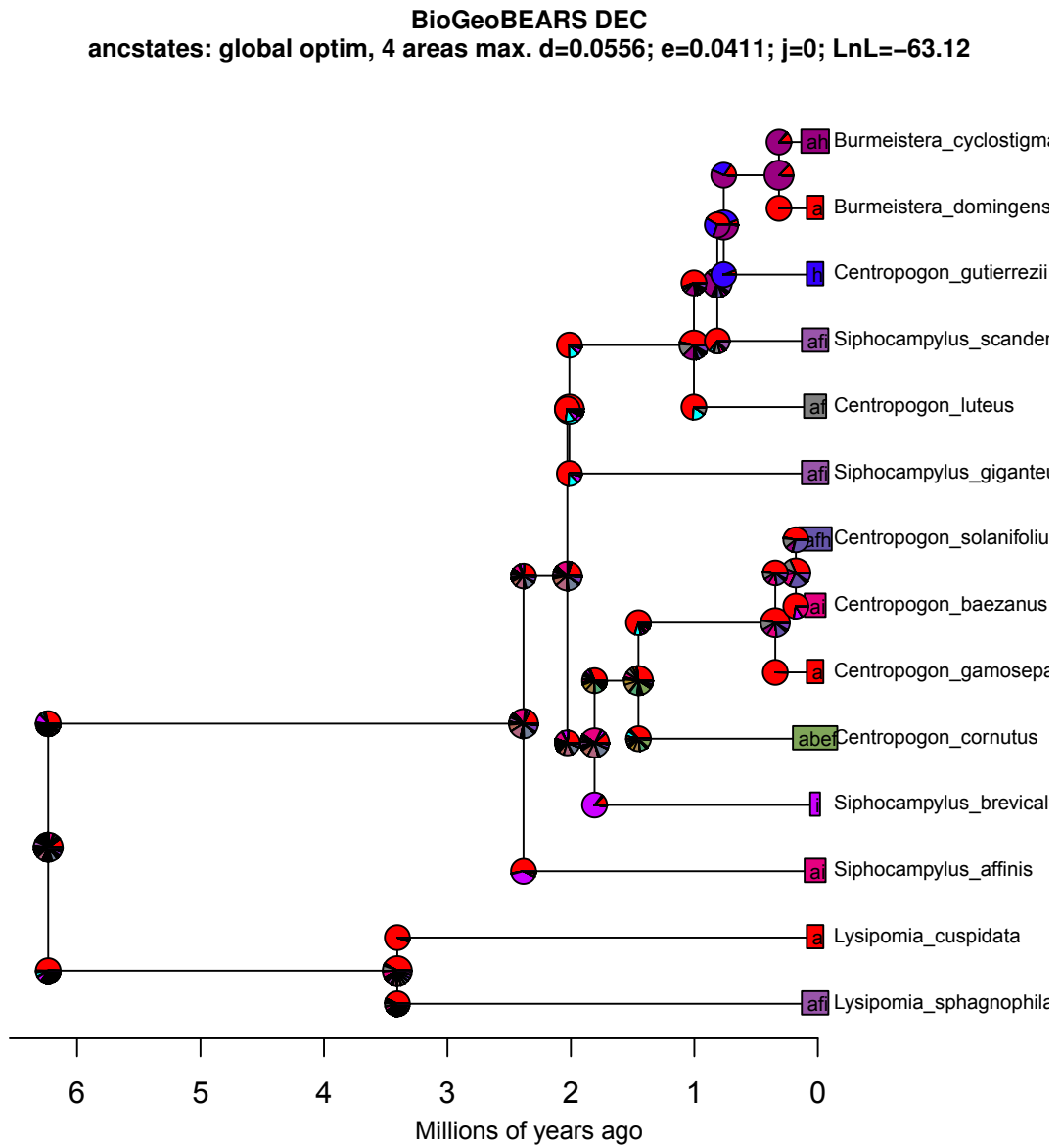


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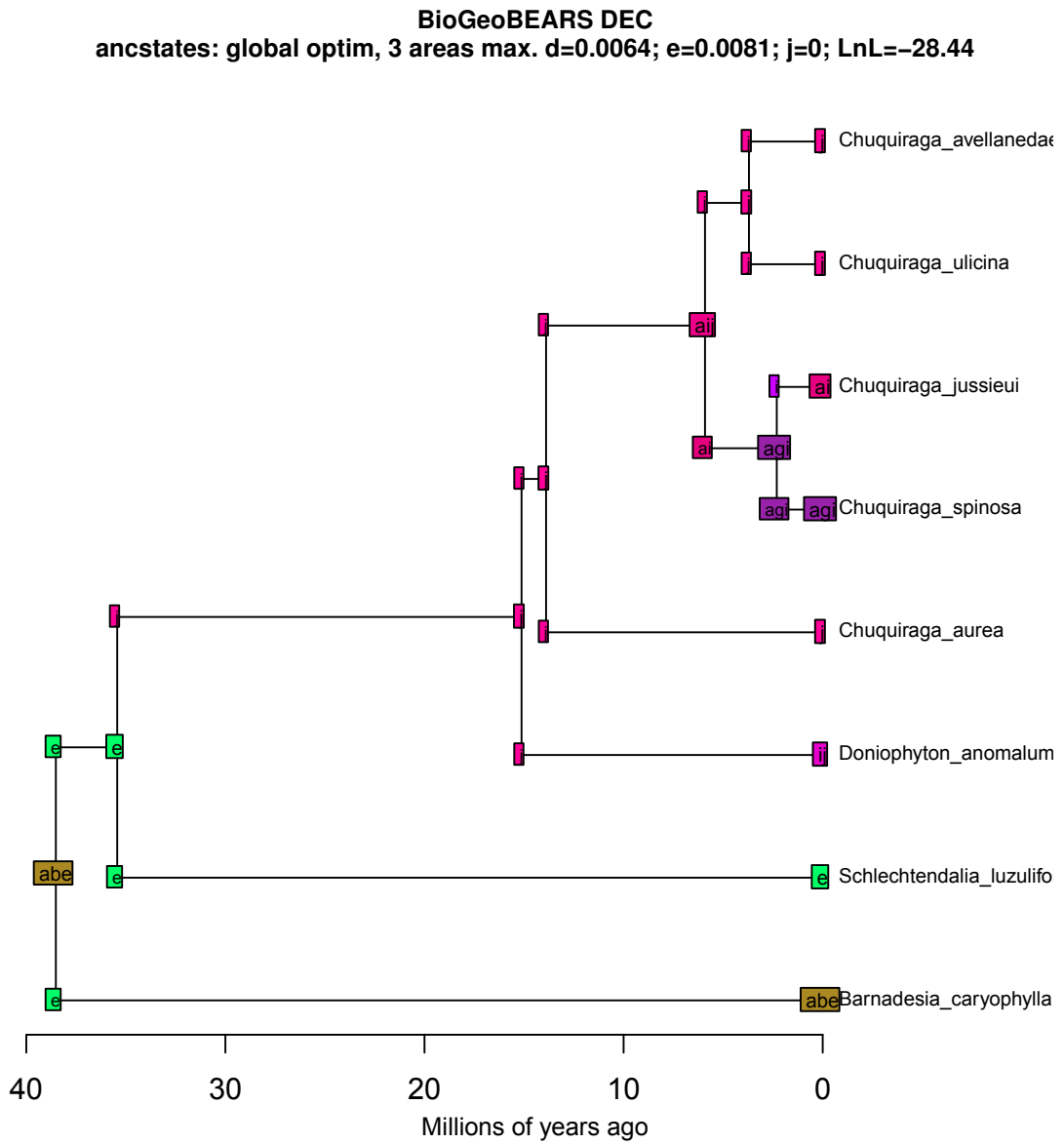


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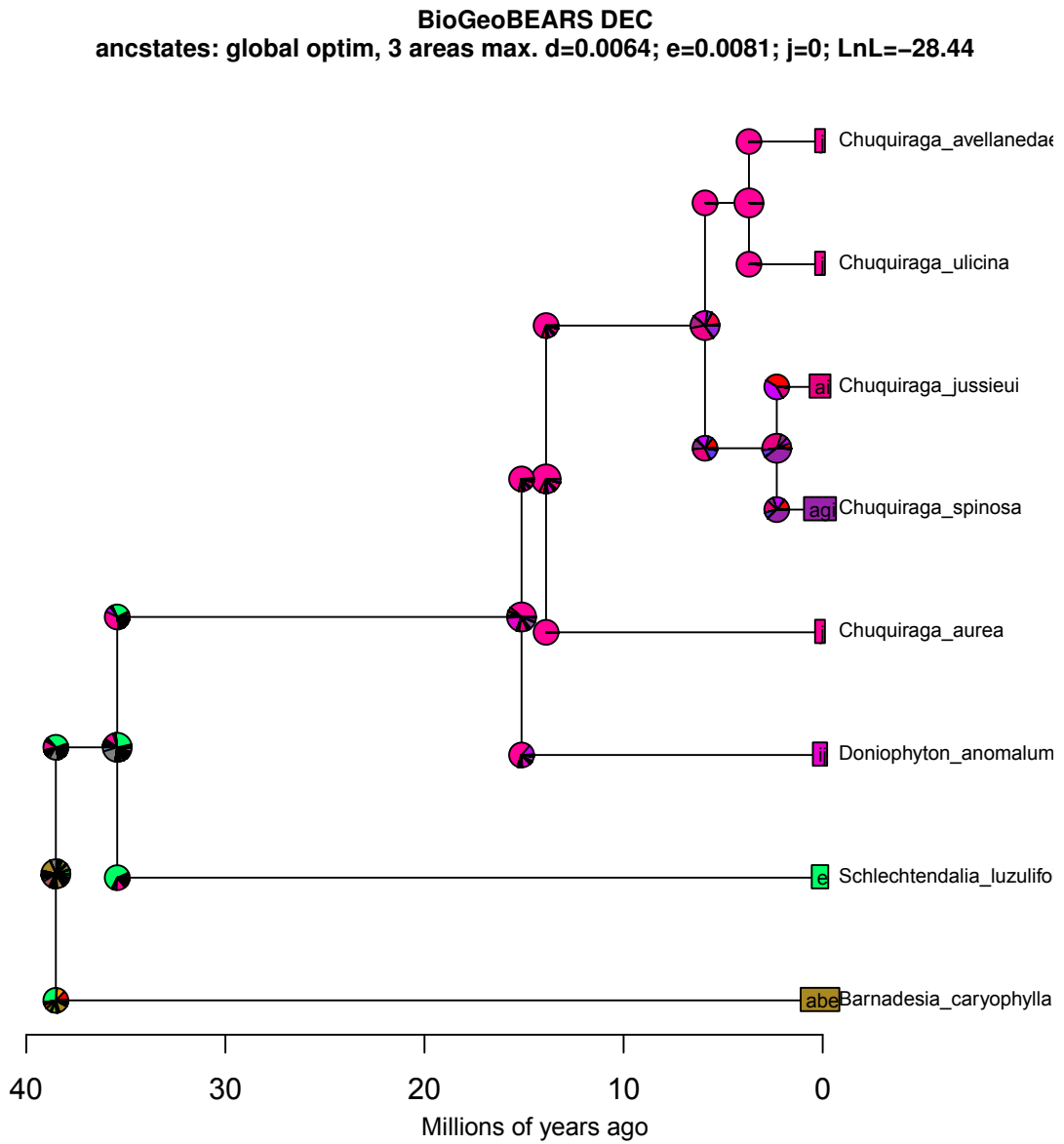


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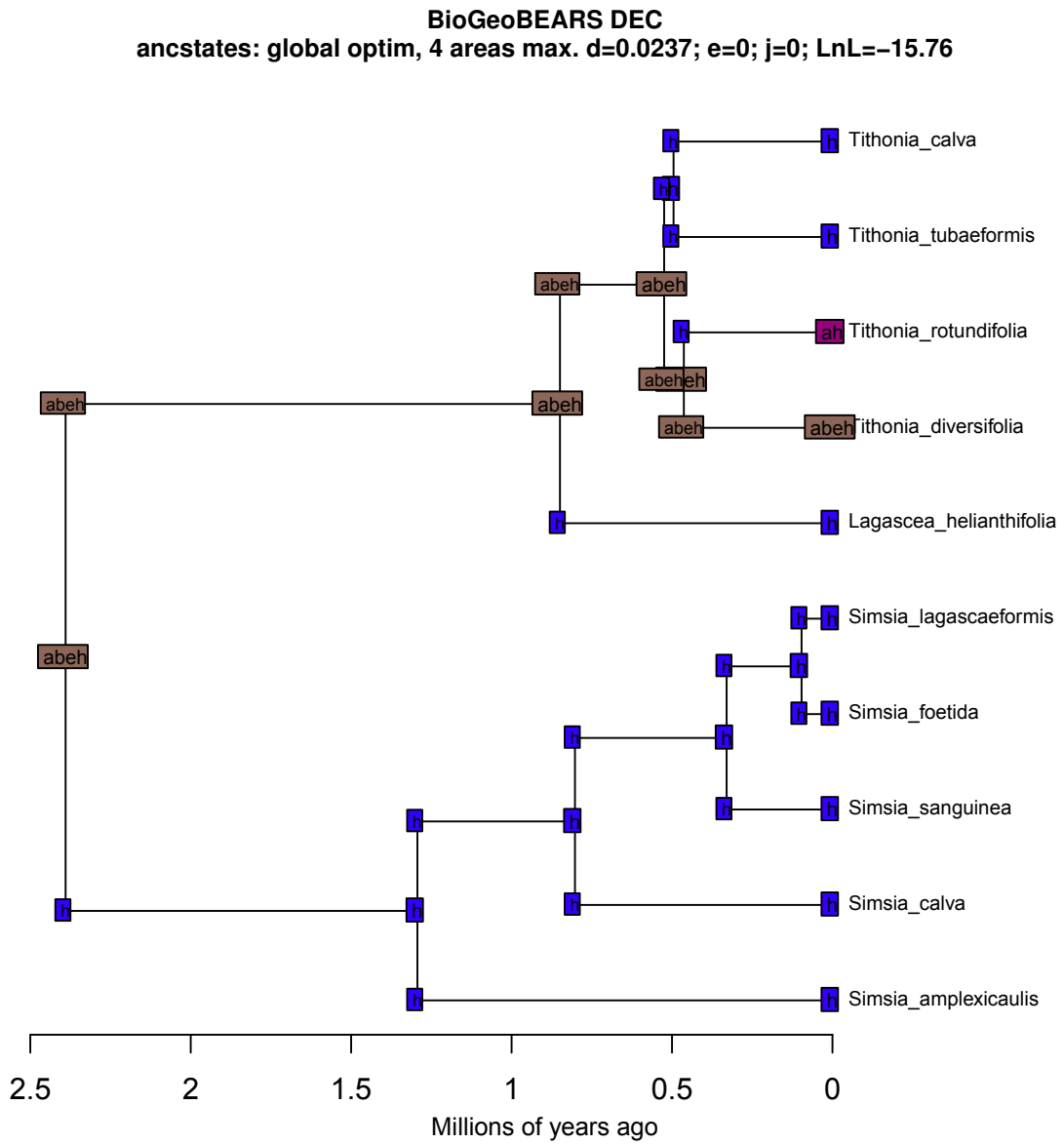


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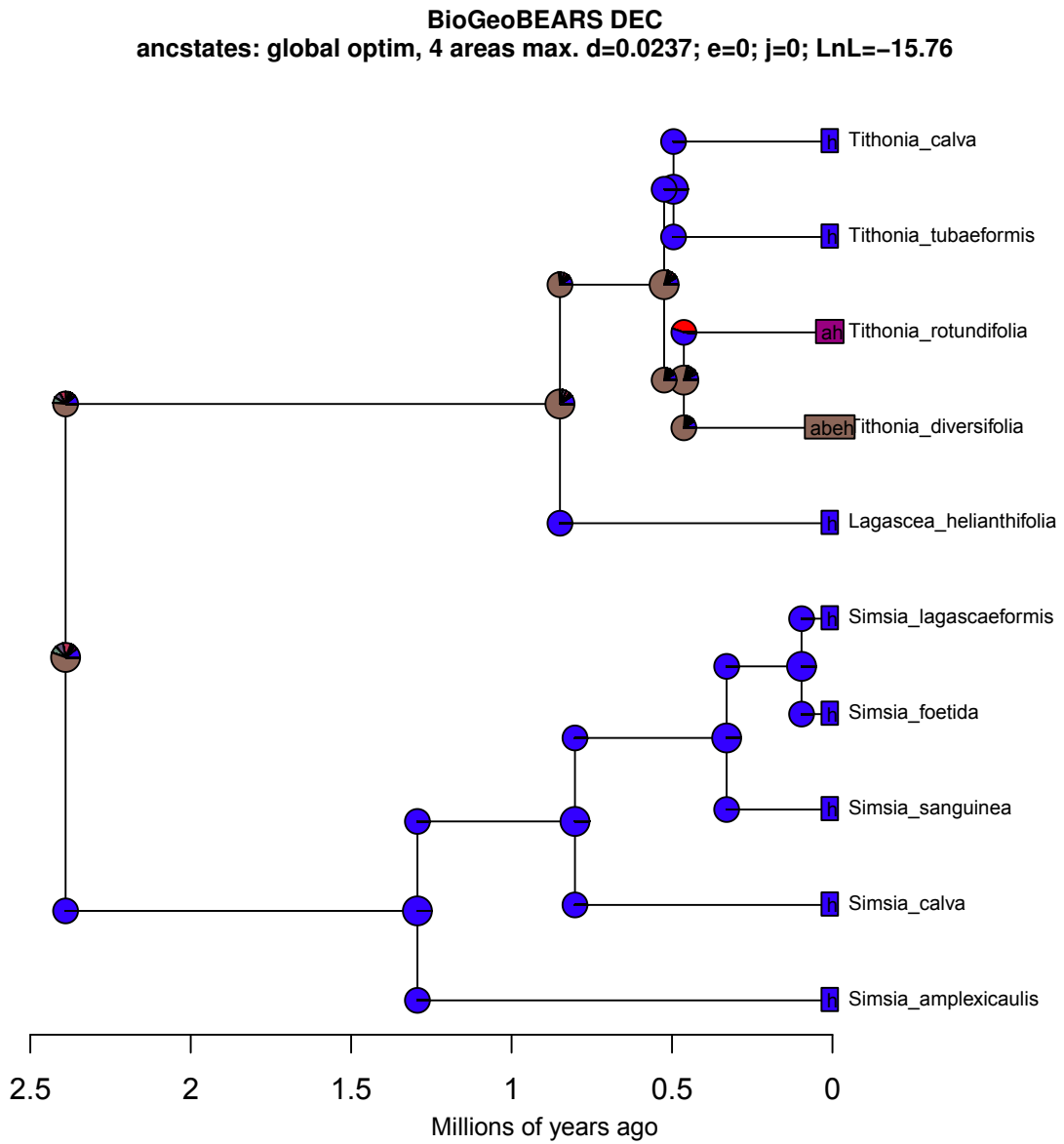


Figure S4: Clades of frogs

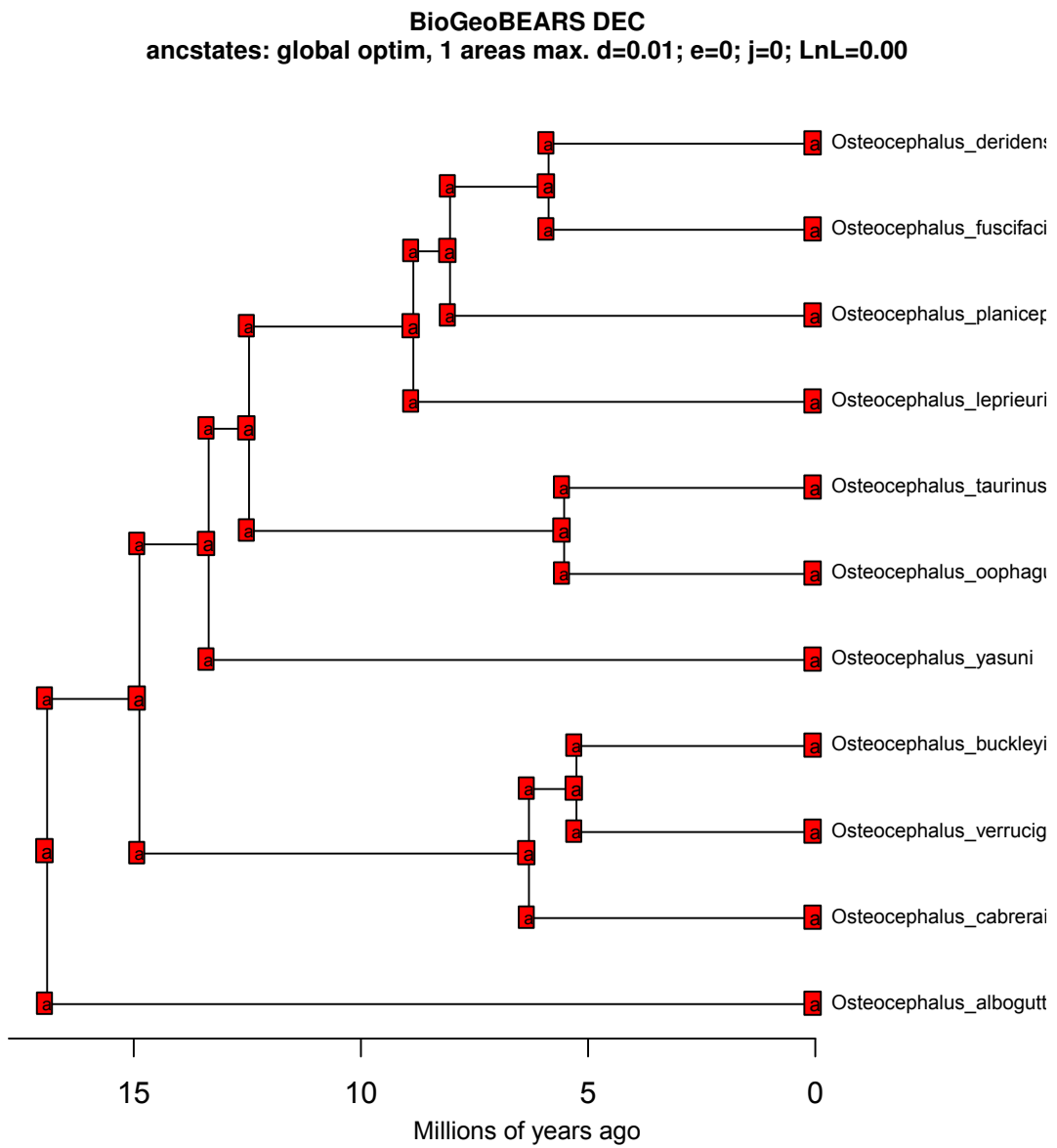


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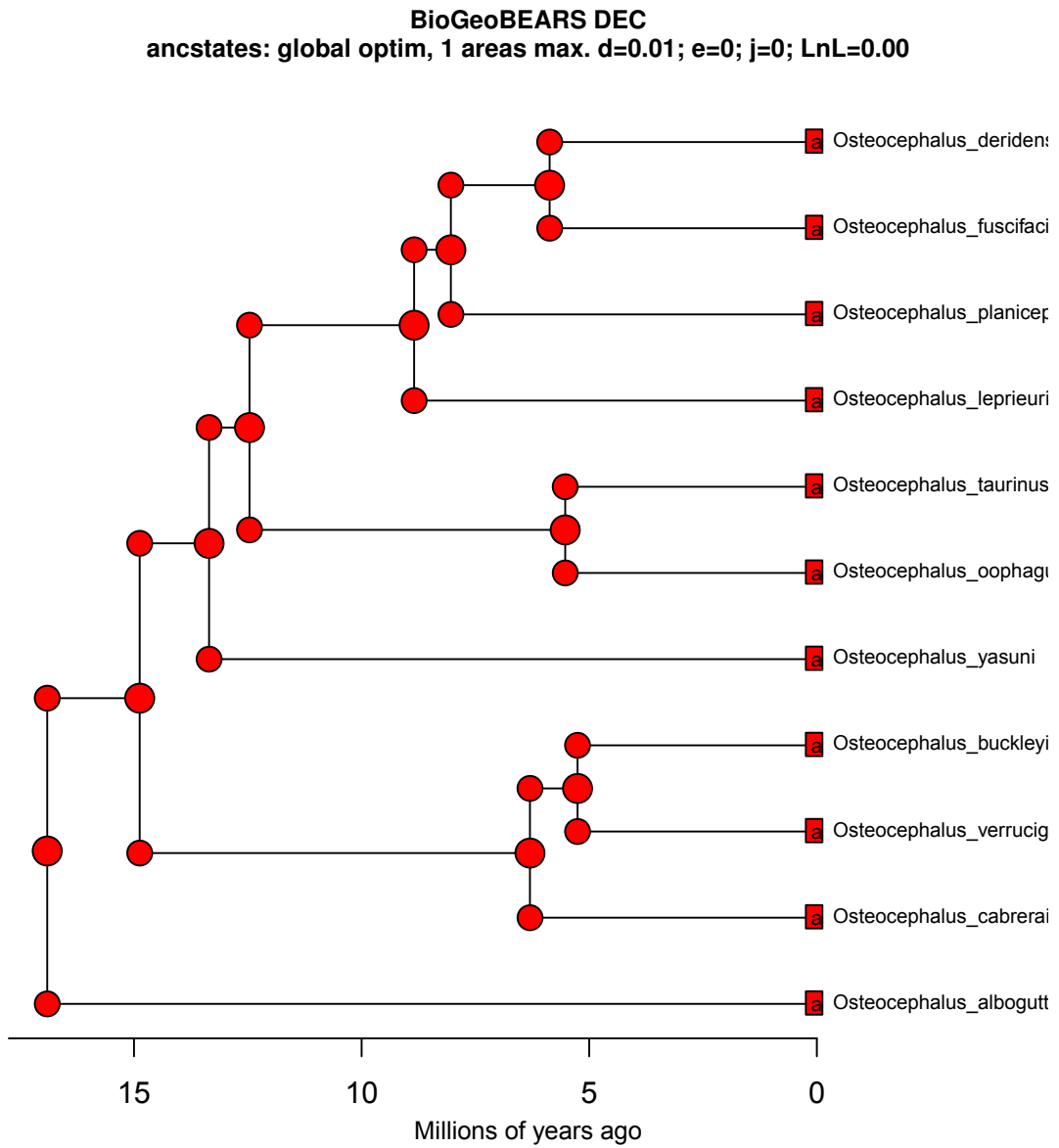


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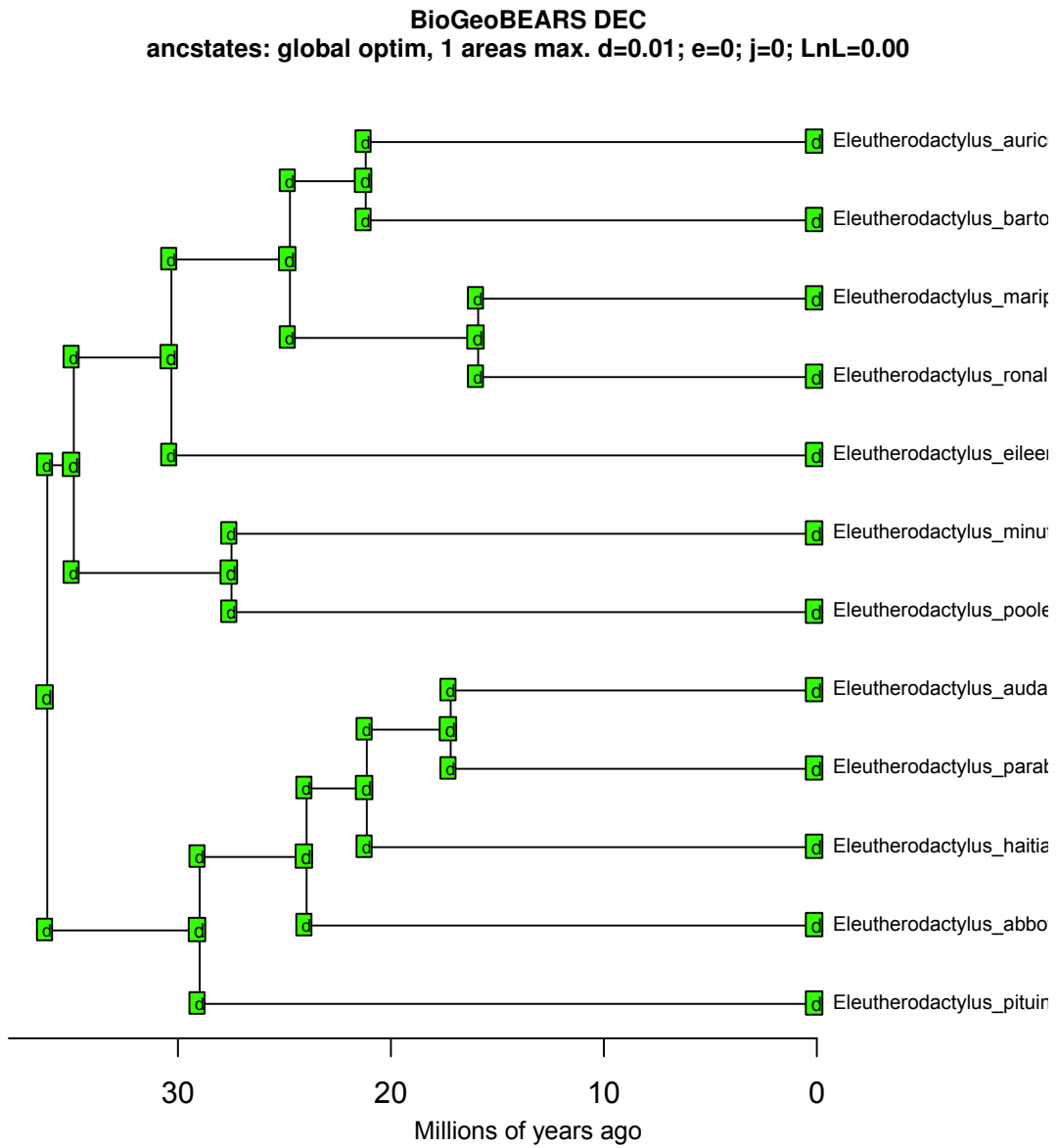


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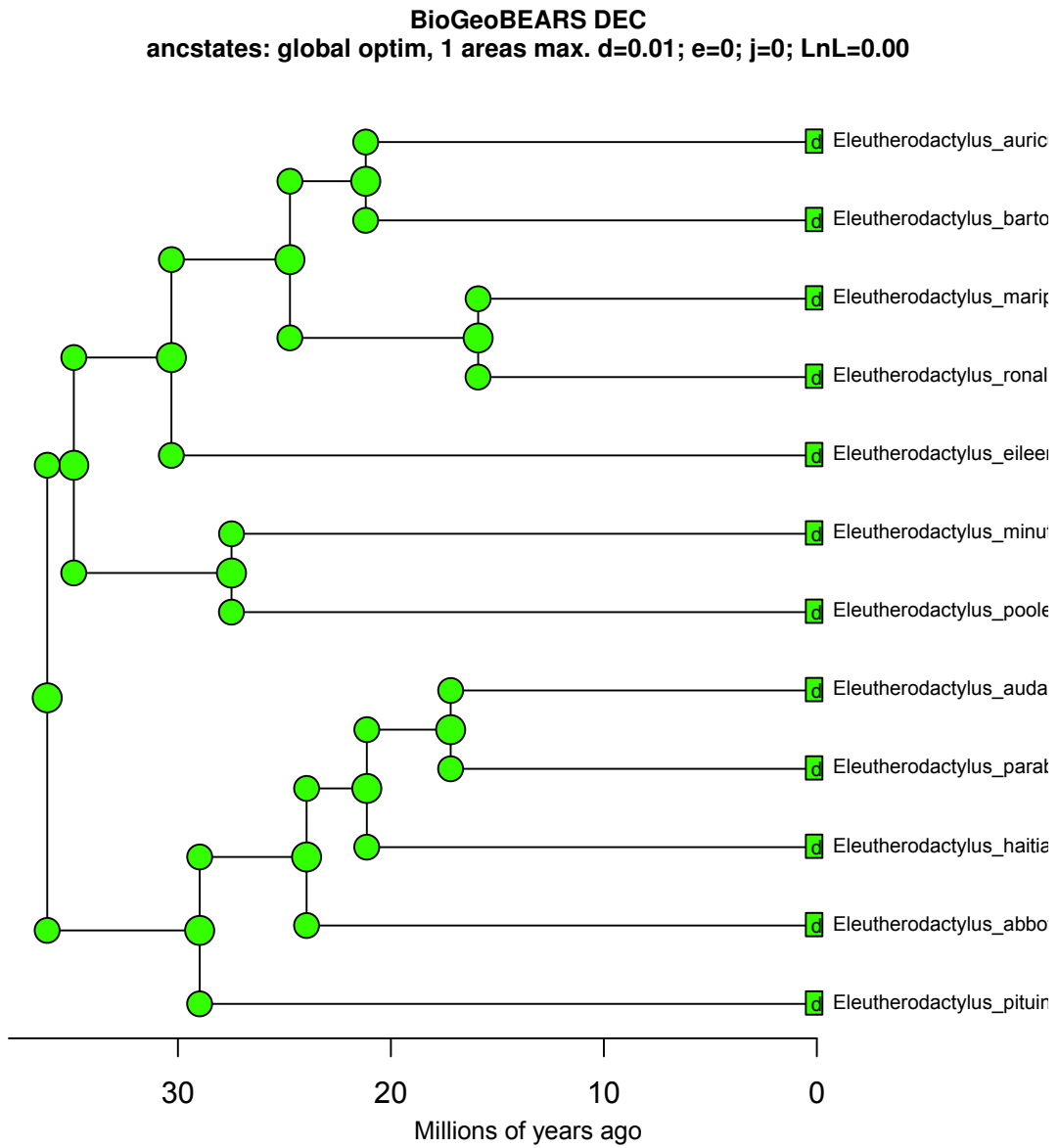


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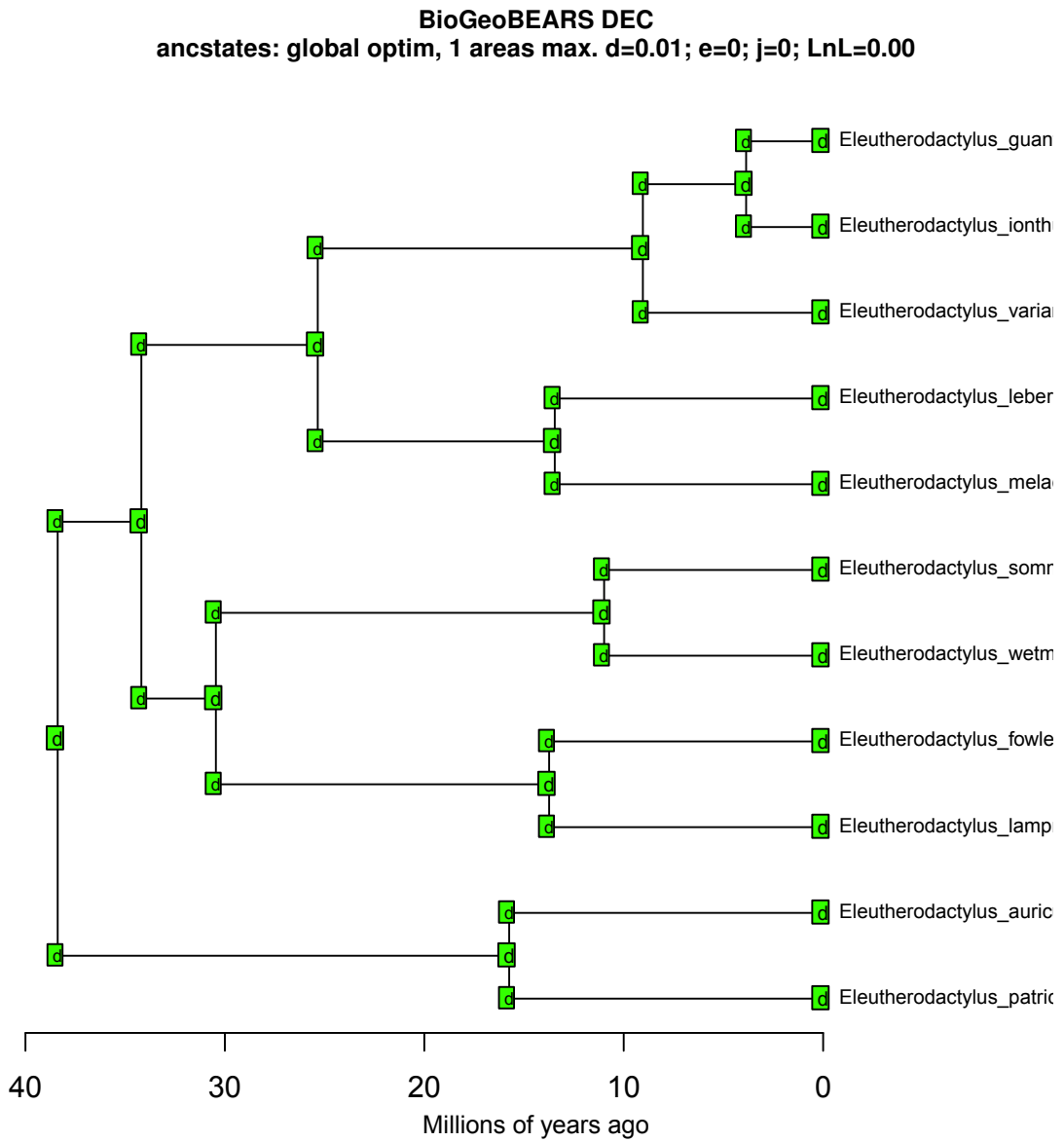


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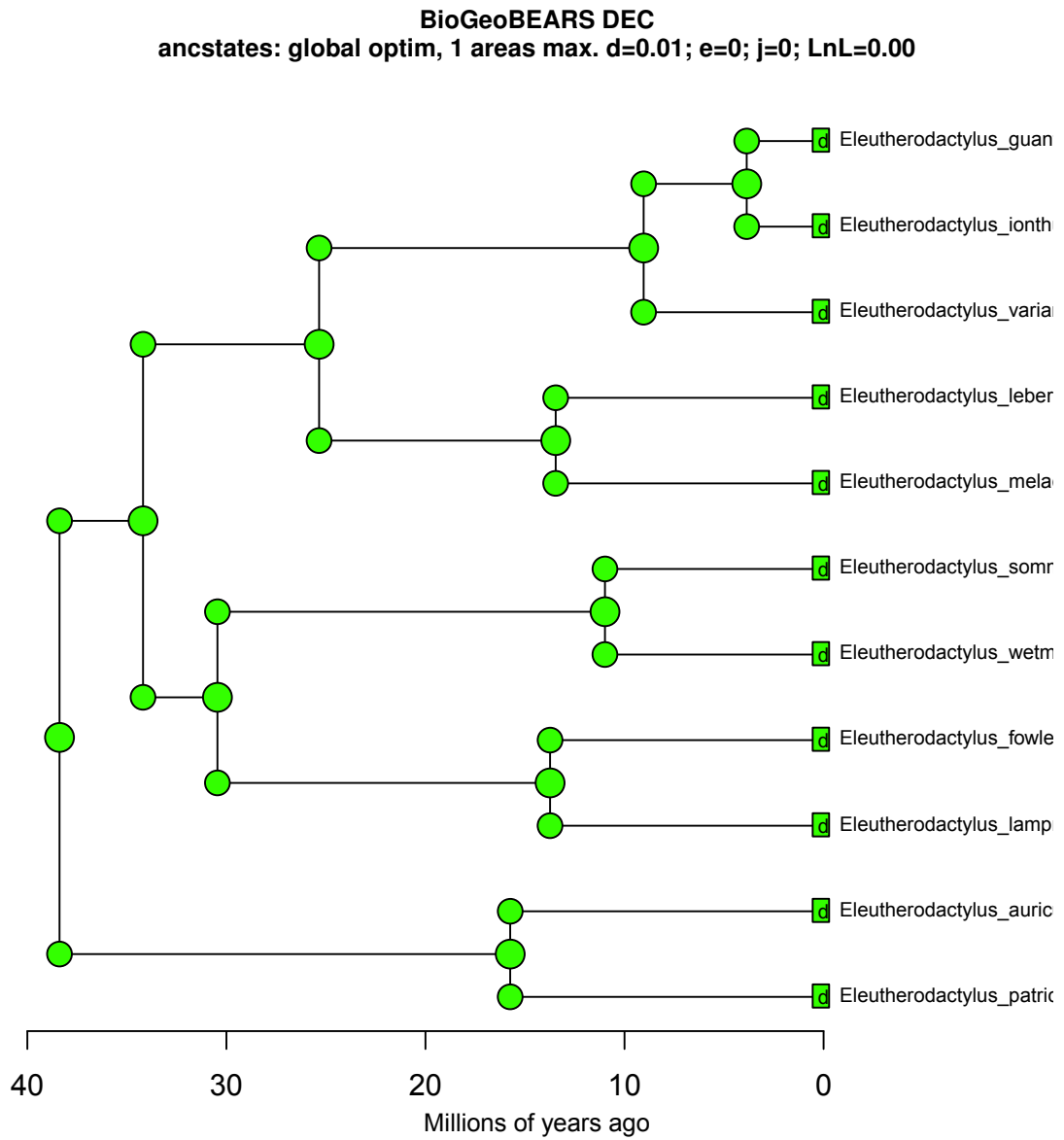


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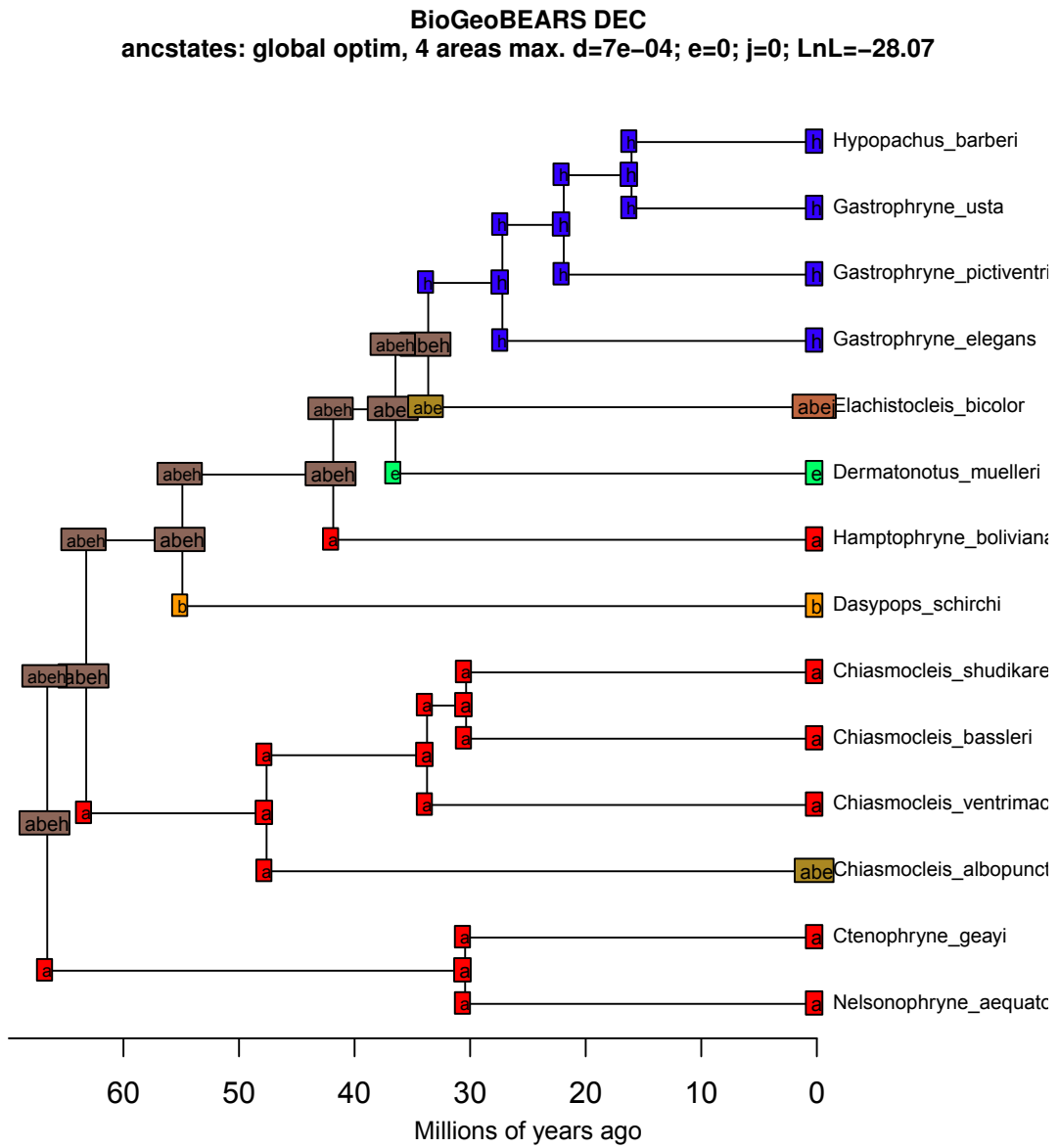


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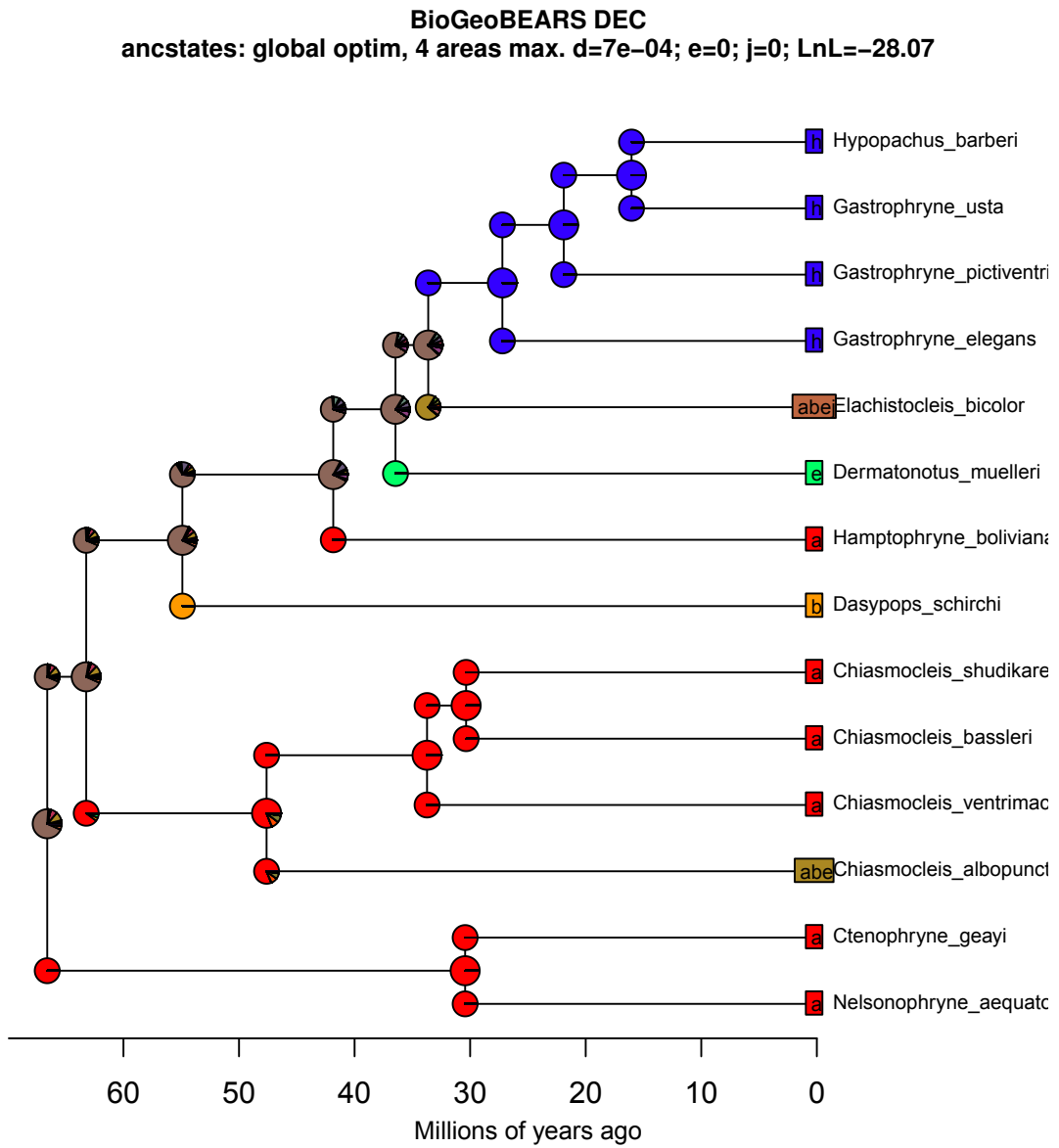


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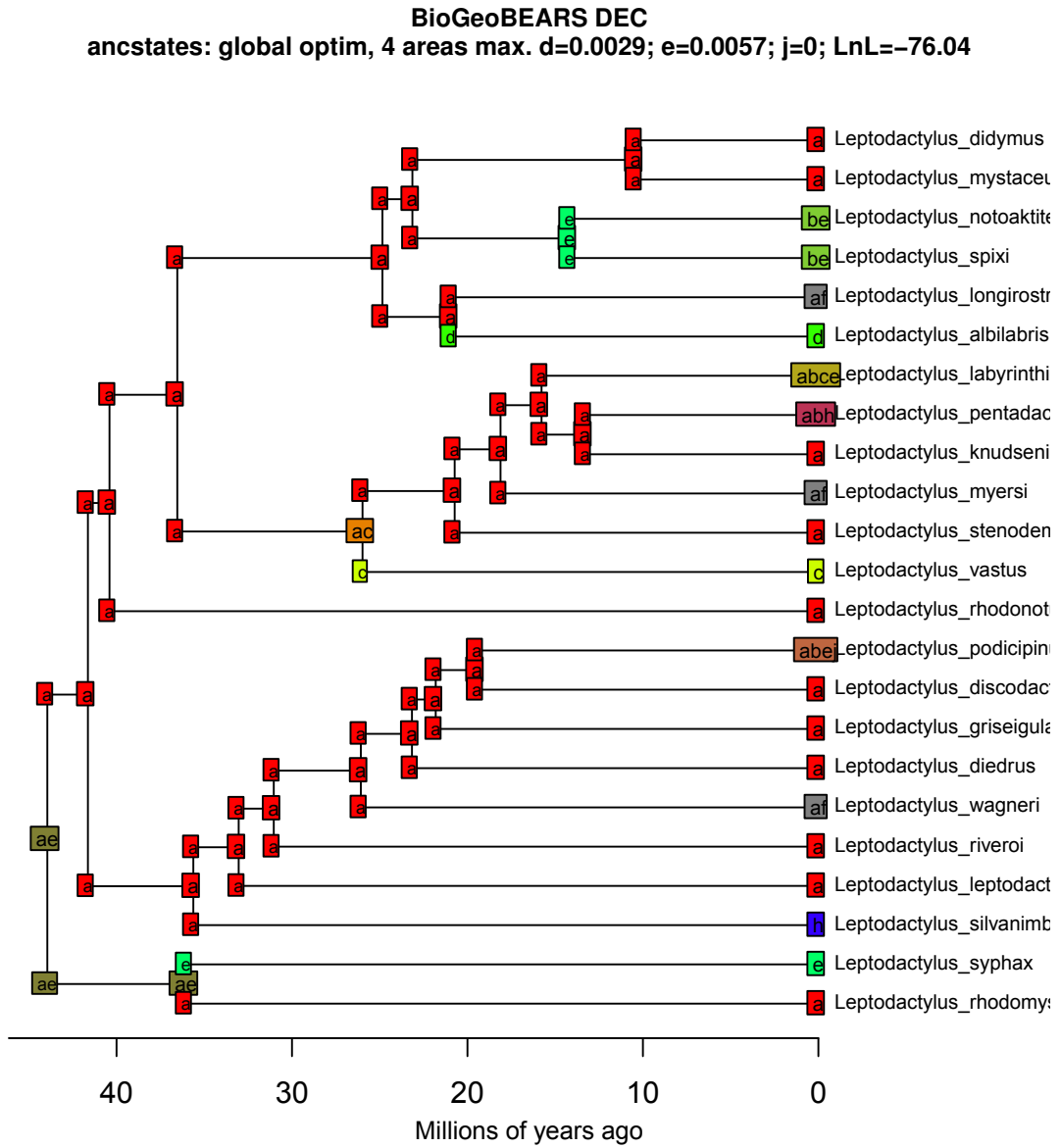


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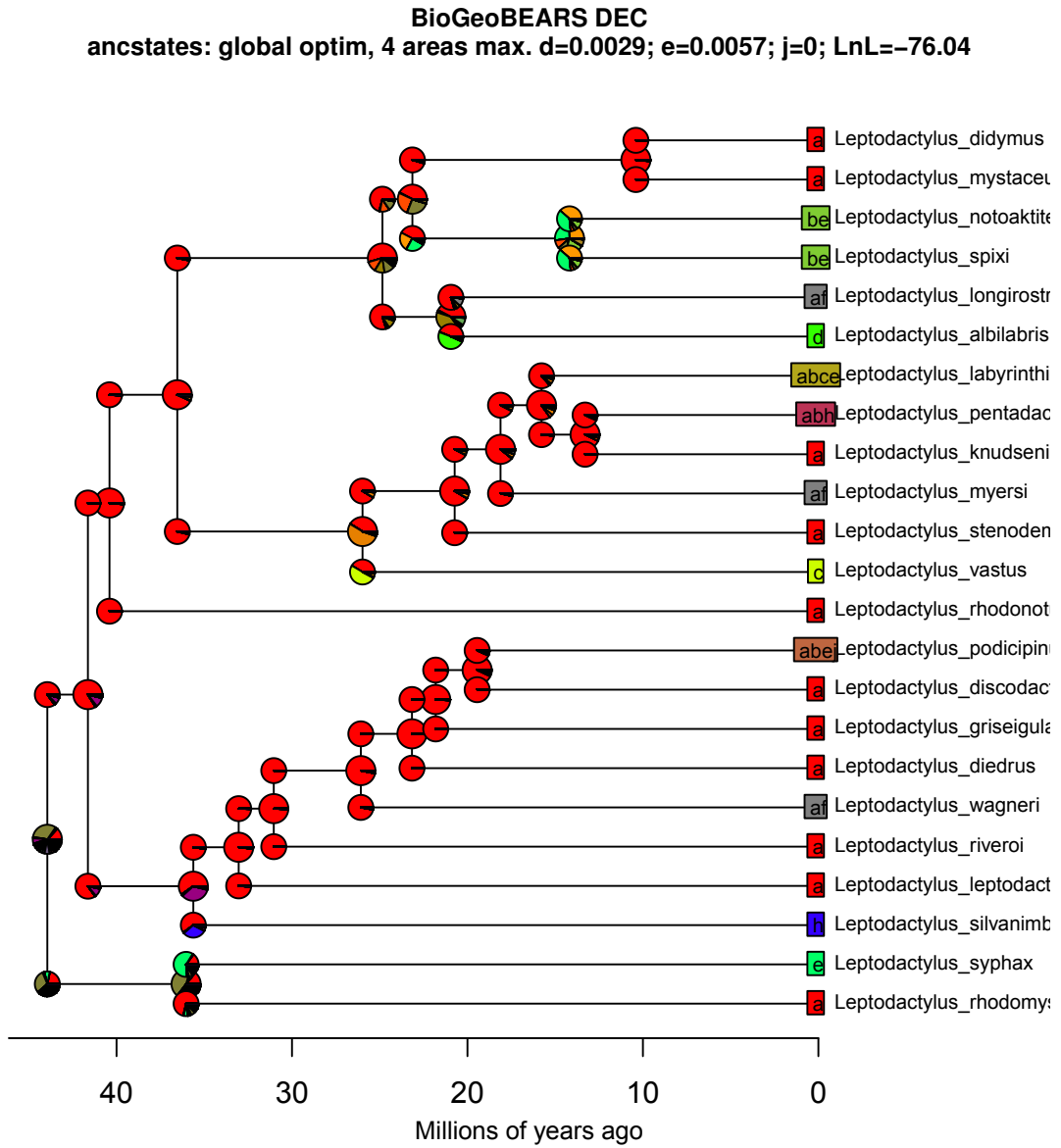


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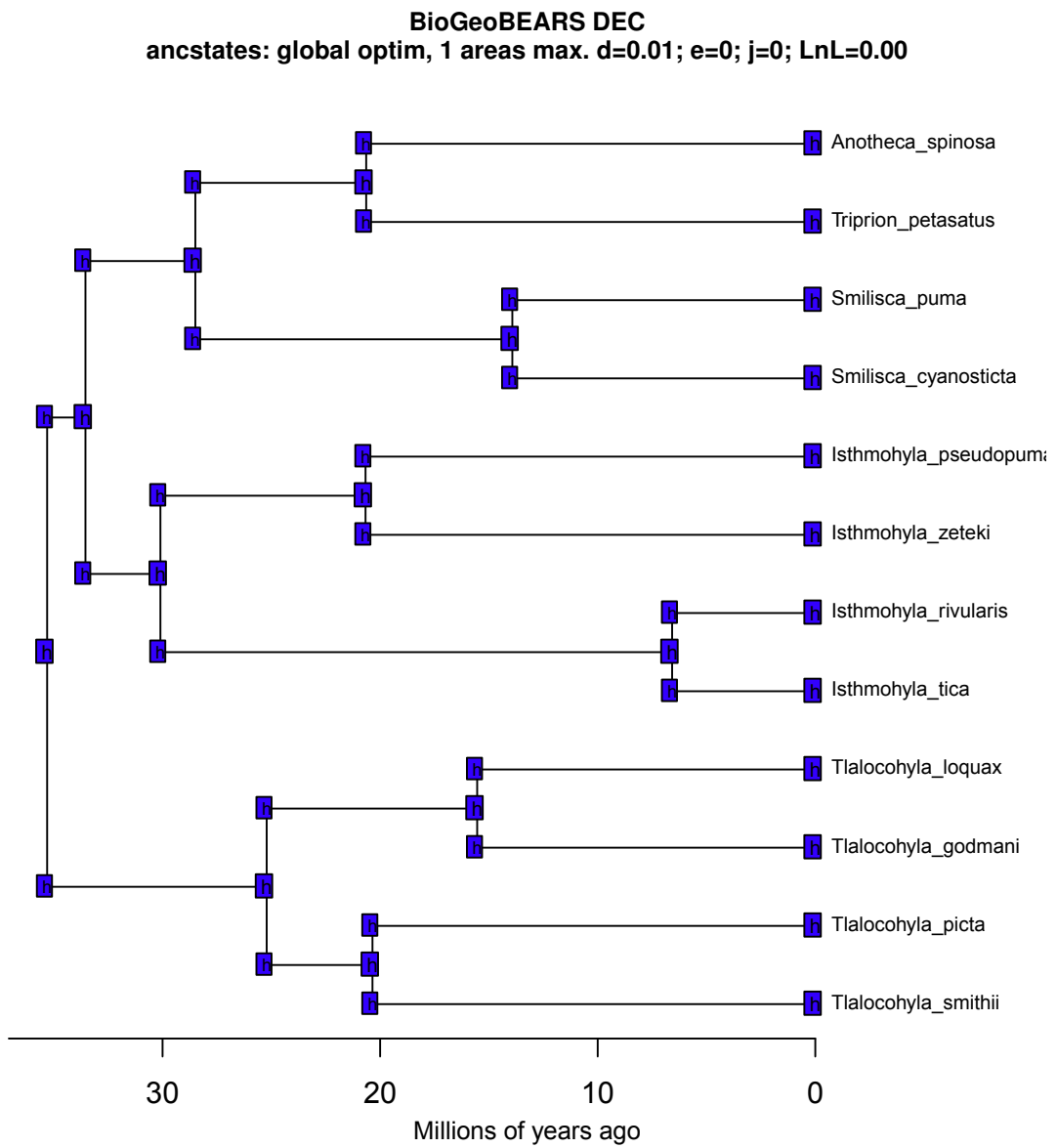


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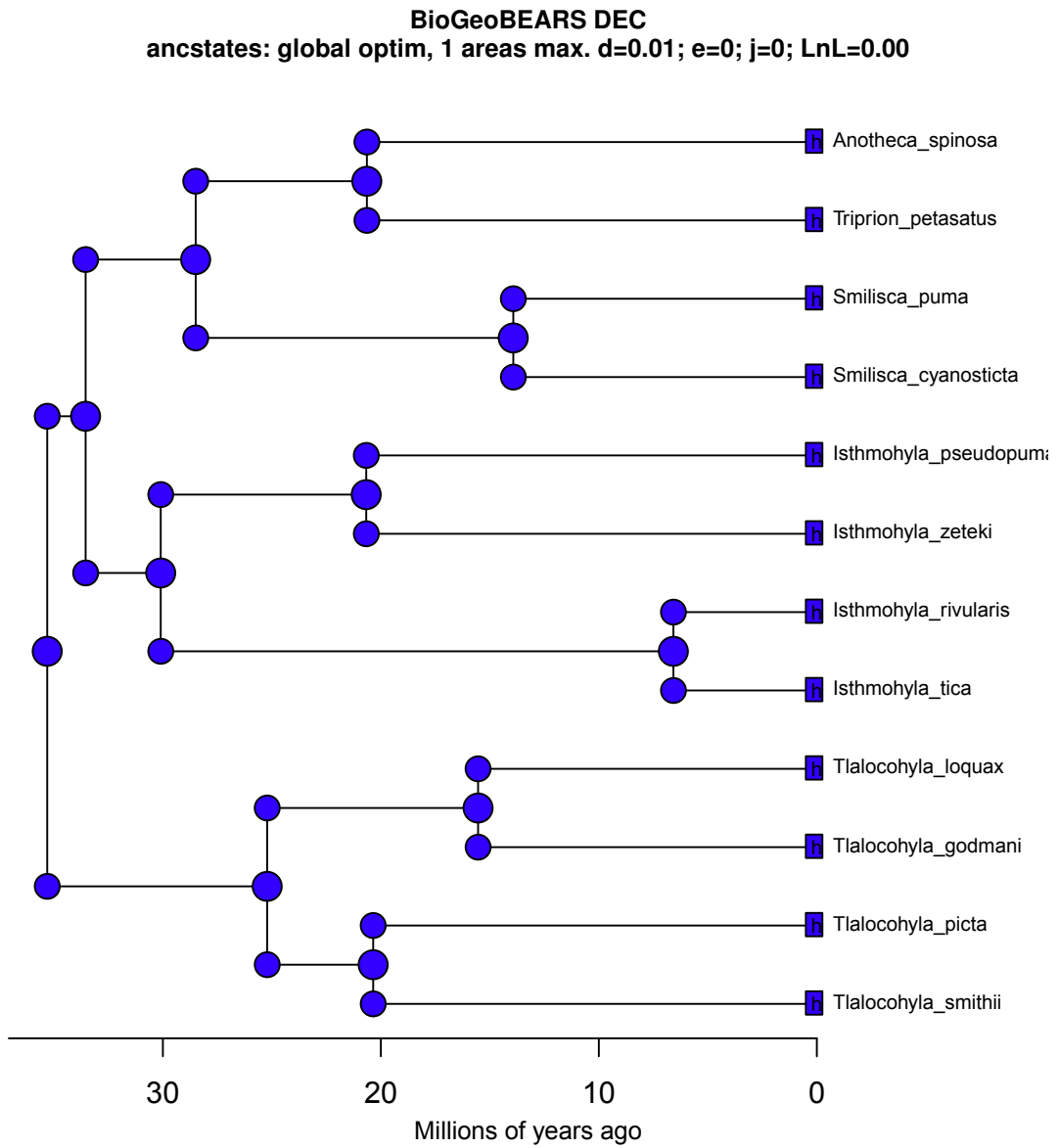


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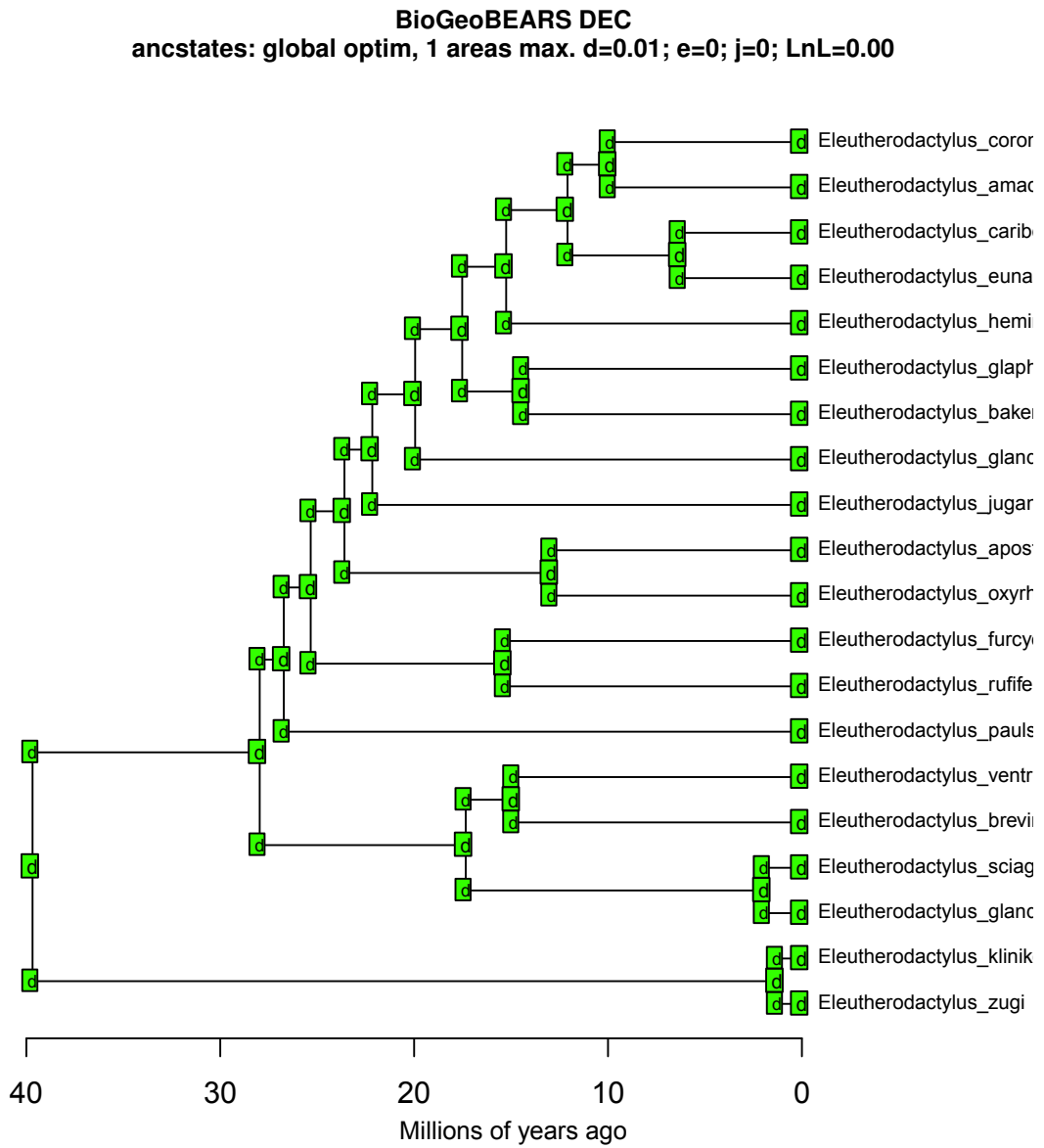


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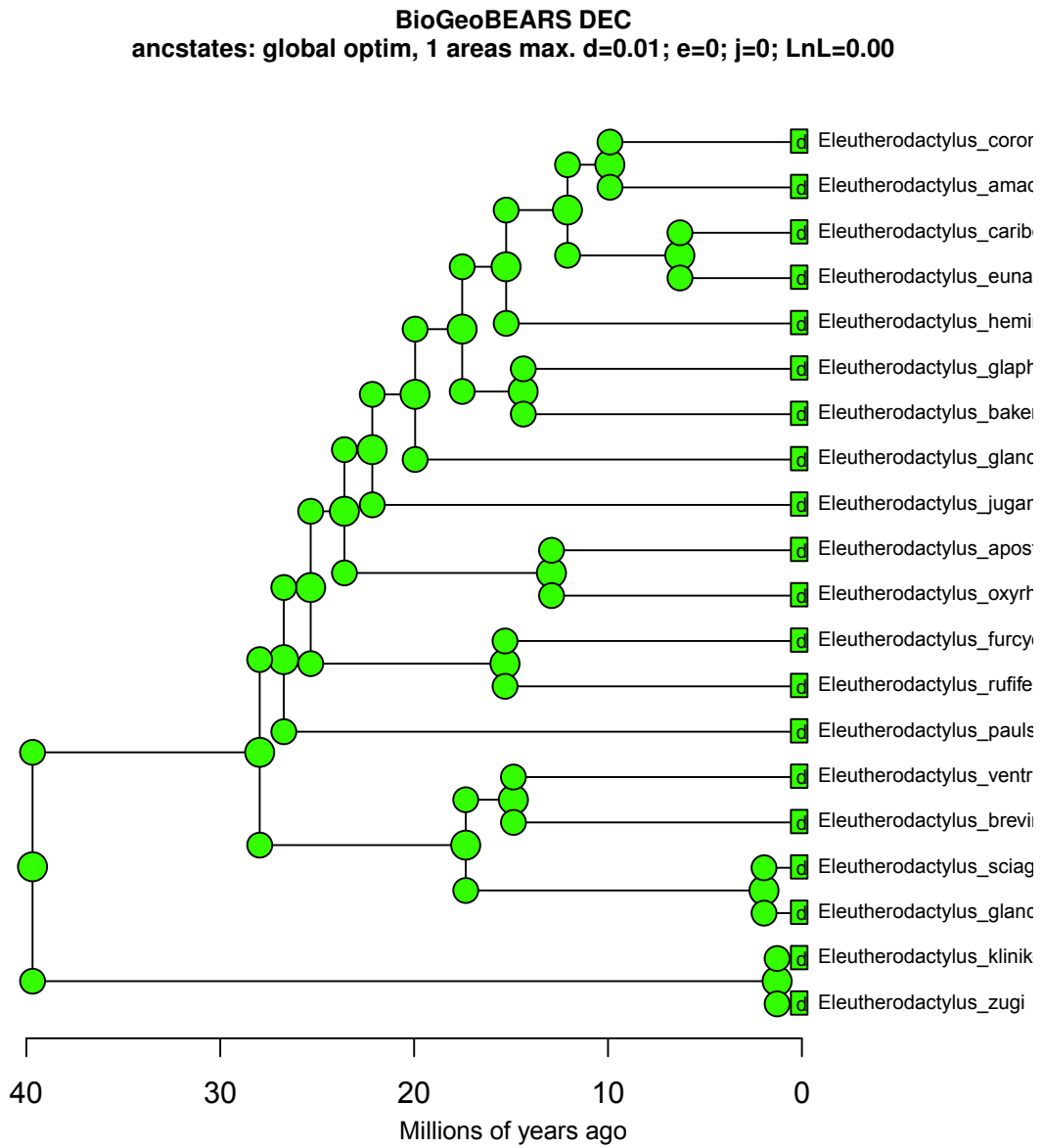


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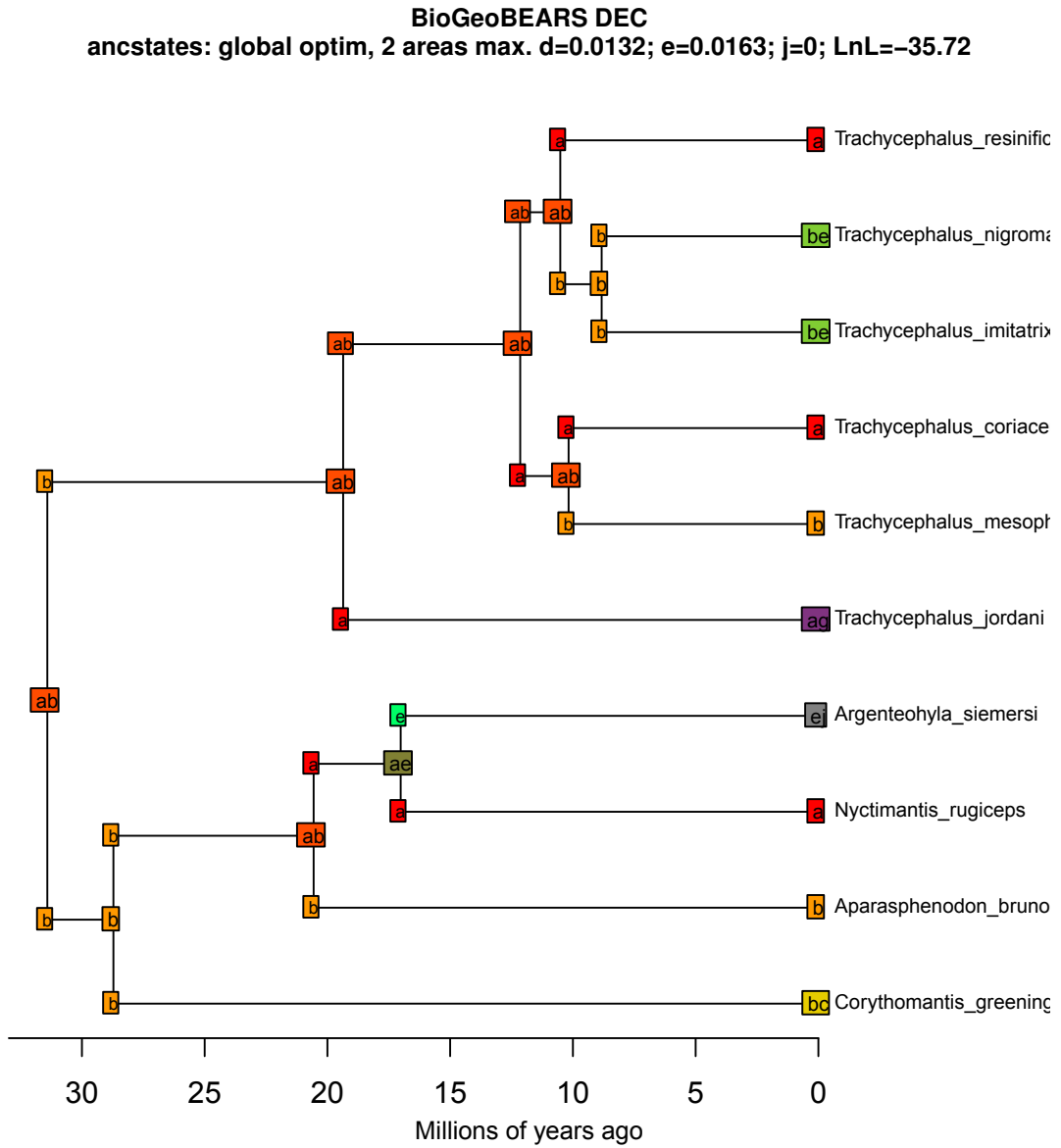


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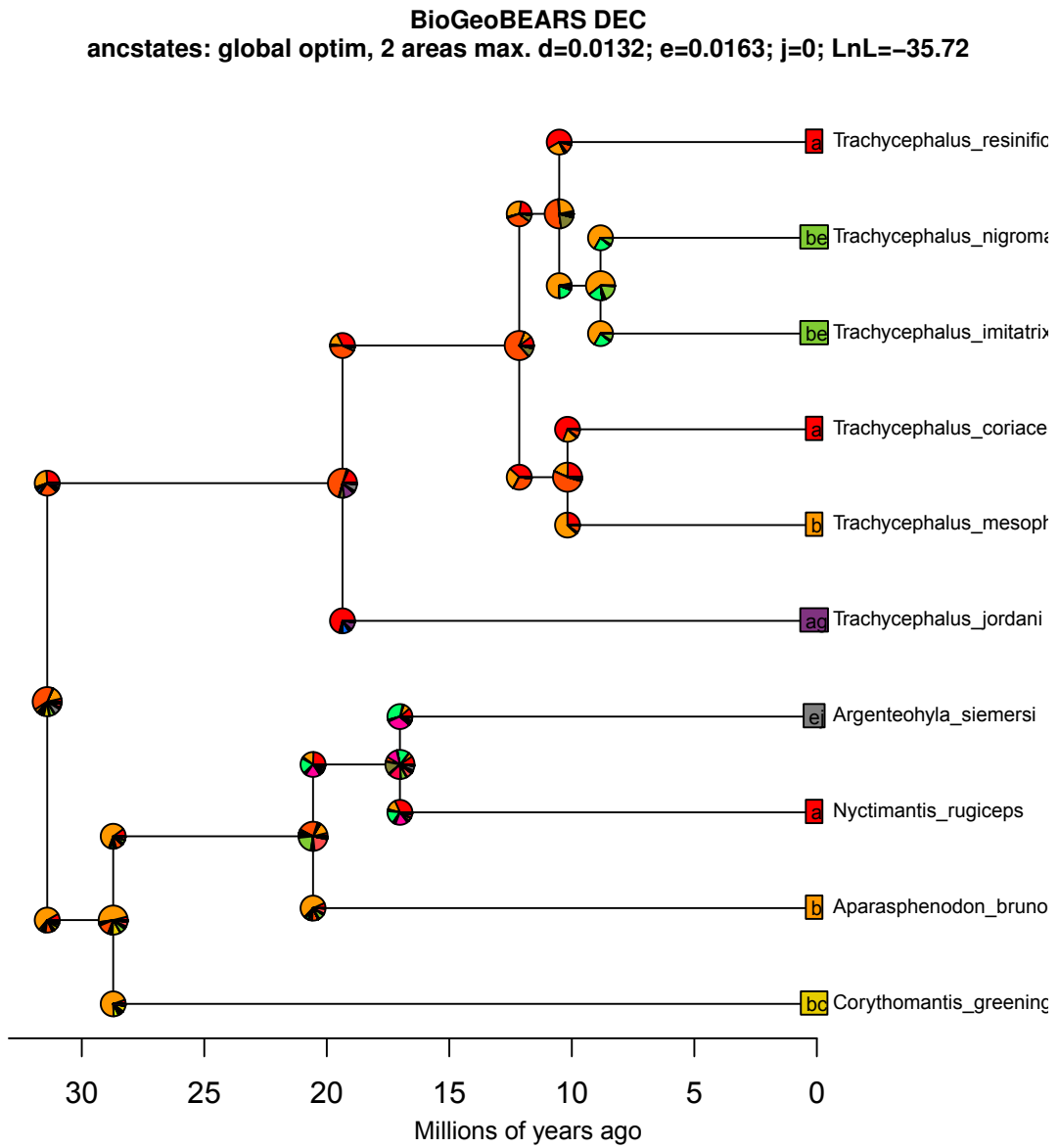


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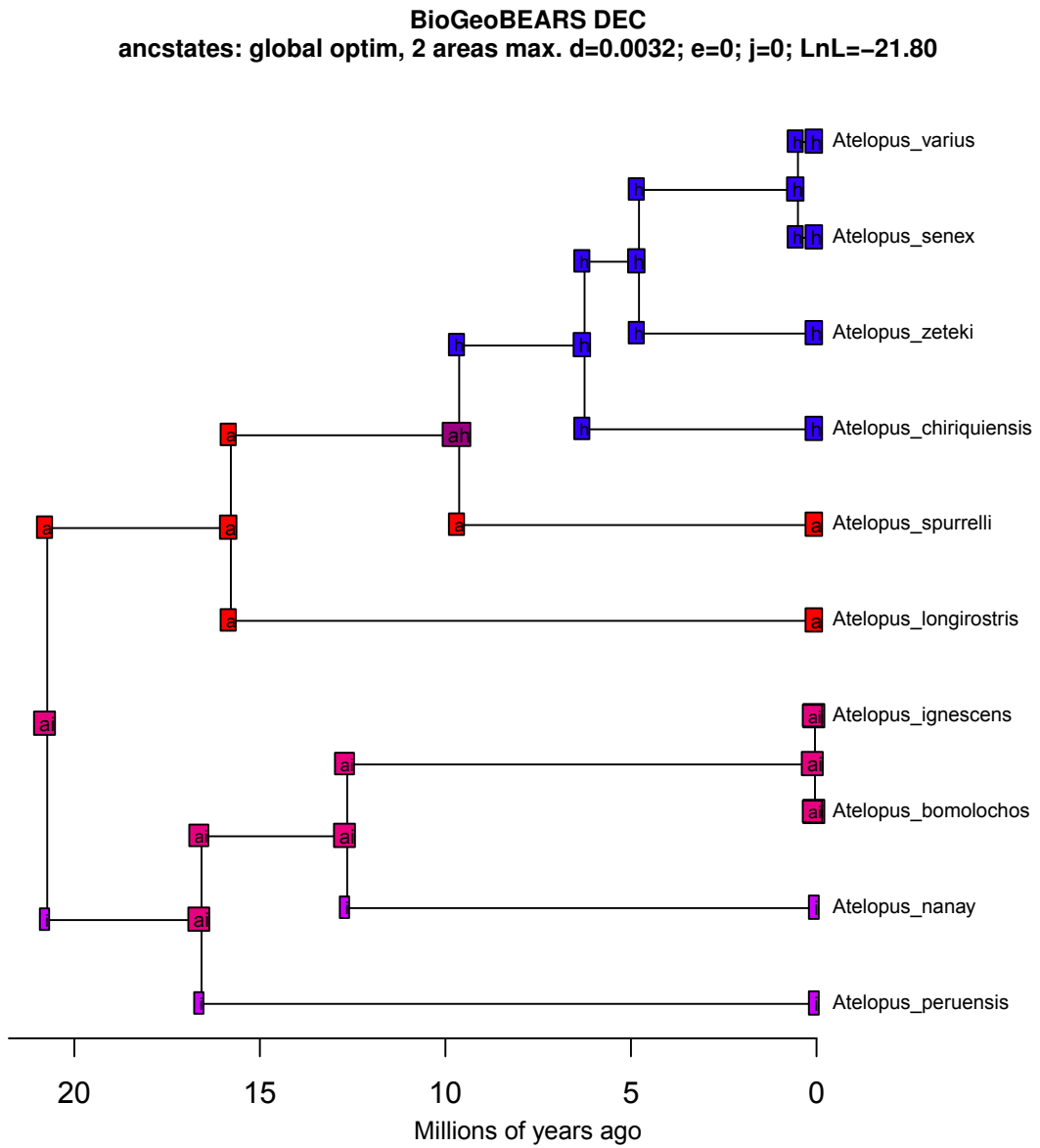


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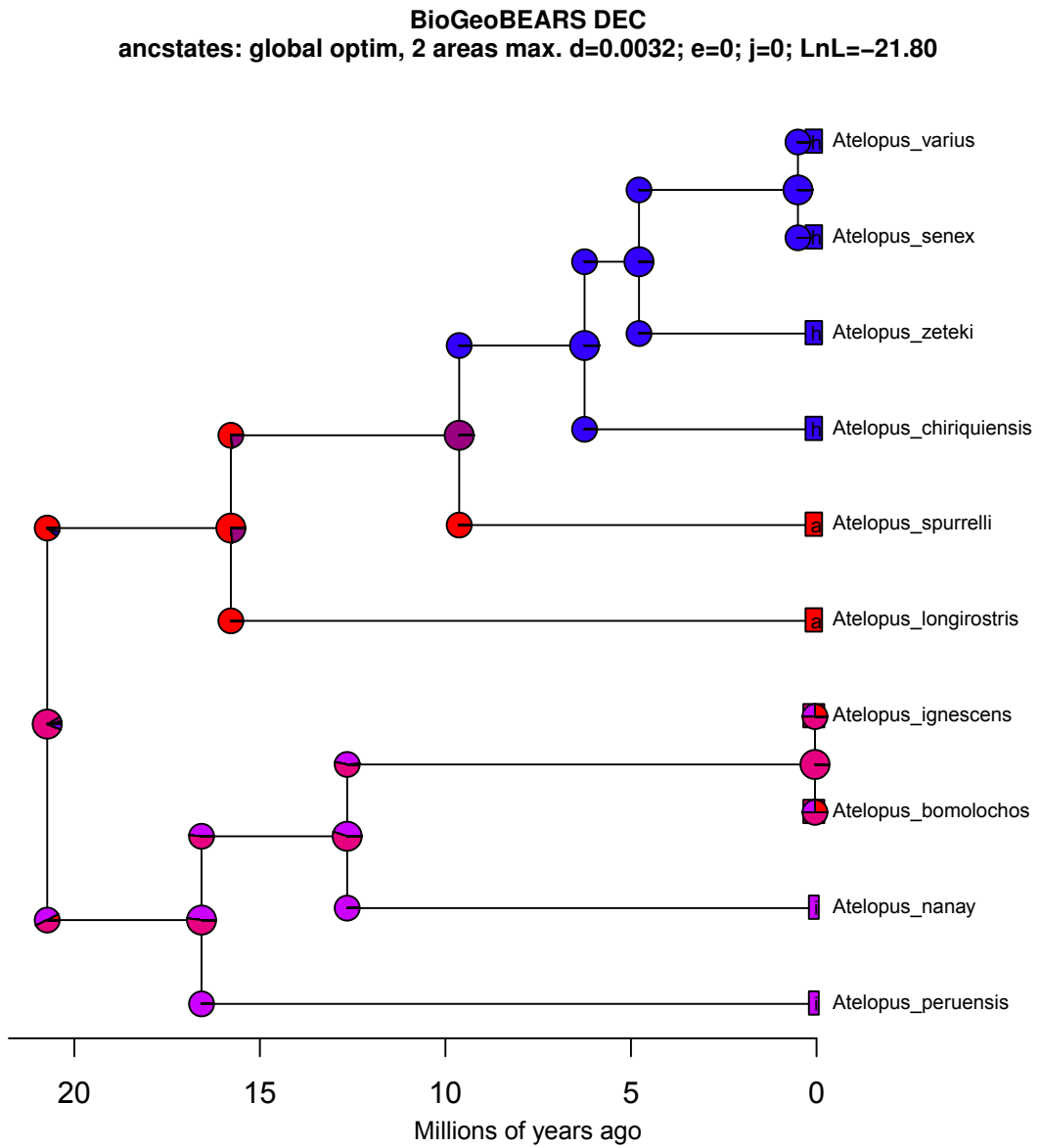


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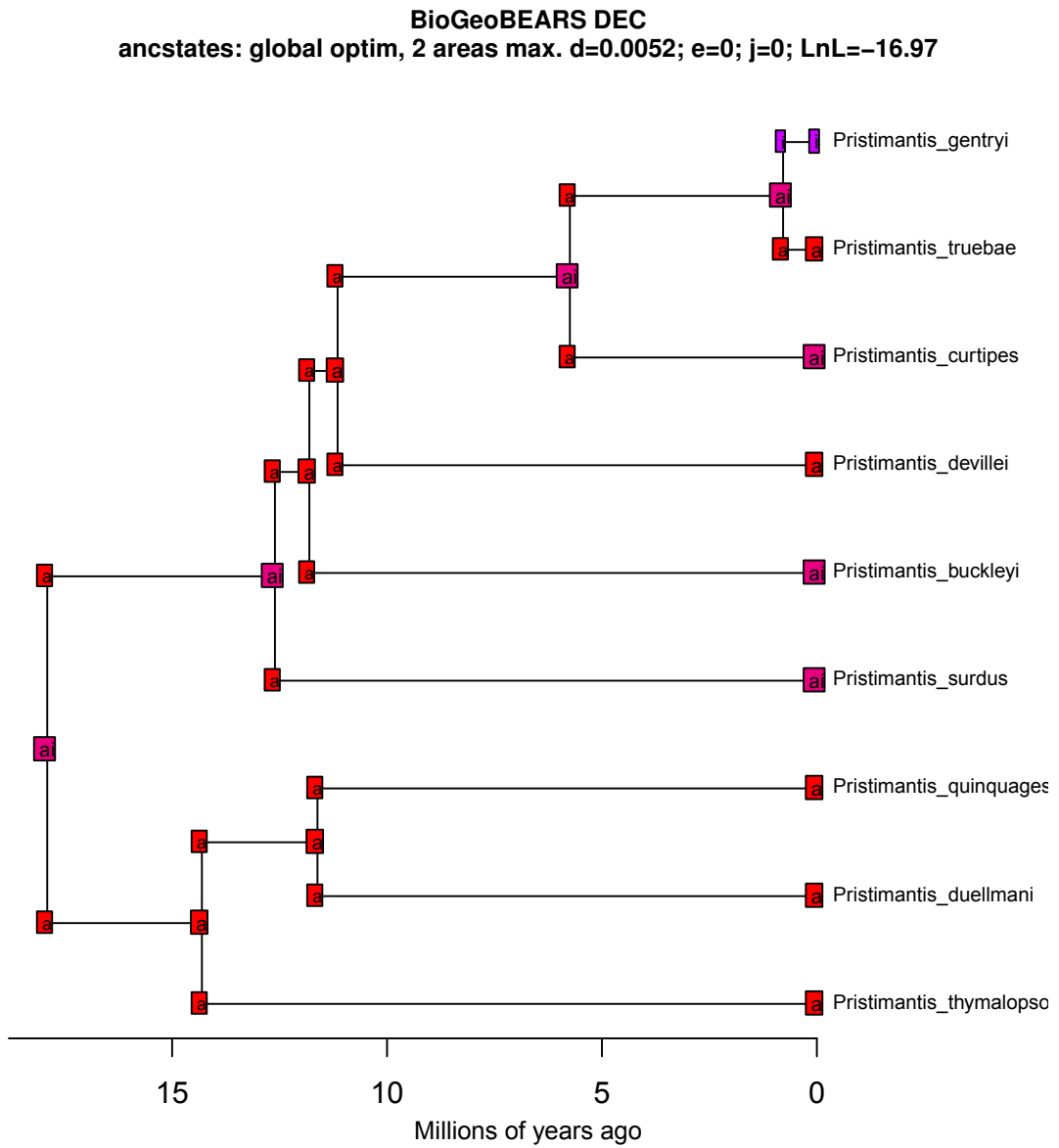


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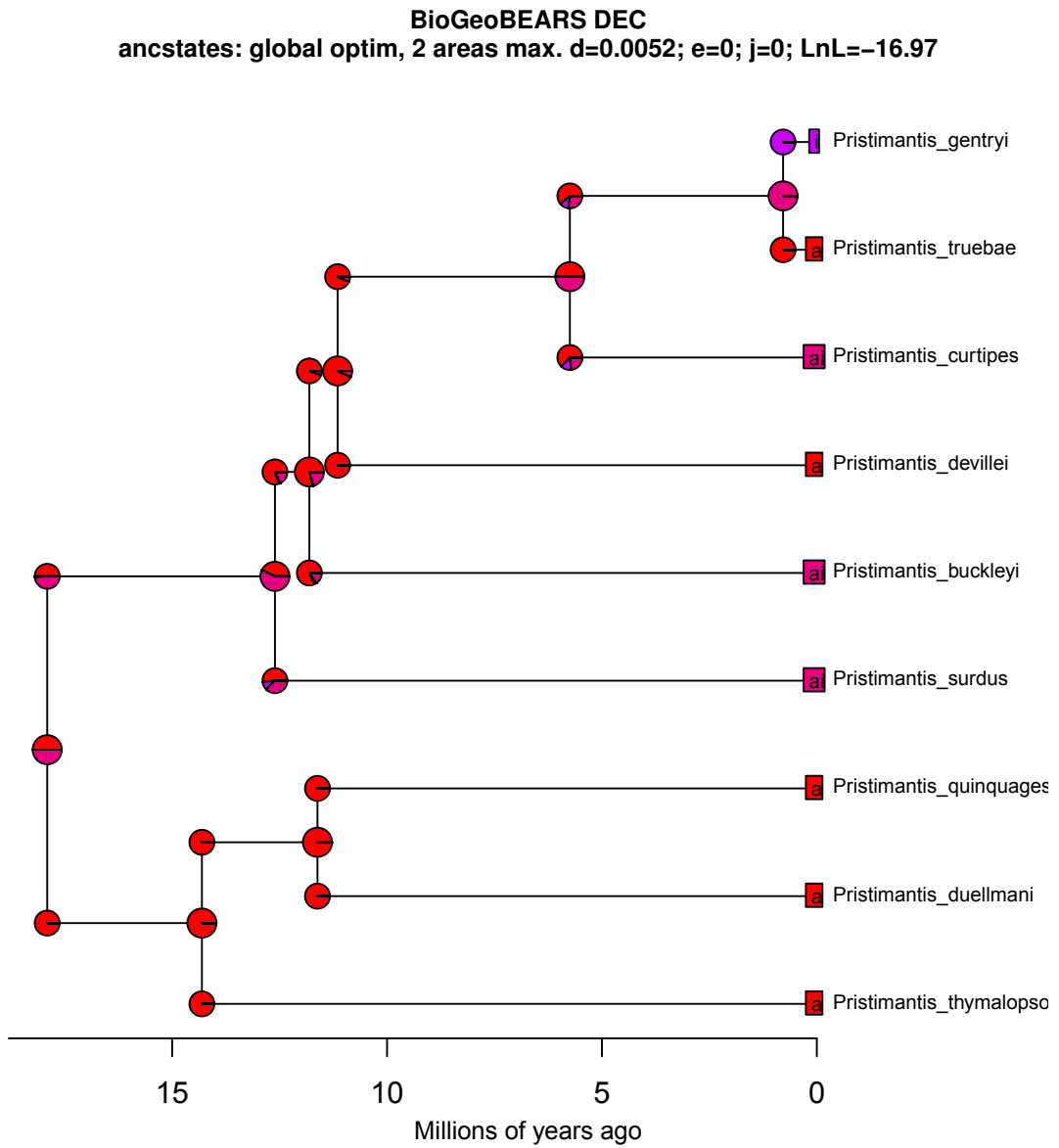


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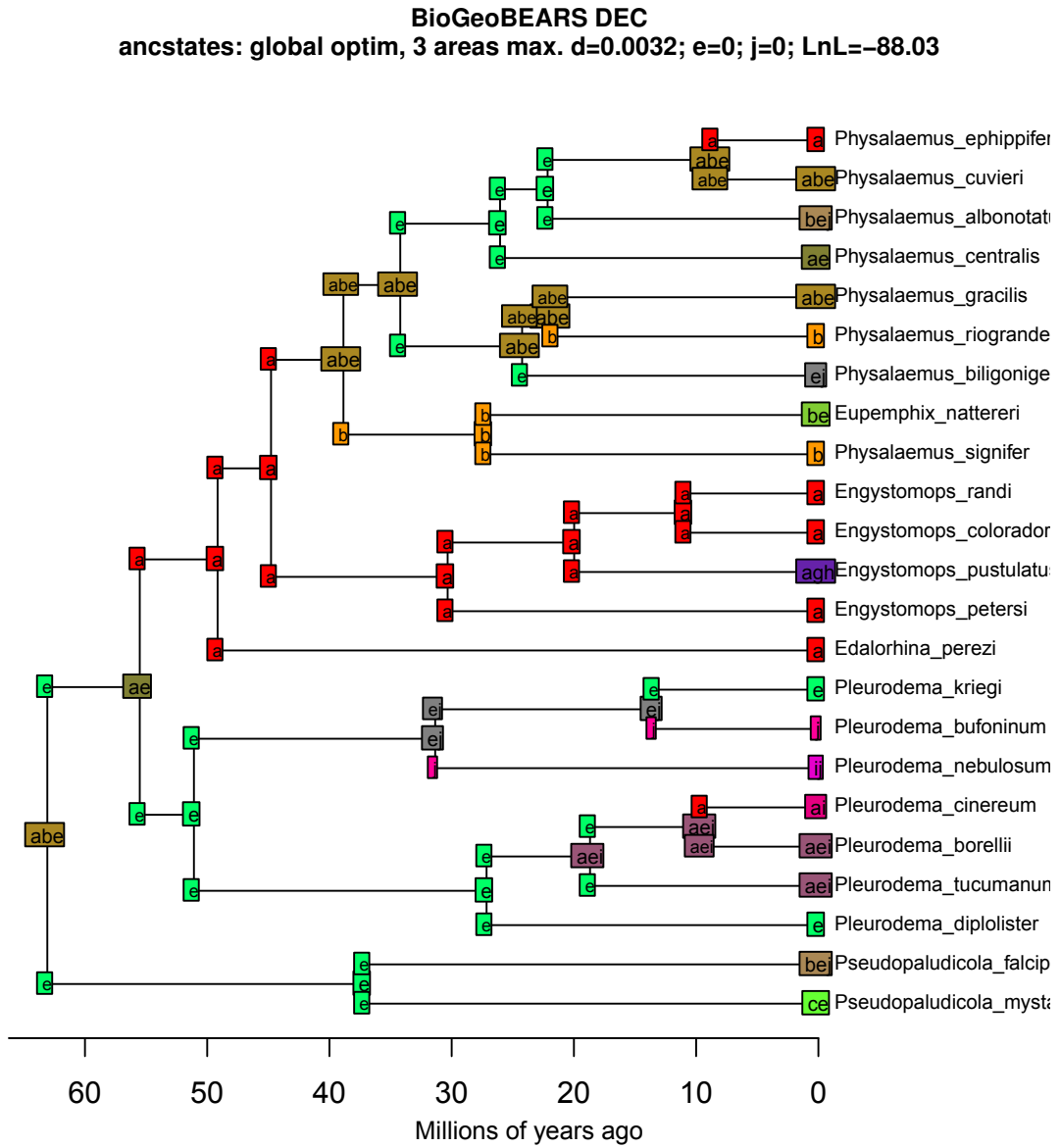


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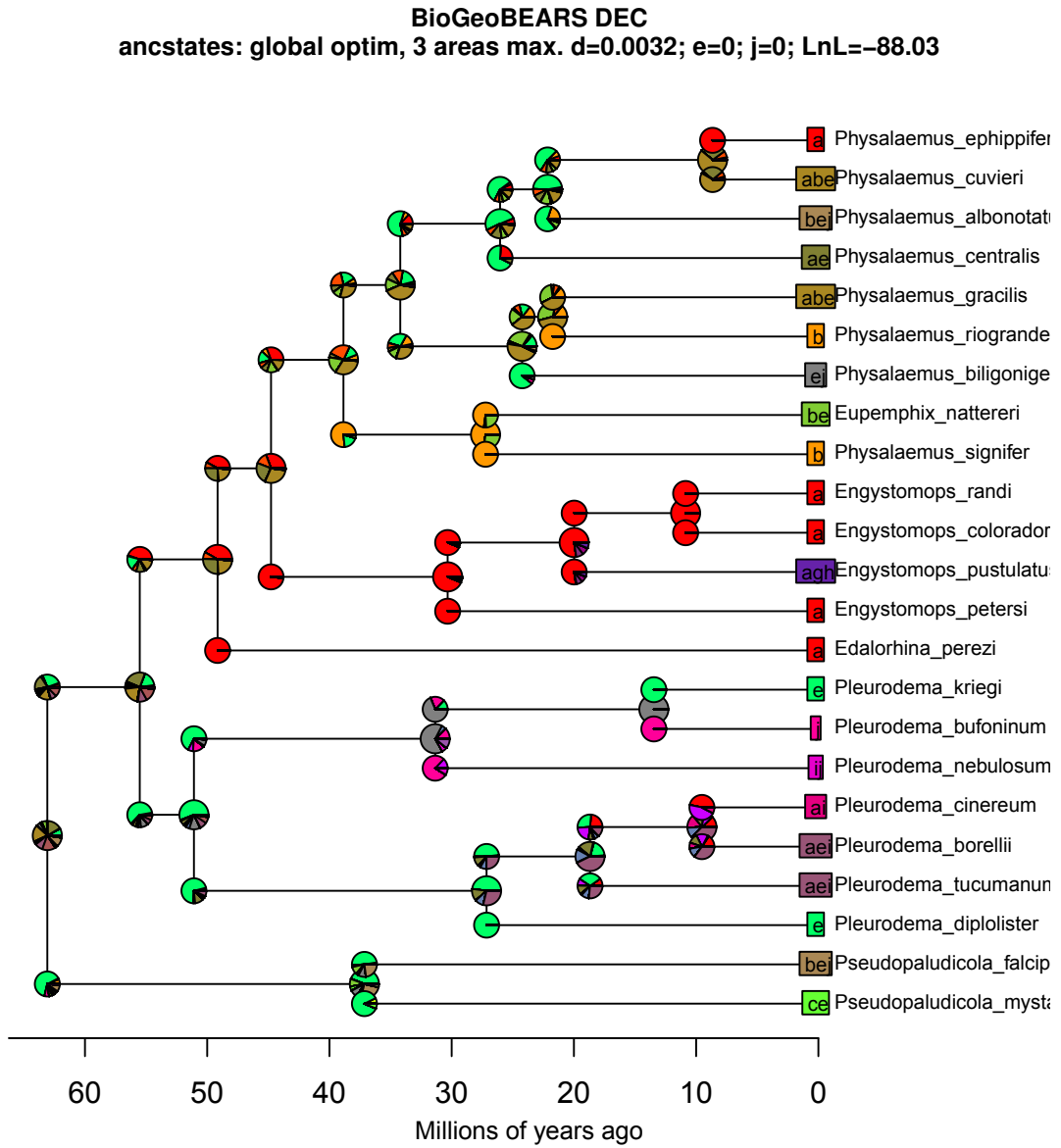


Figure S5: Clades of birds

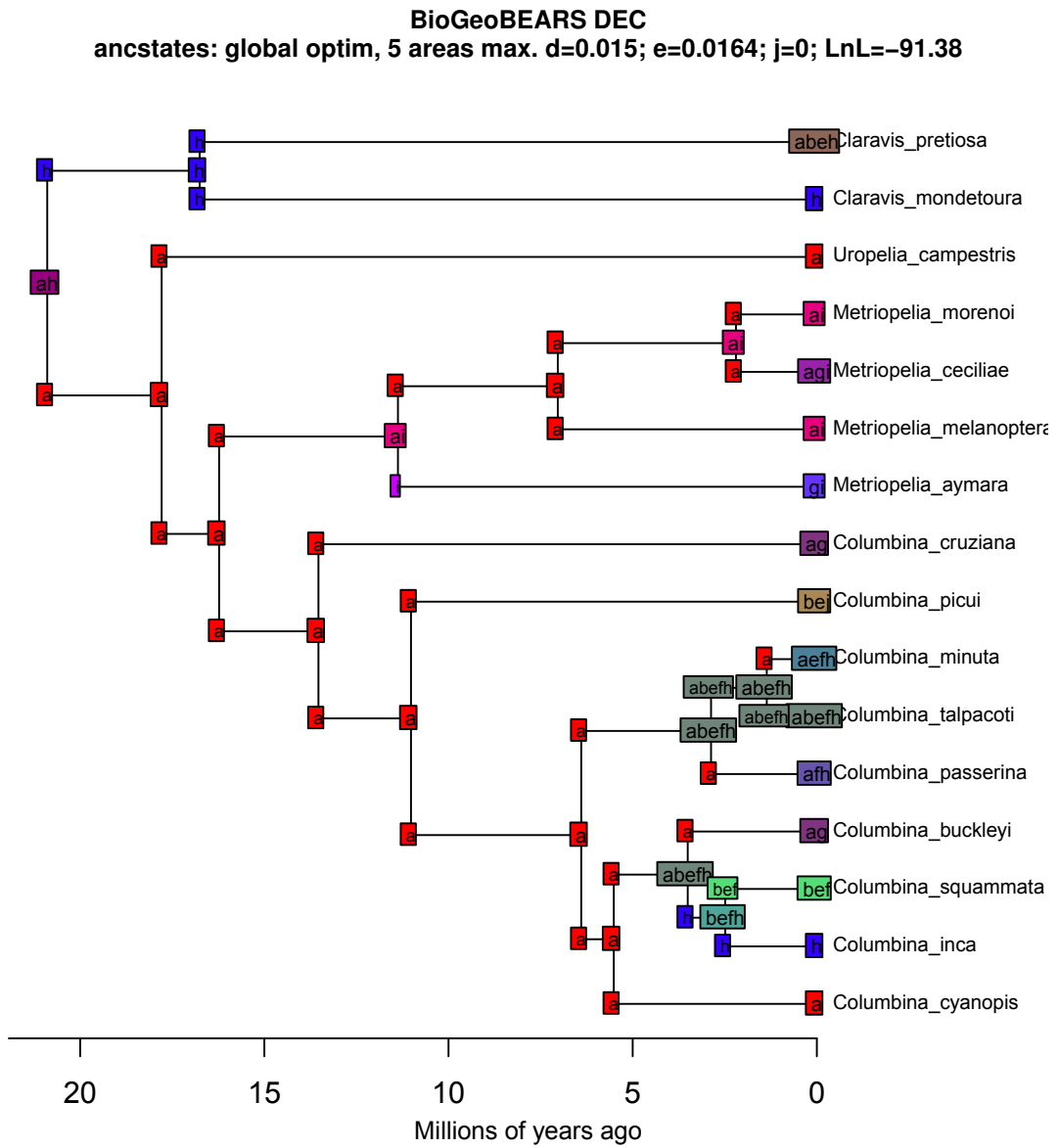


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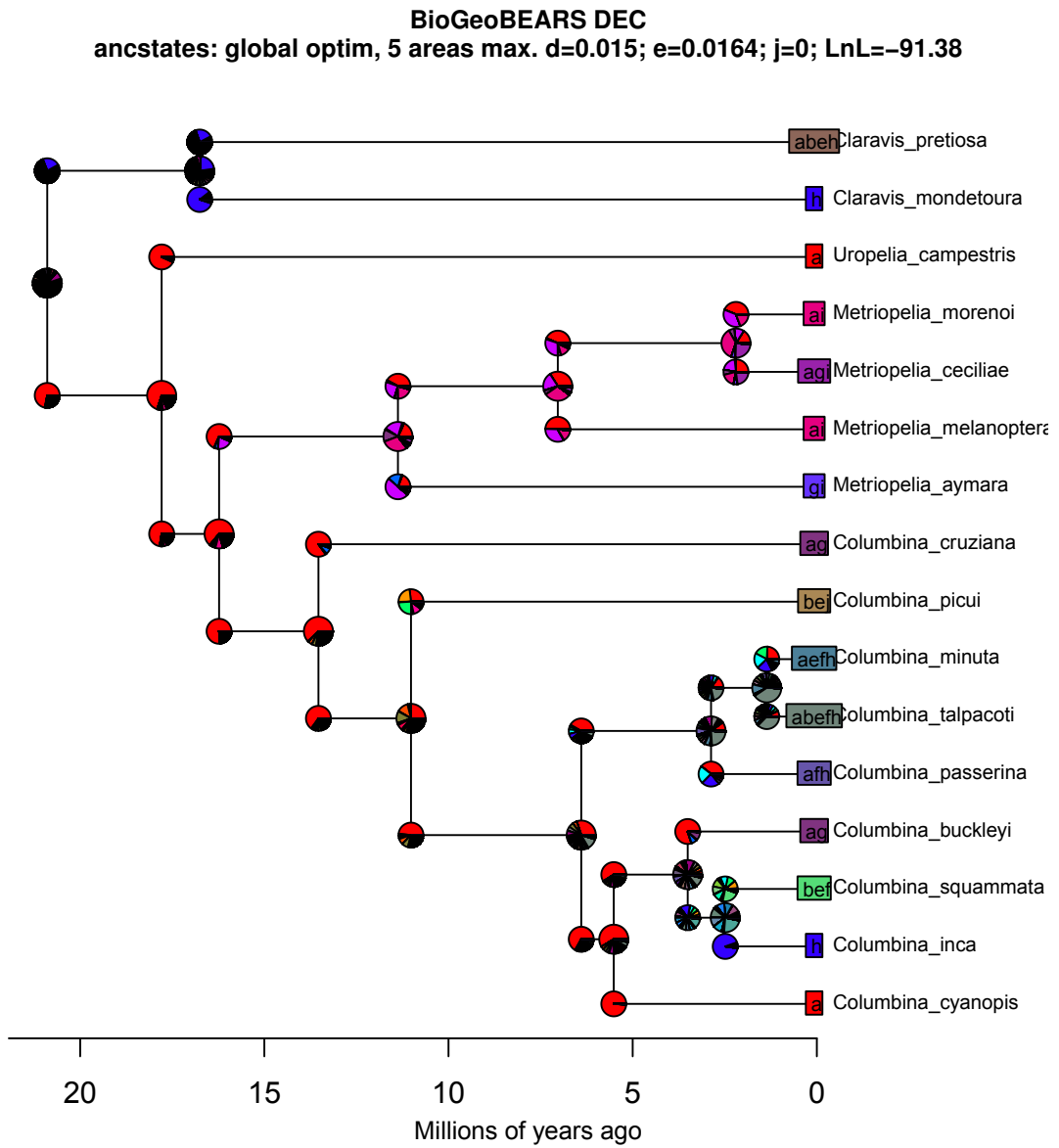


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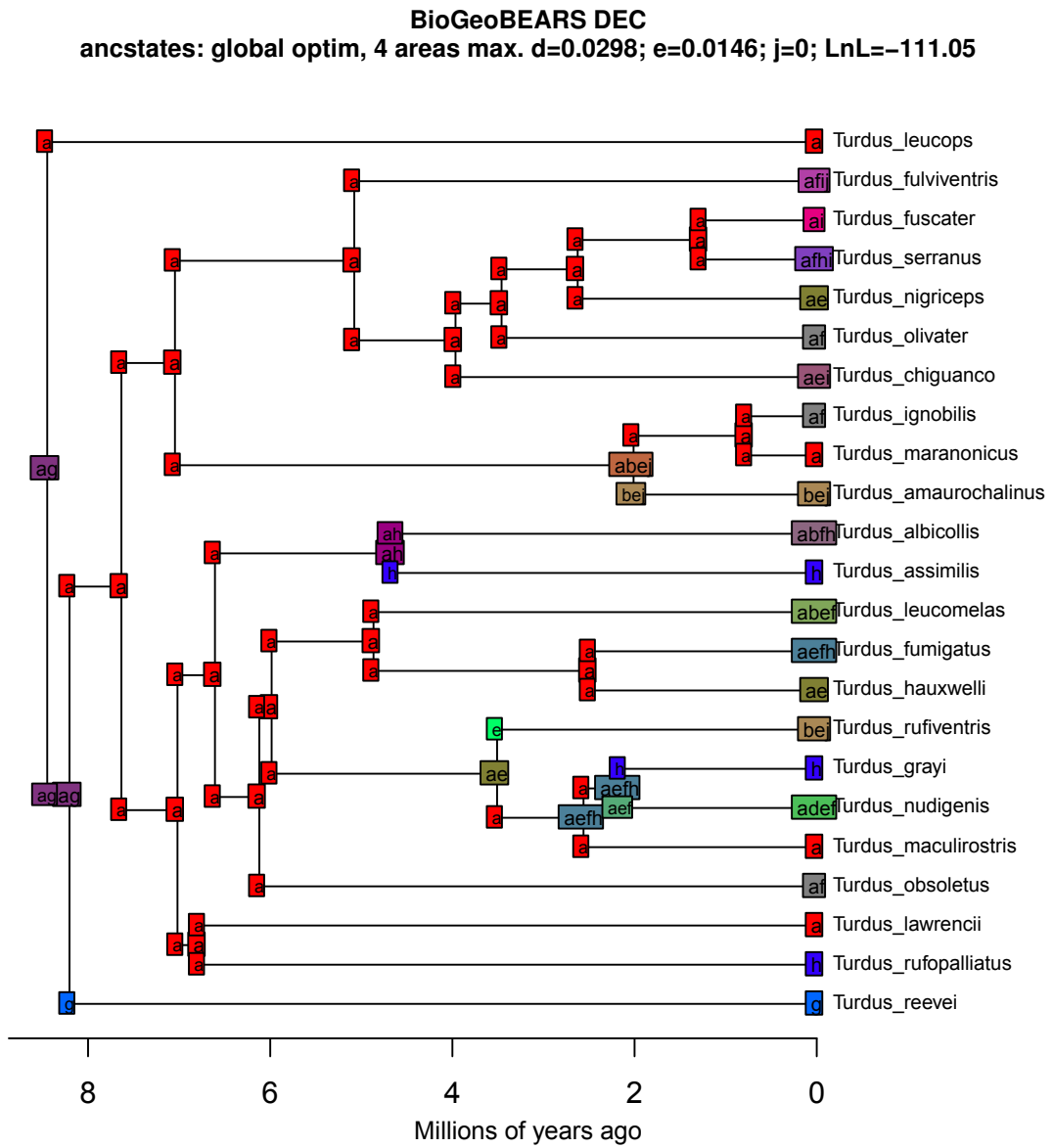


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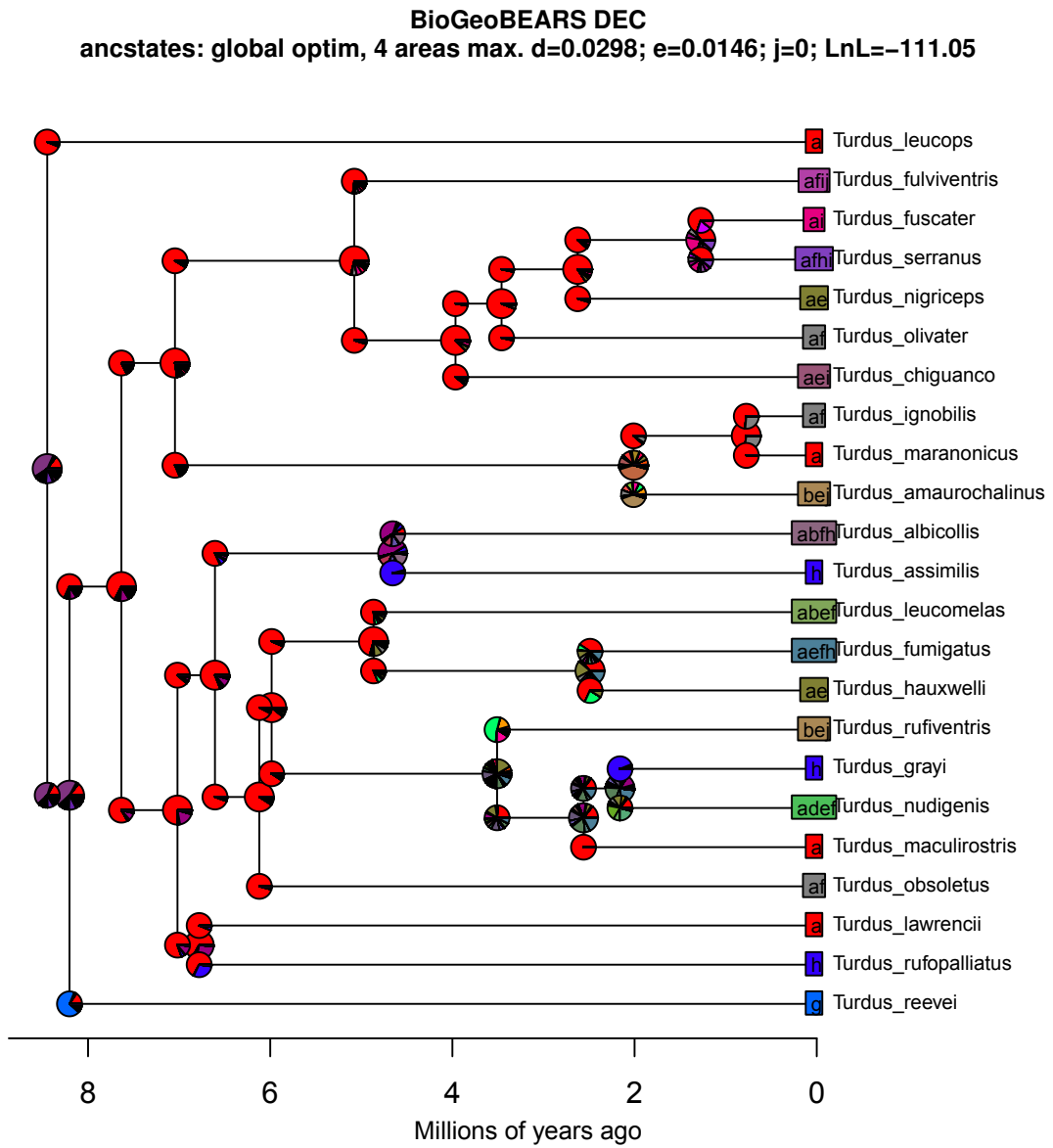


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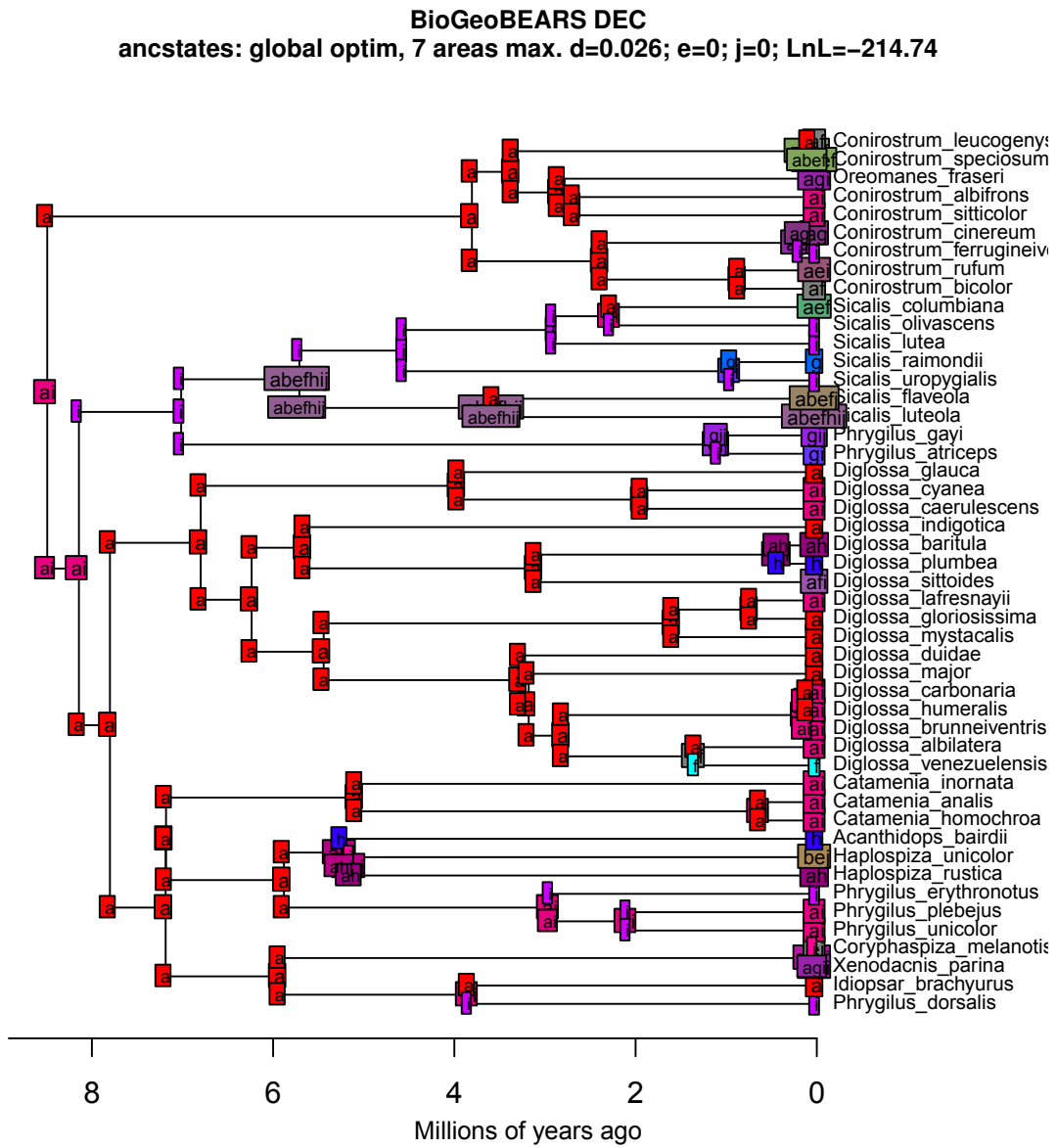


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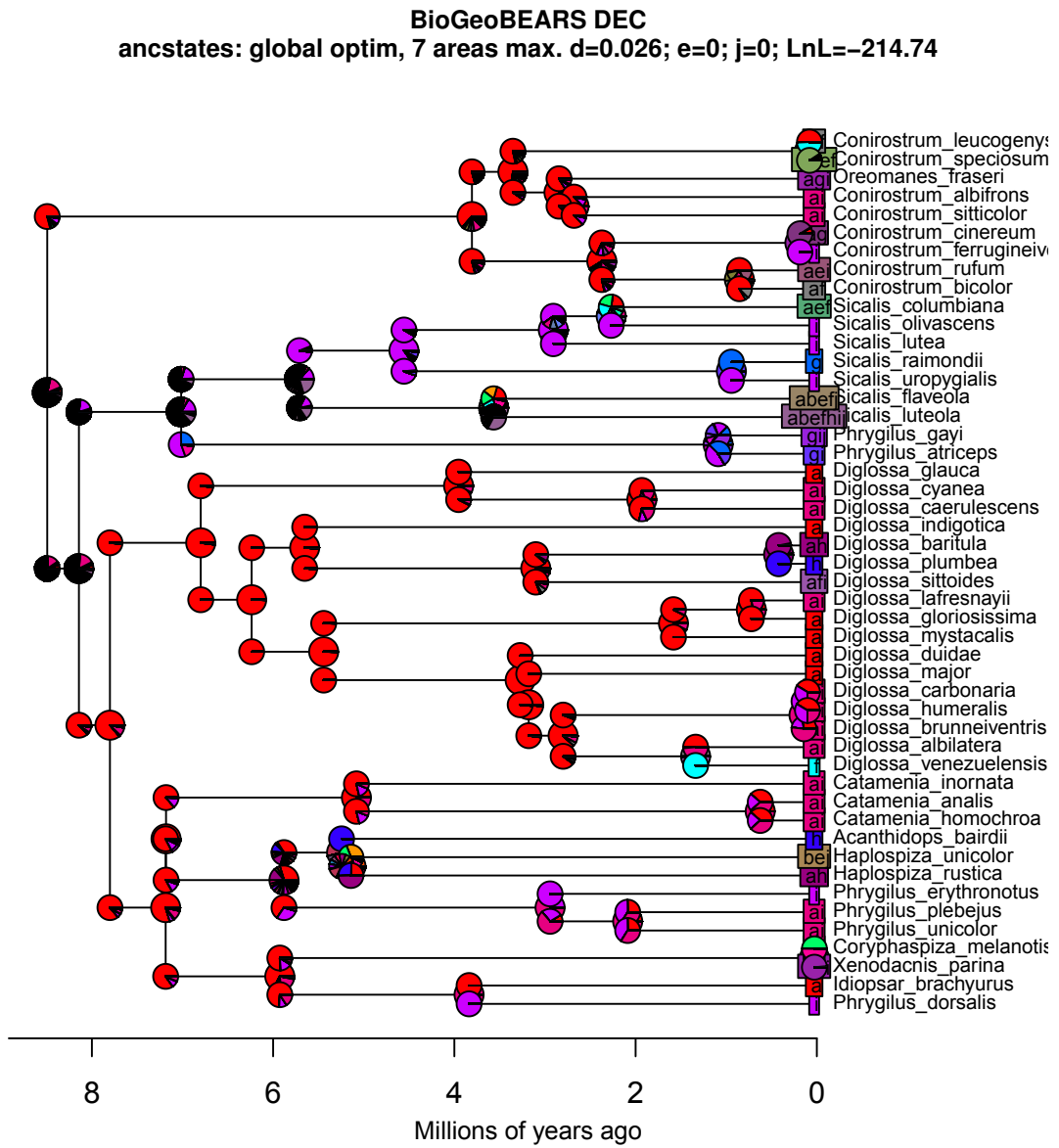


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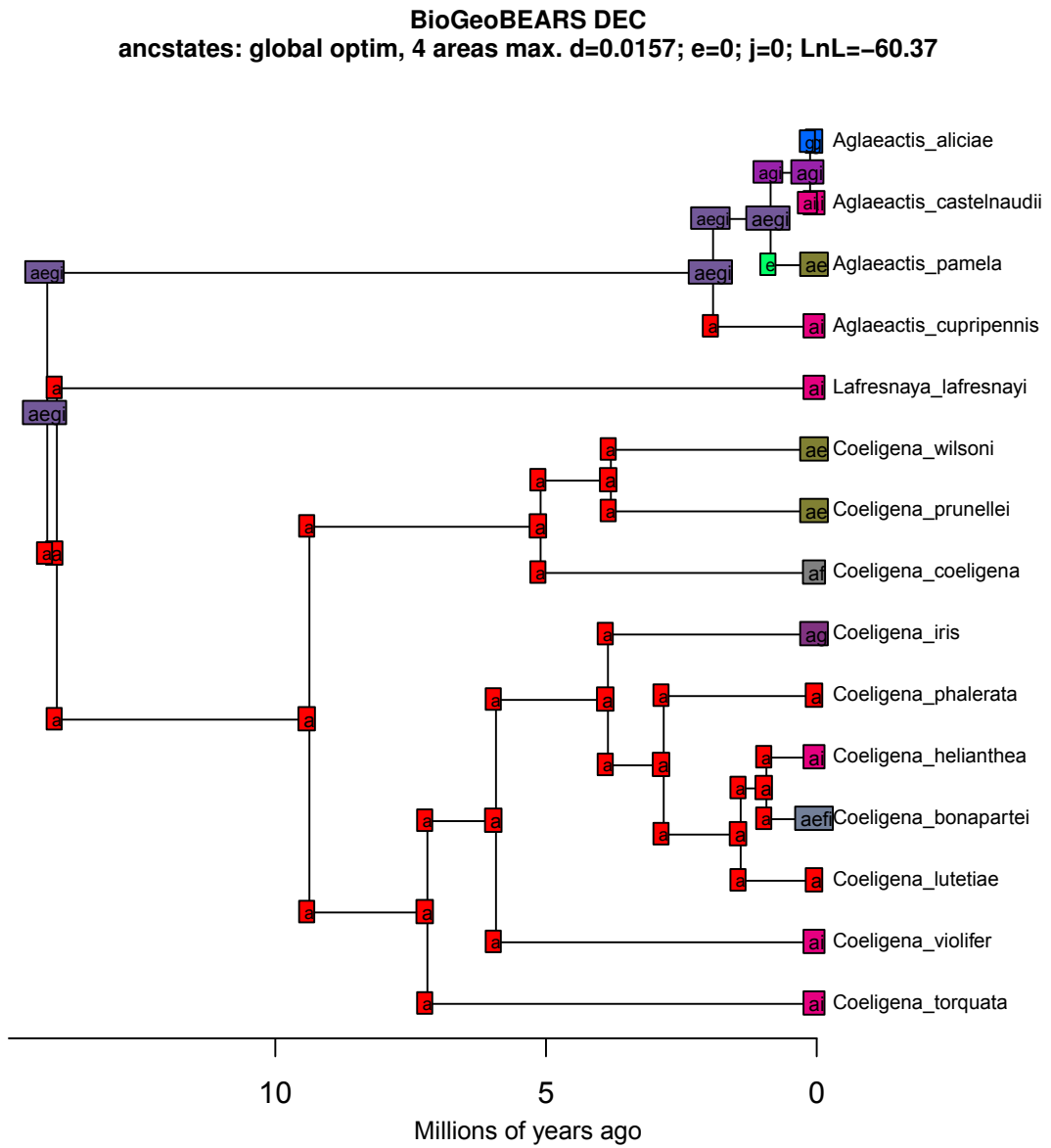


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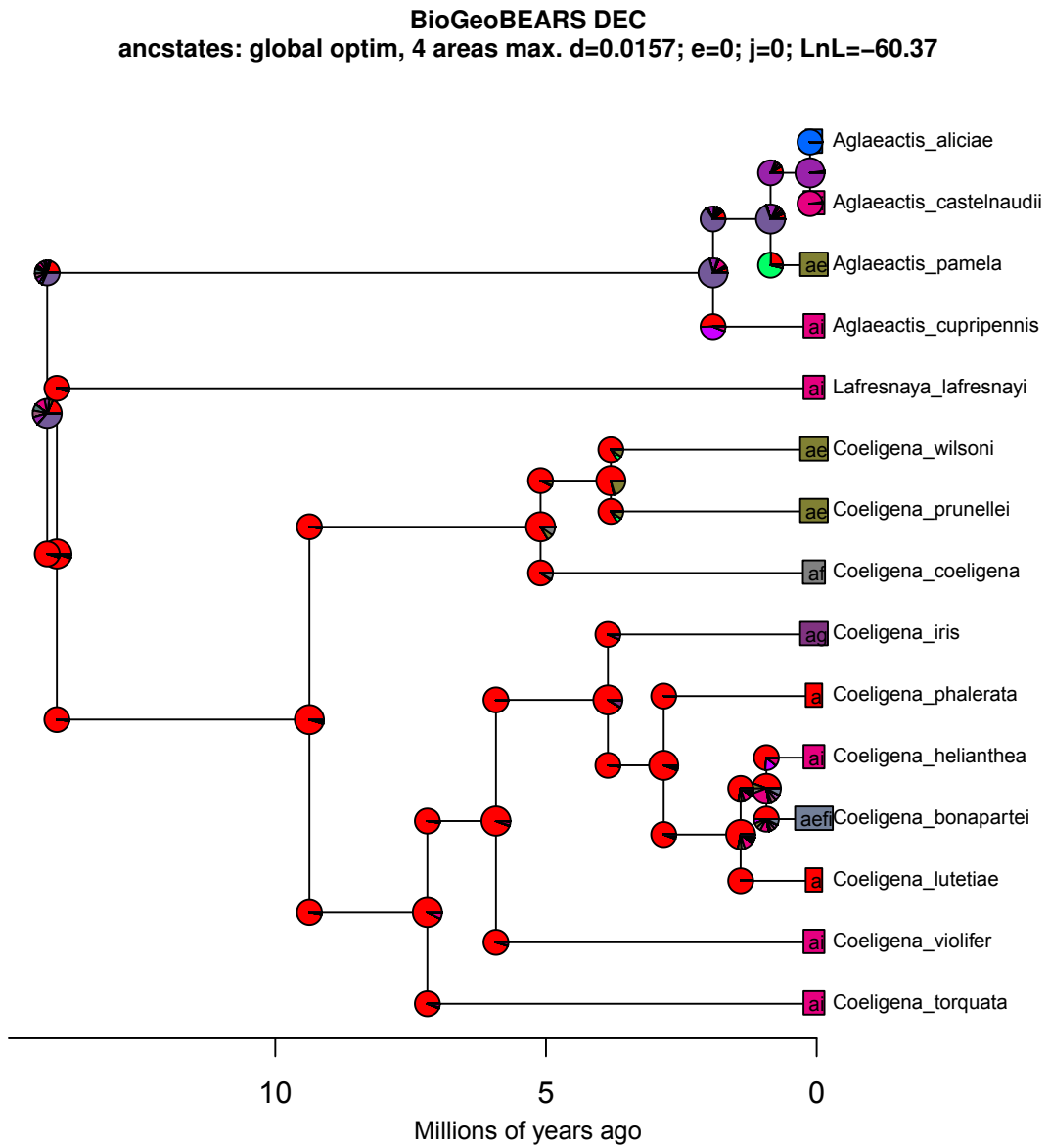


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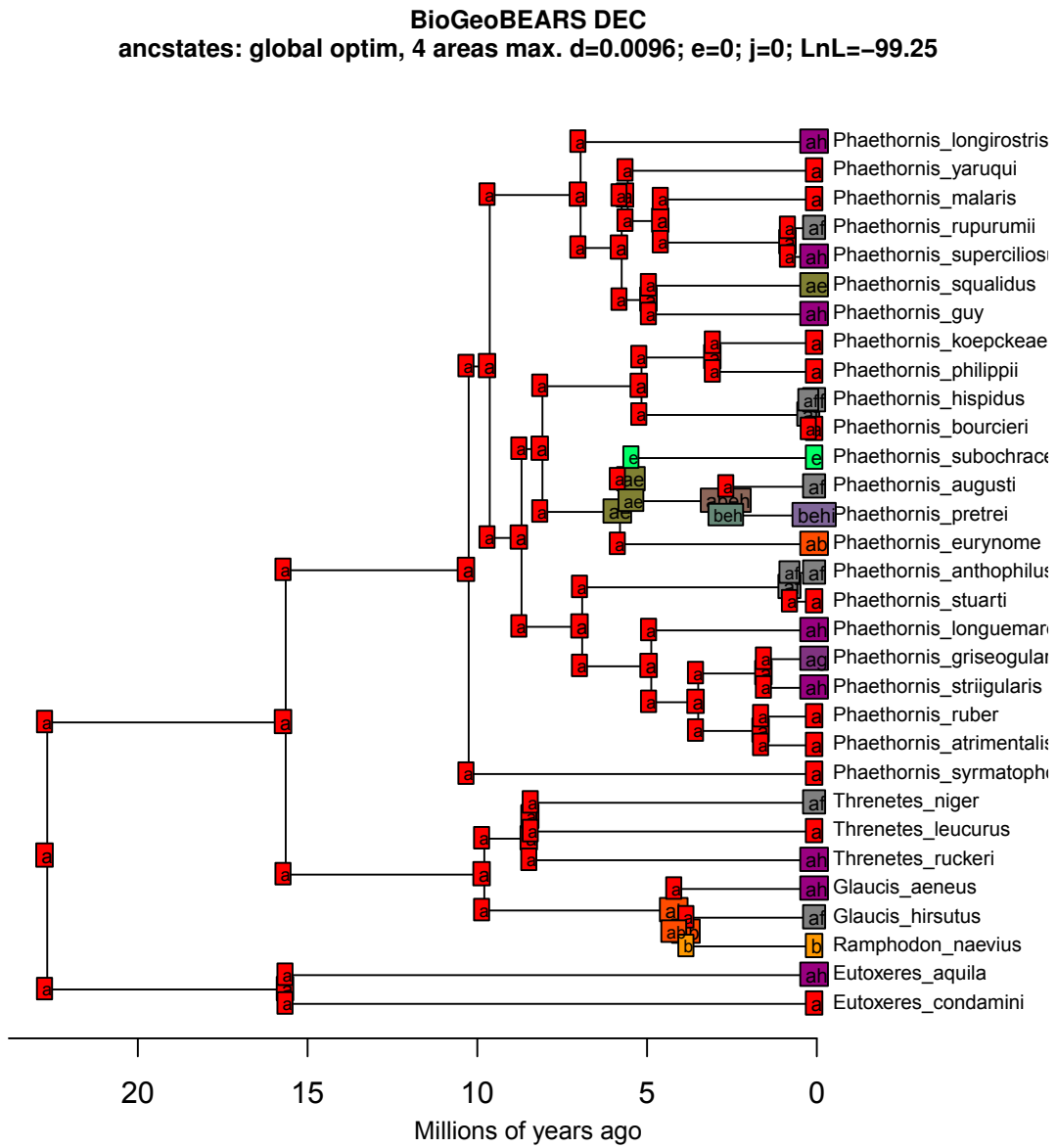


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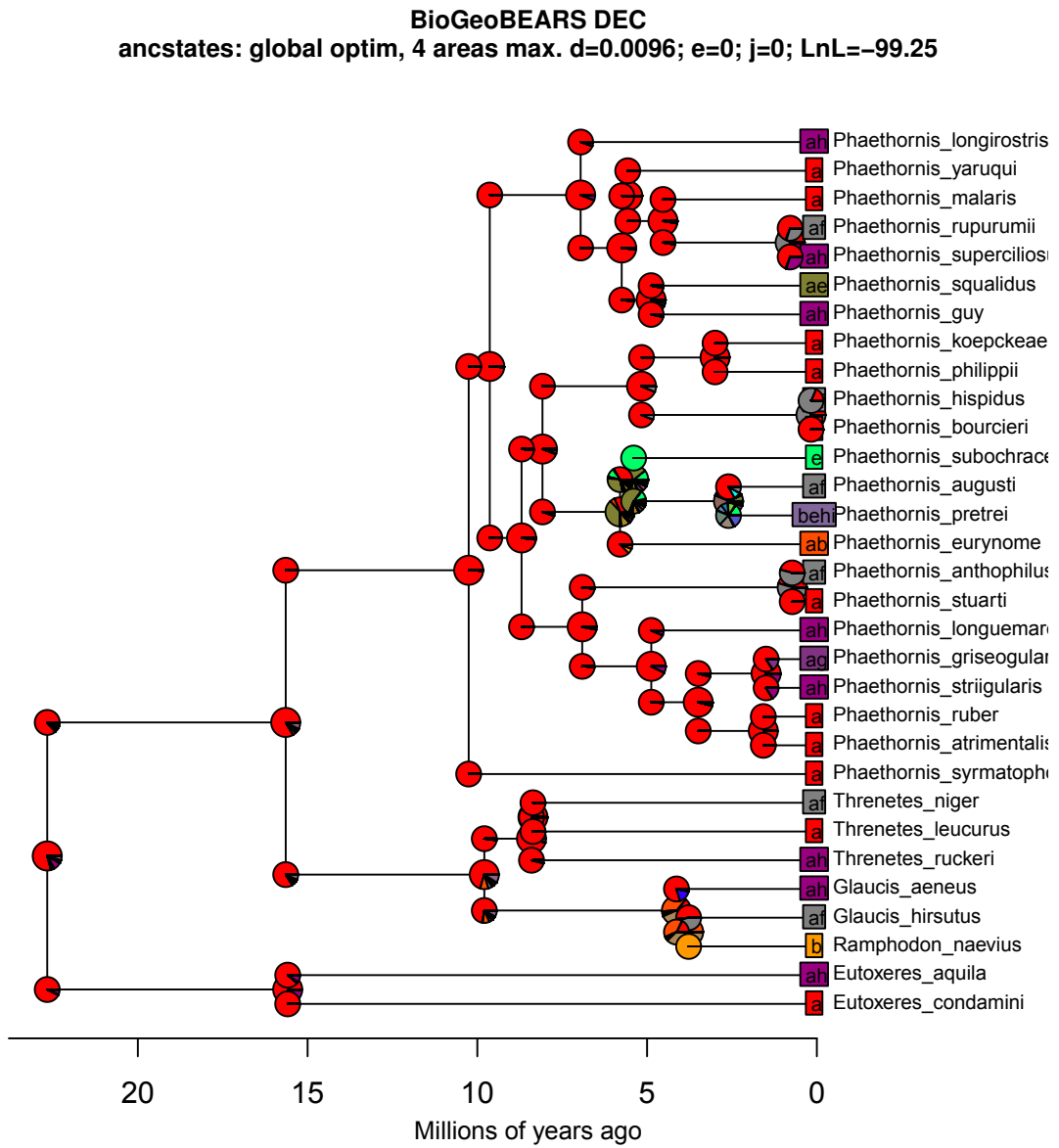


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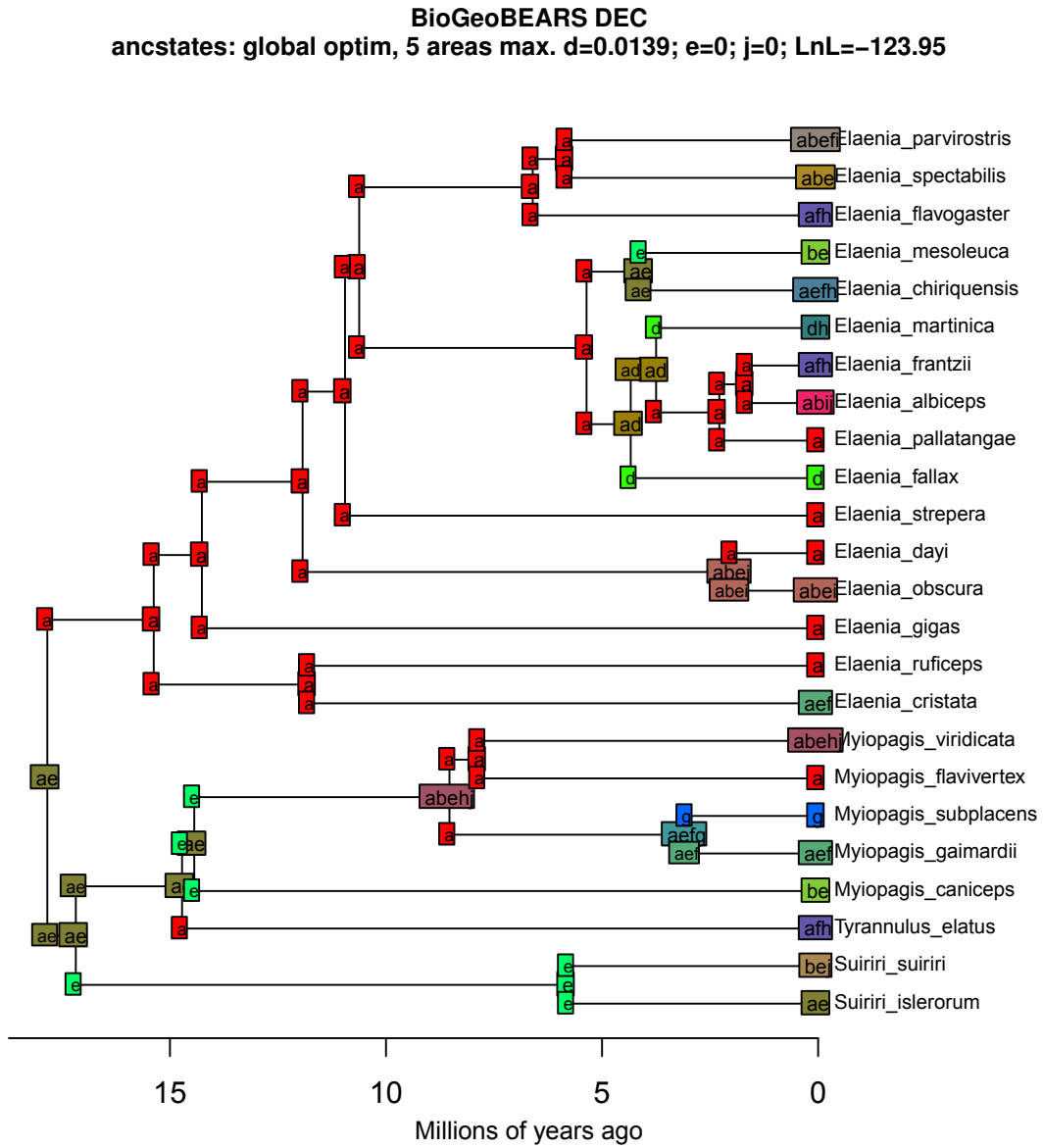


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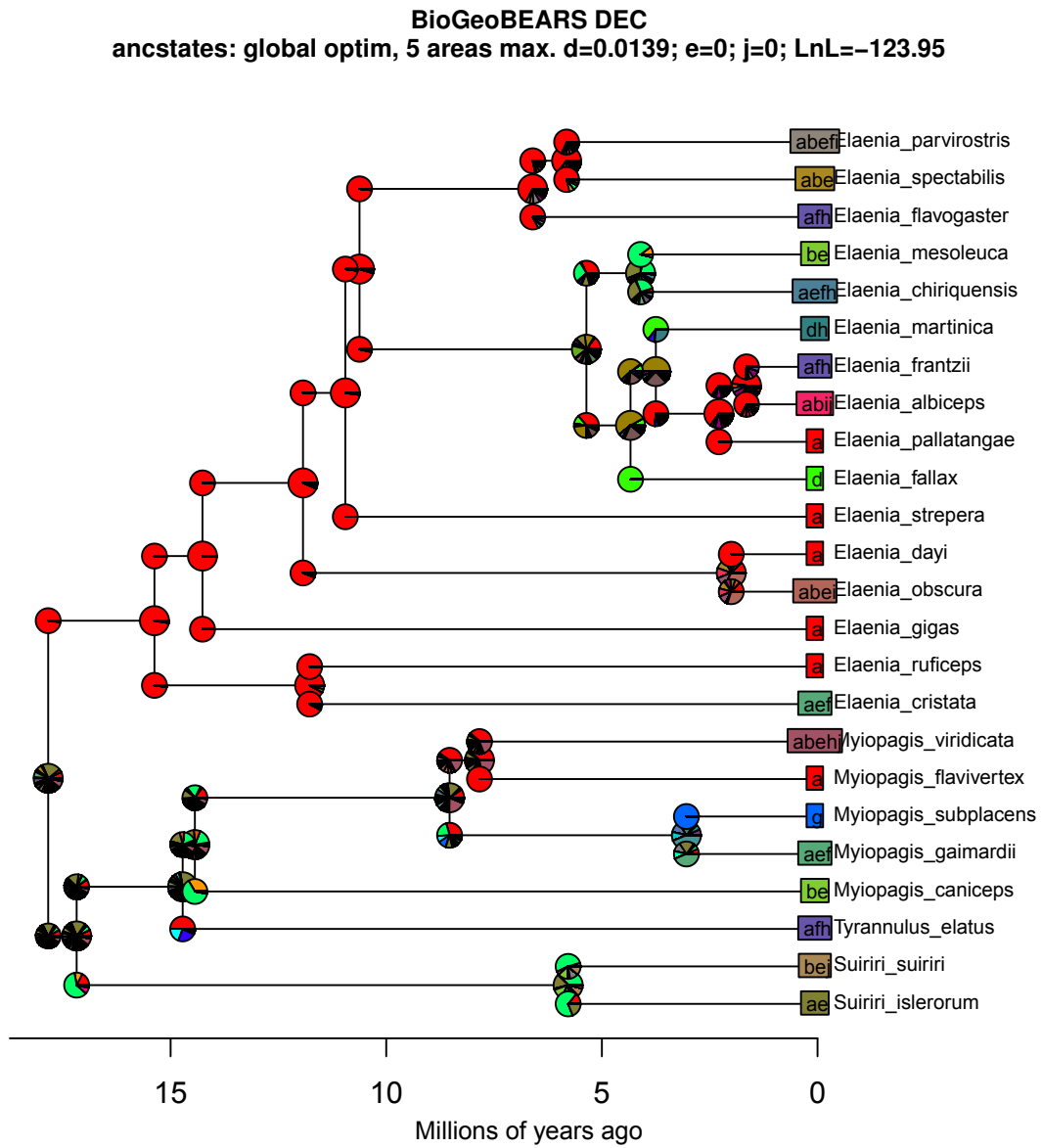


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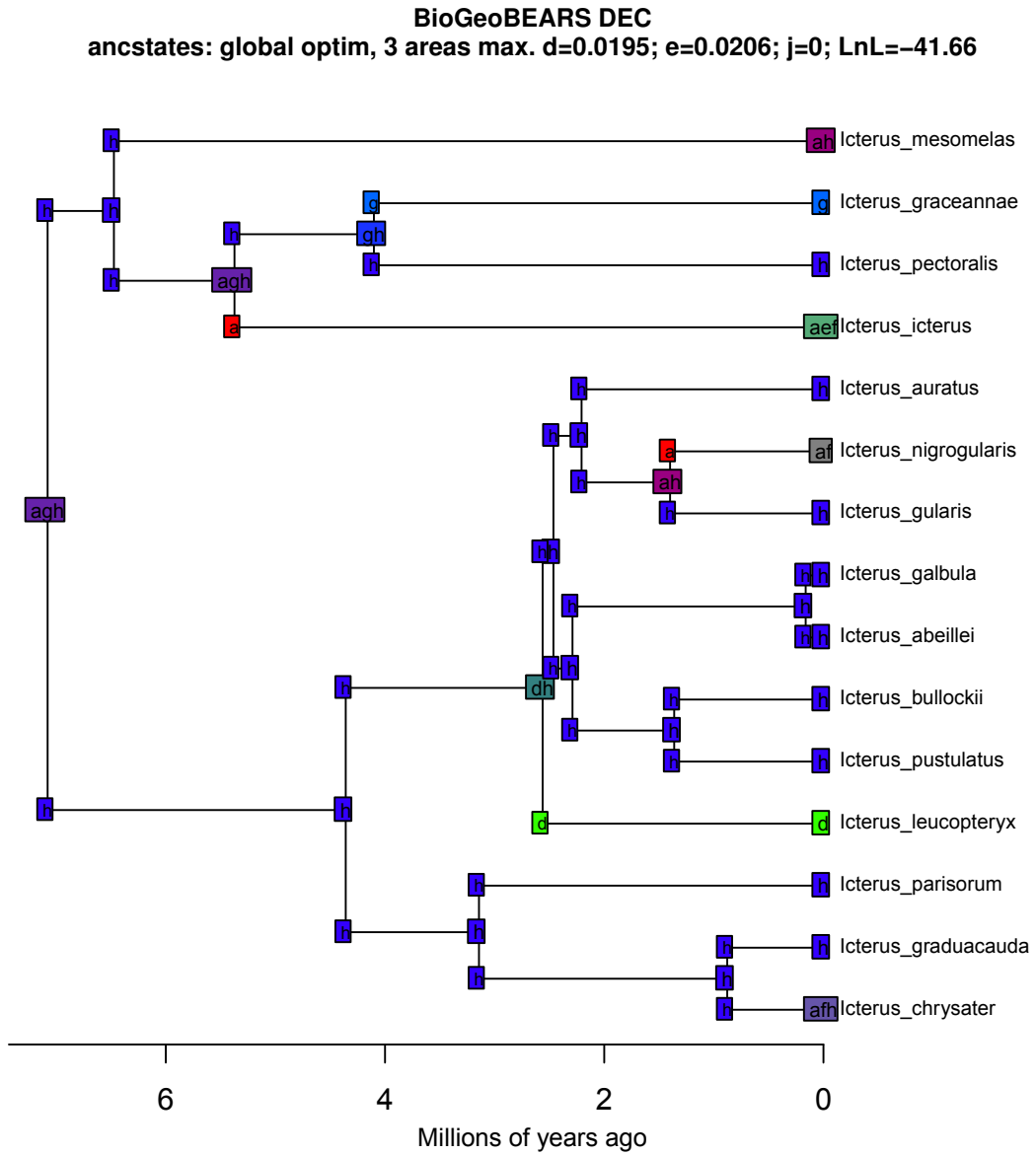


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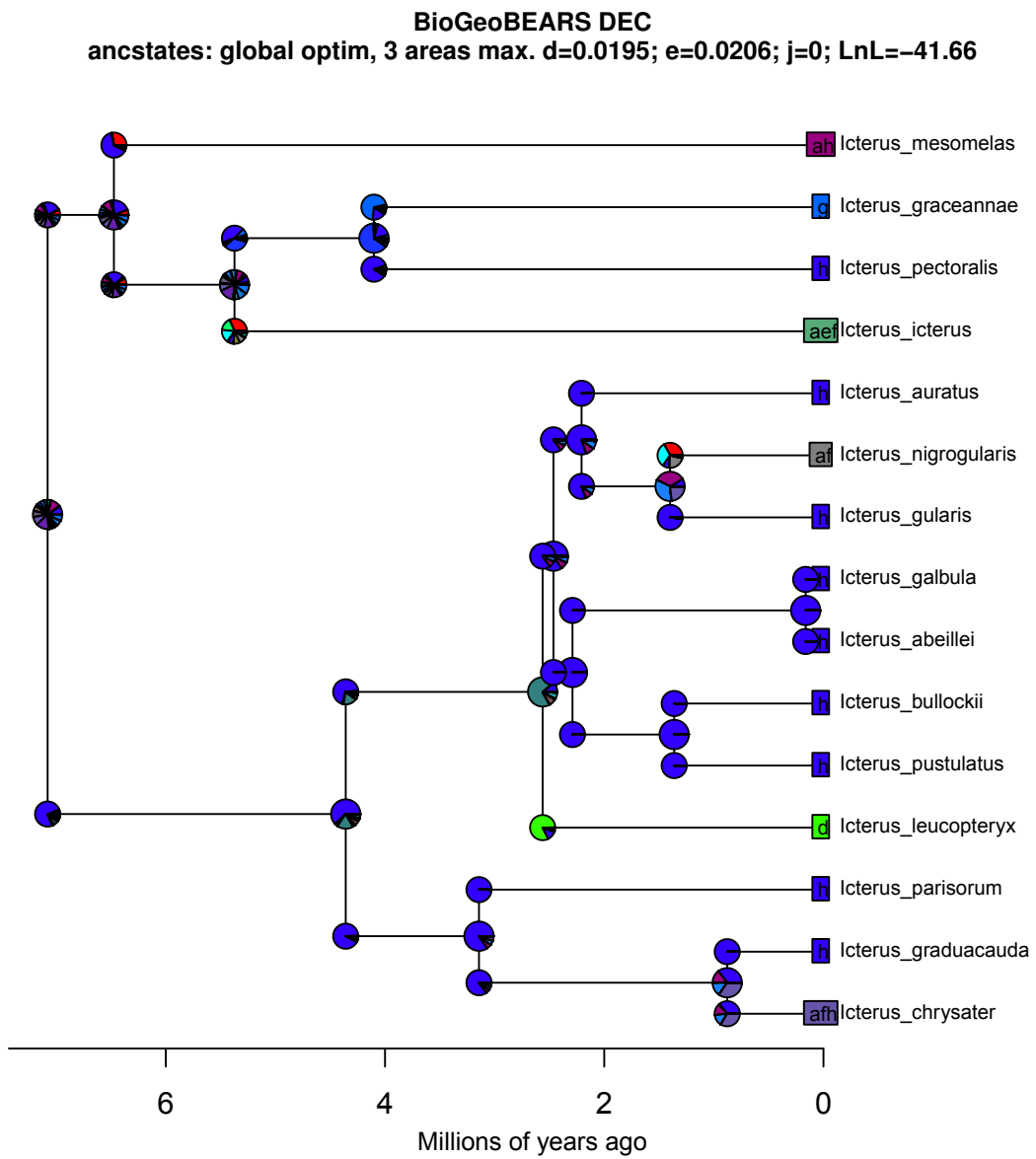


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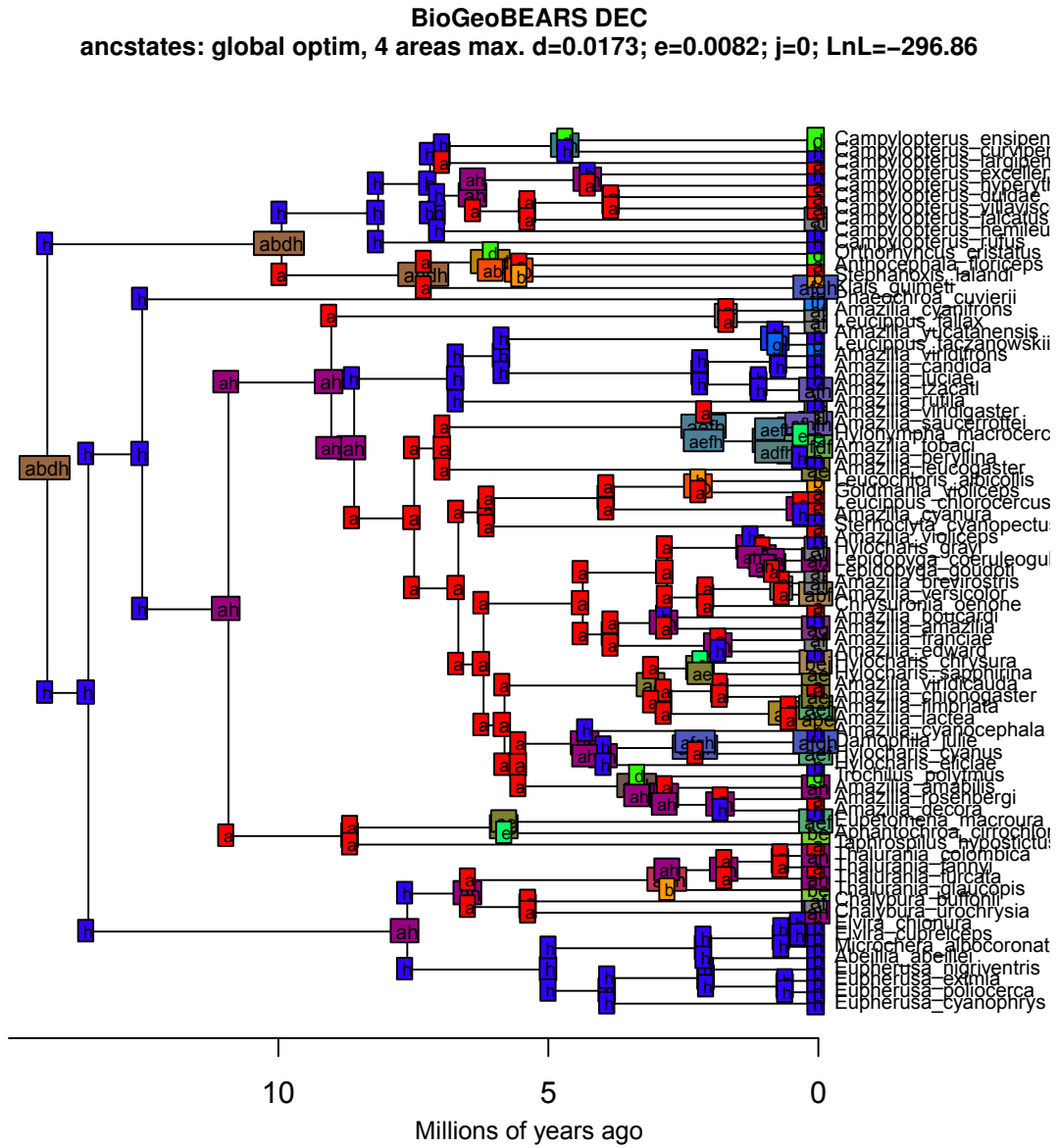


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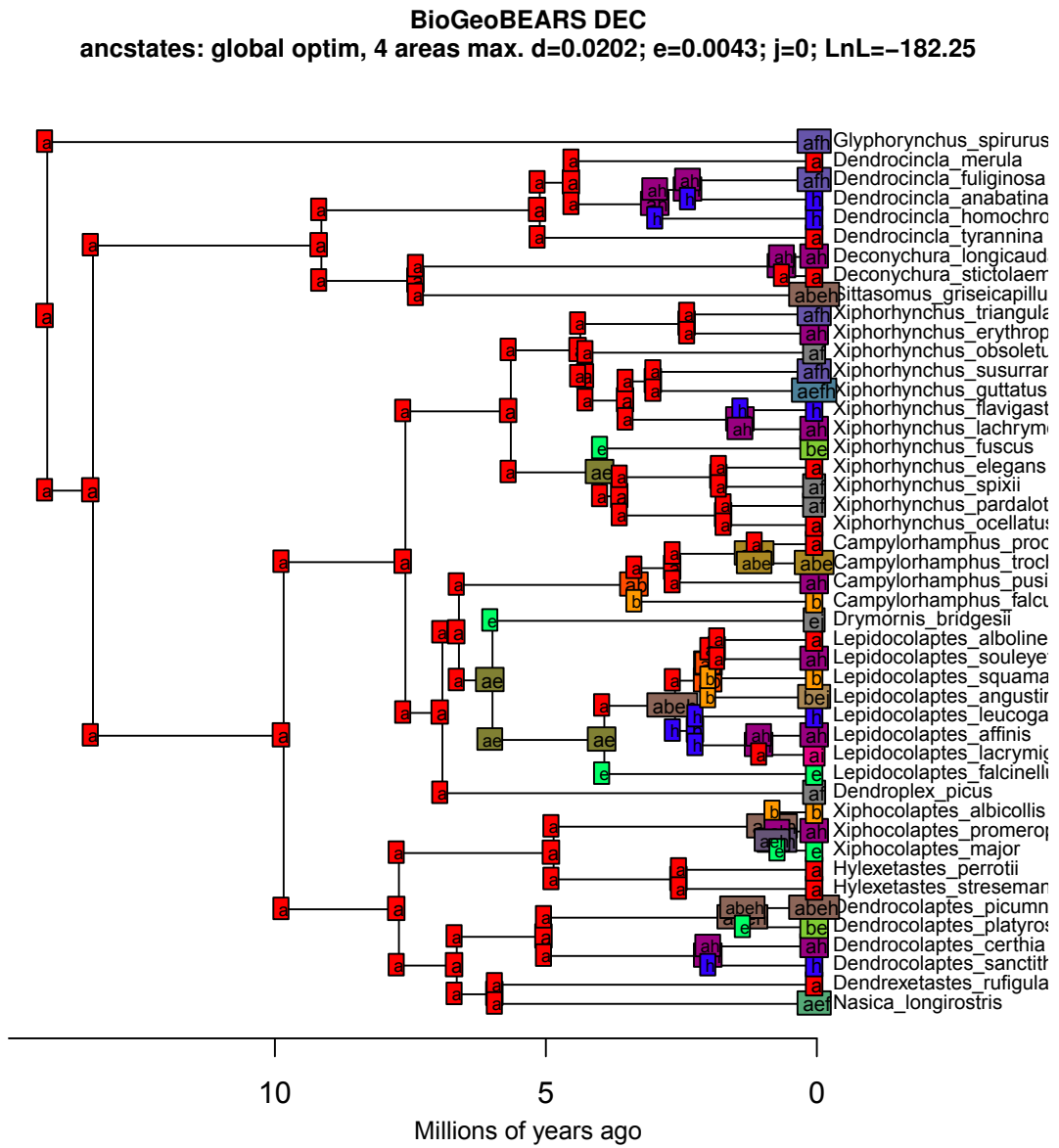


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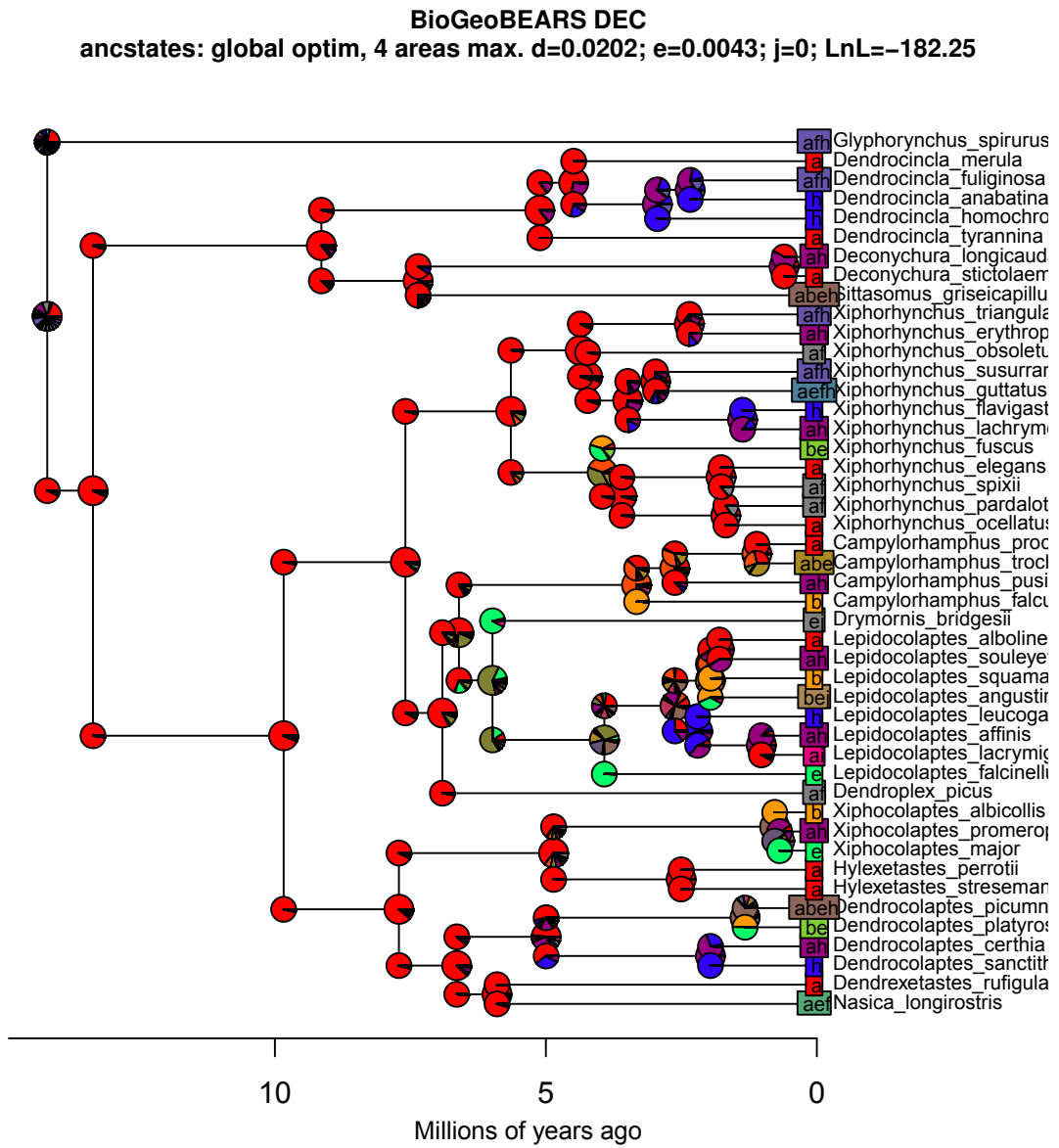


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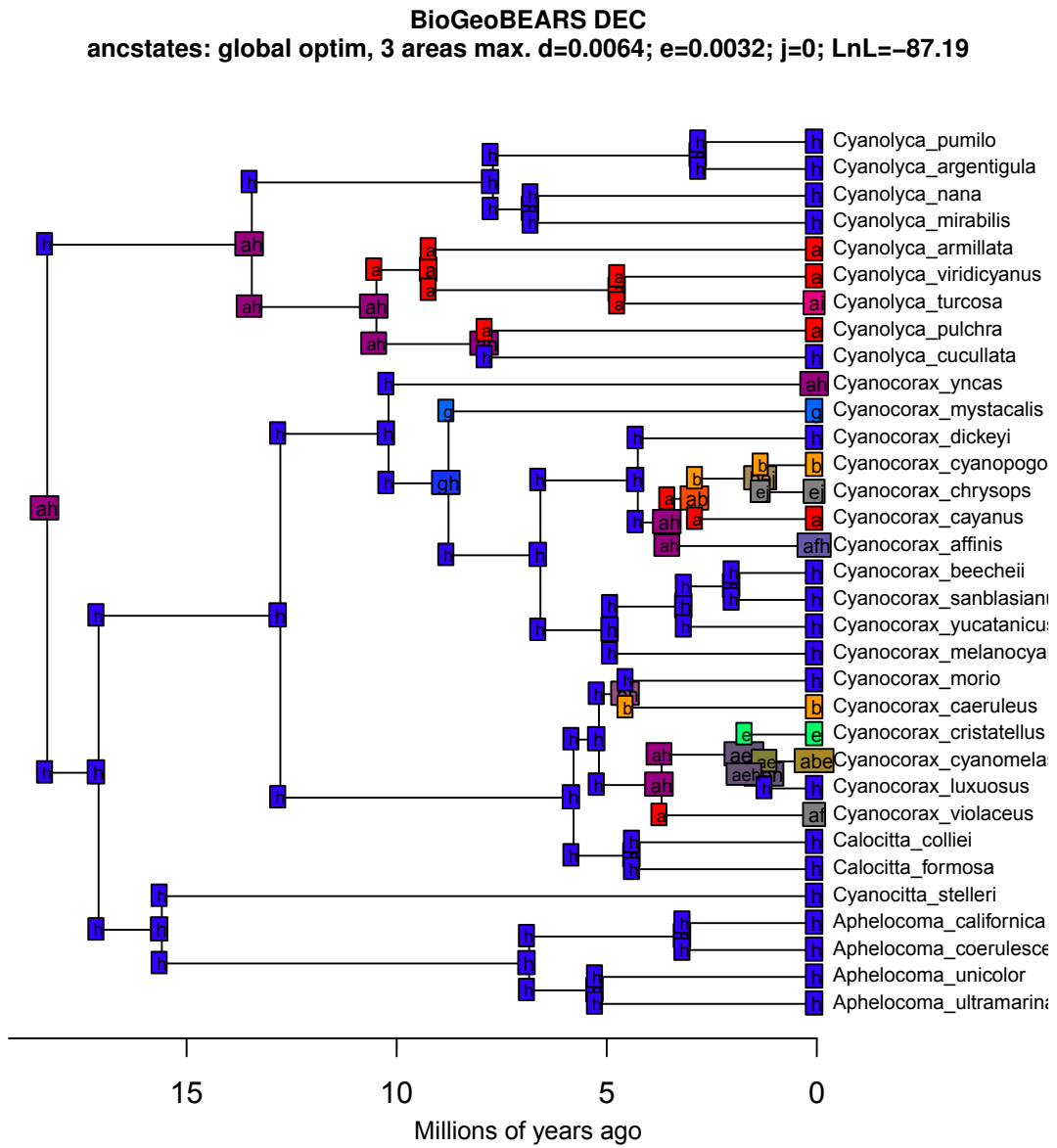


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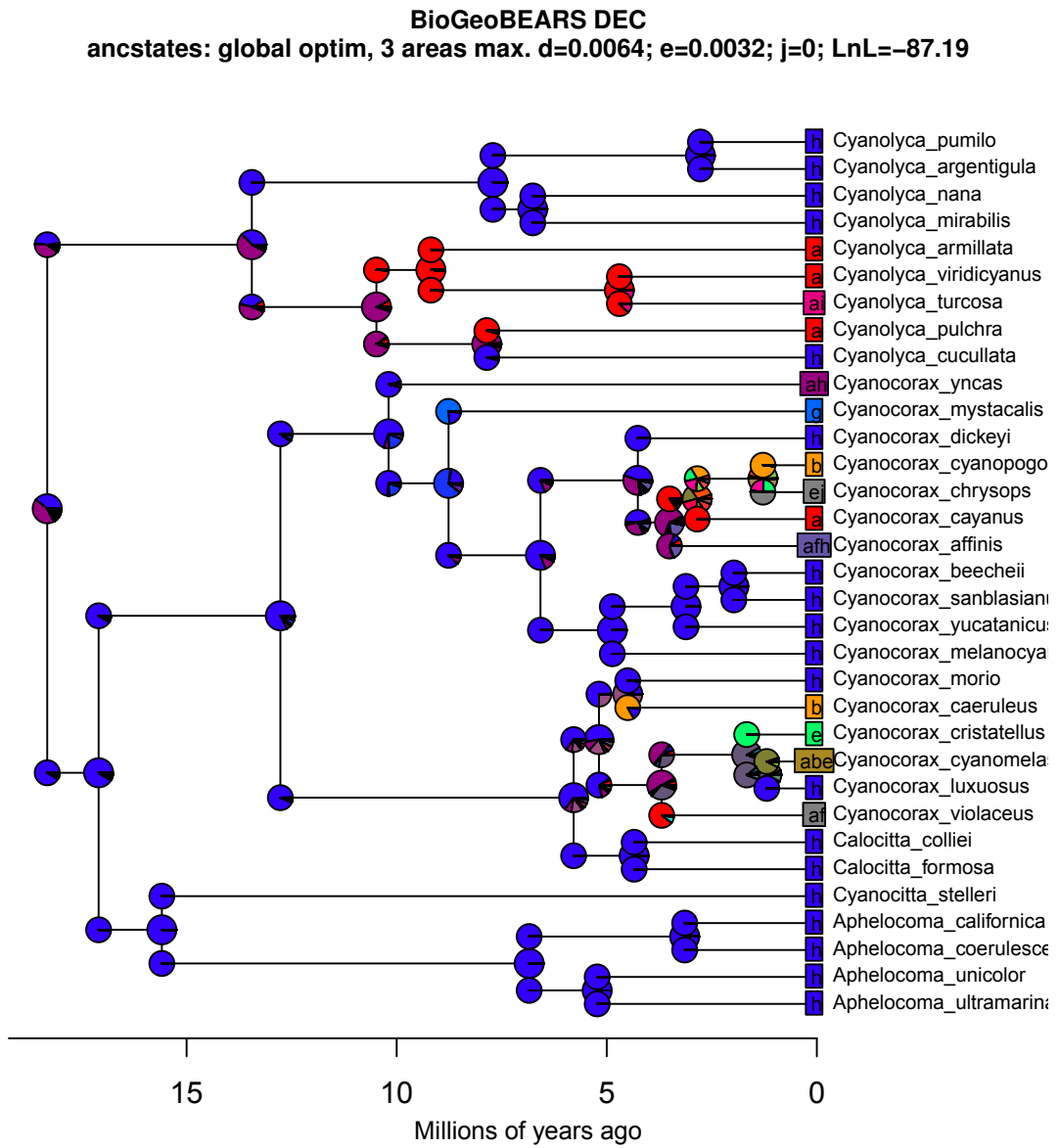


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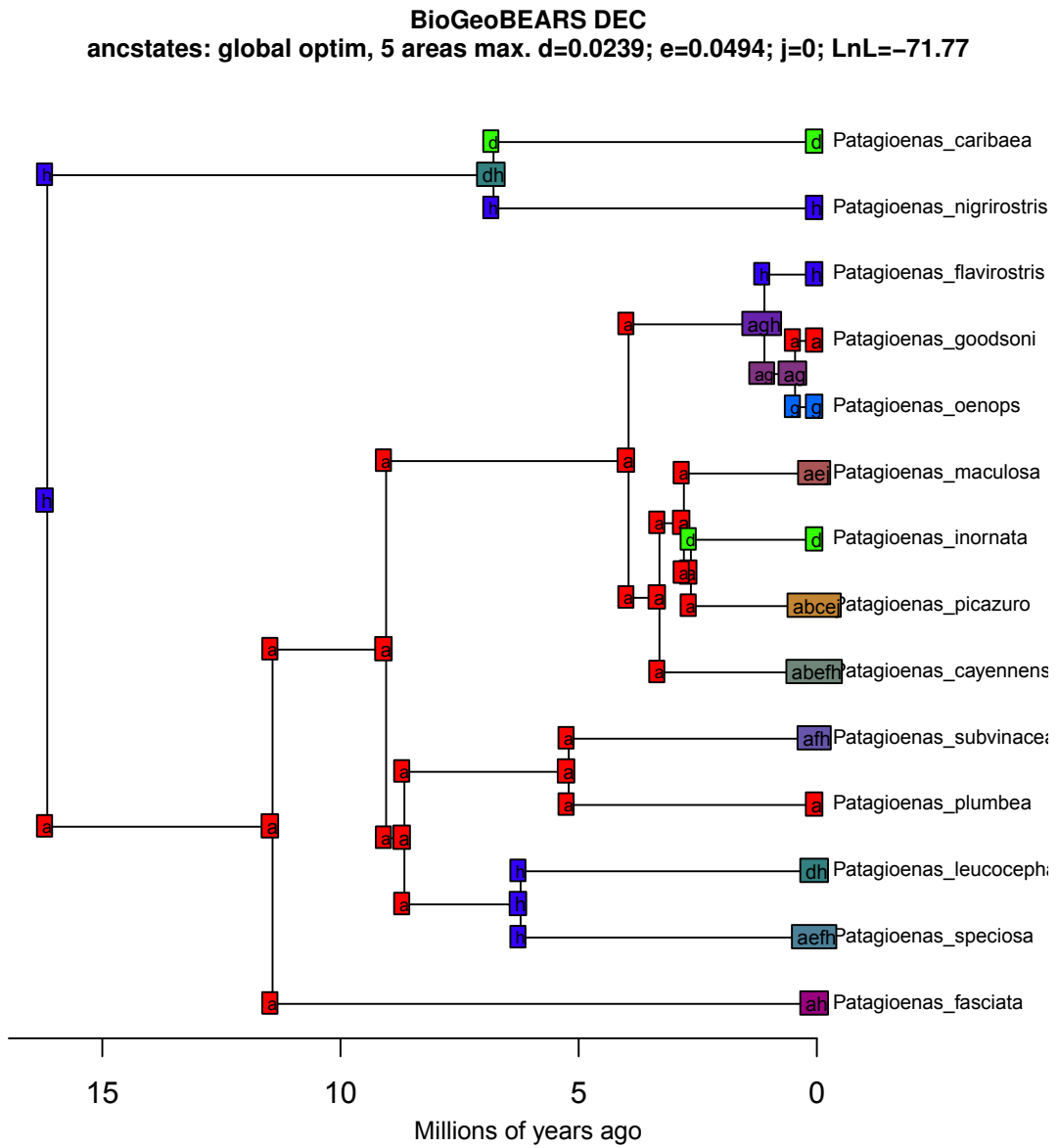


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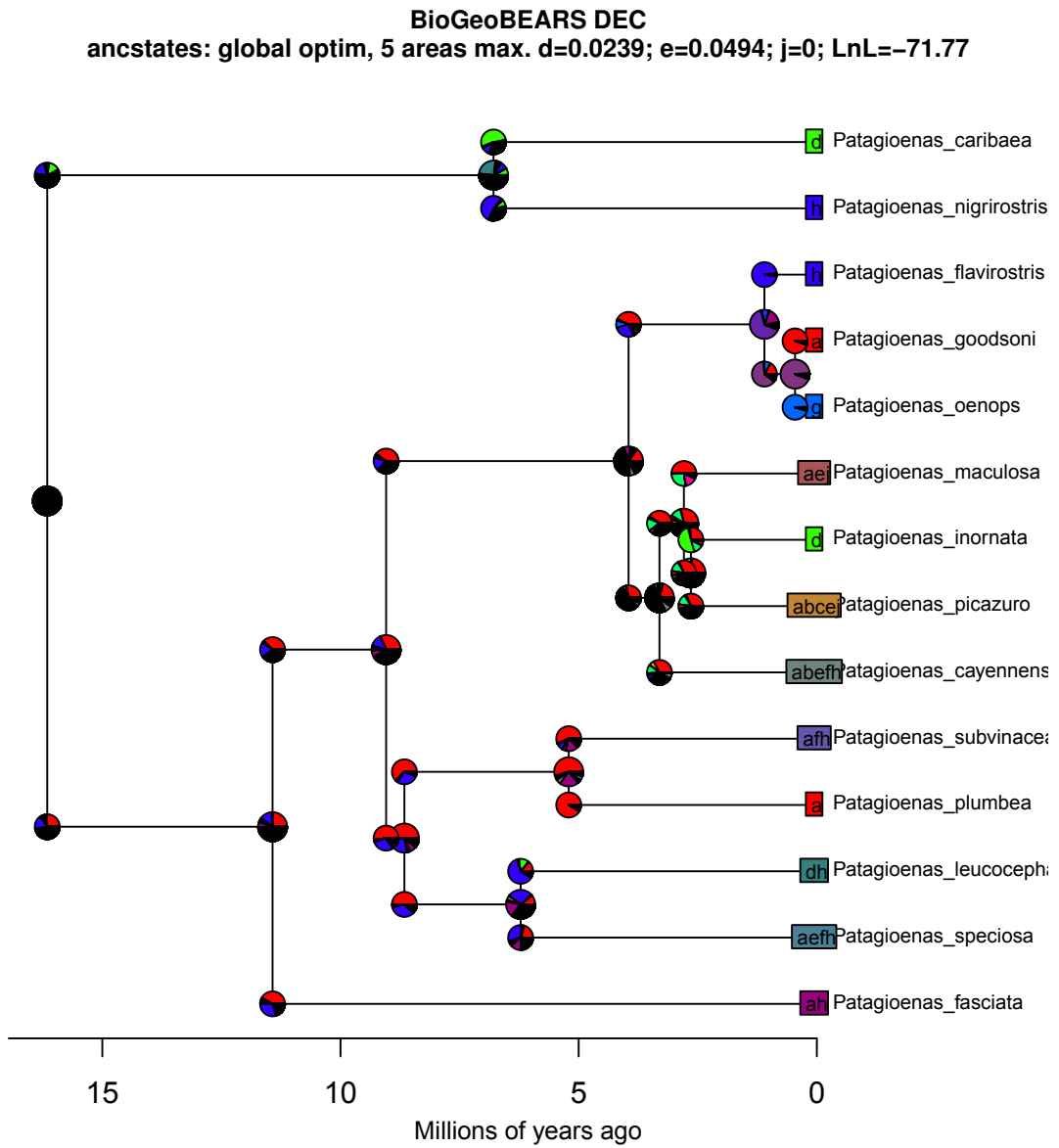


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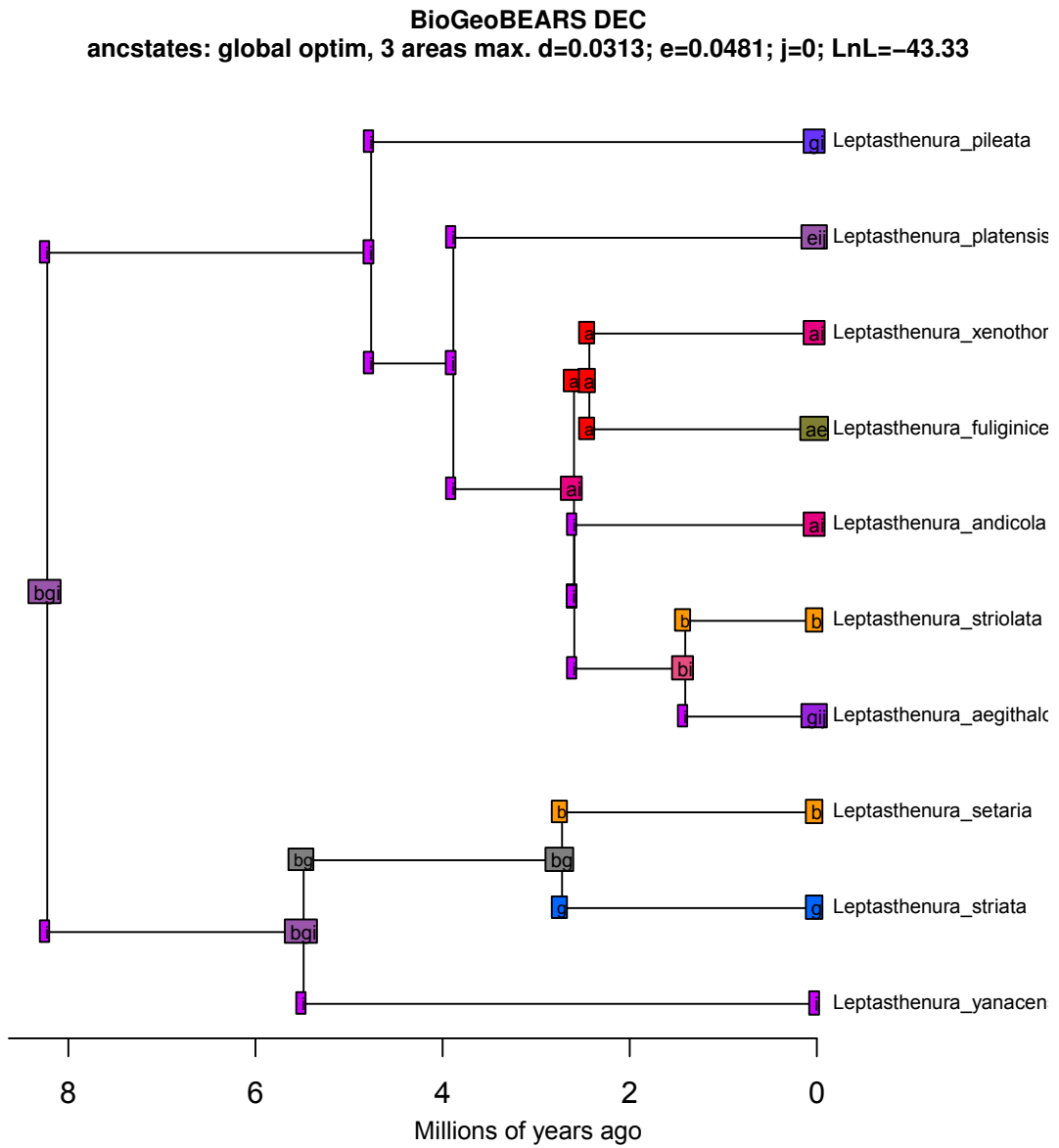


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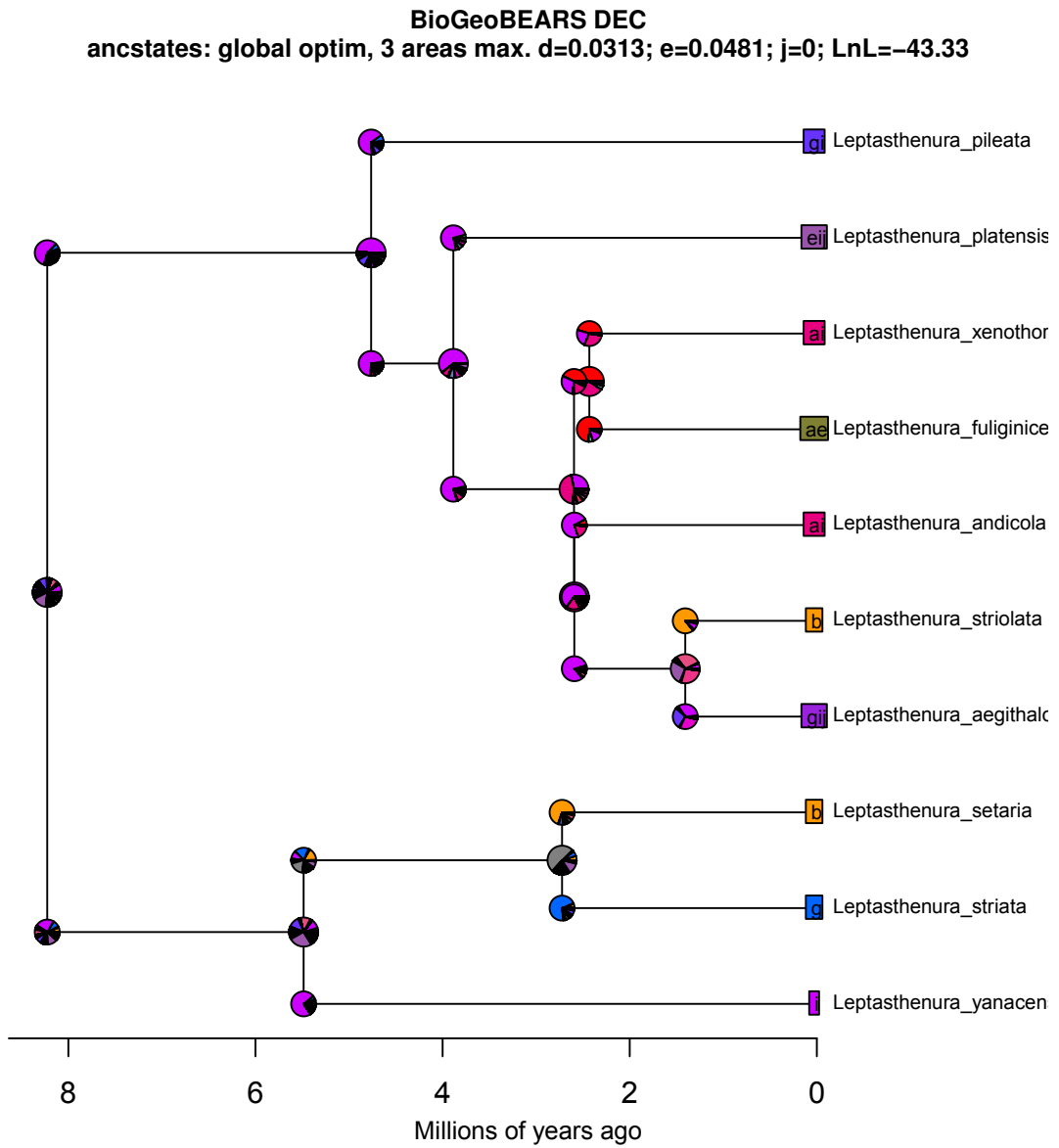


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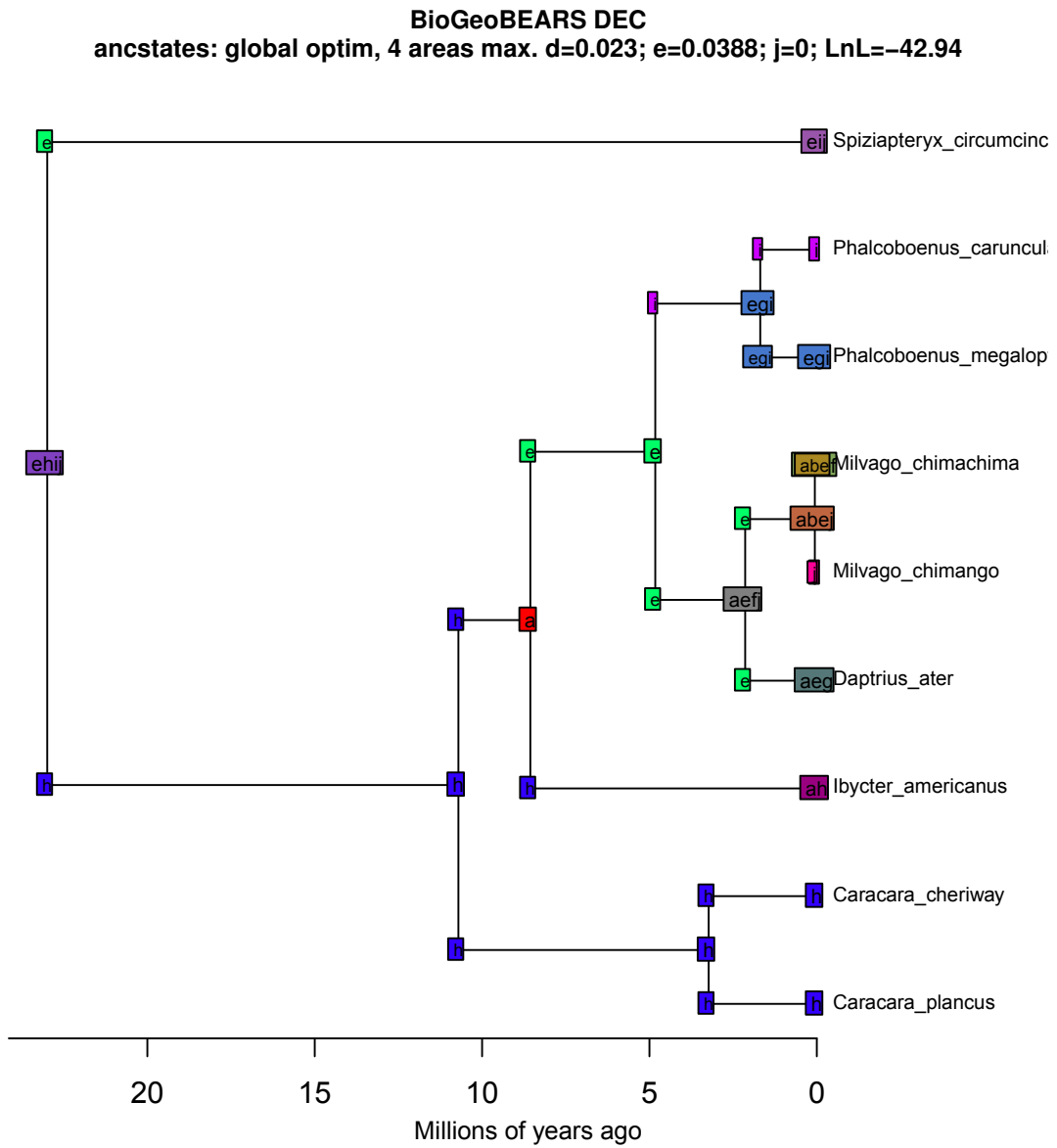


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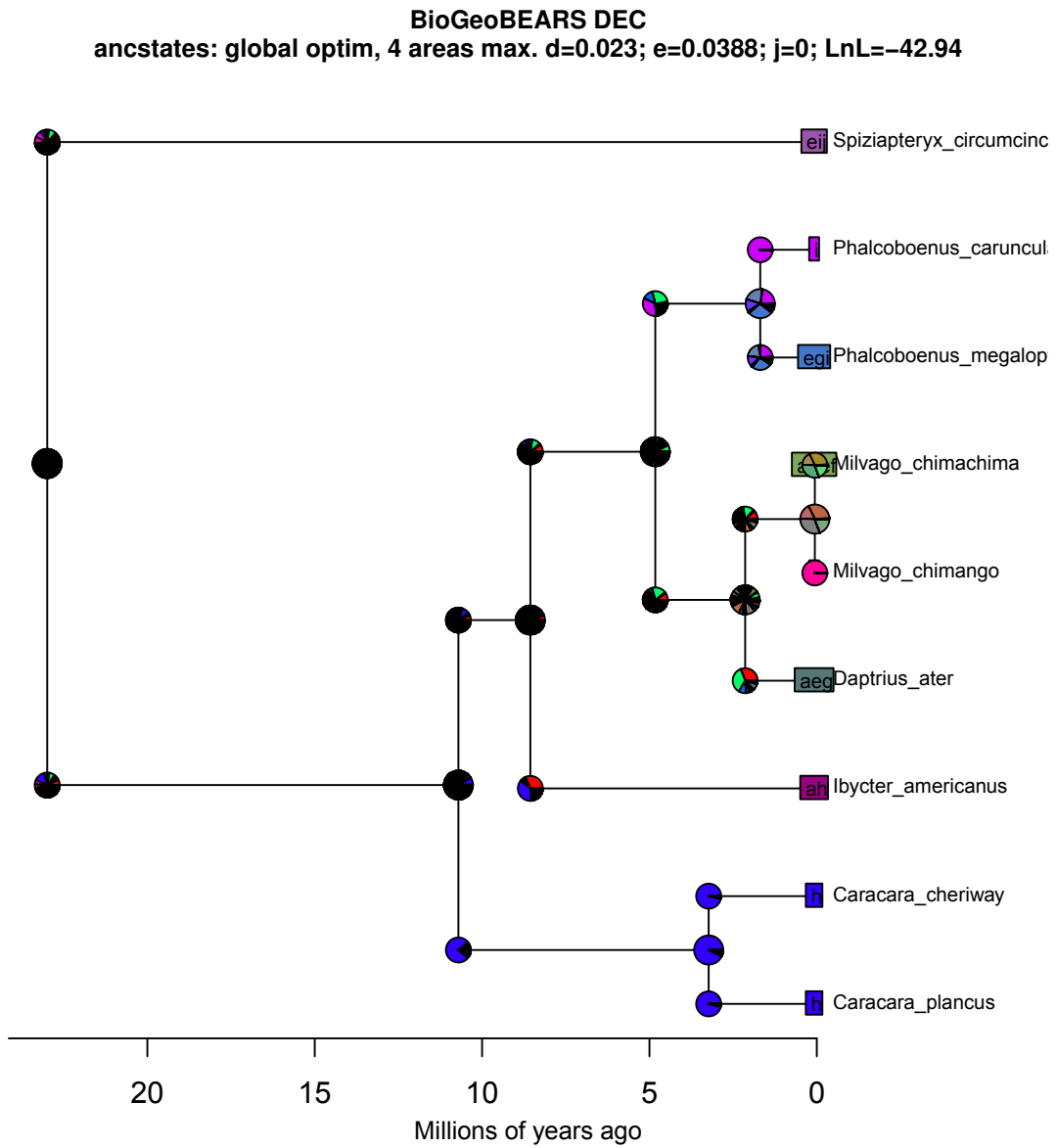


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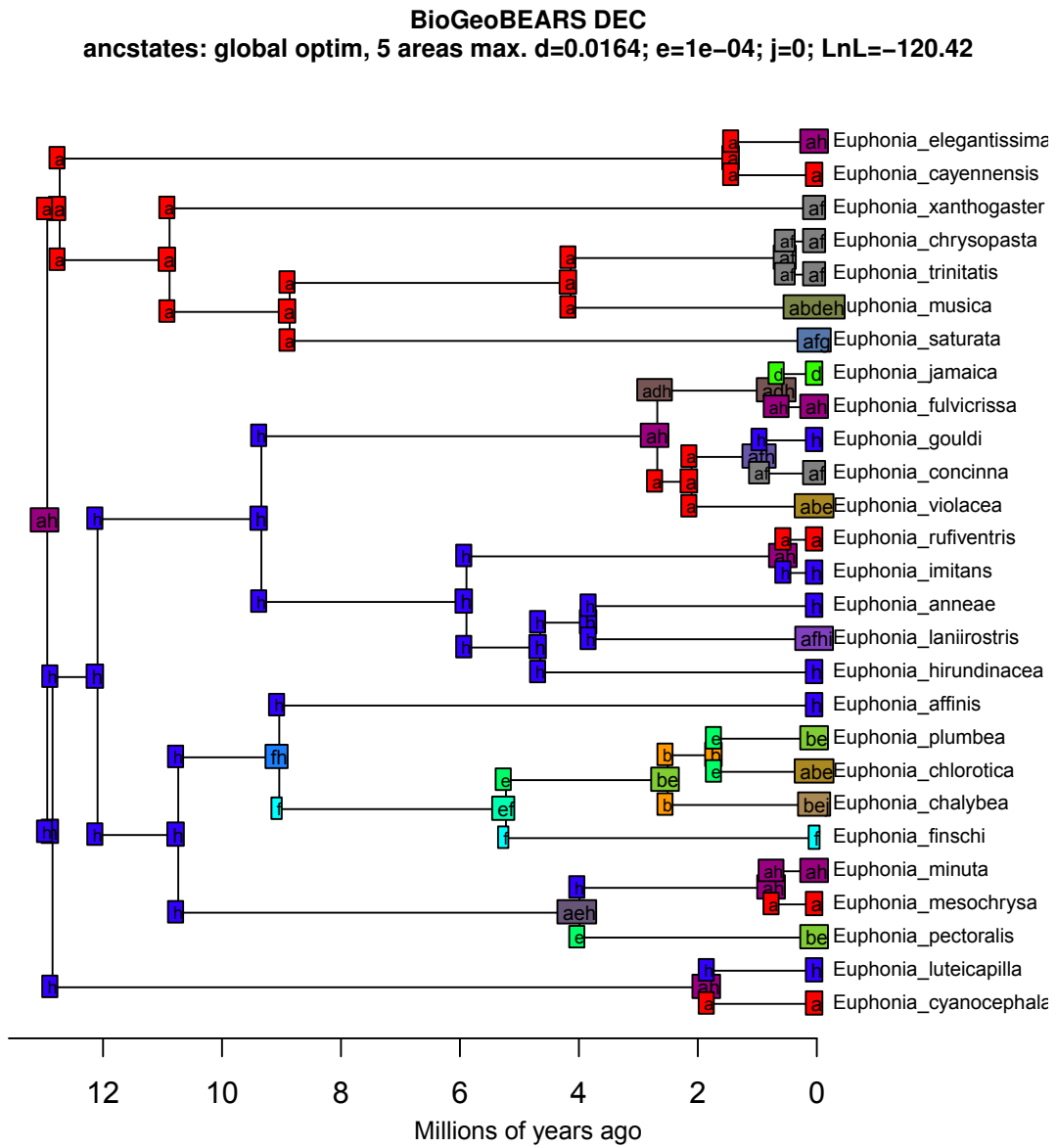


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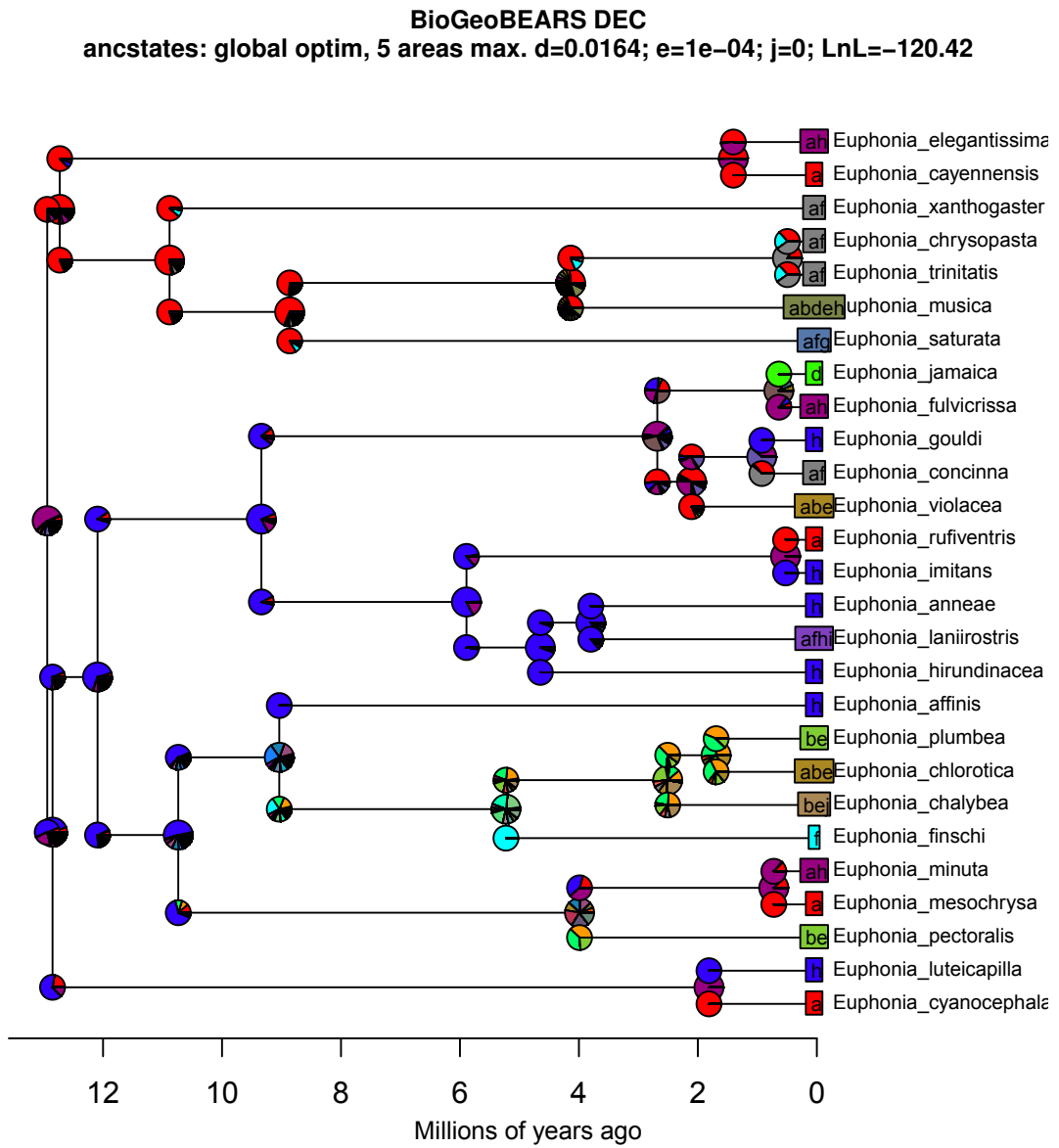


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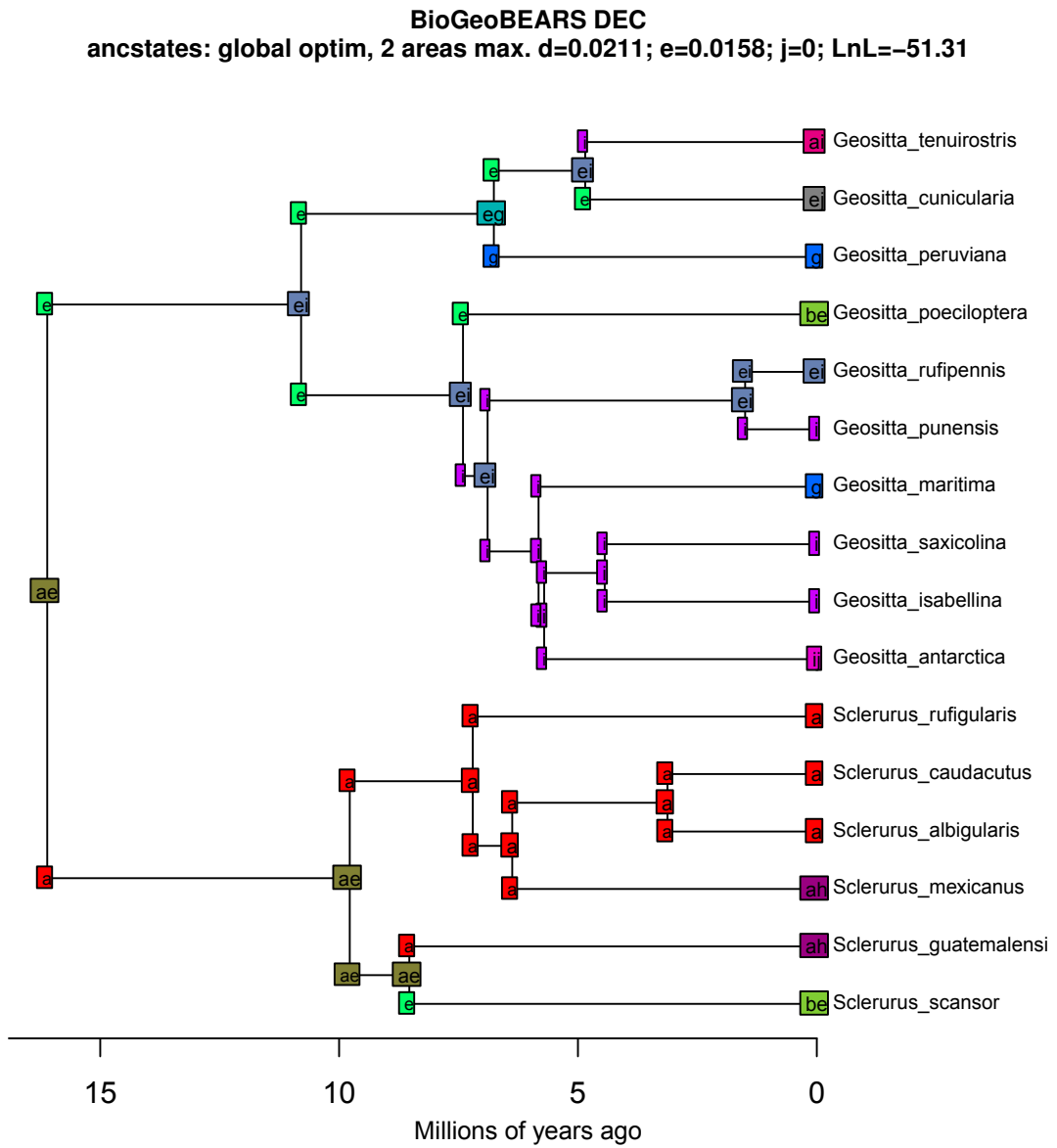


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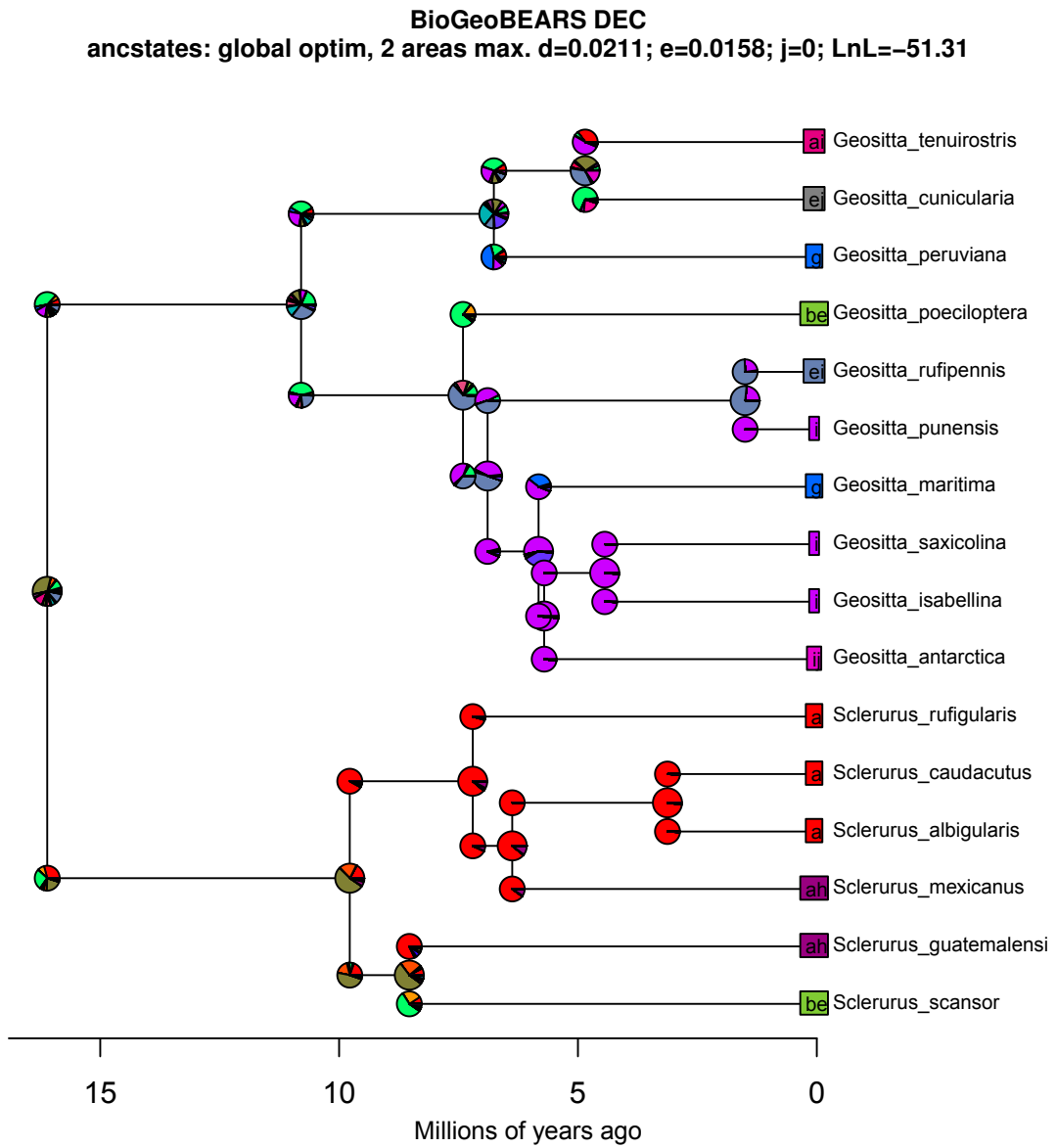


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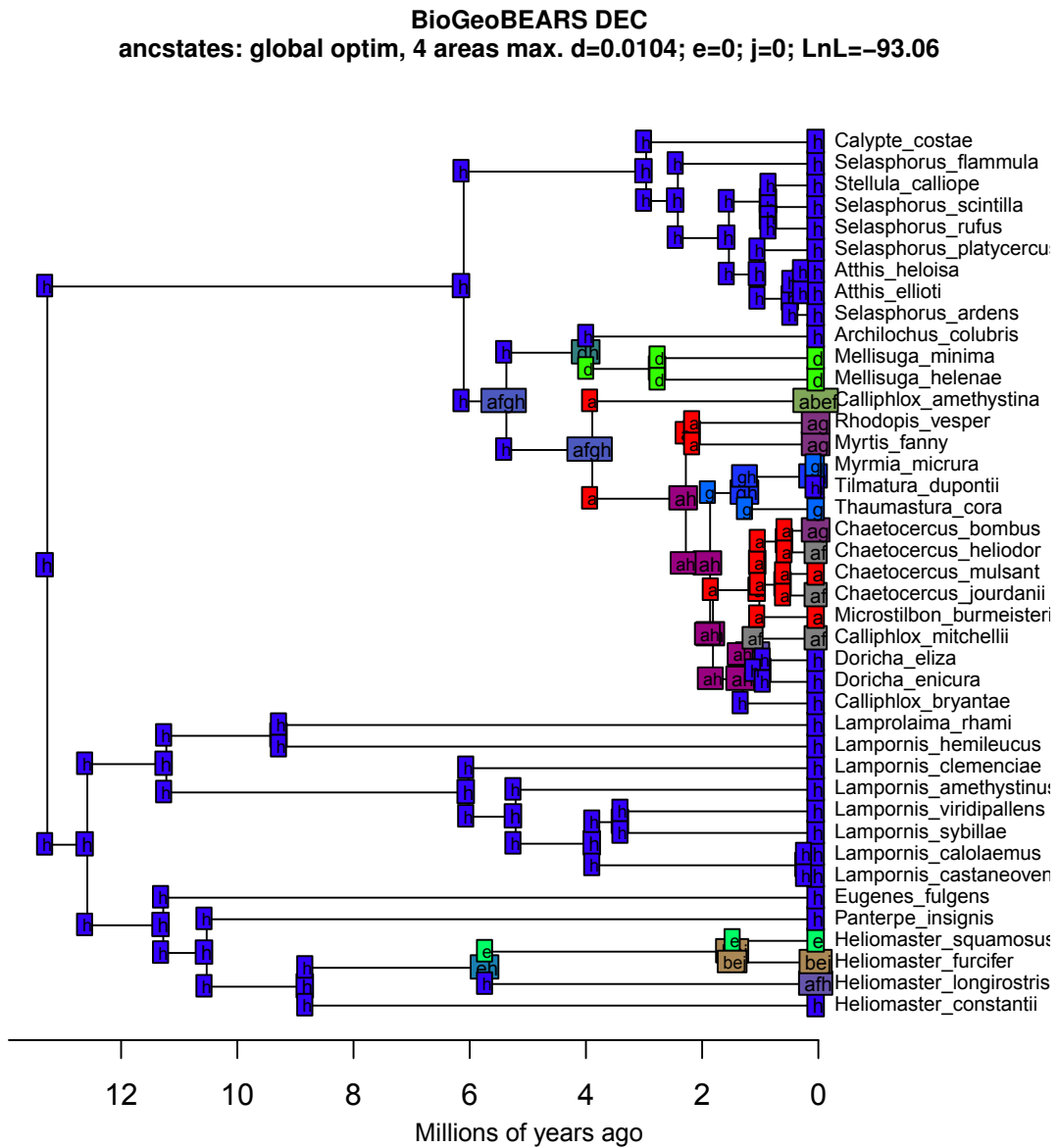


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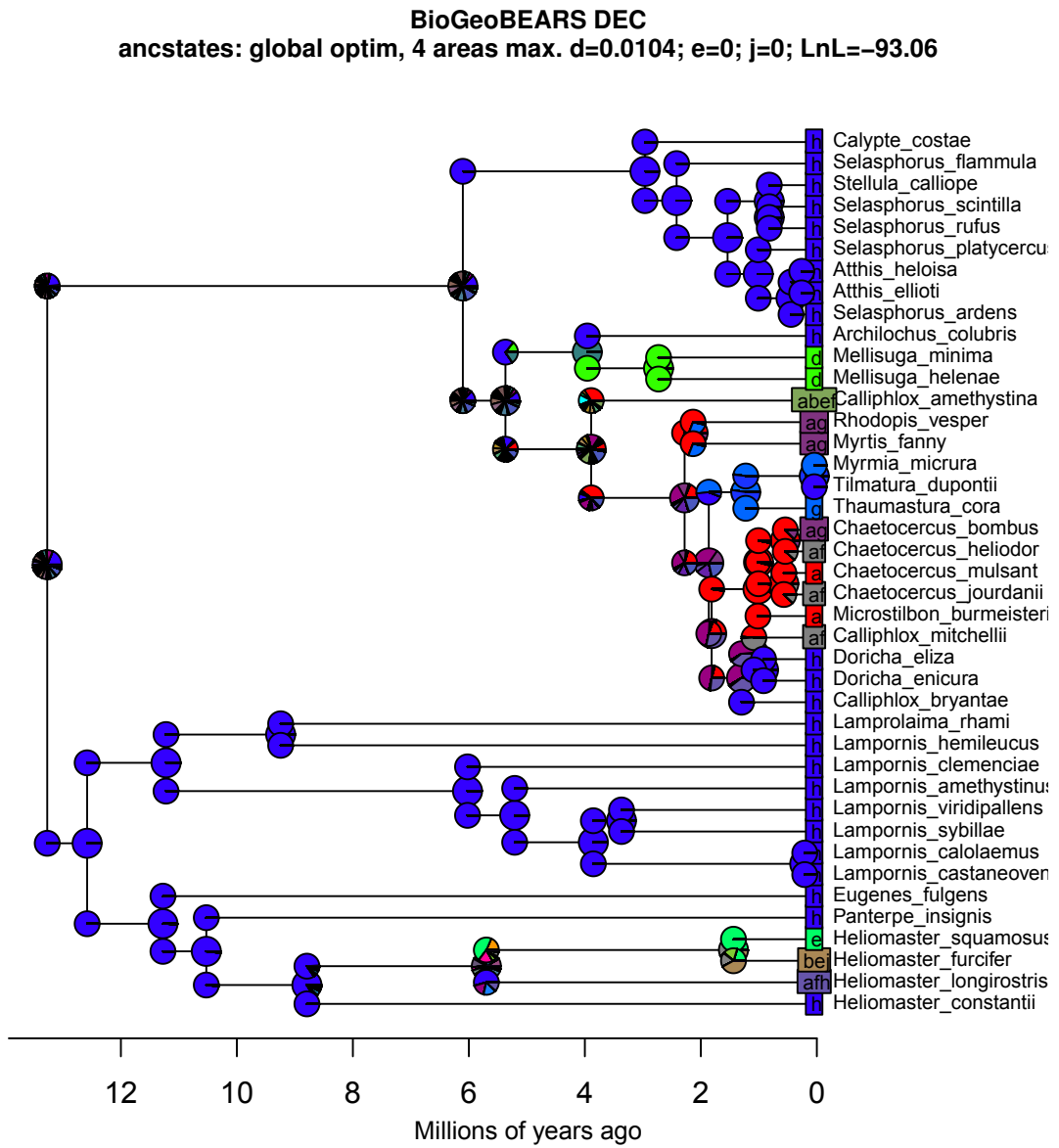


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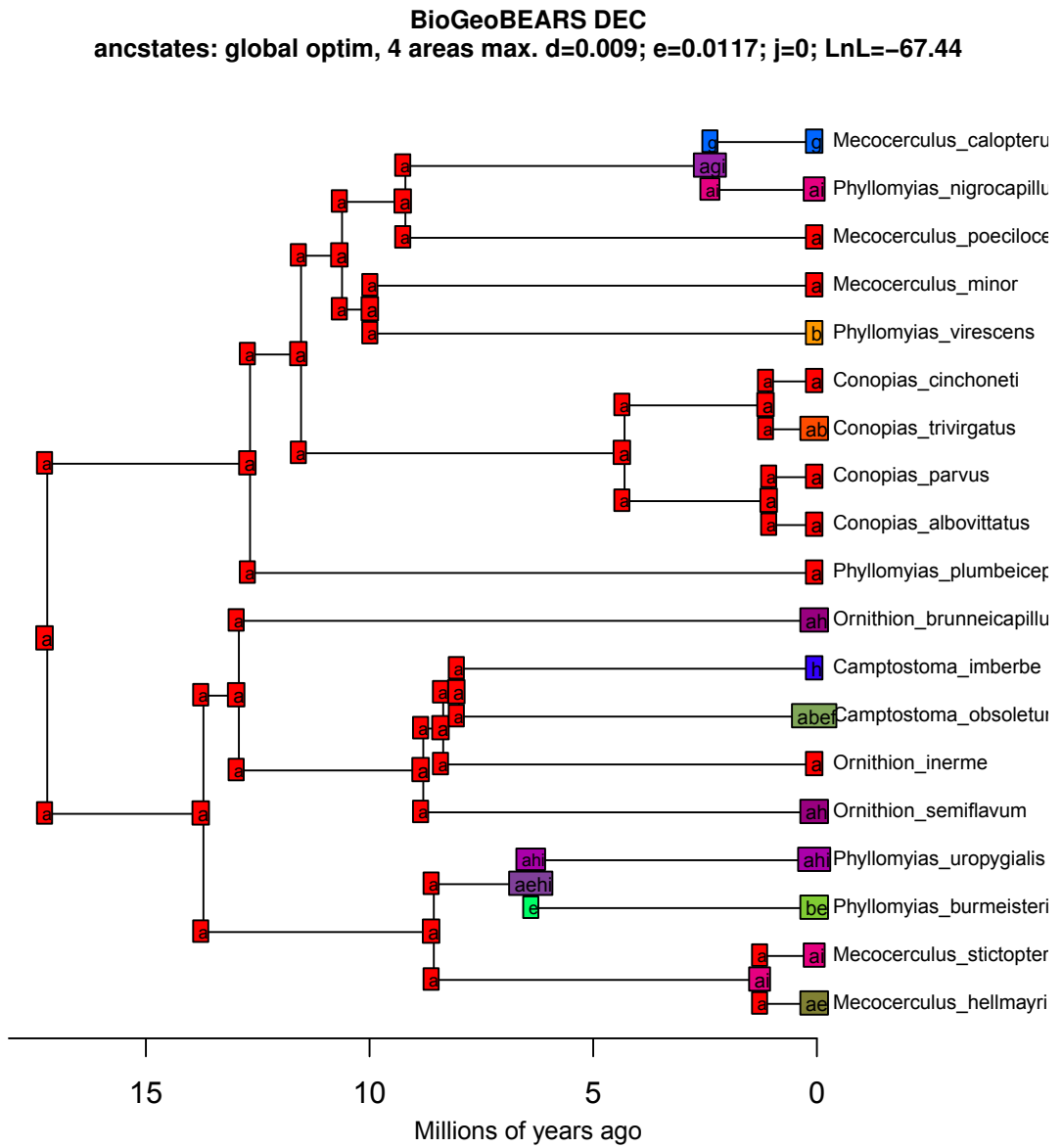


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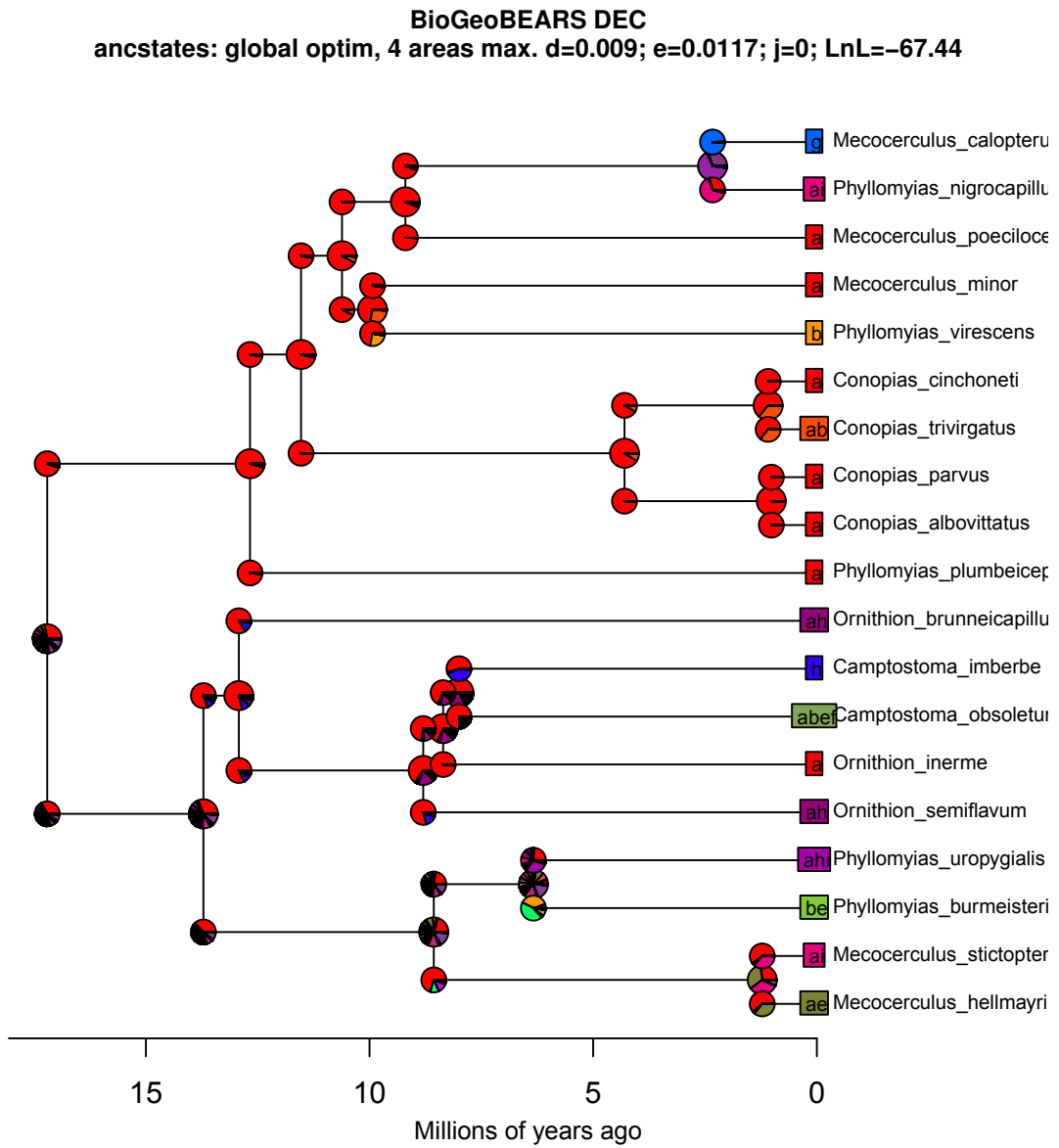


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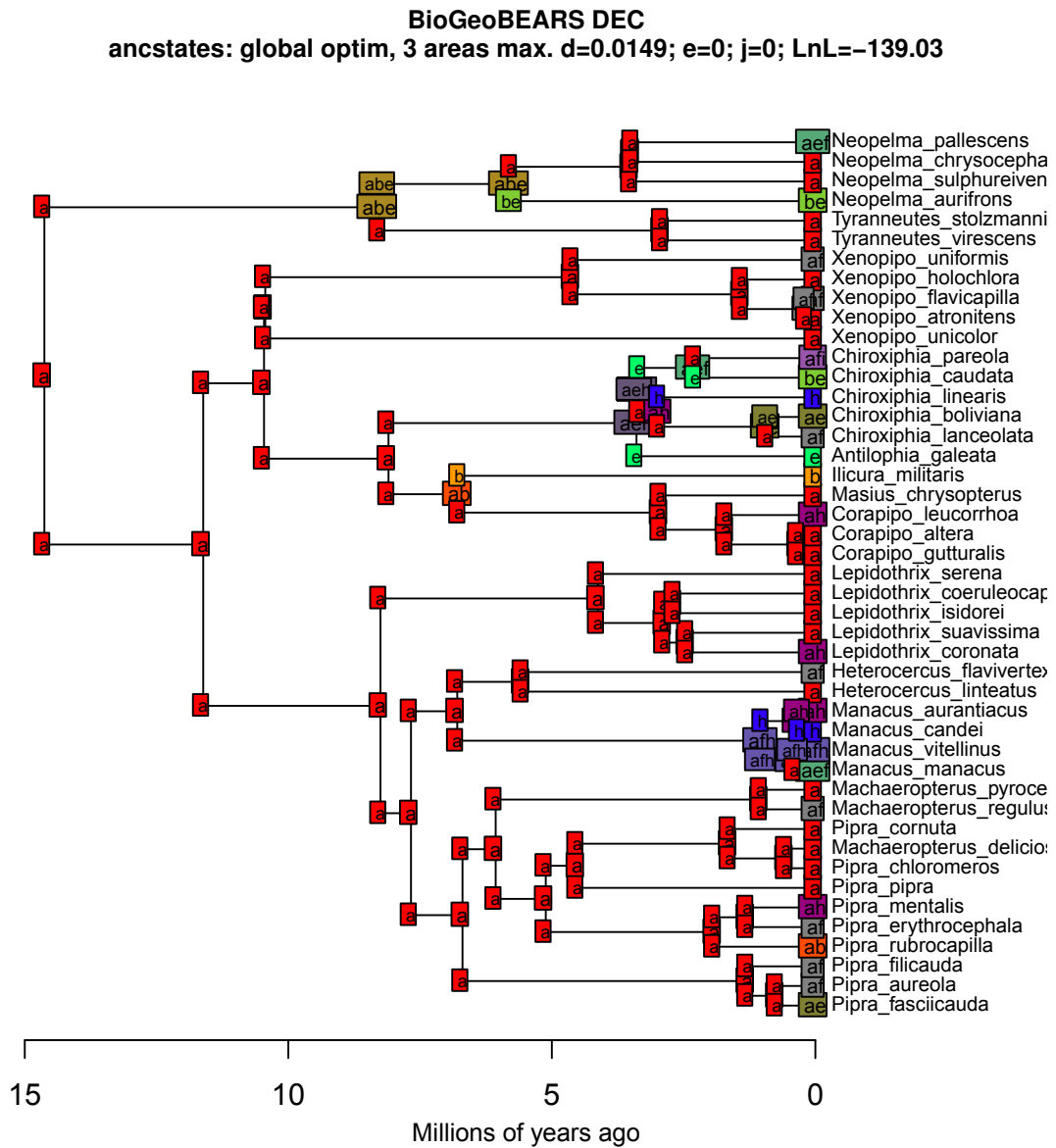


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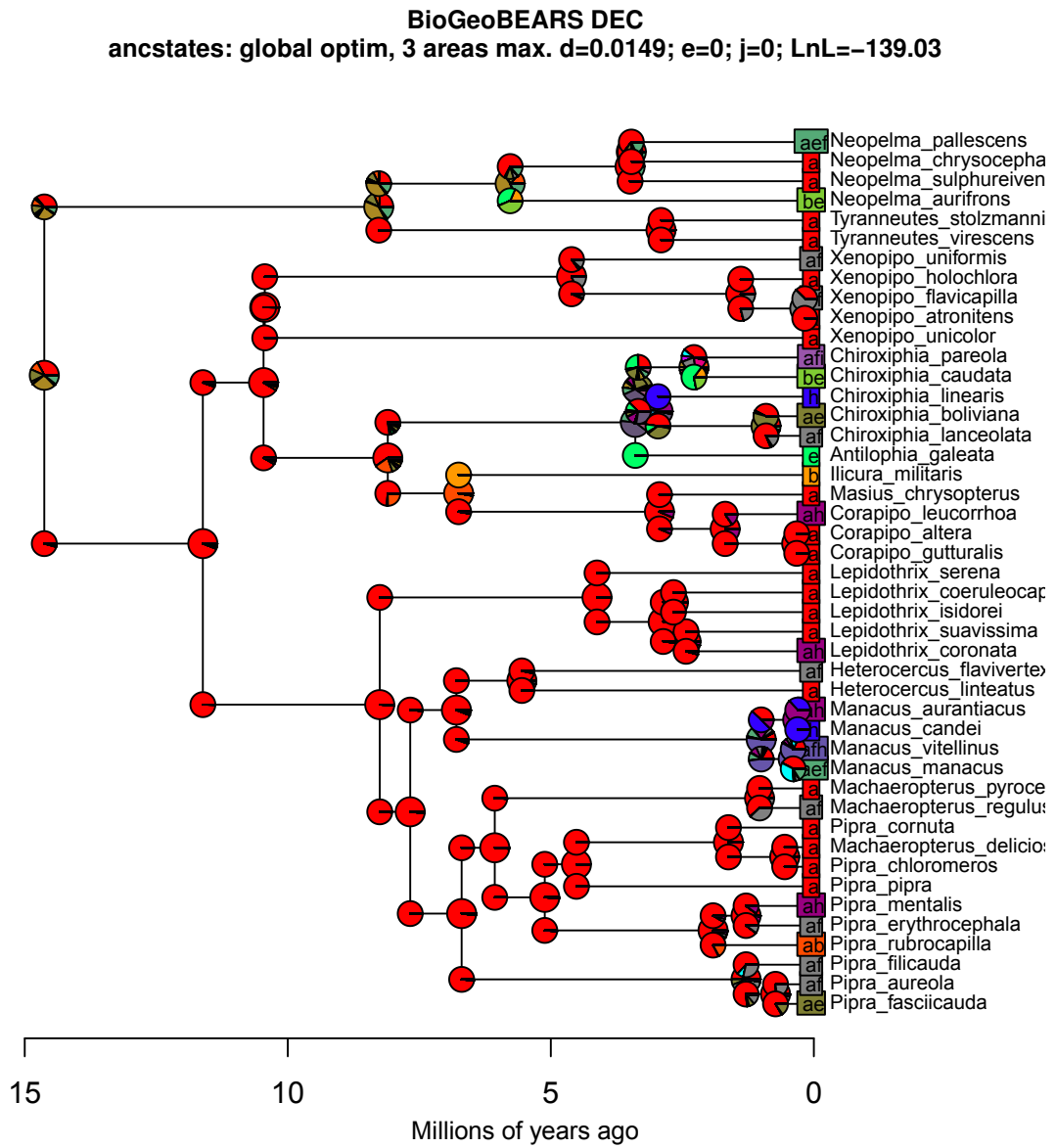


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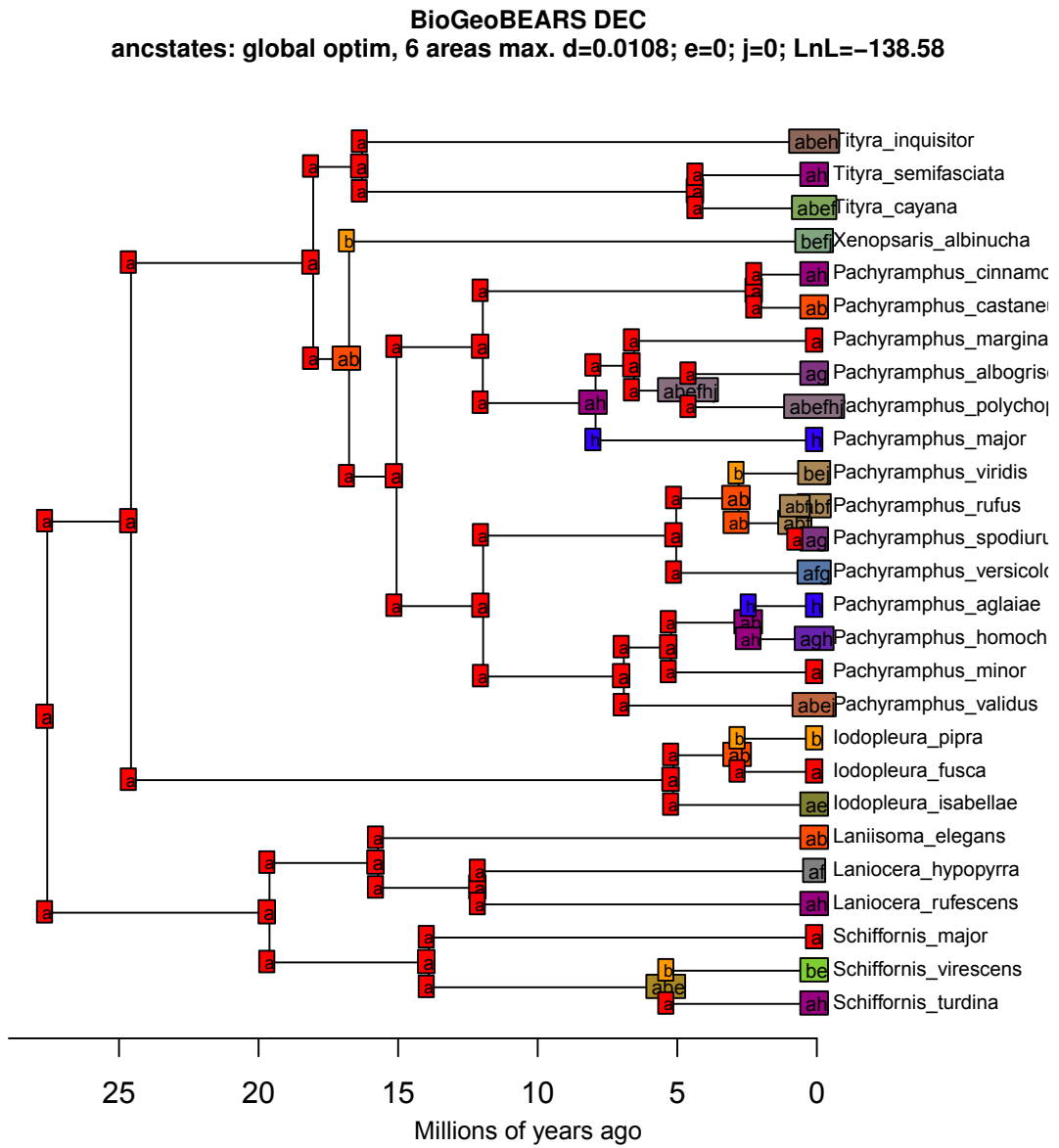


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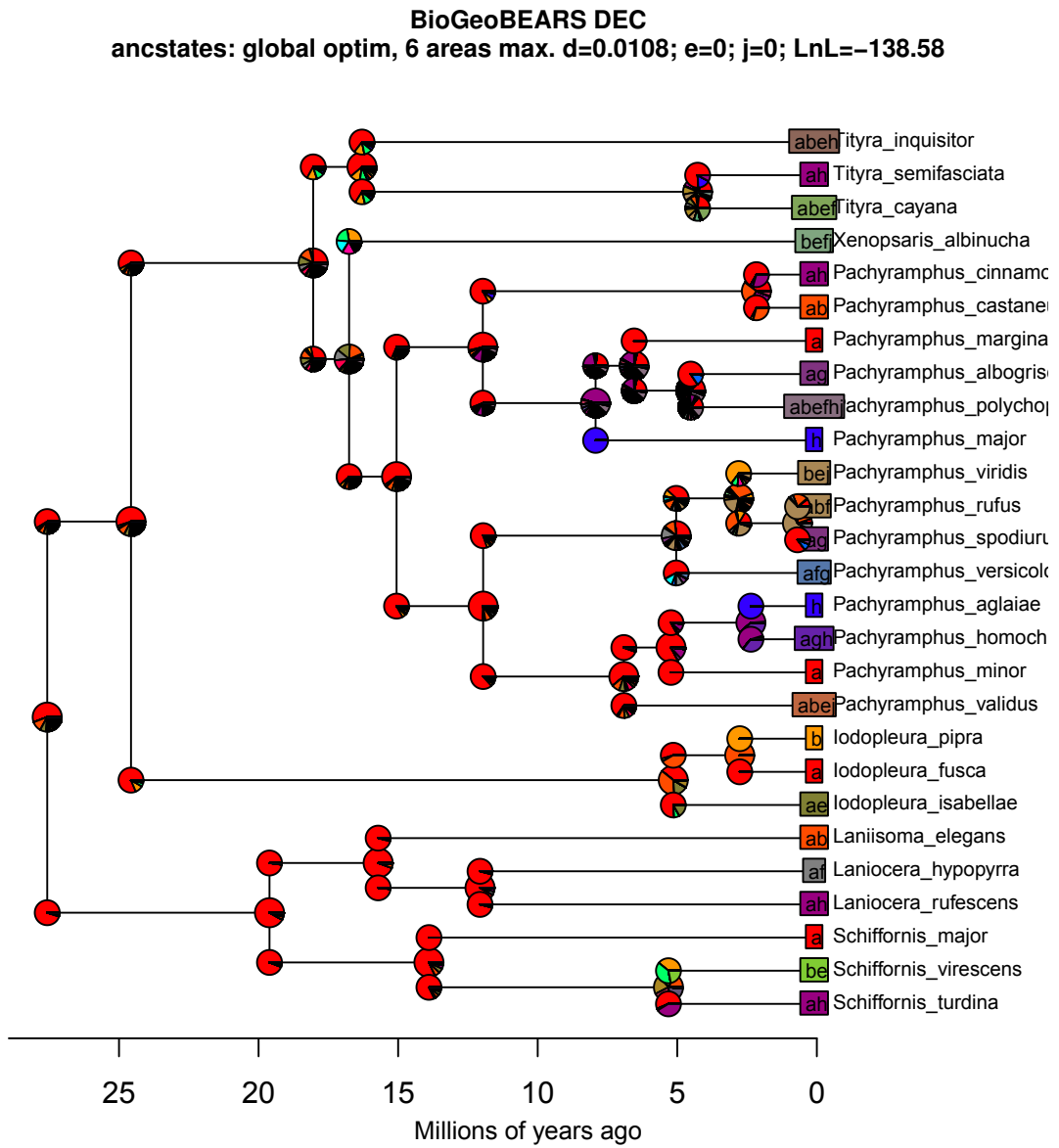


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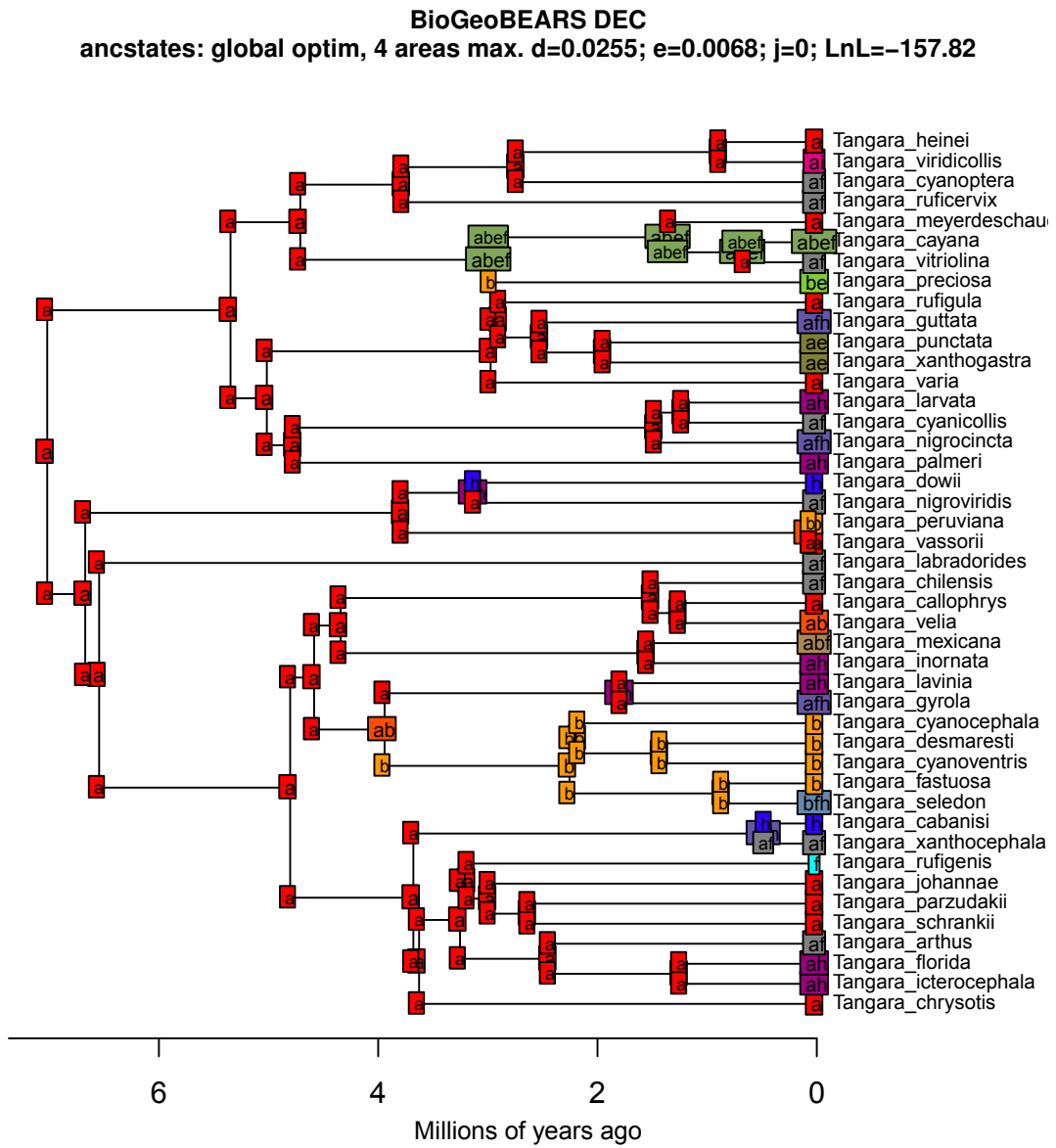


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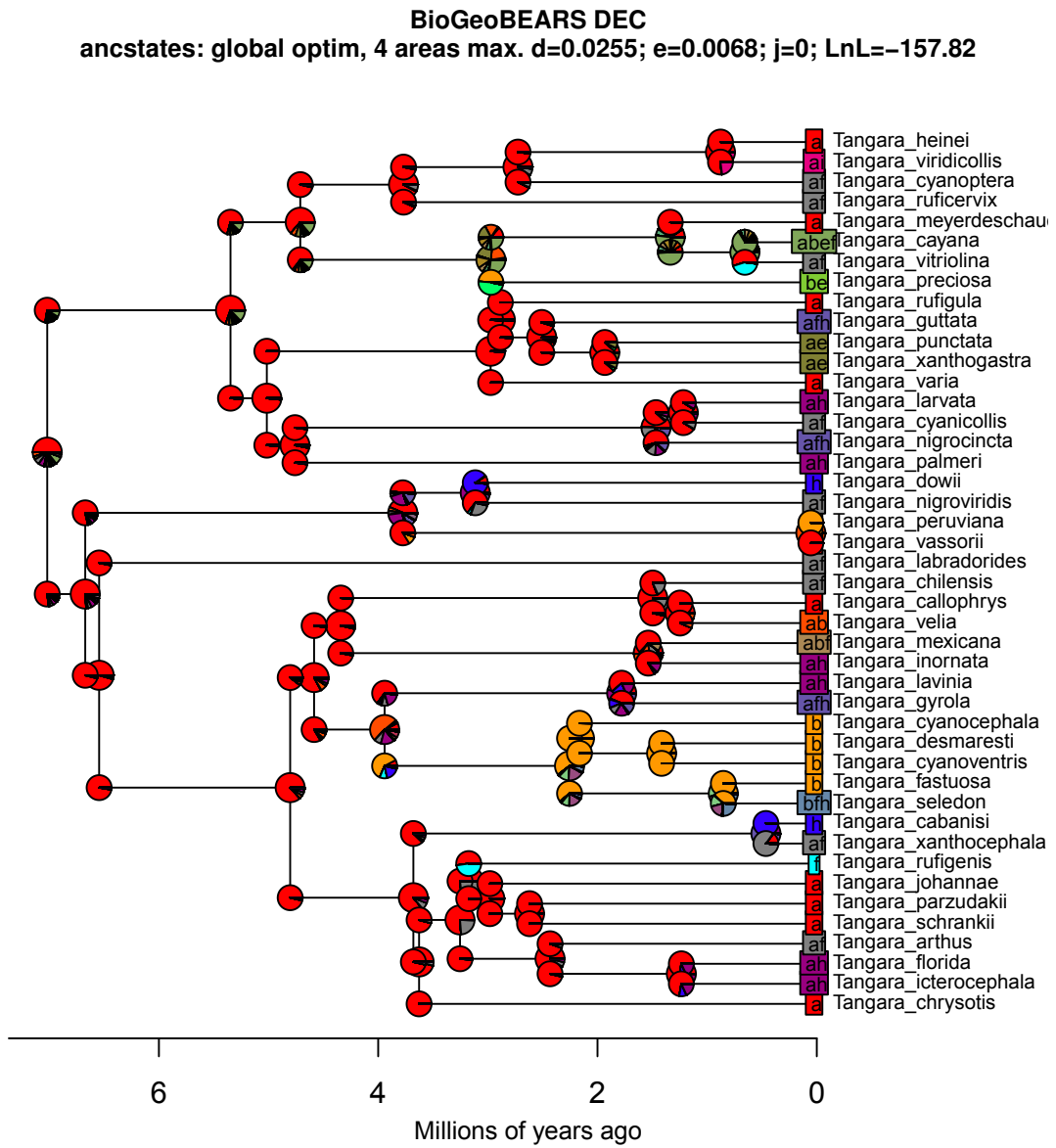


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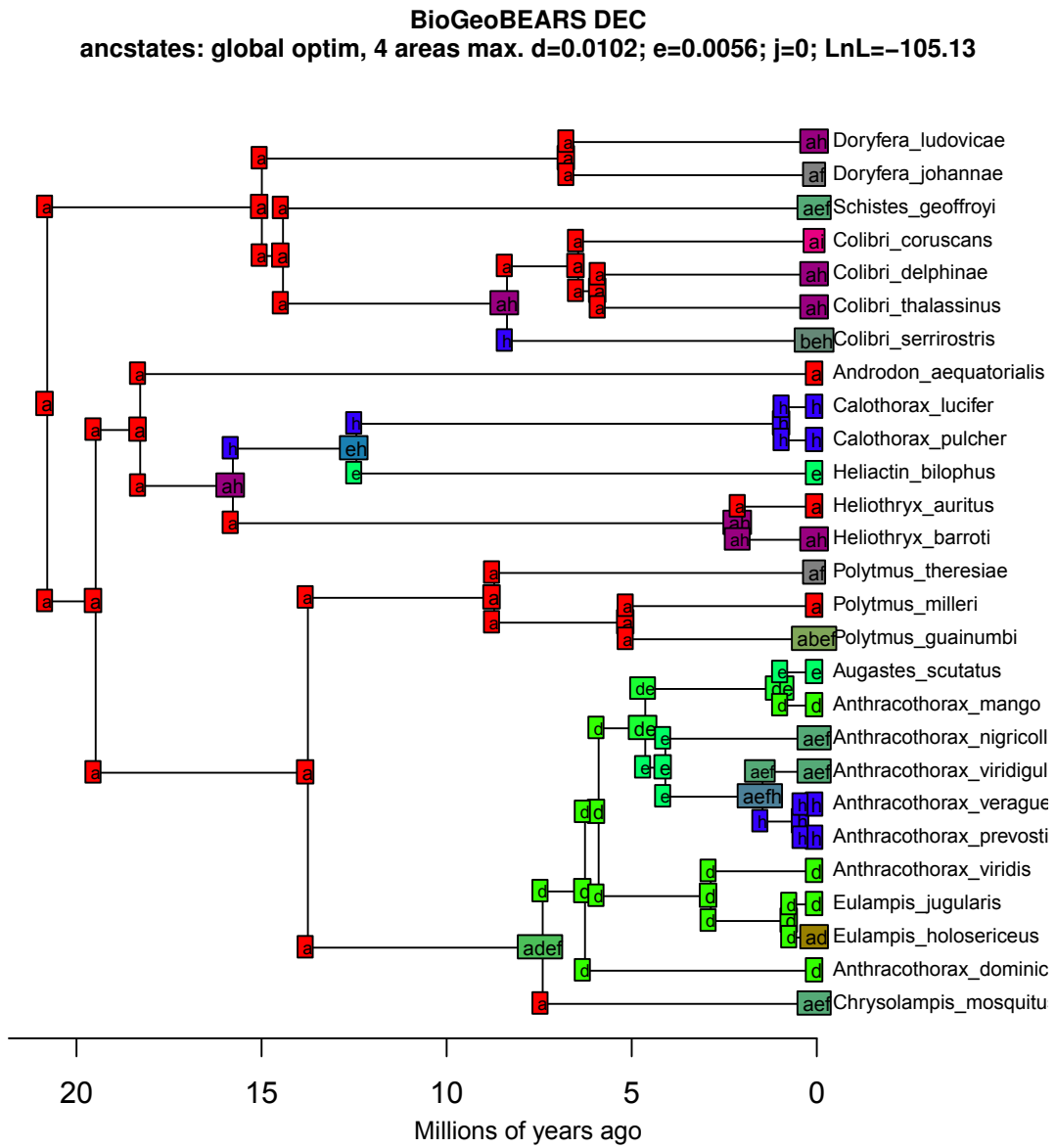


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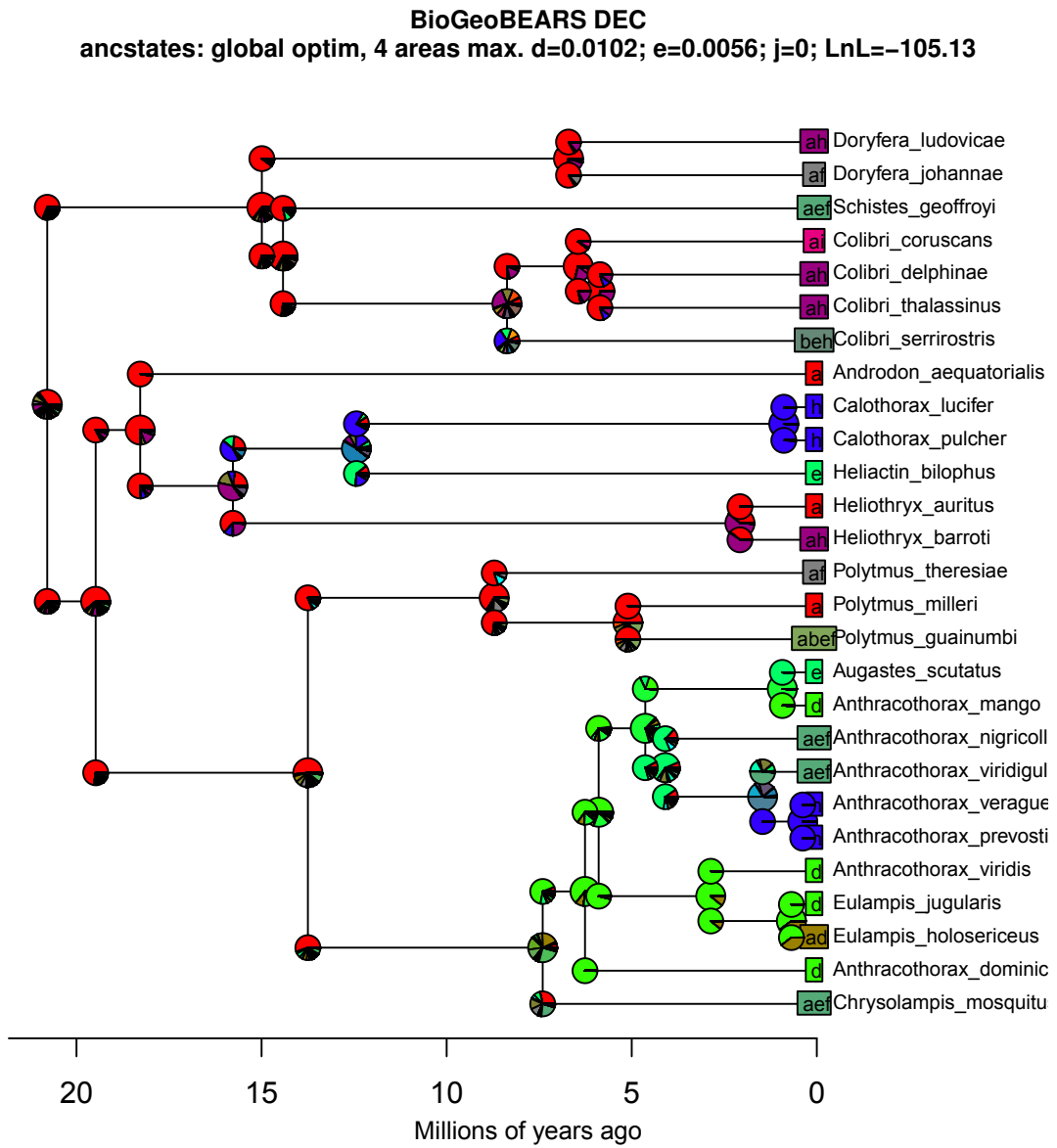


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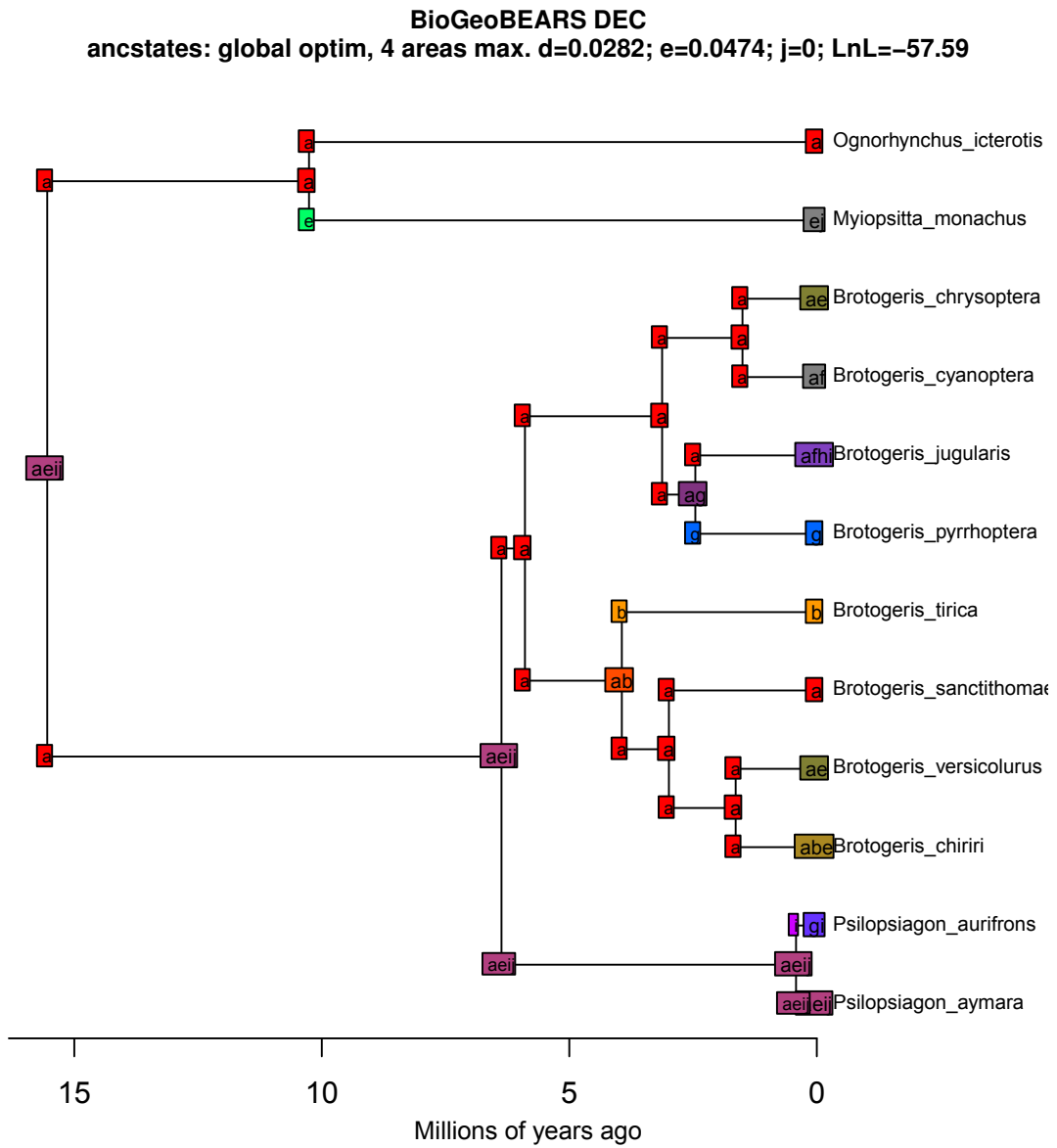


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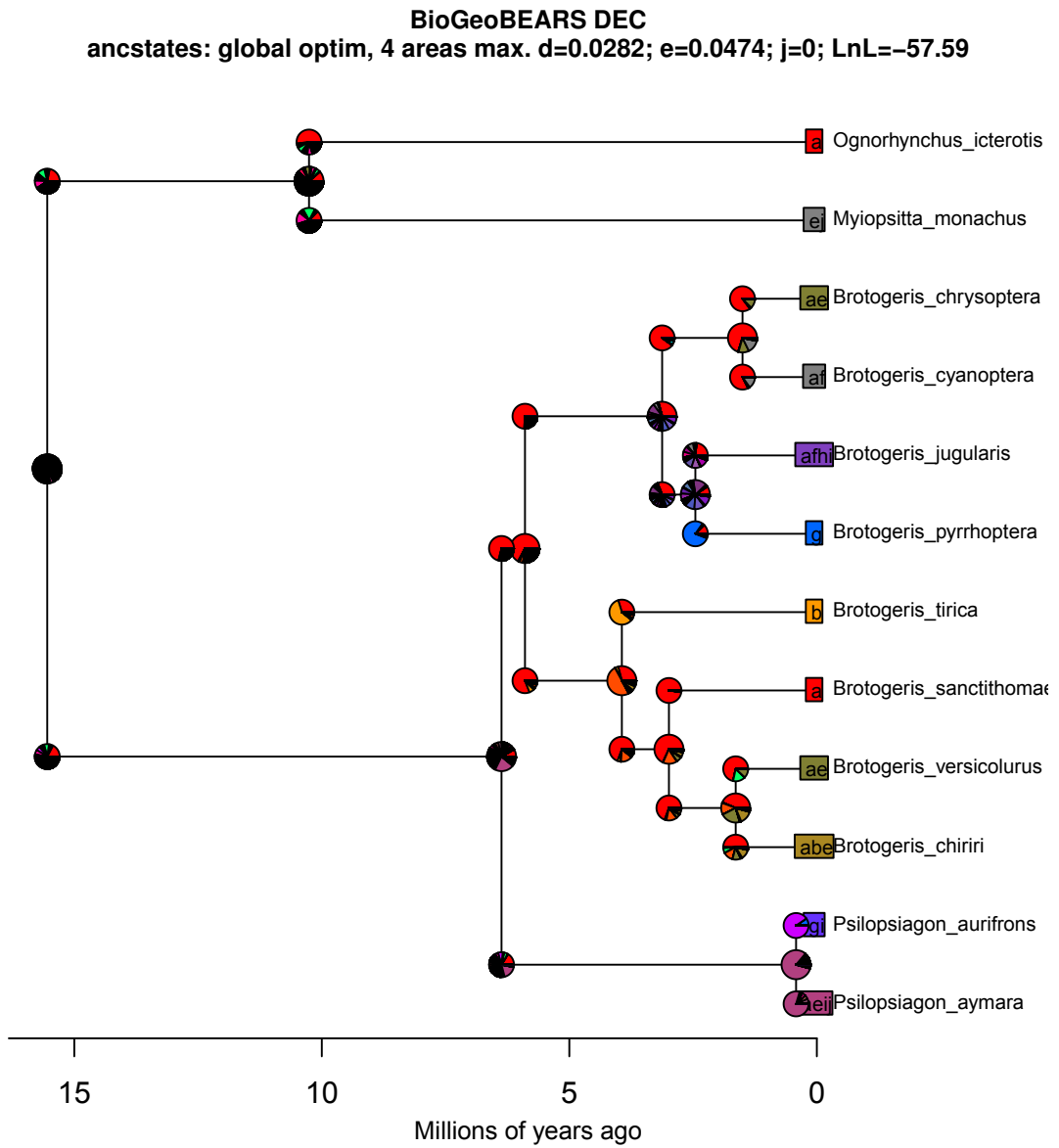


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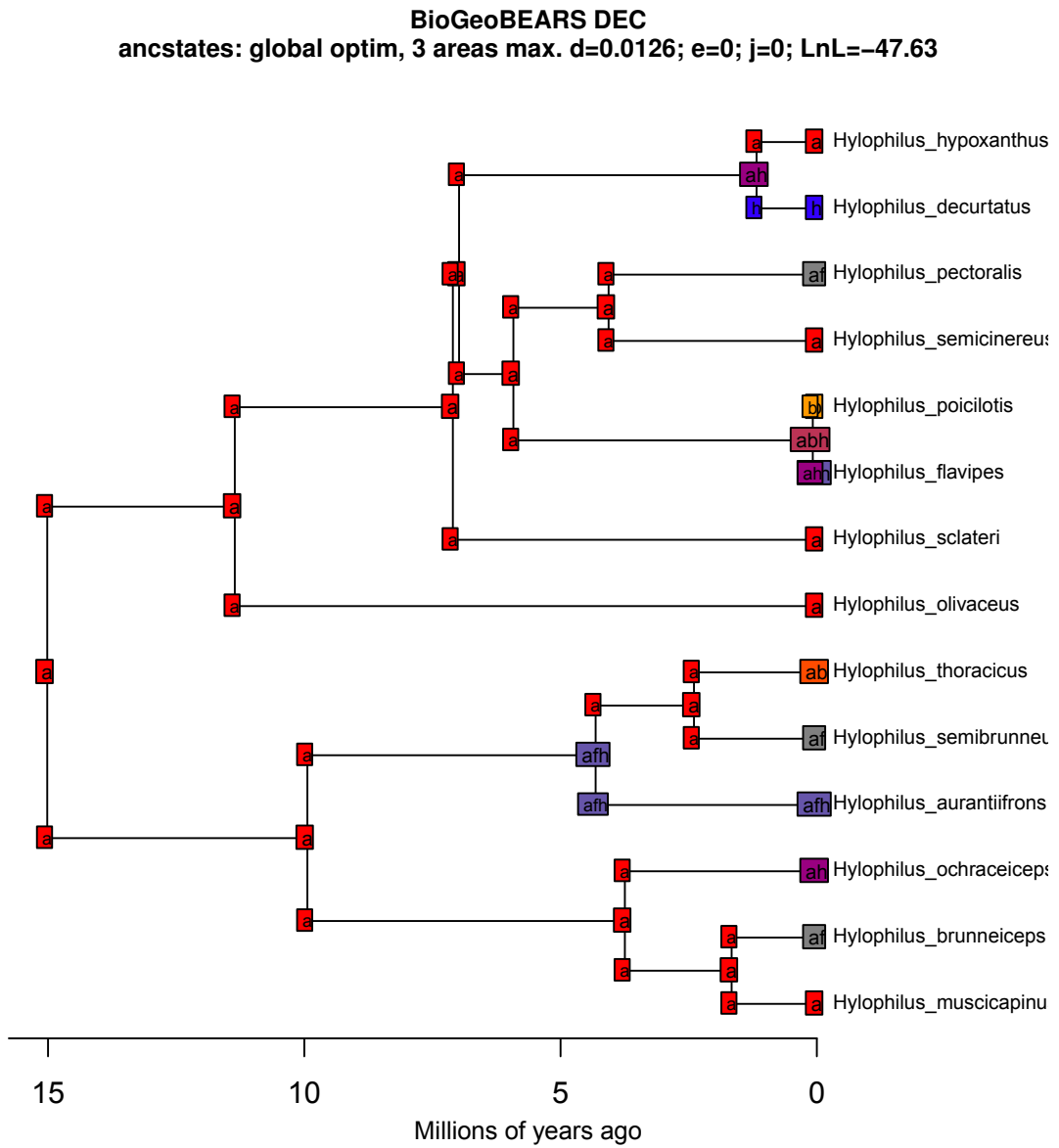


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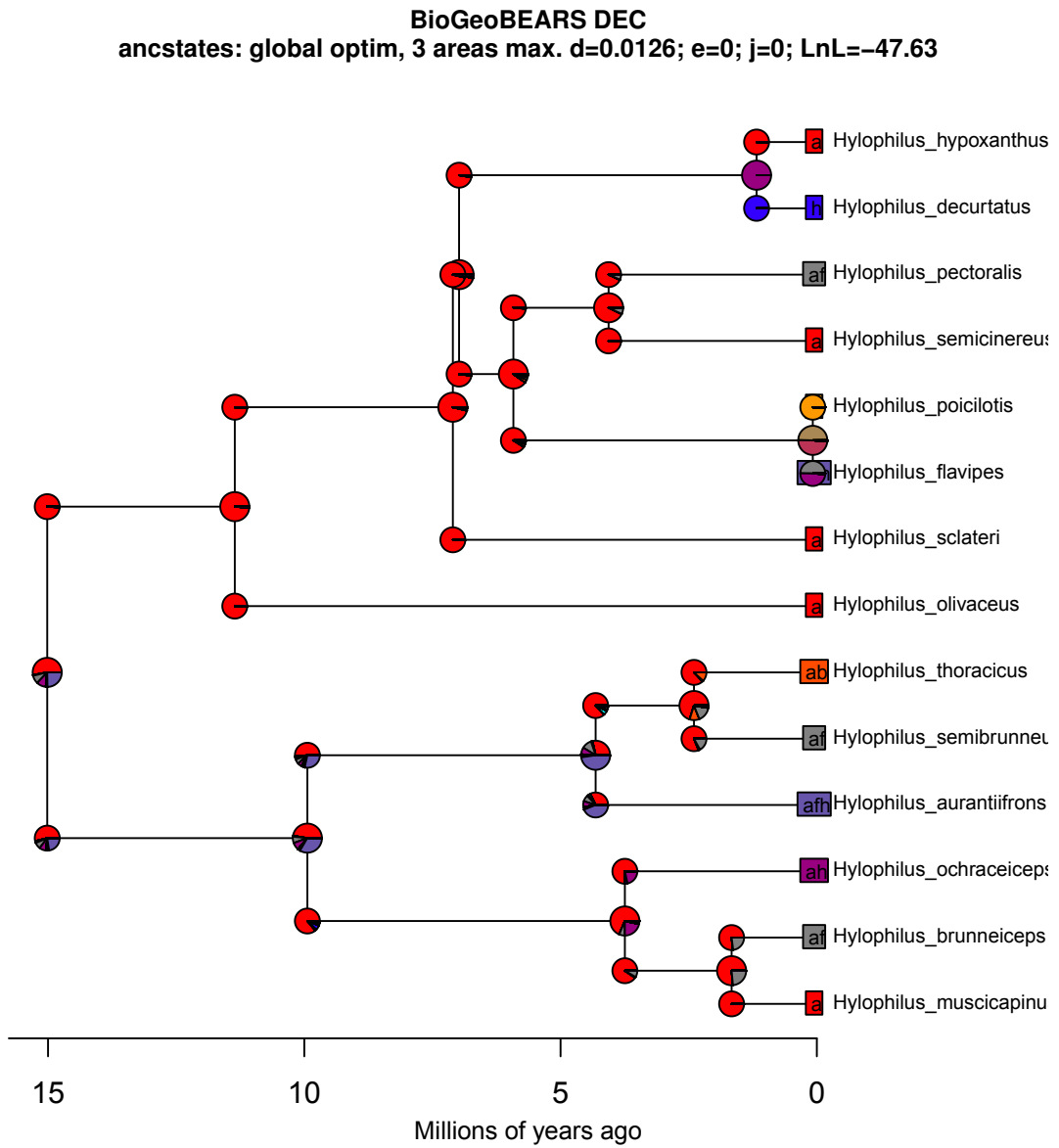


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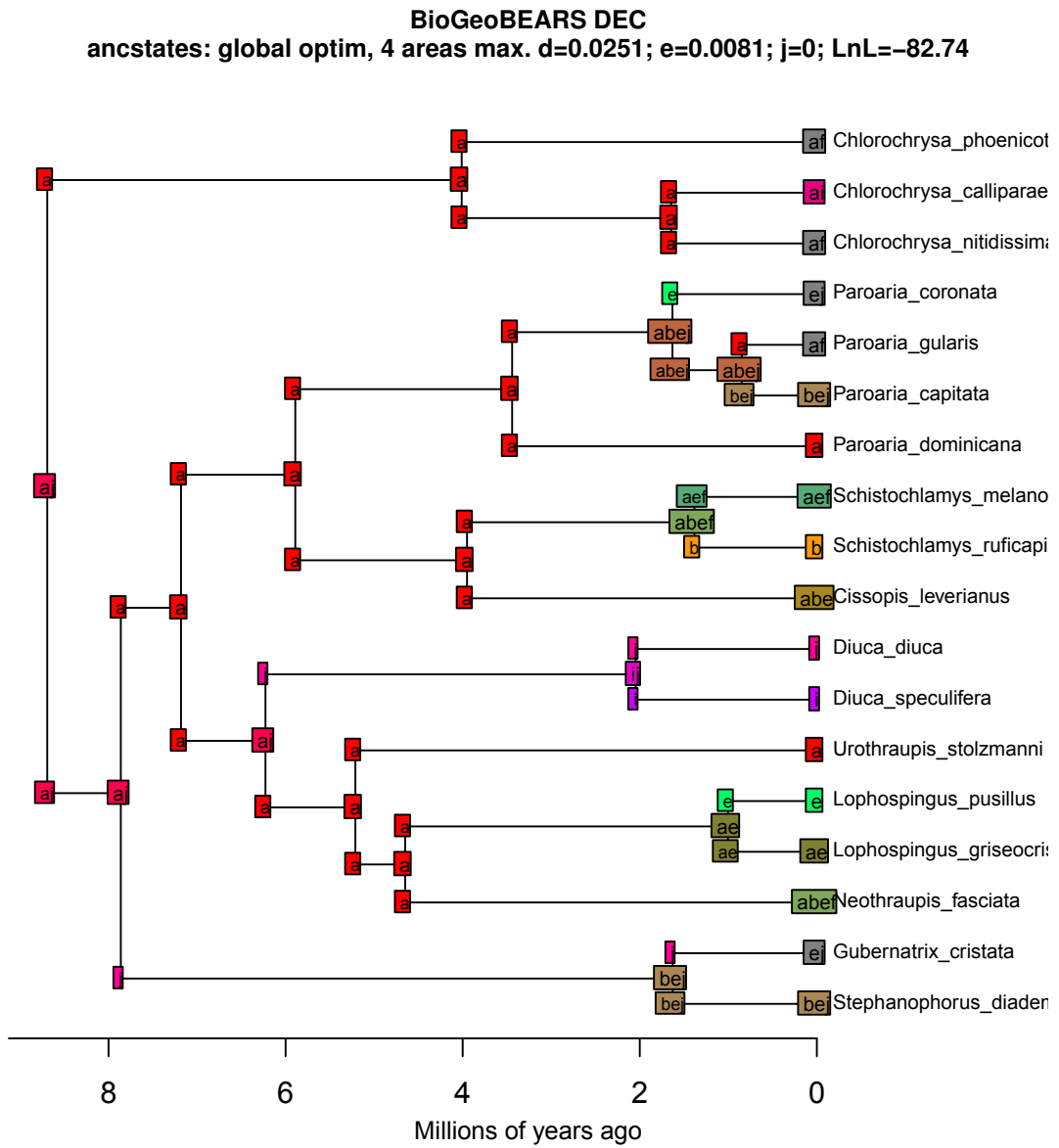


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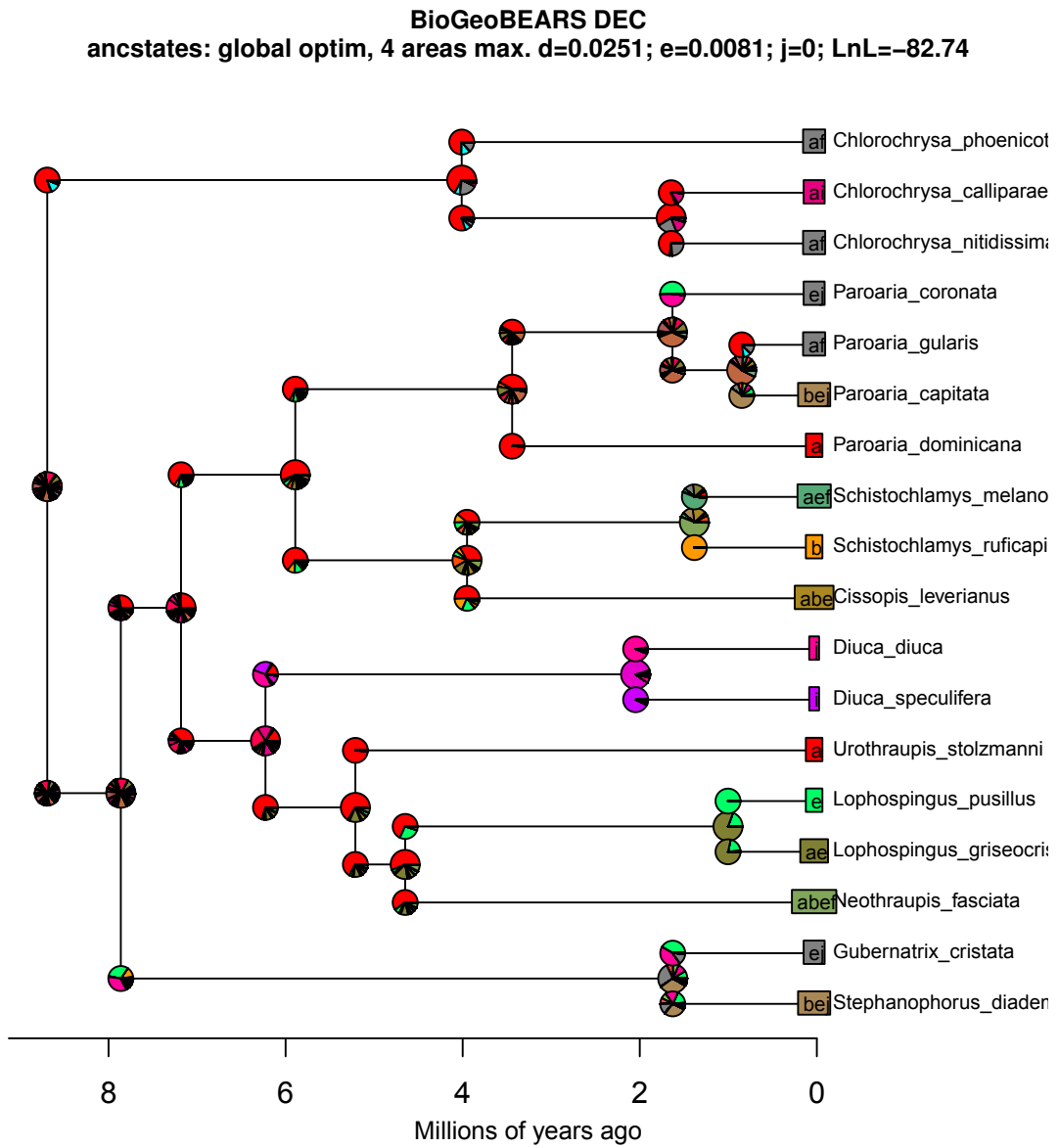


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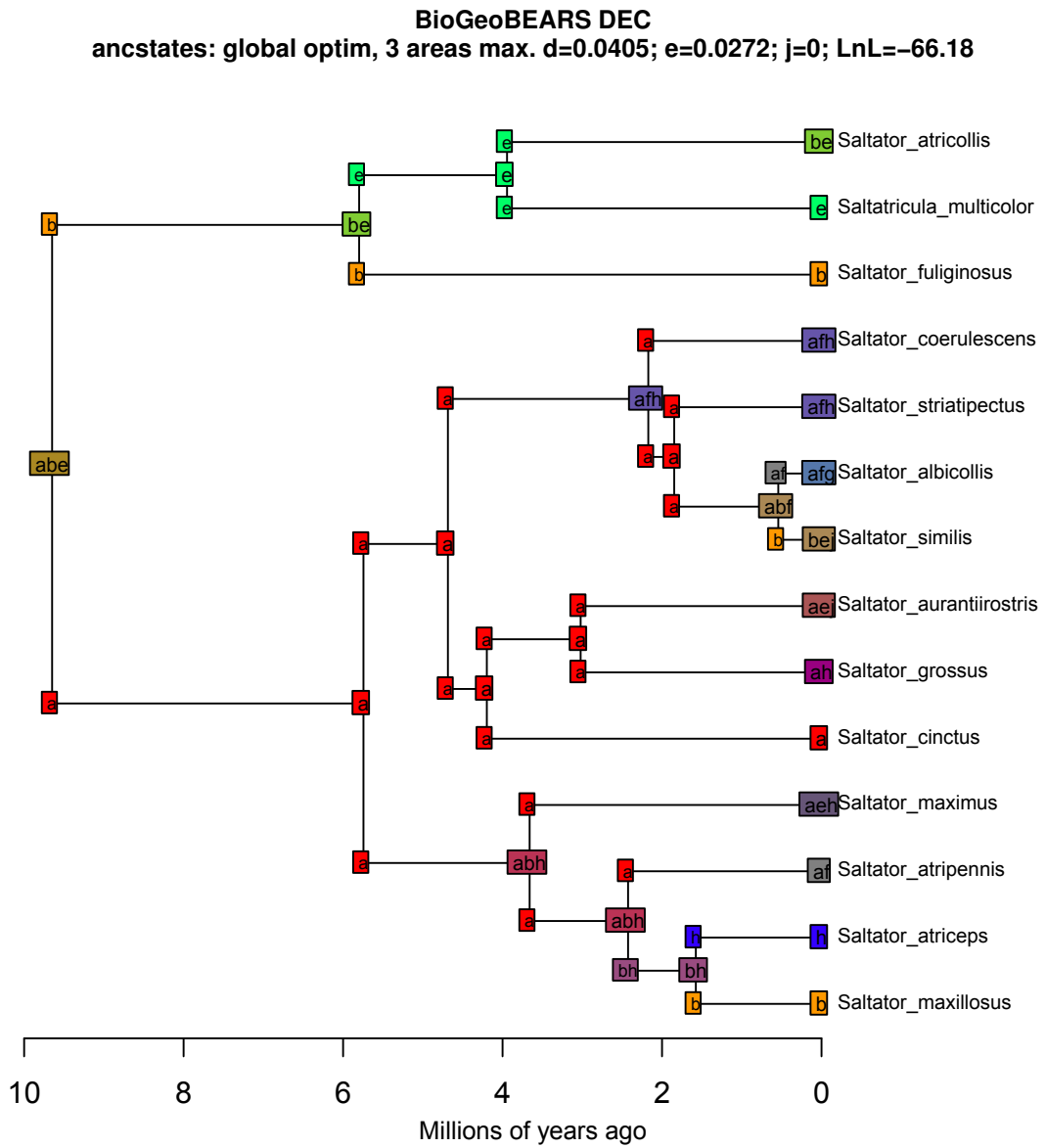


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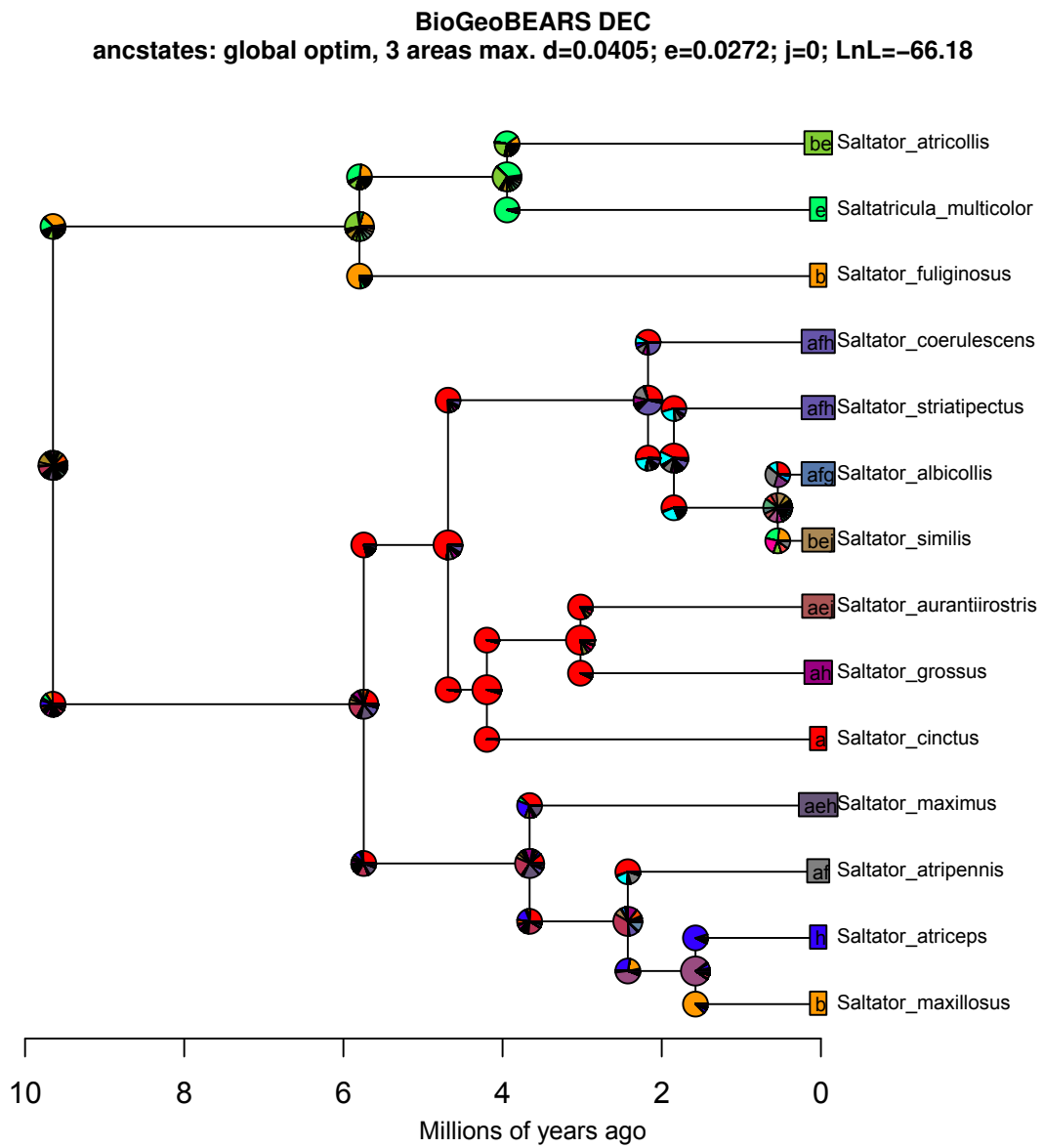


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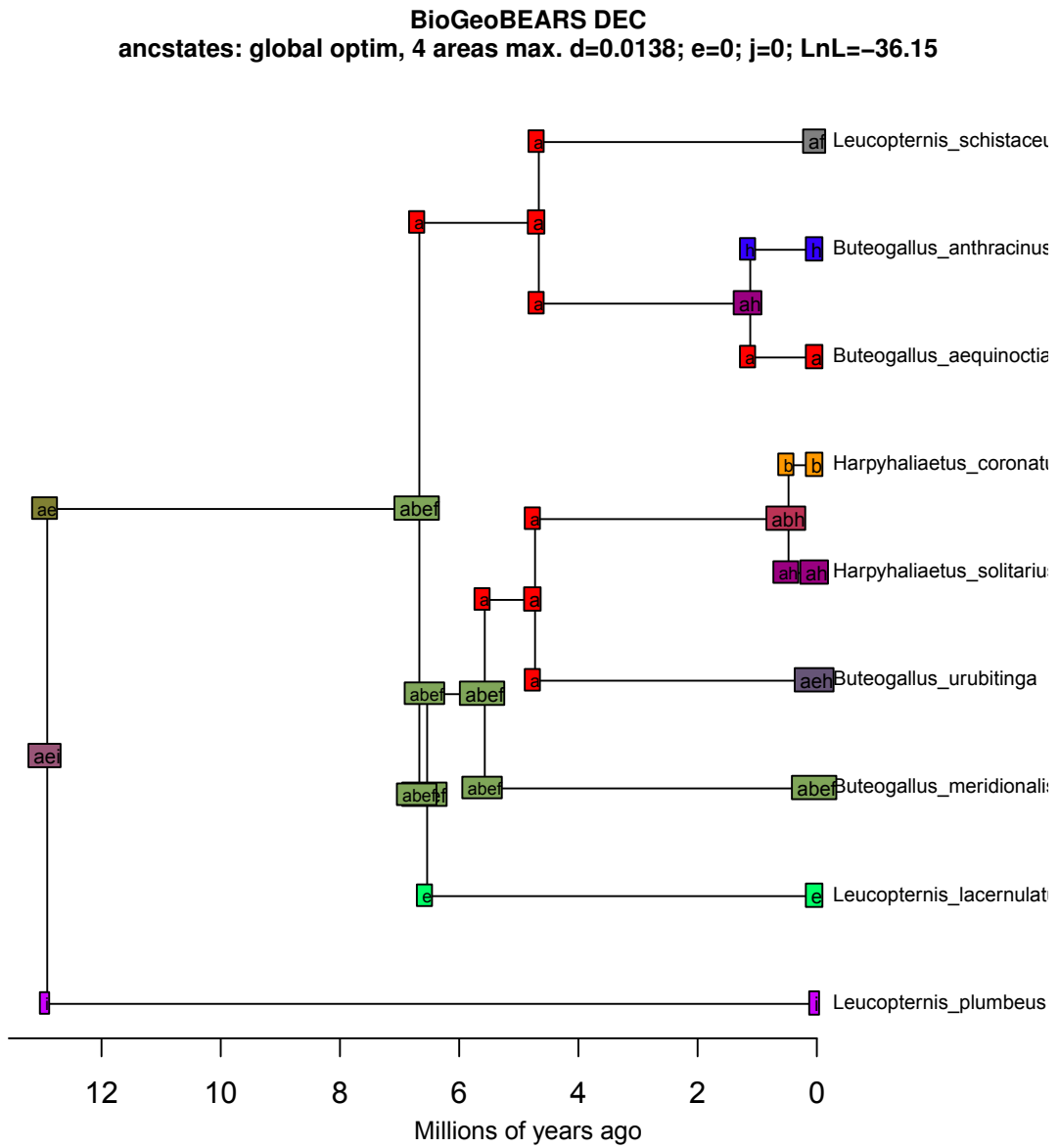


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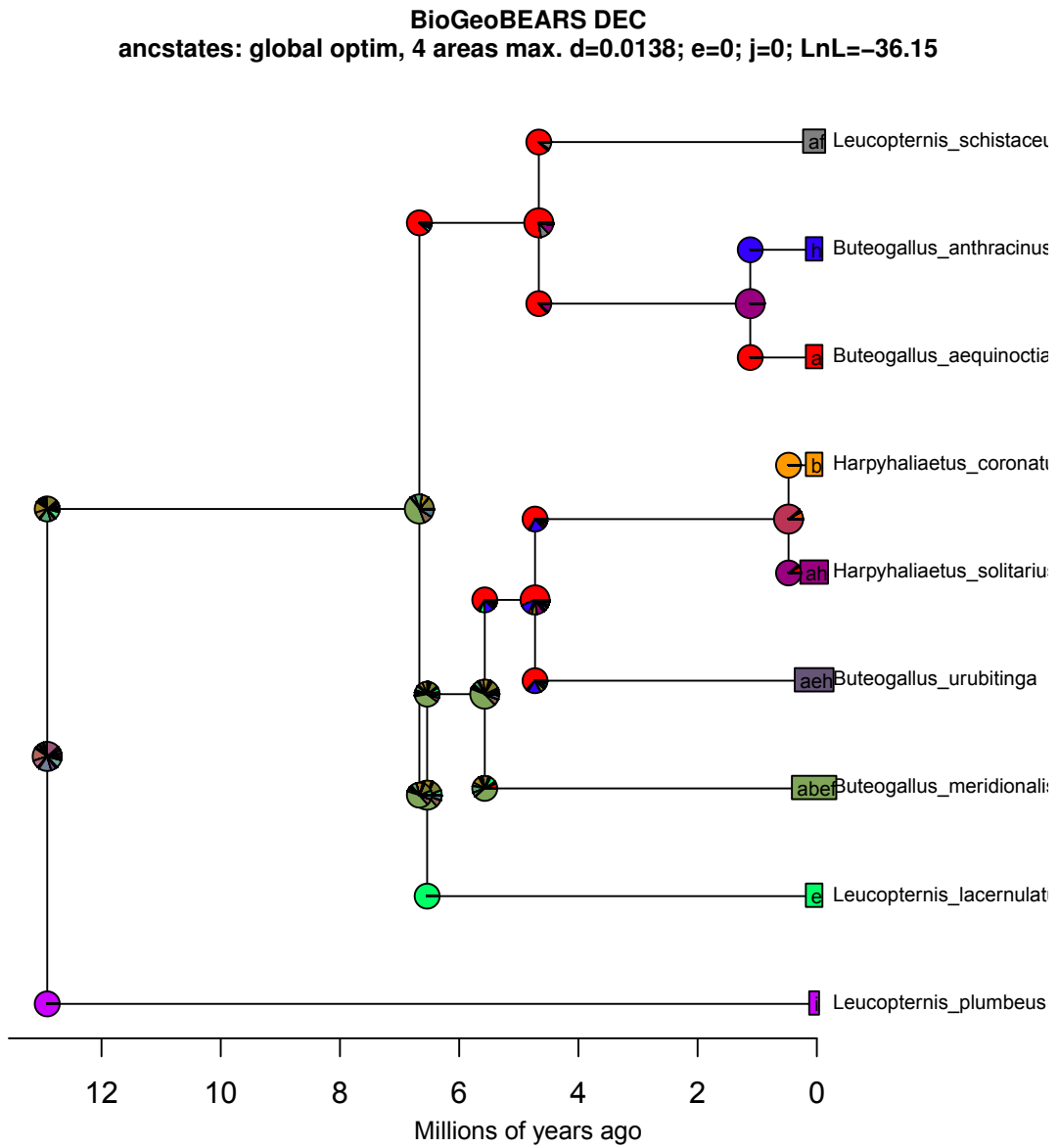


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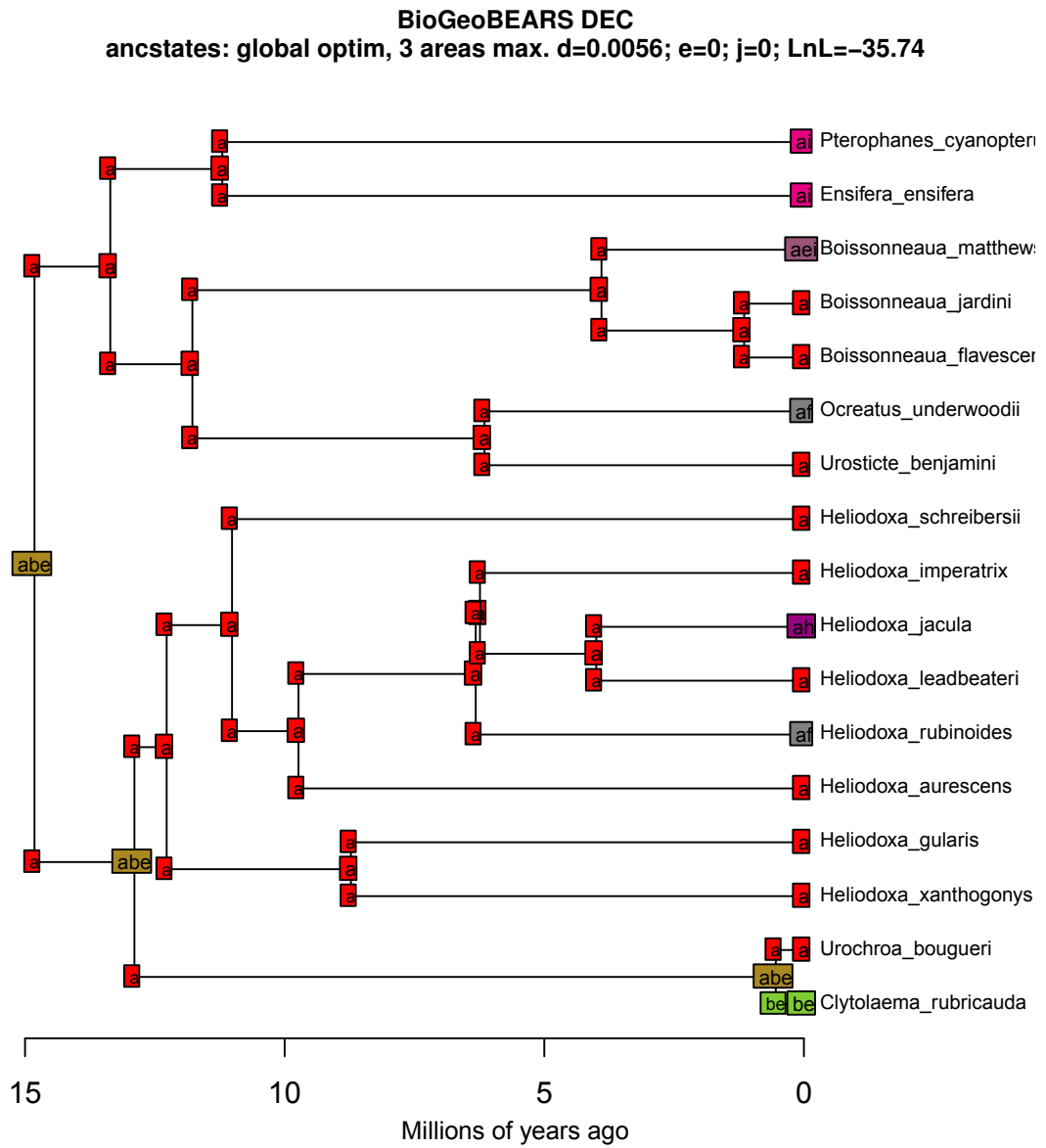


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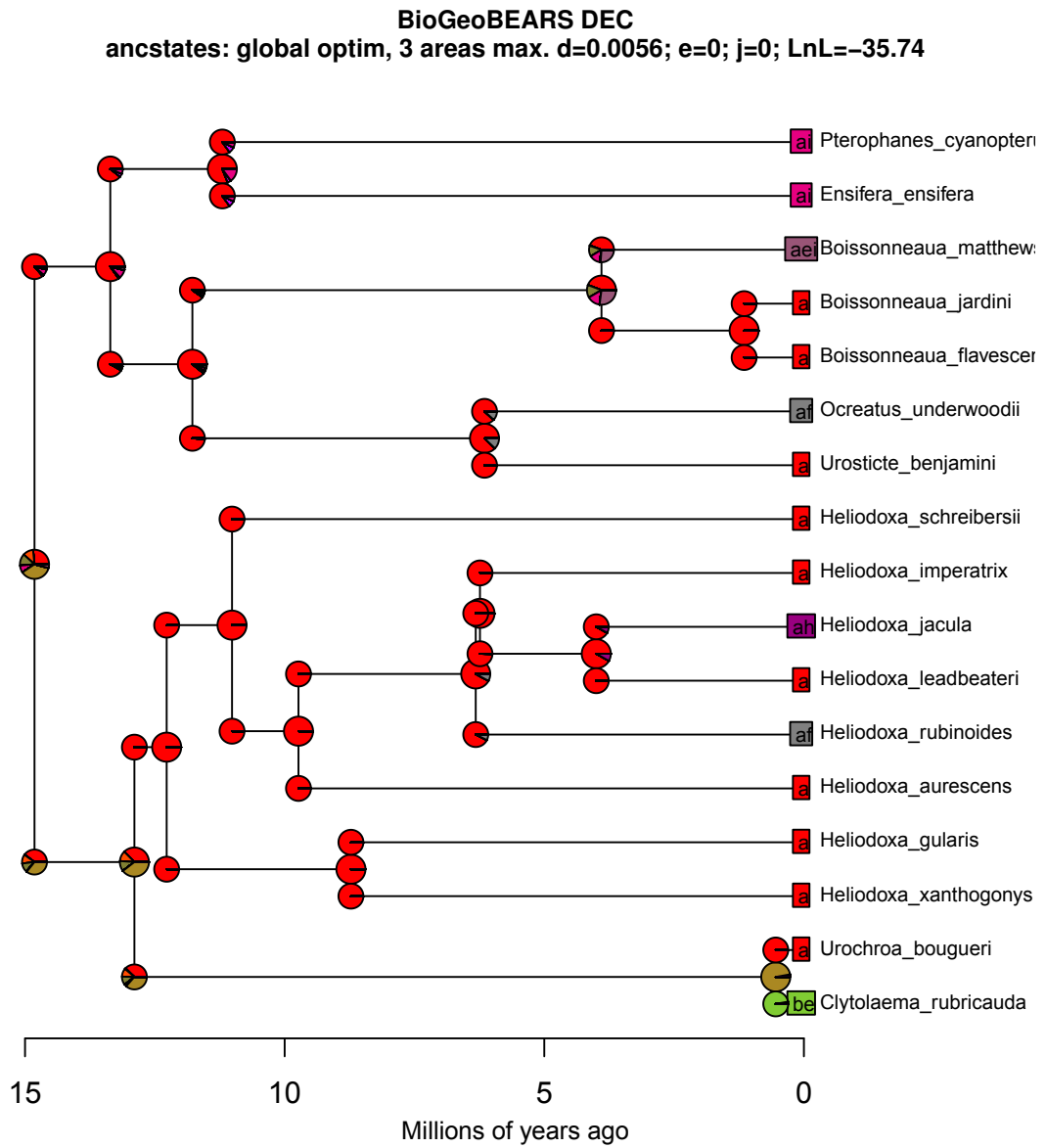


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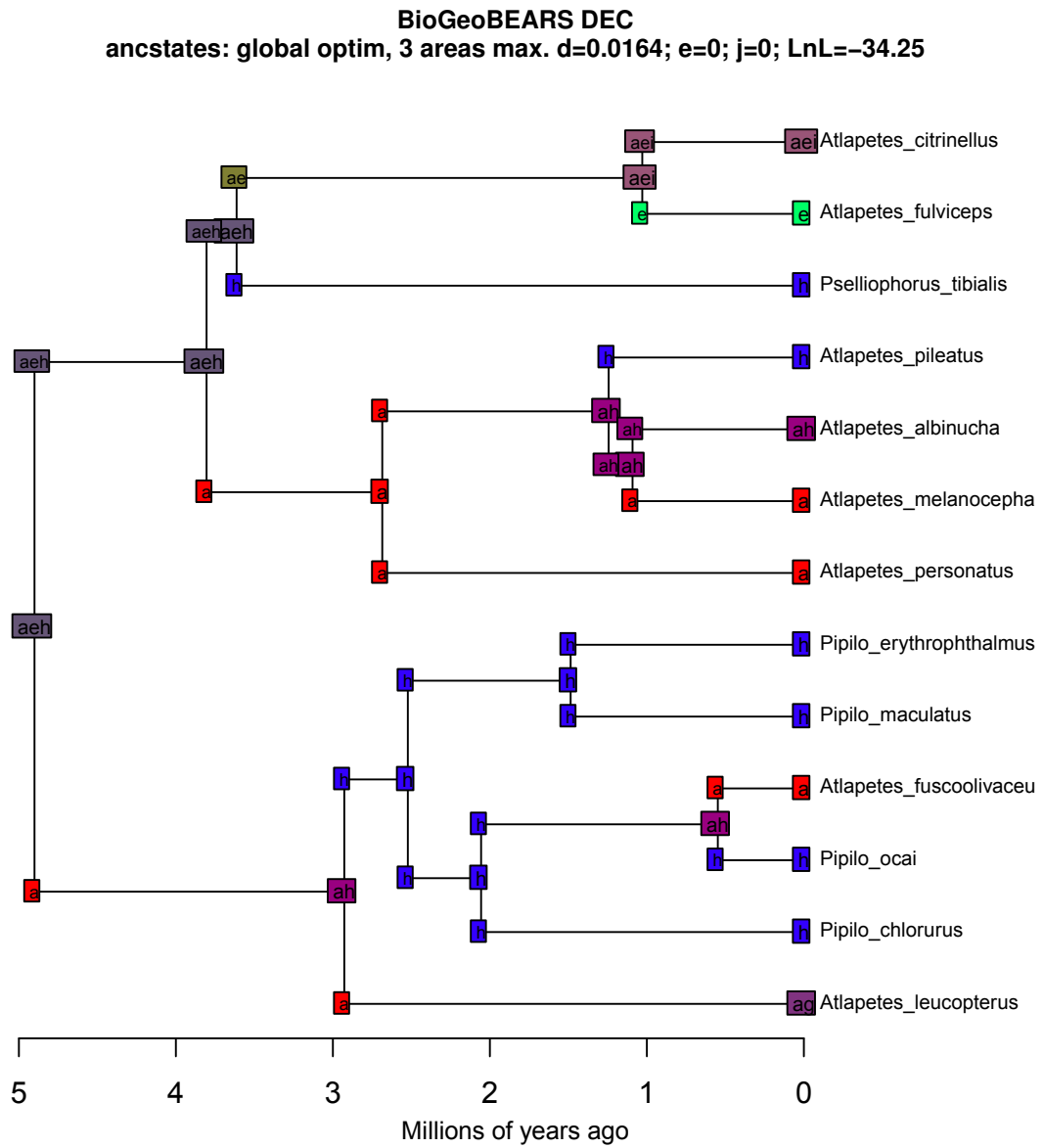


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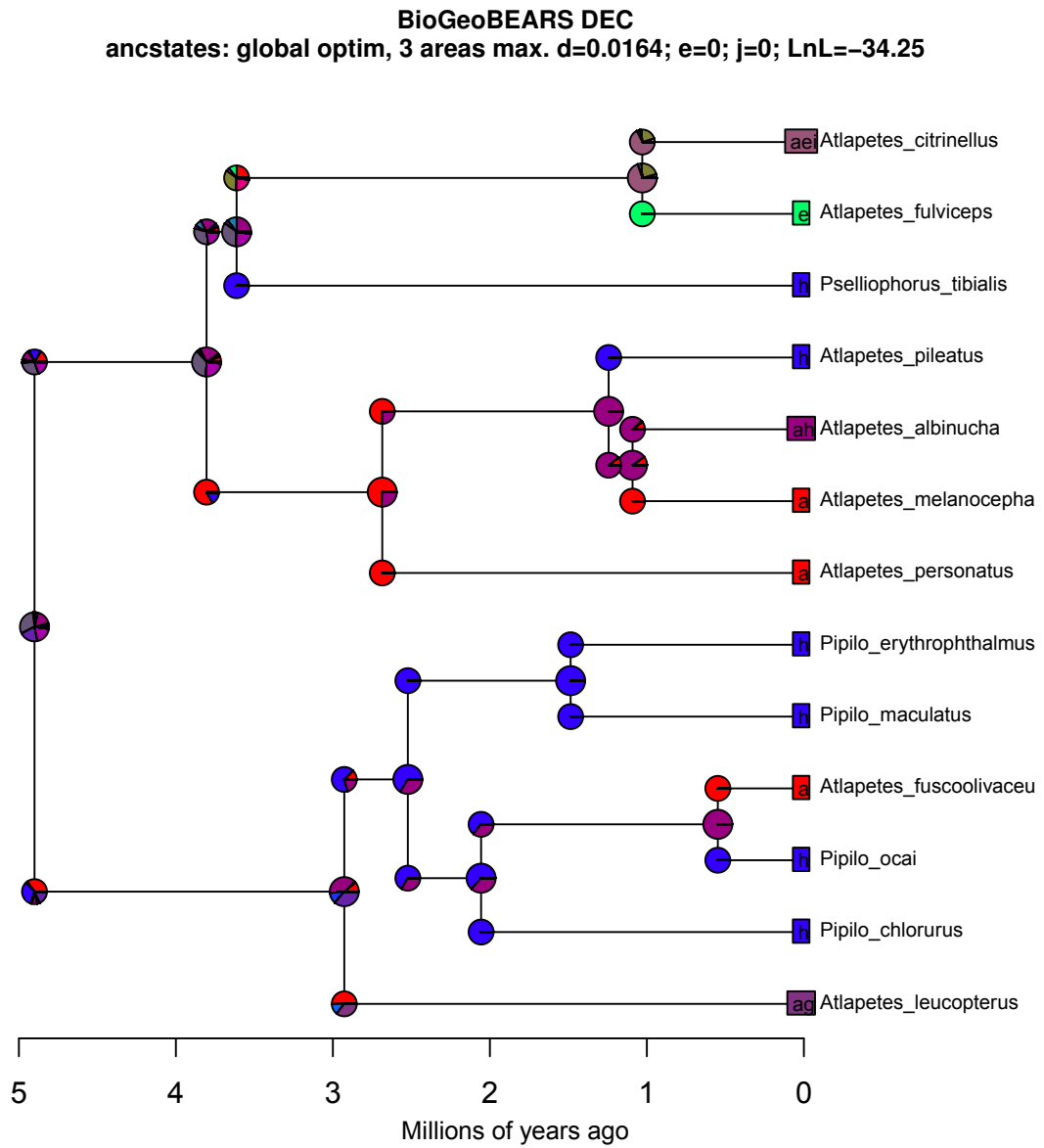


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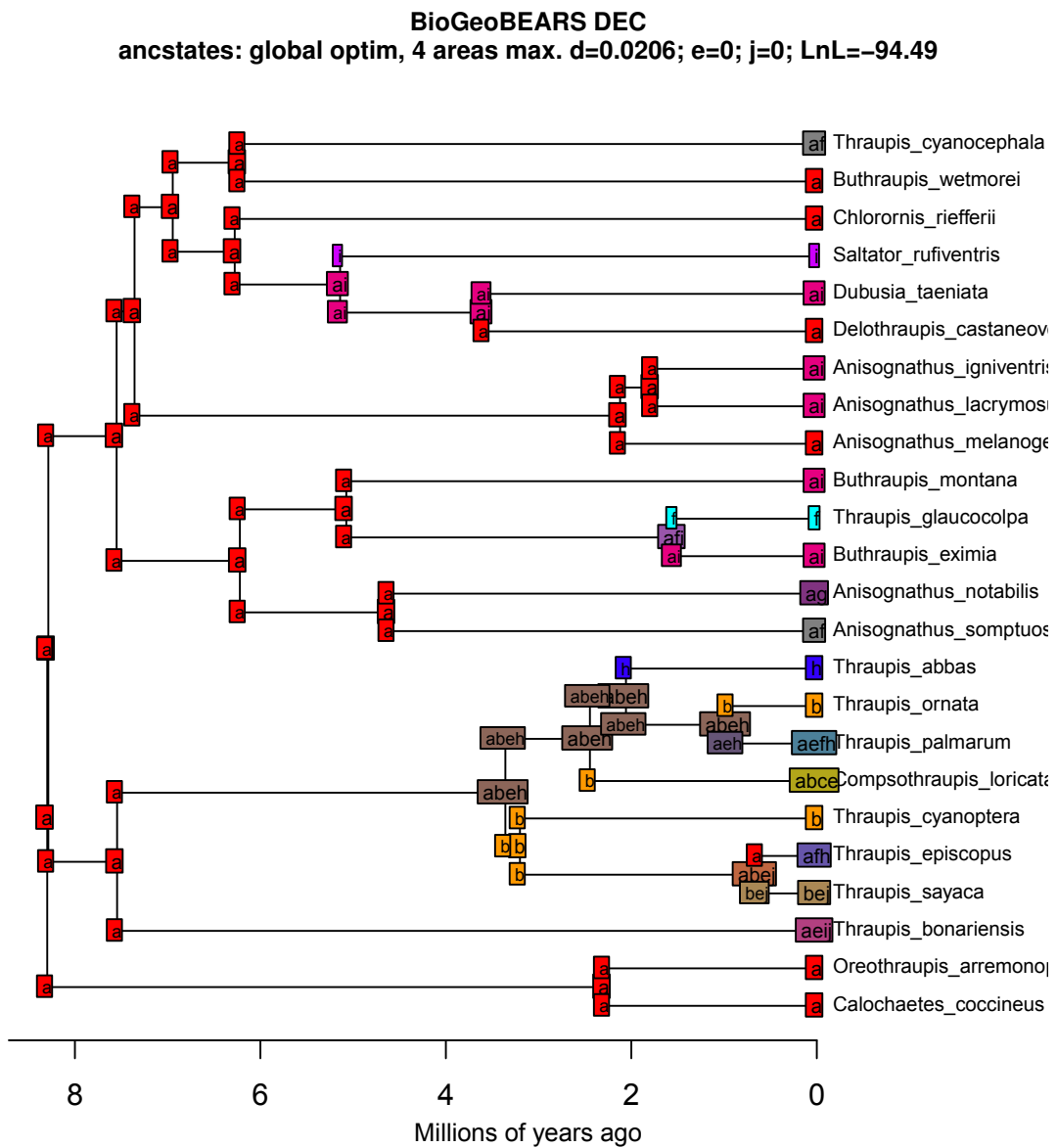


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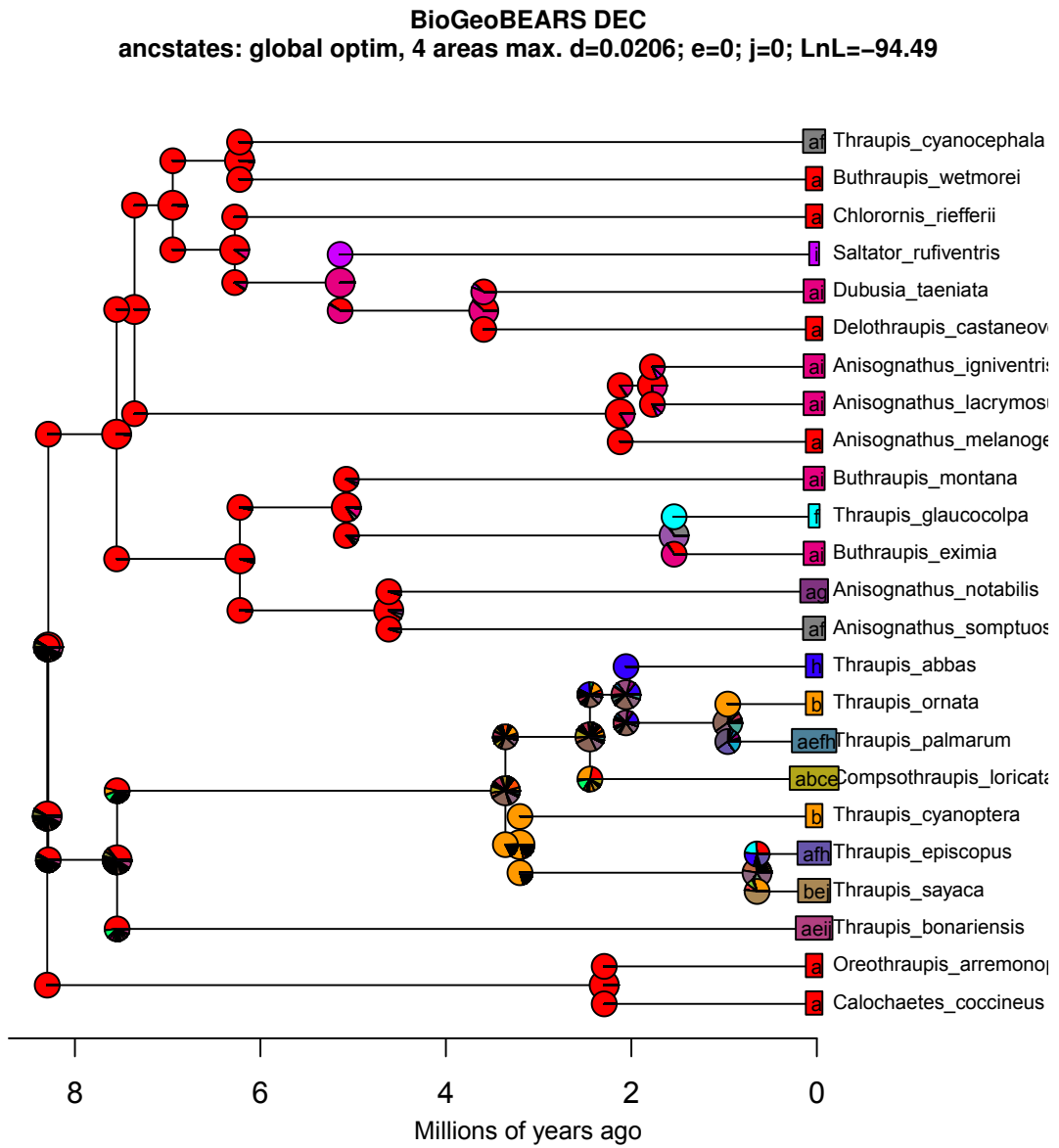


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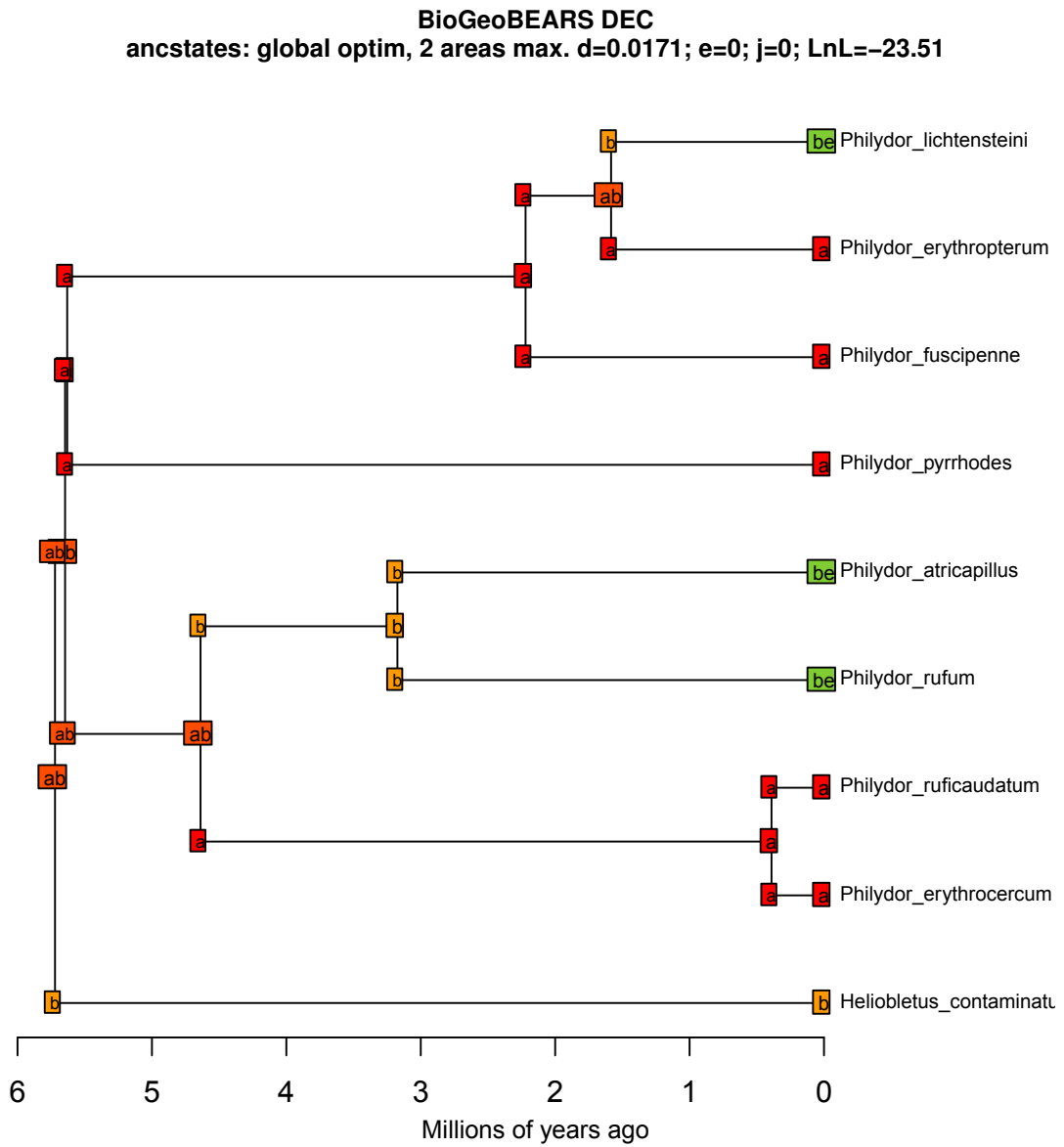


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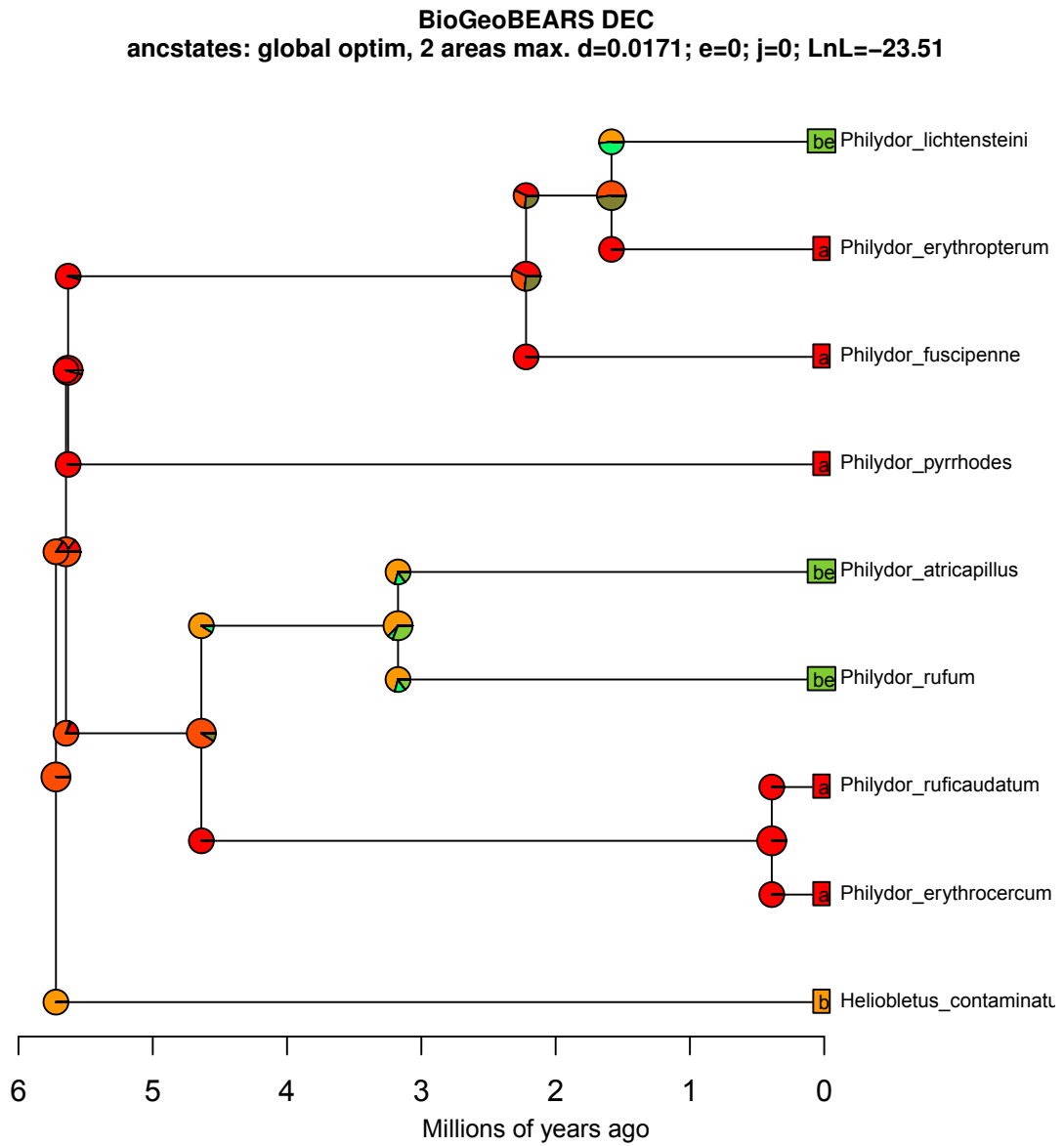


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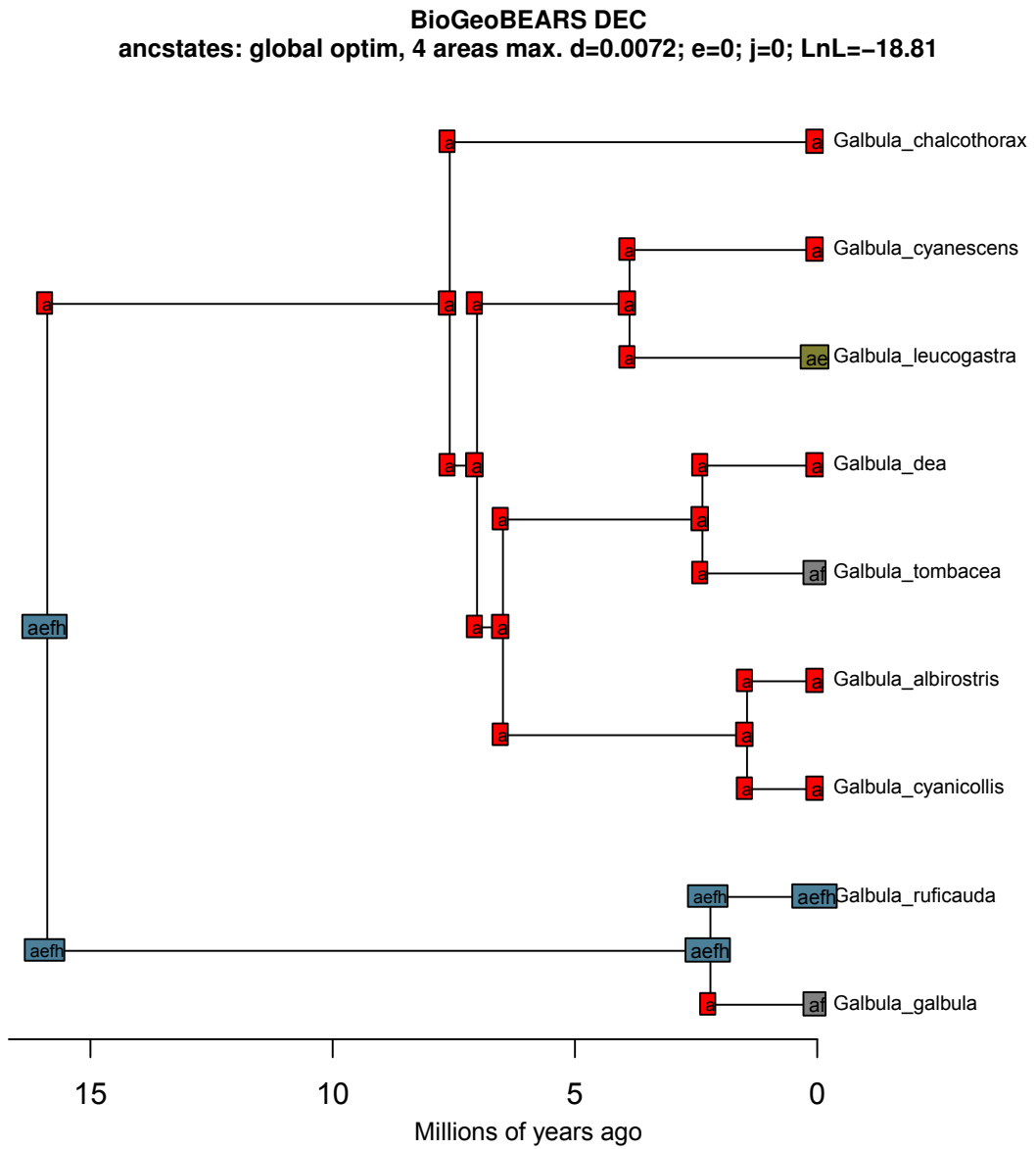


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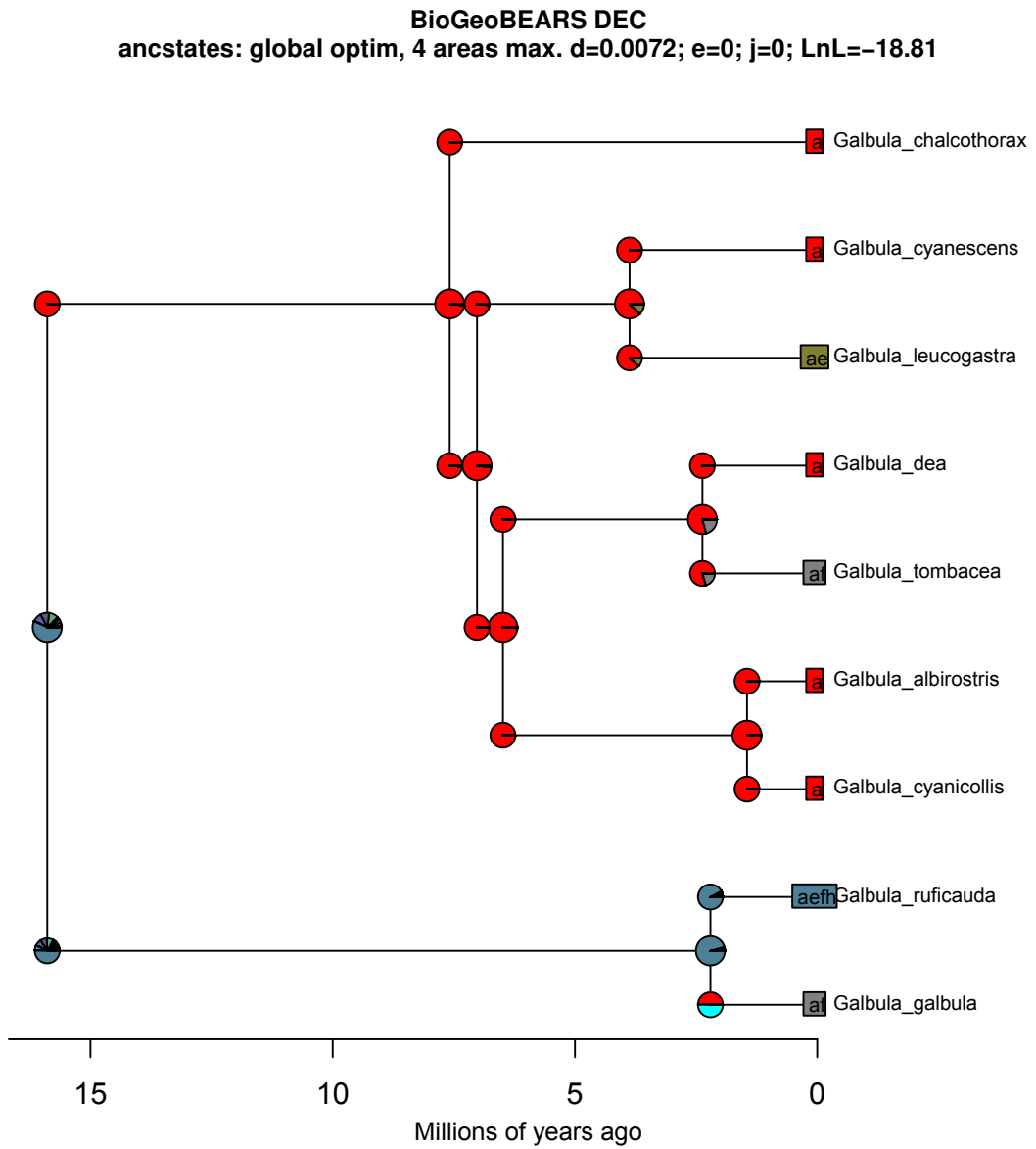


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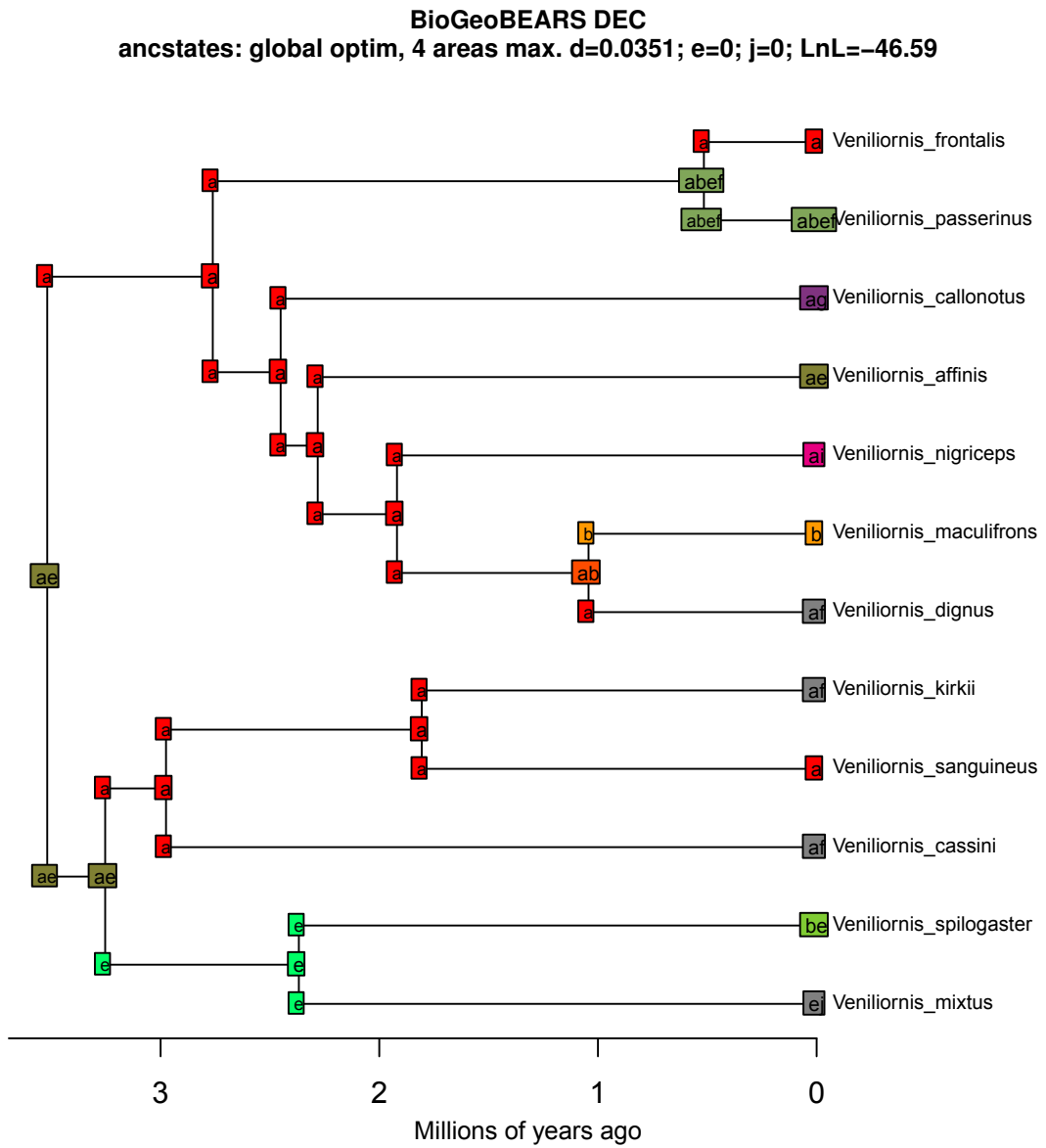


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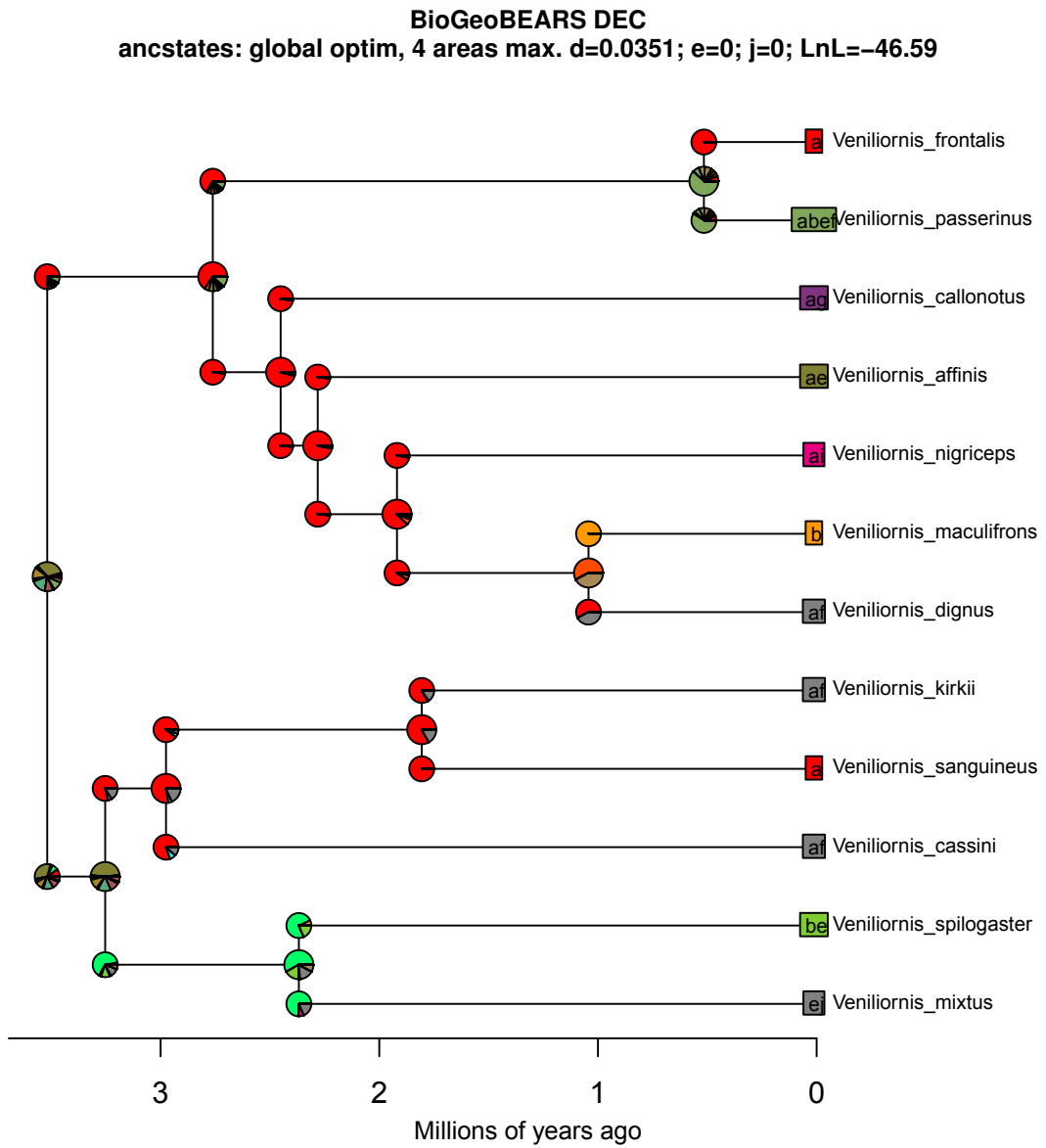


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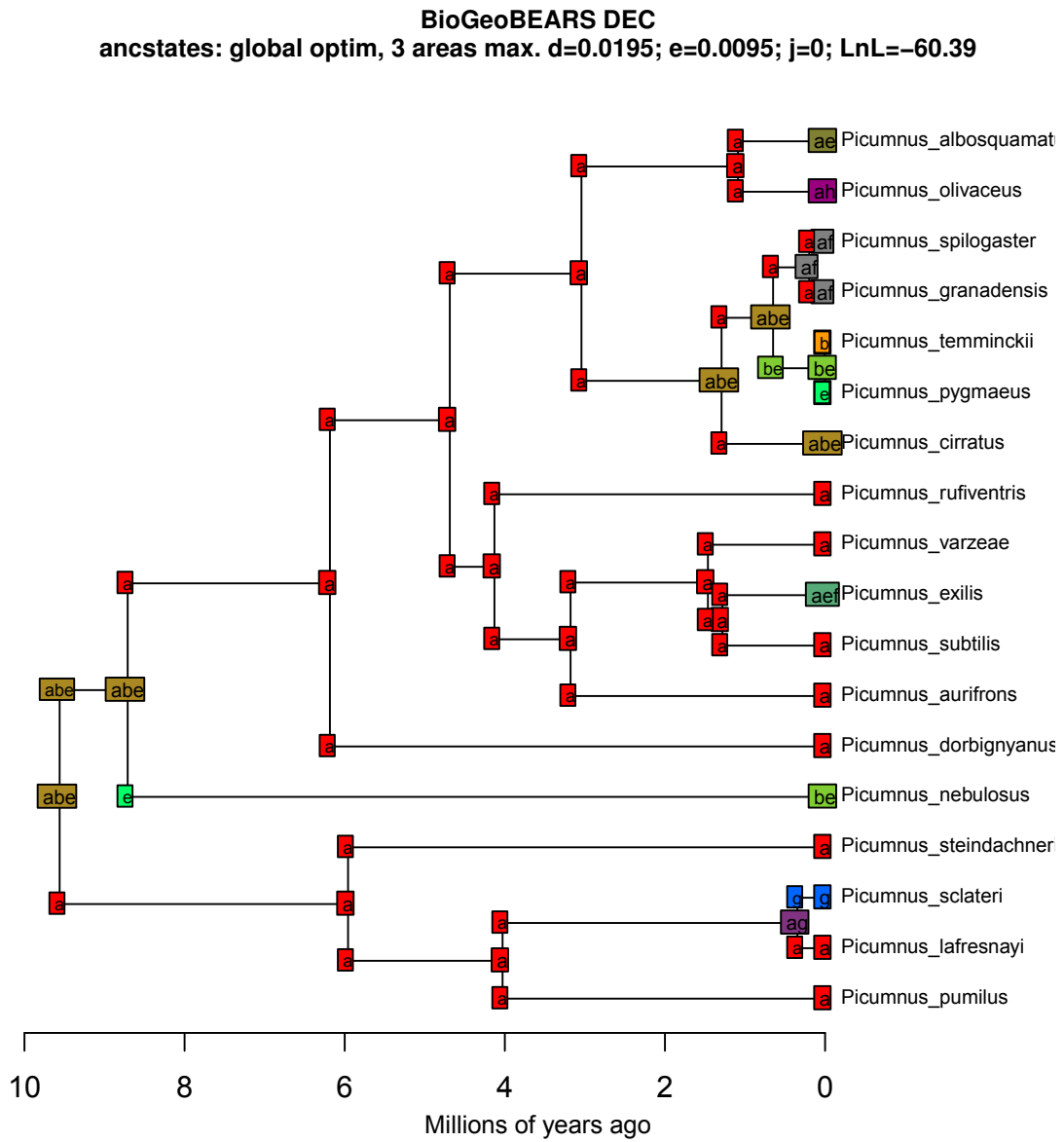


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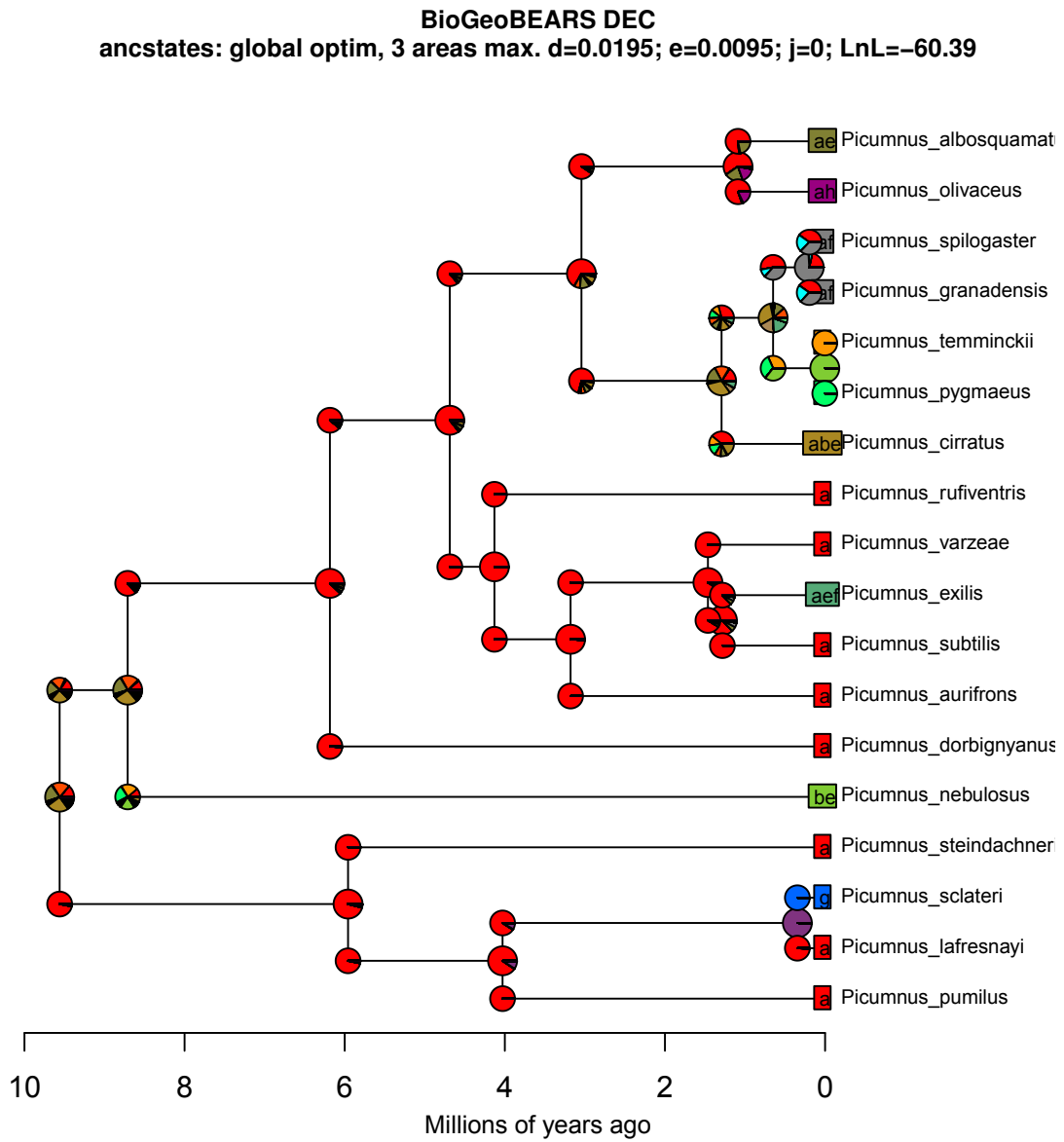


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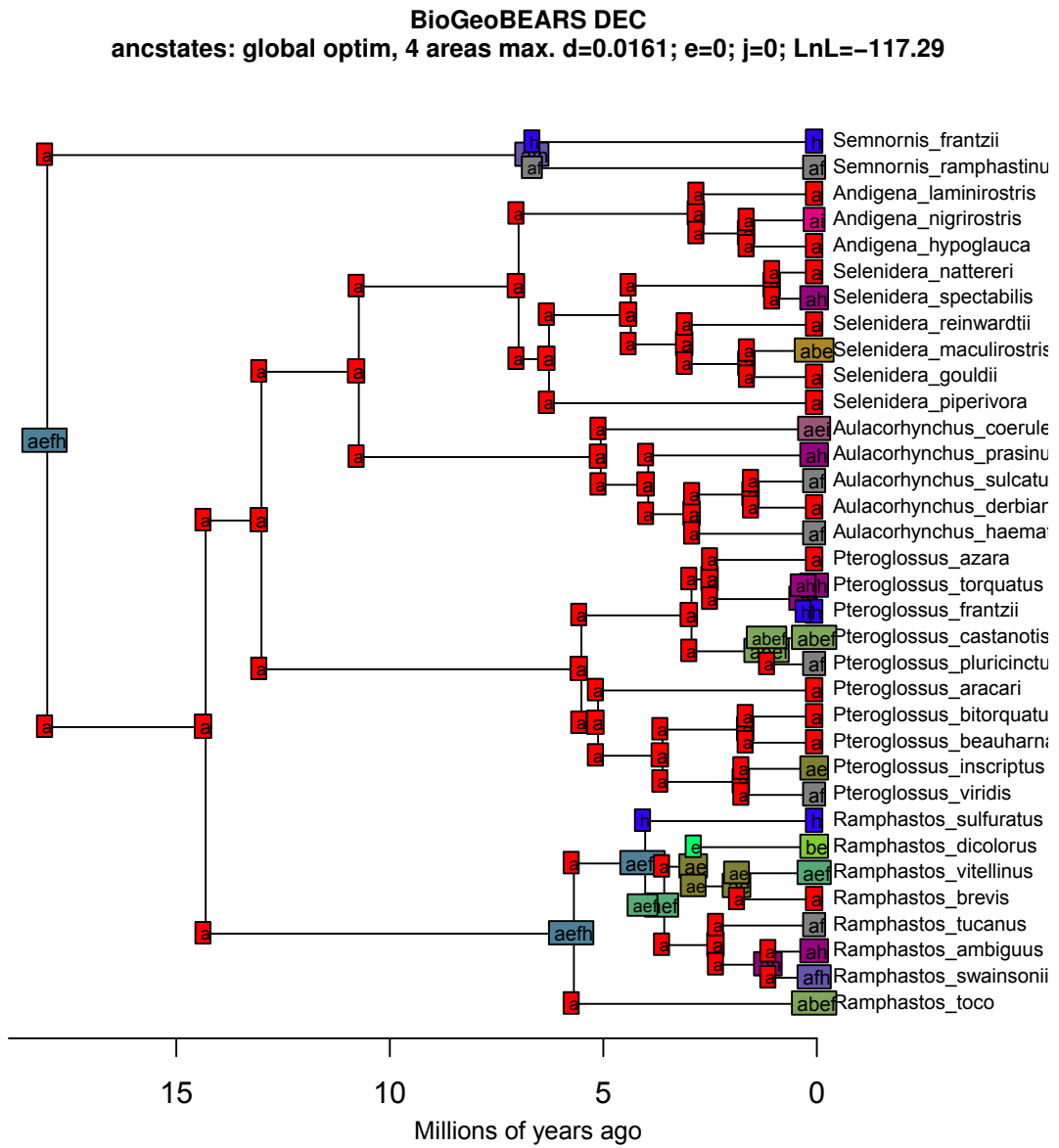


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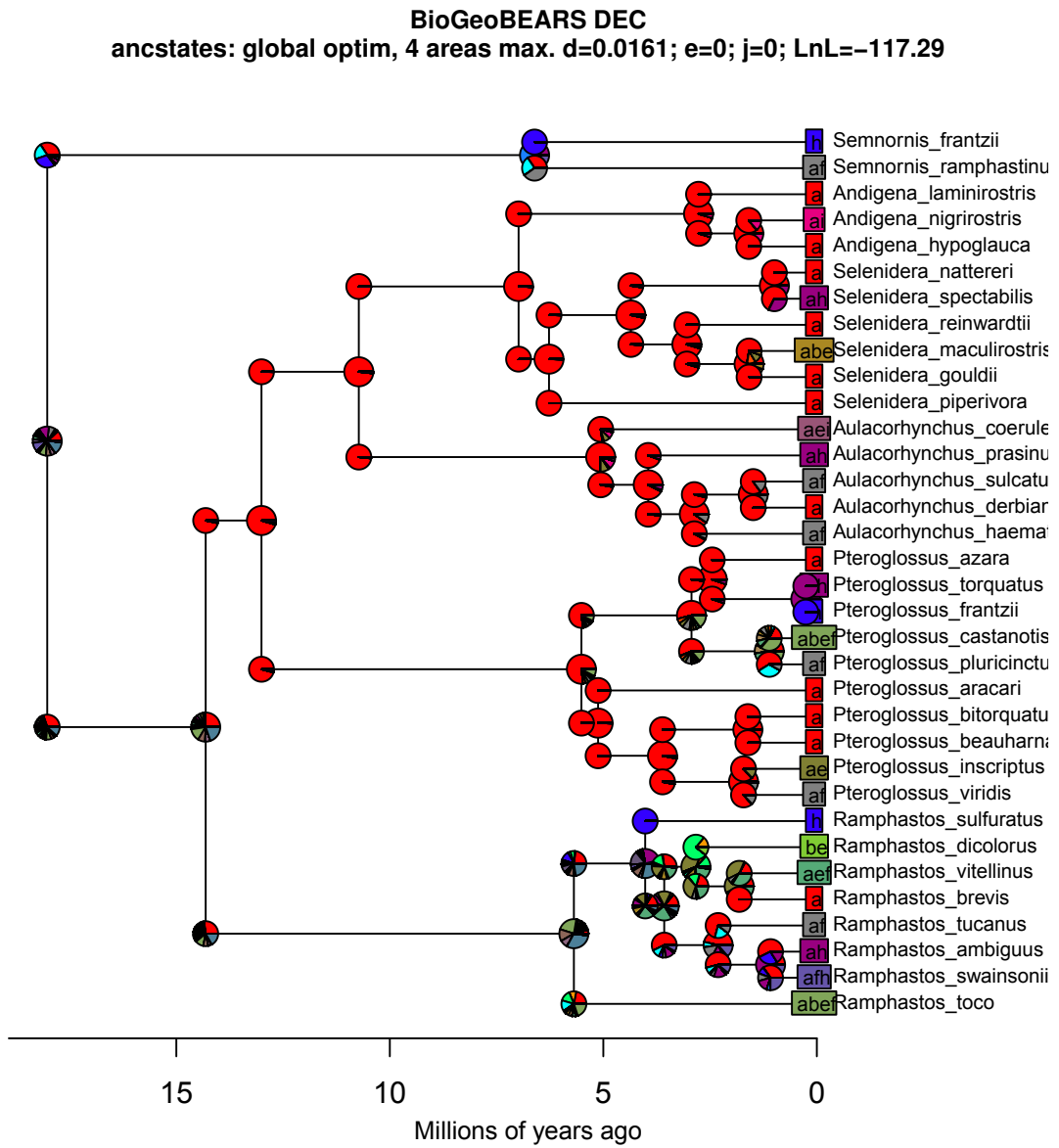


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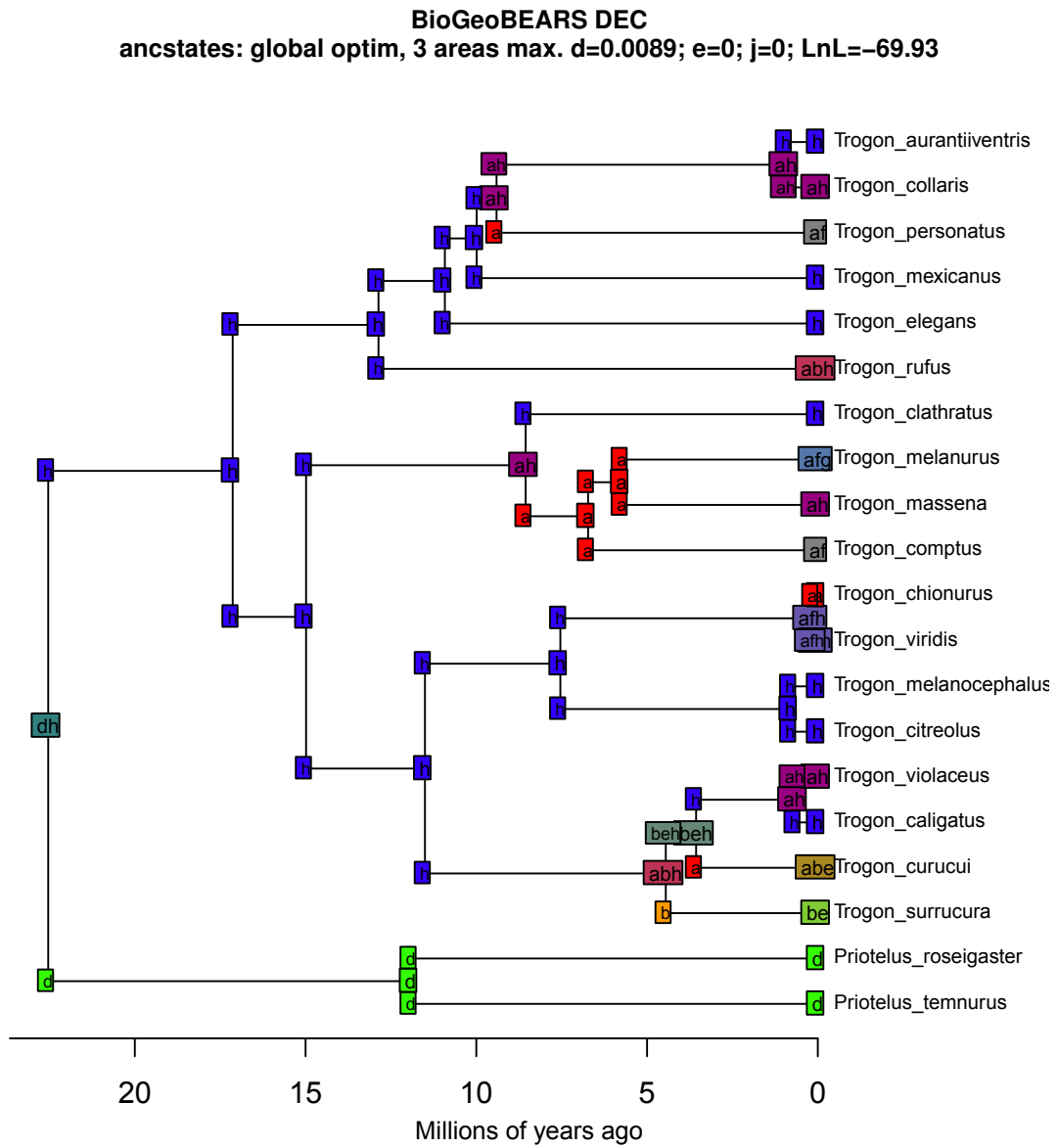


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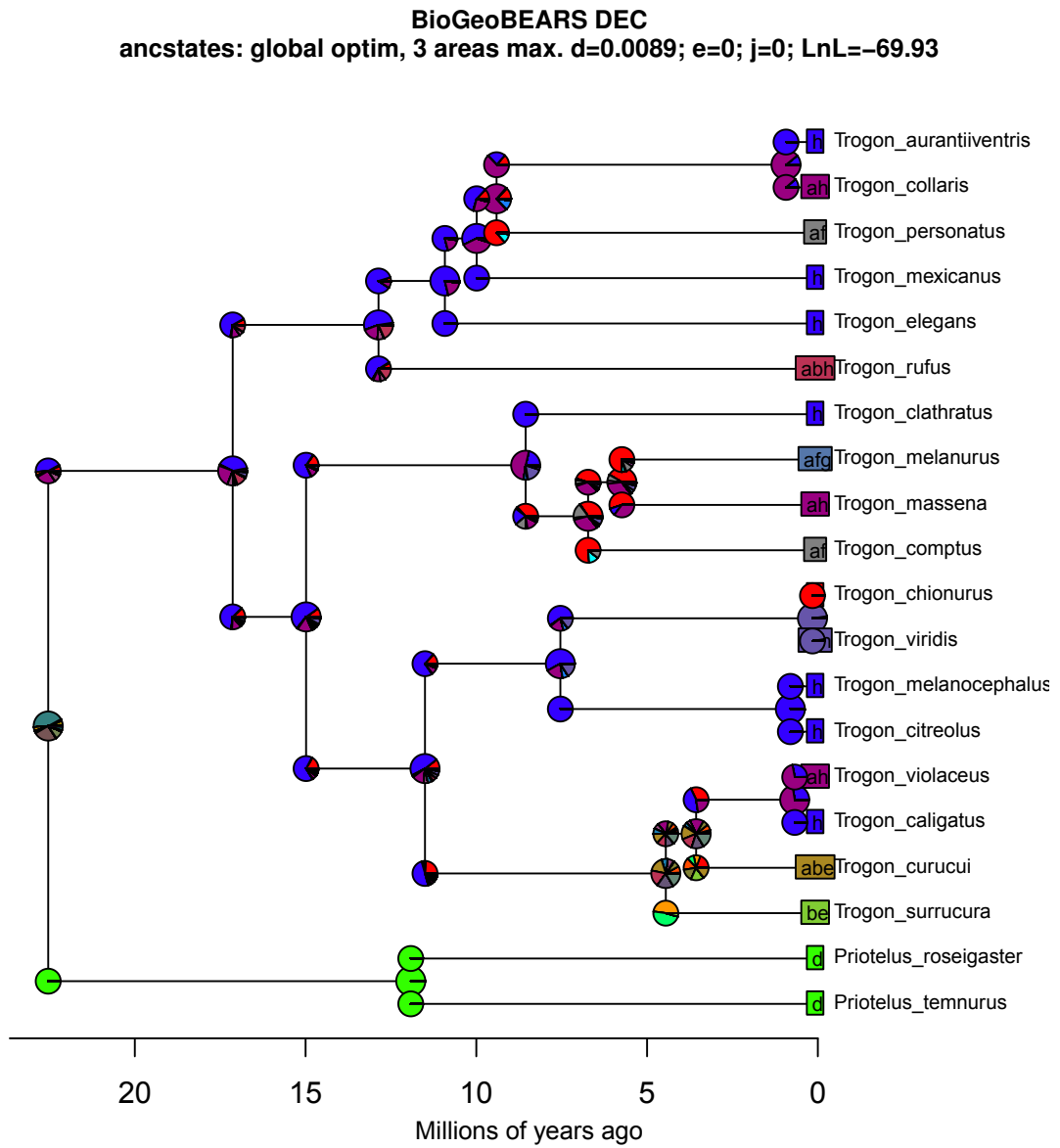


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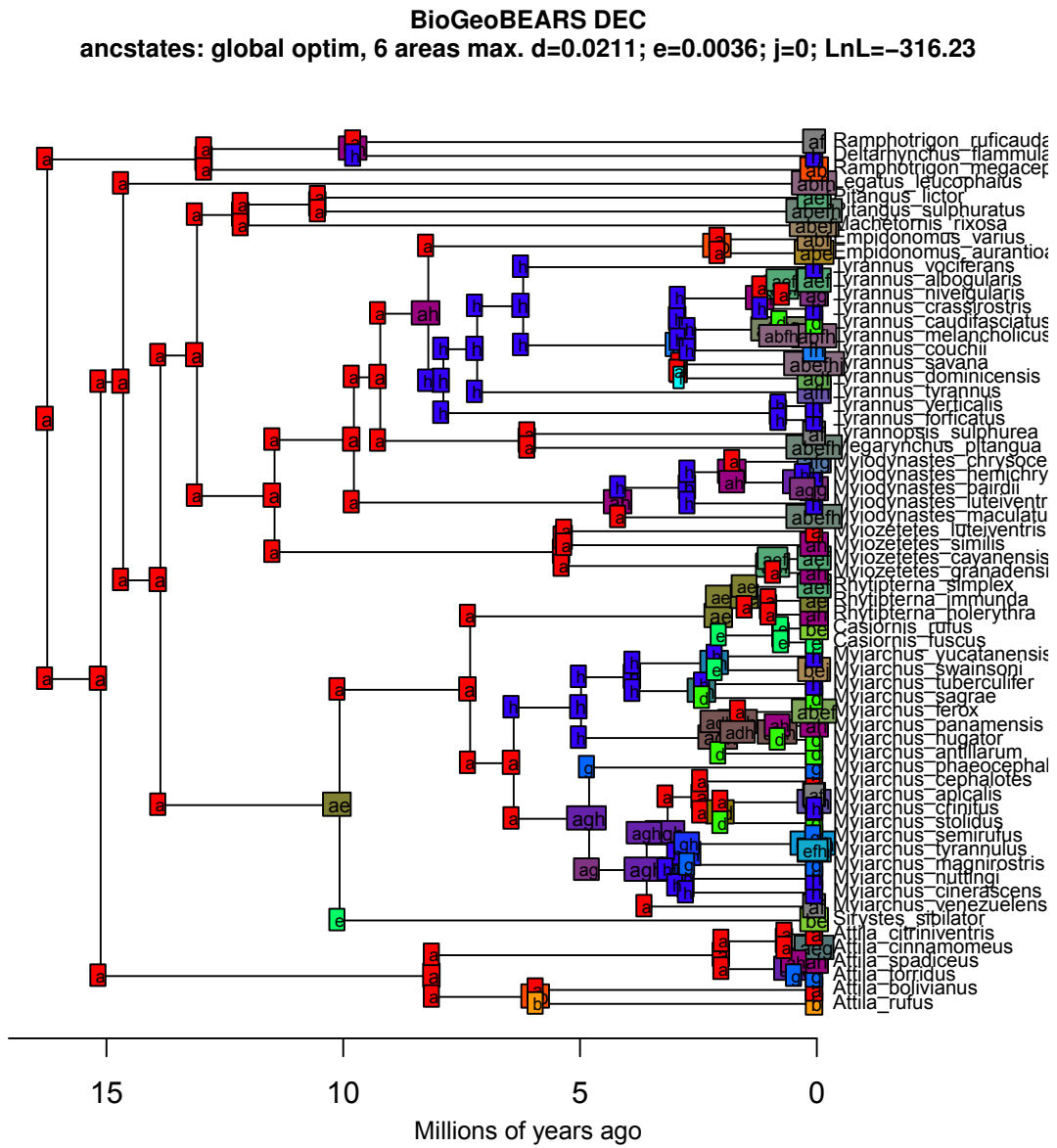


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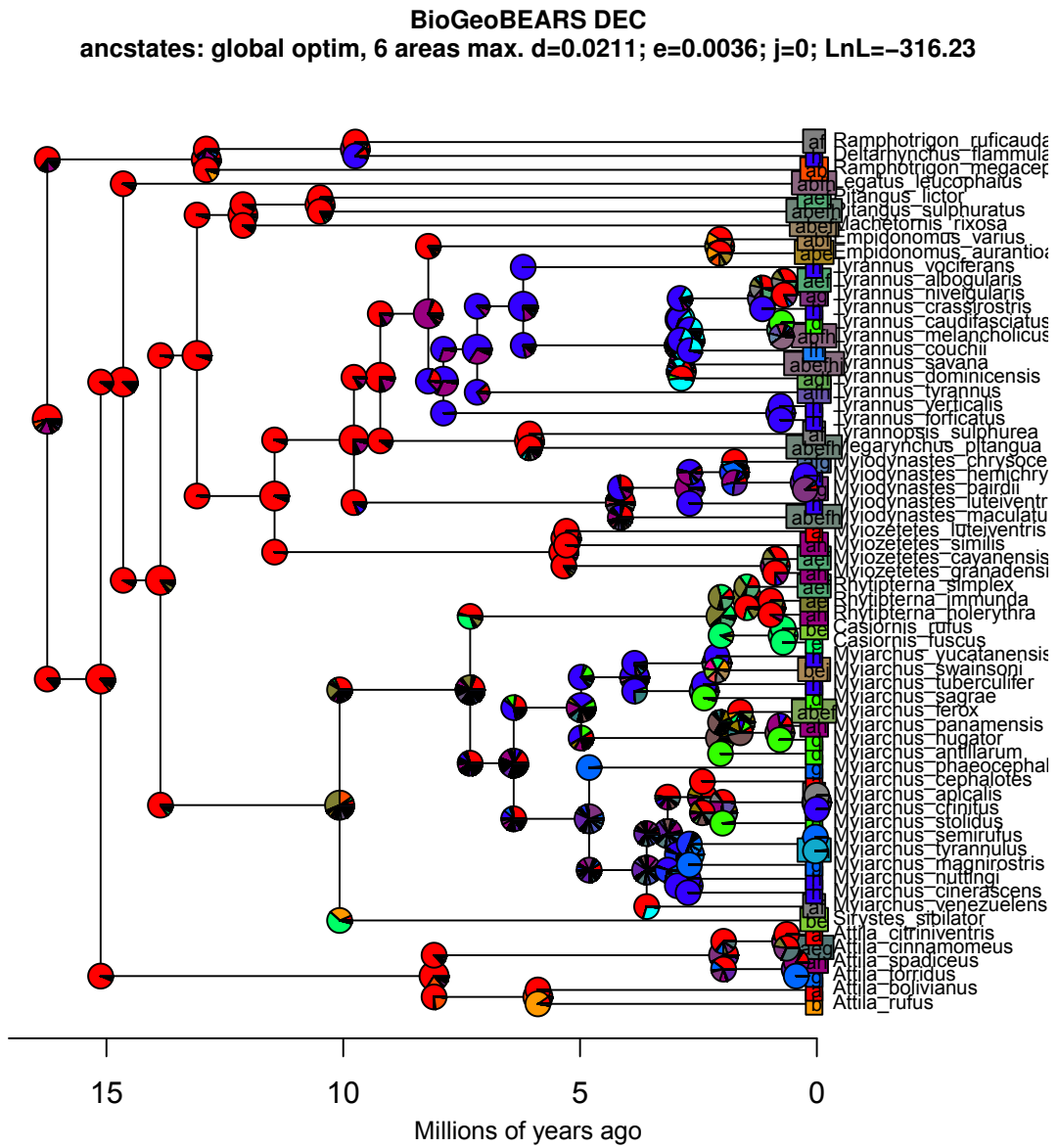


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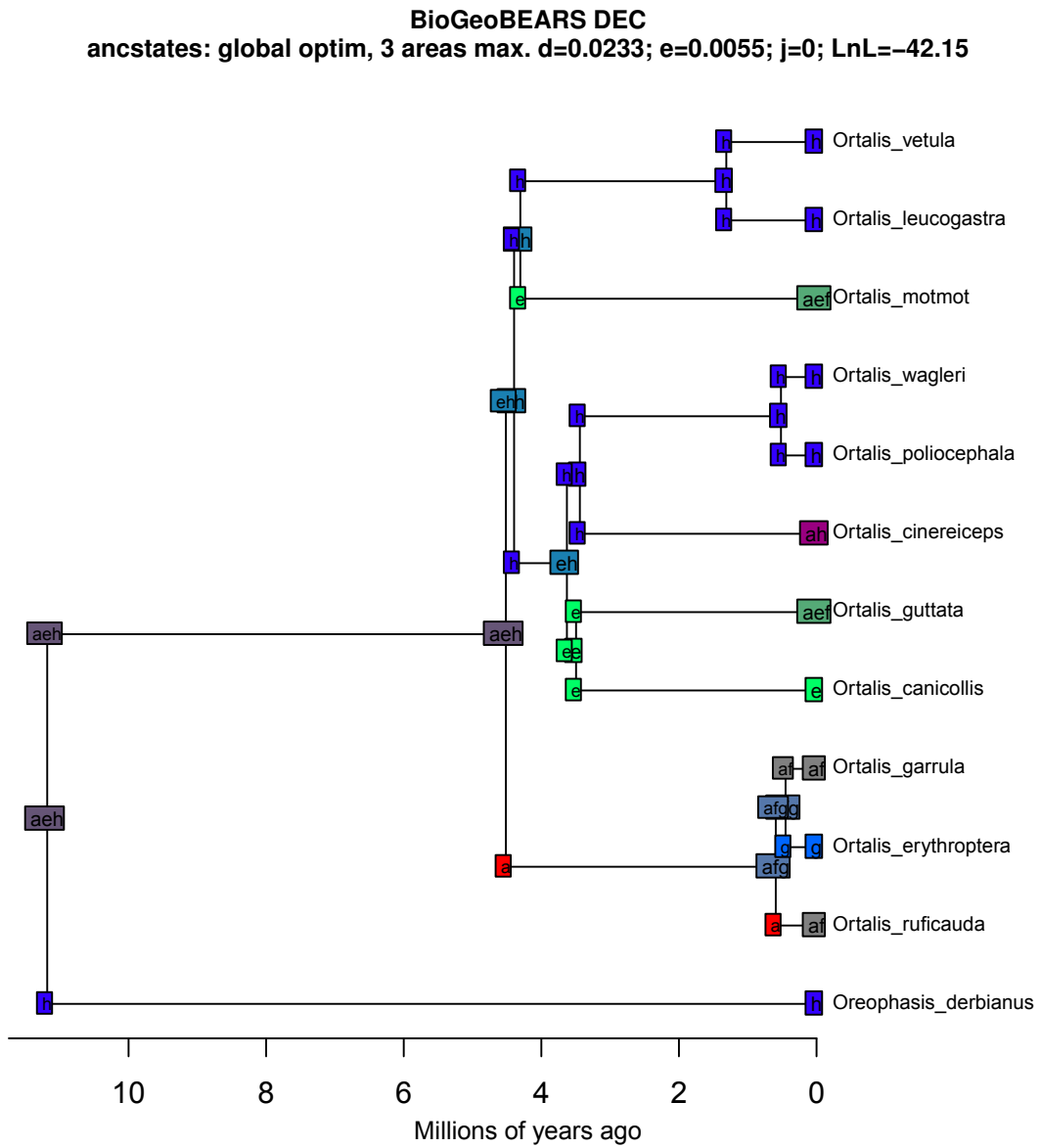


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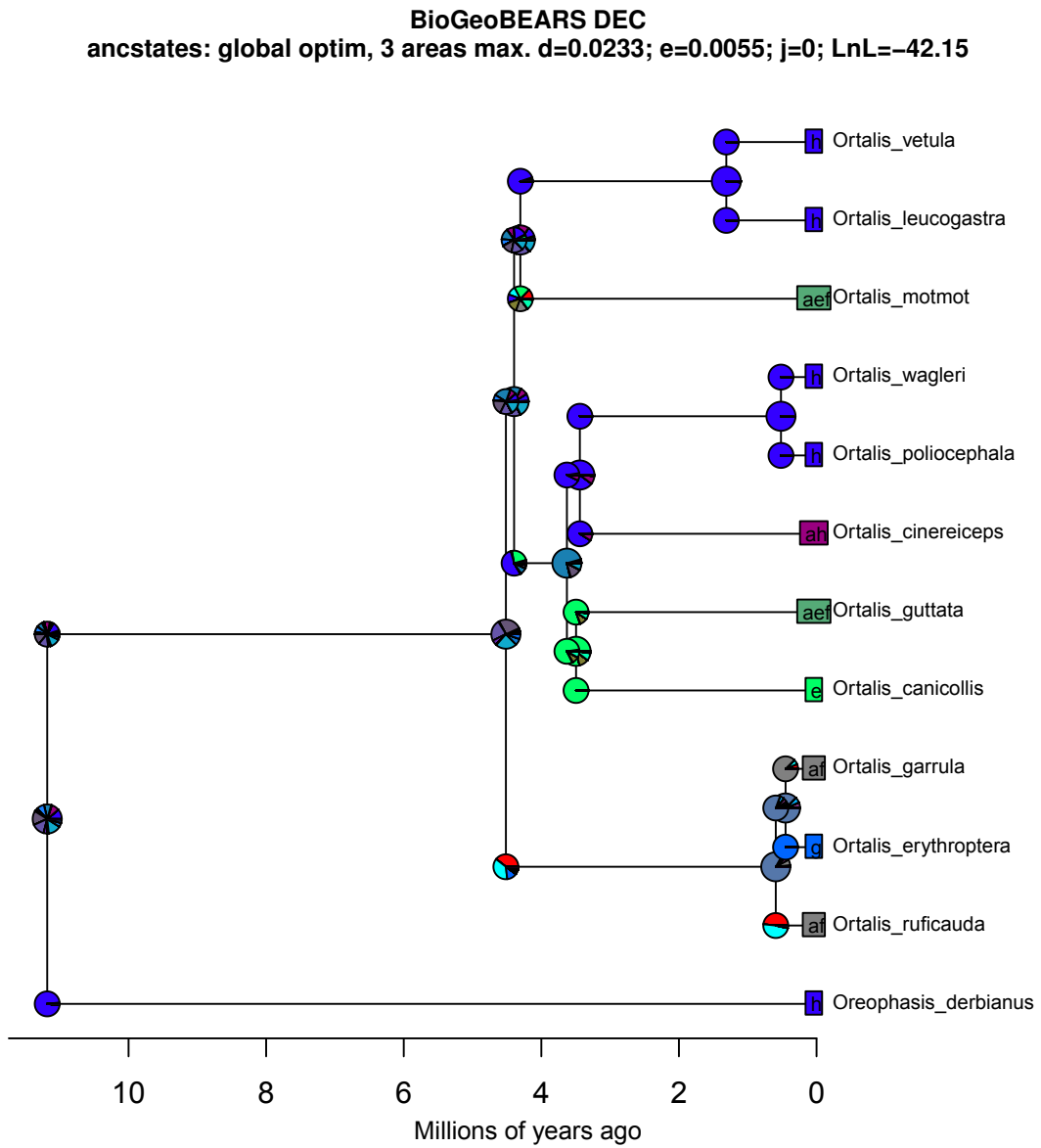


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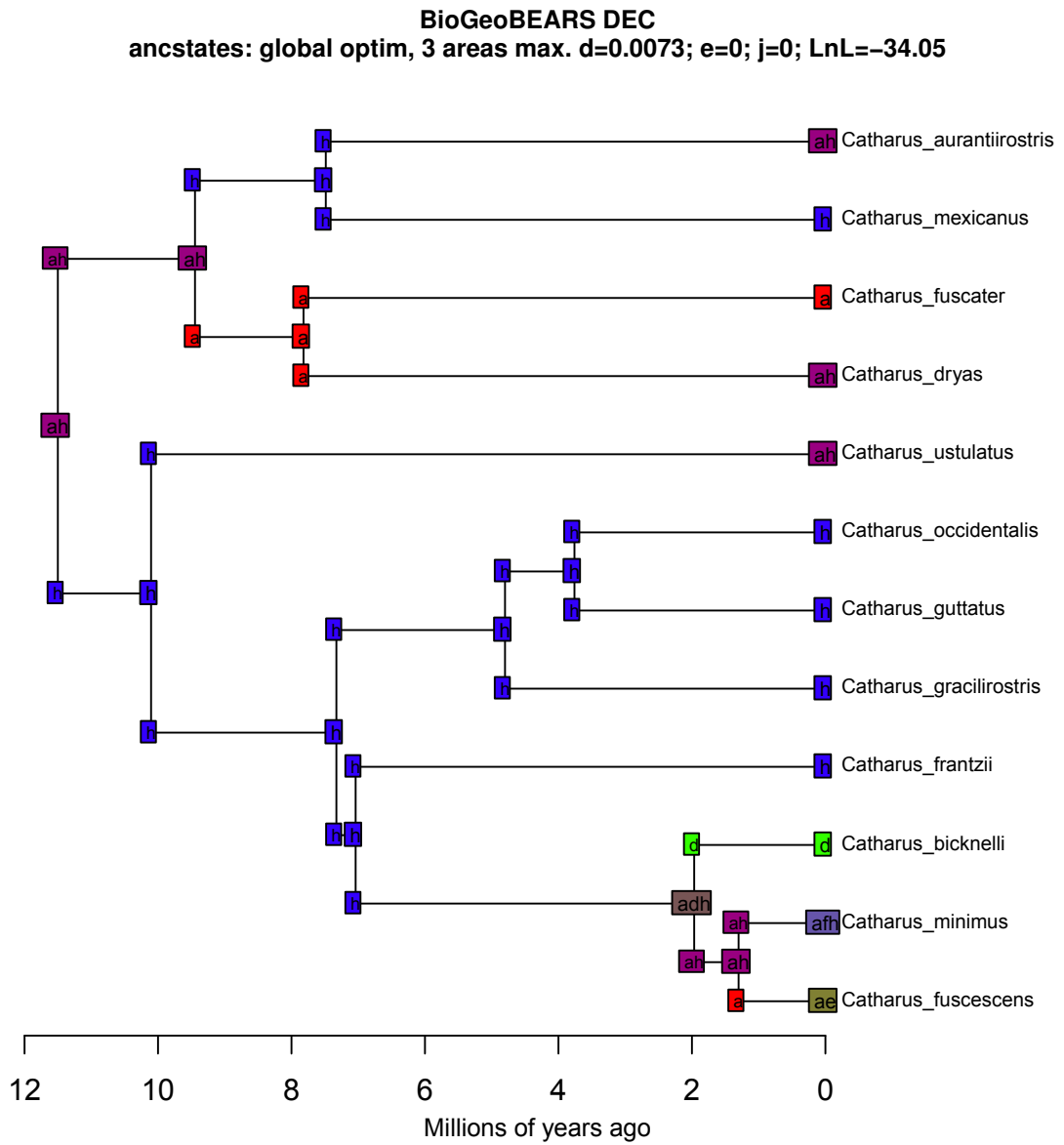


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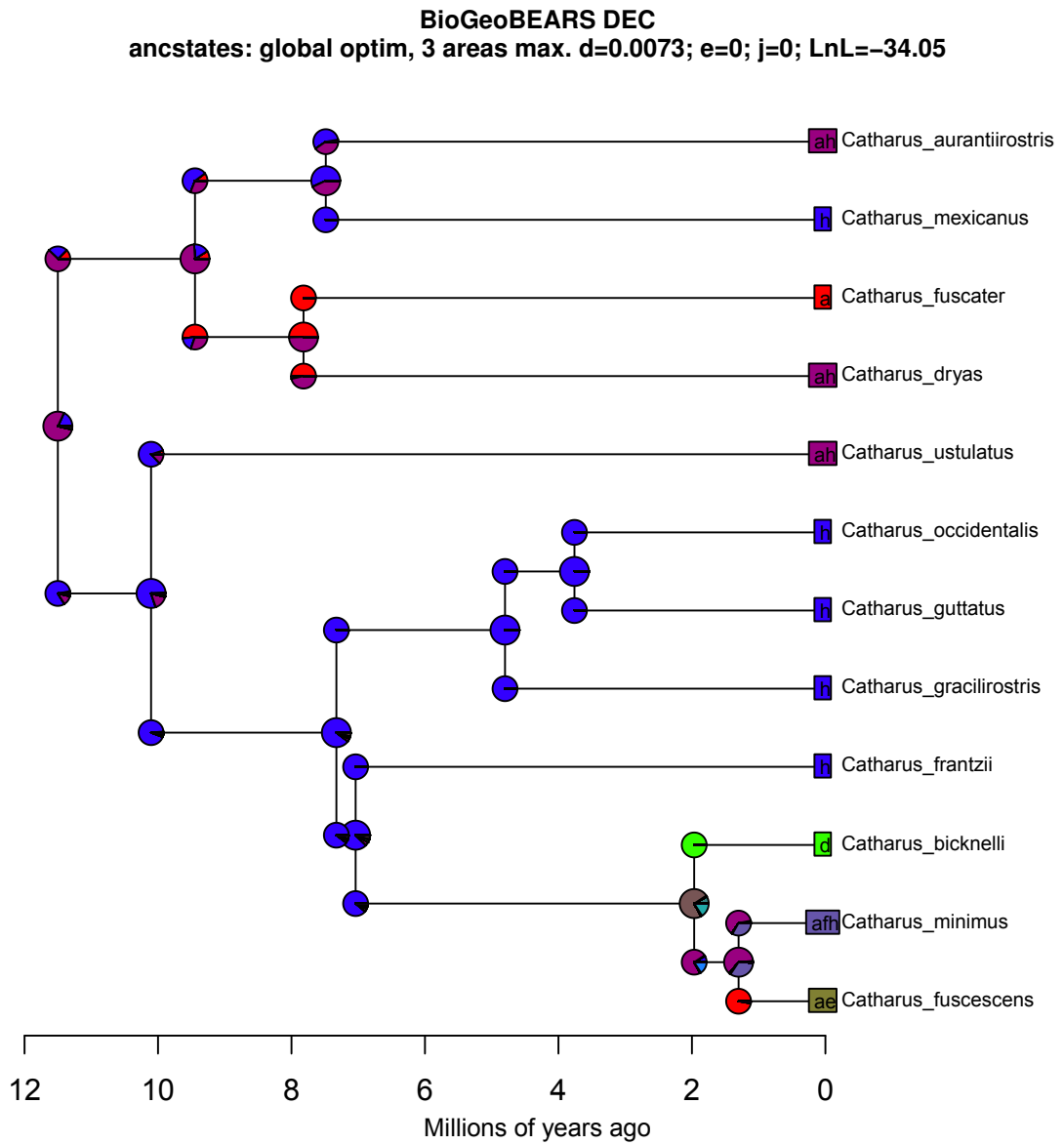


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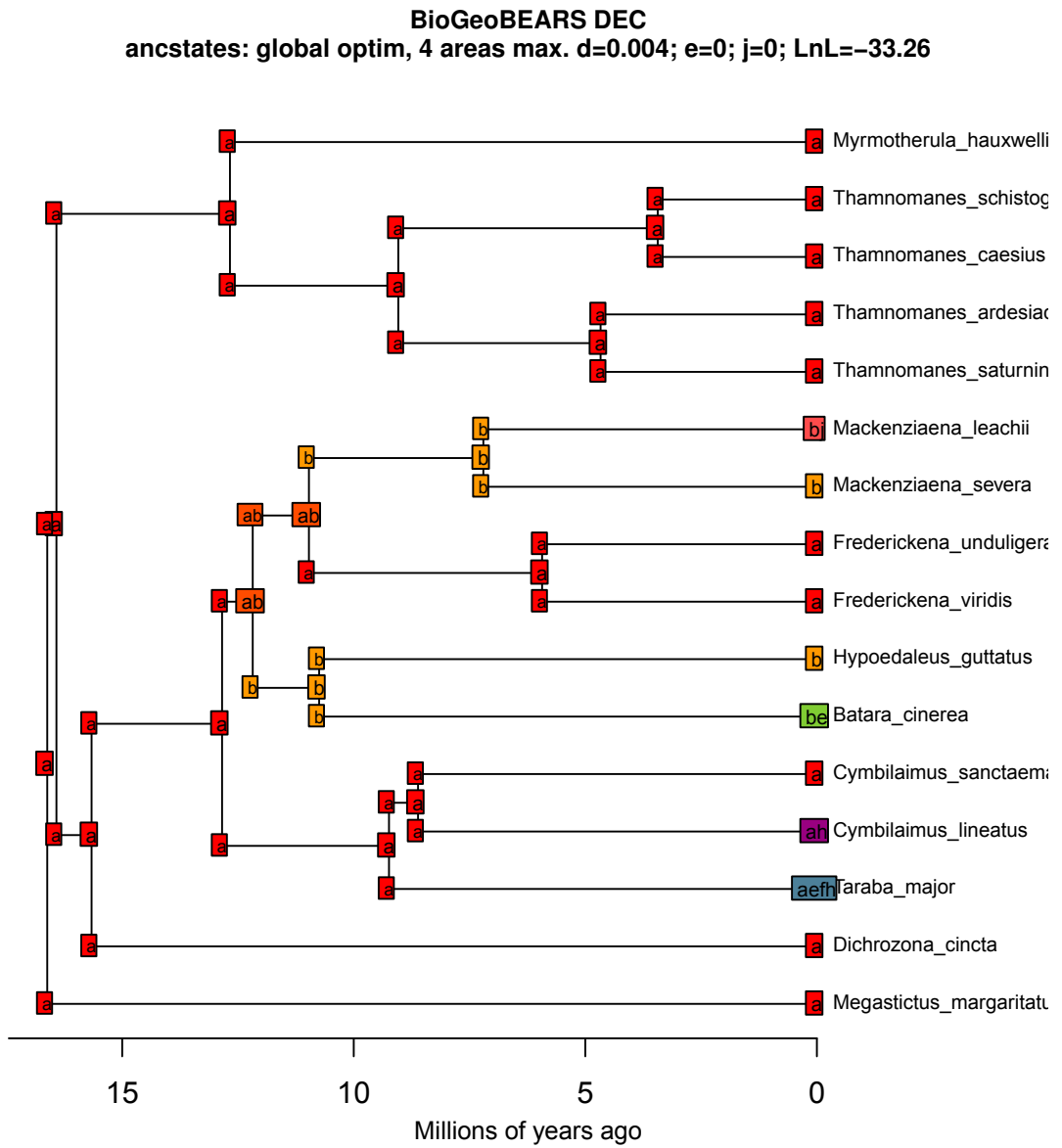


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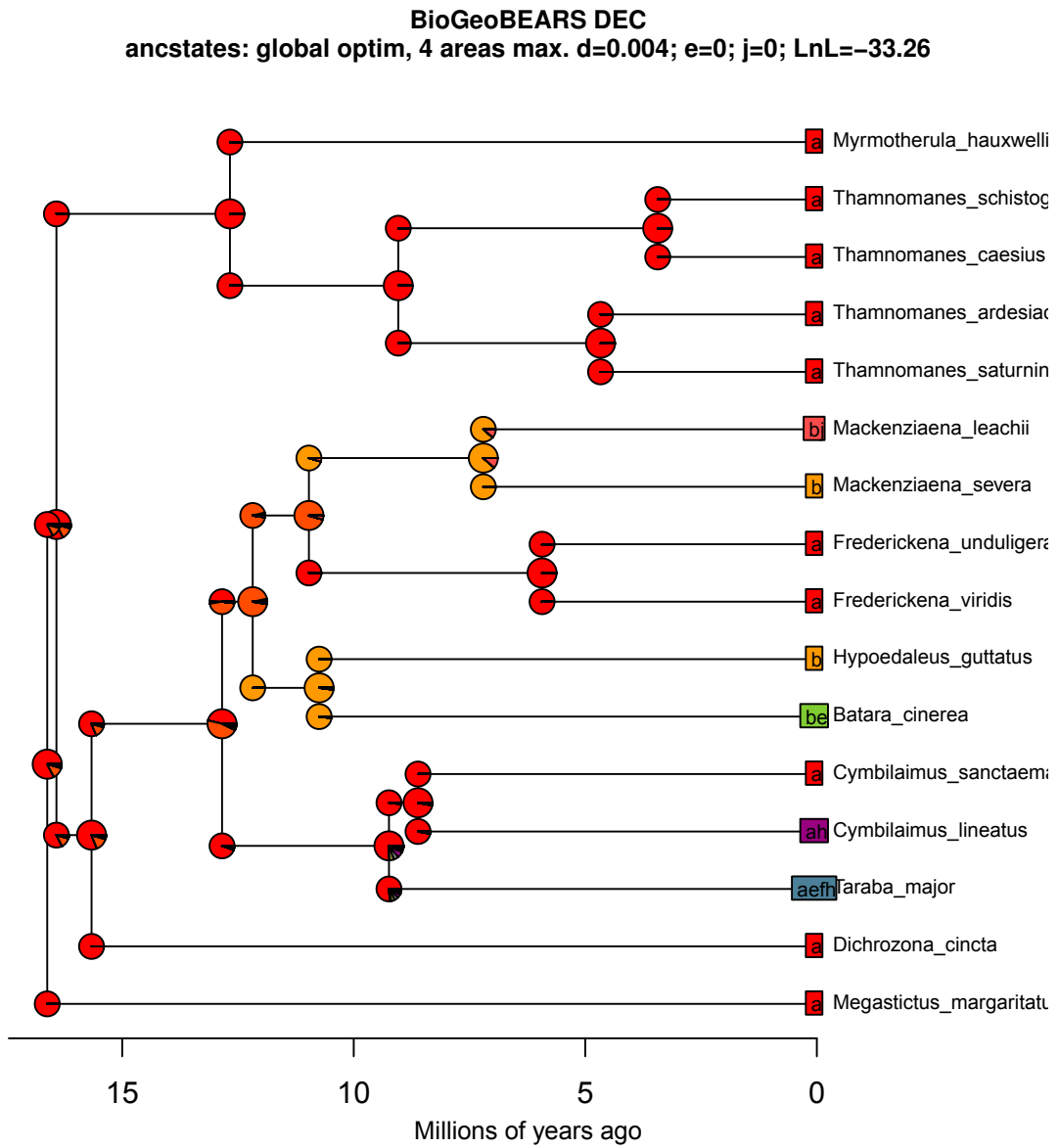


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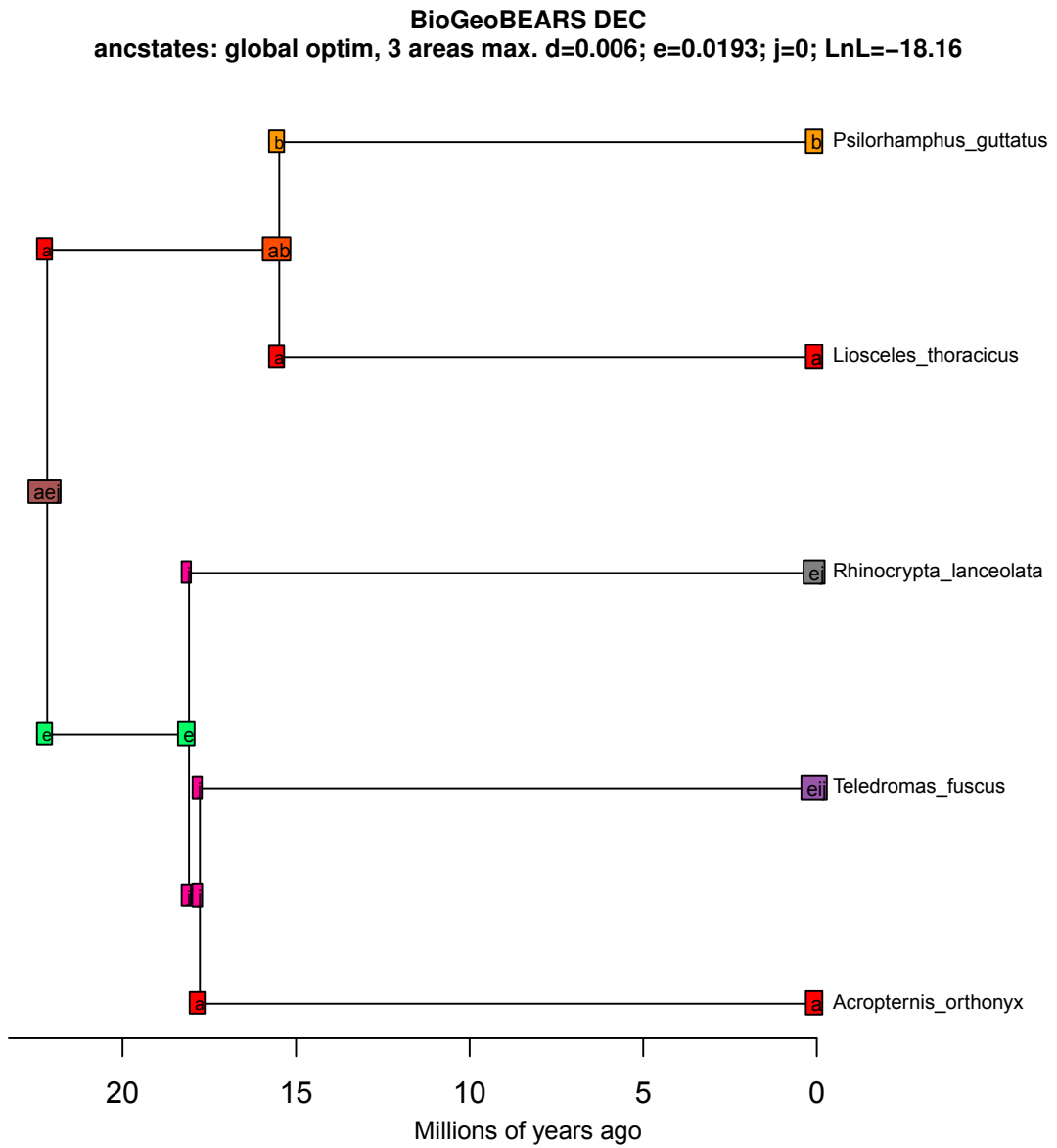


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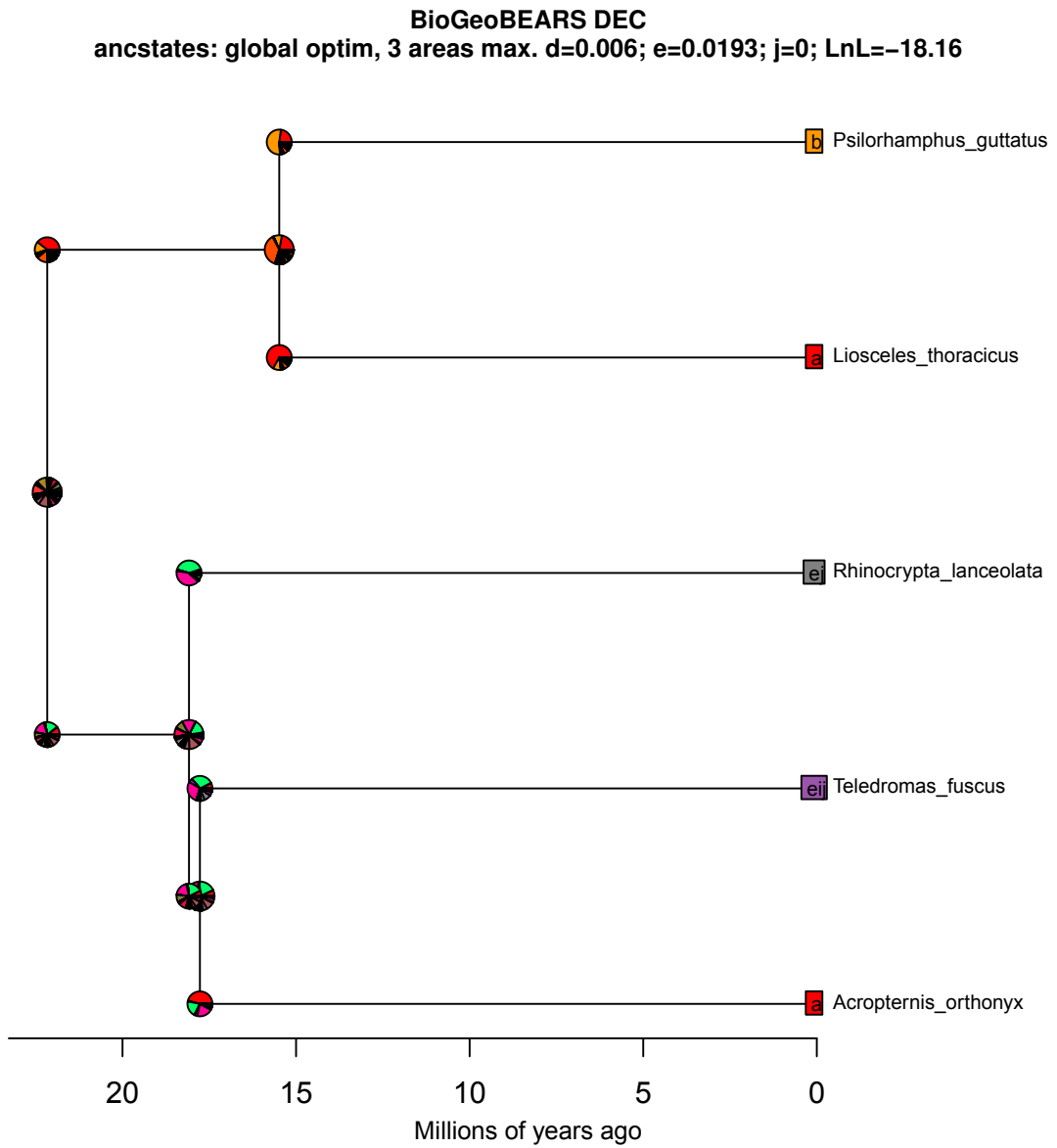


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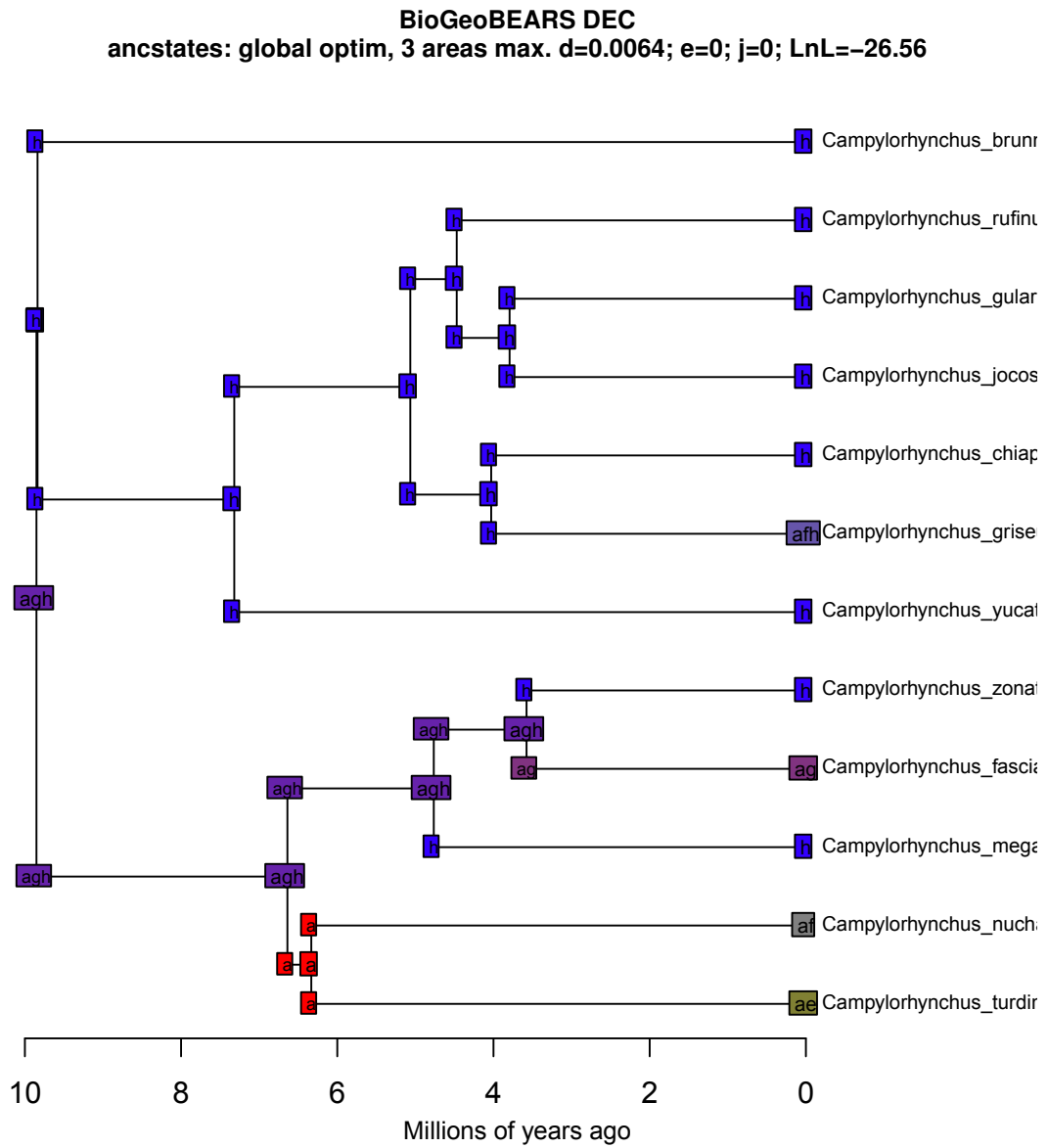


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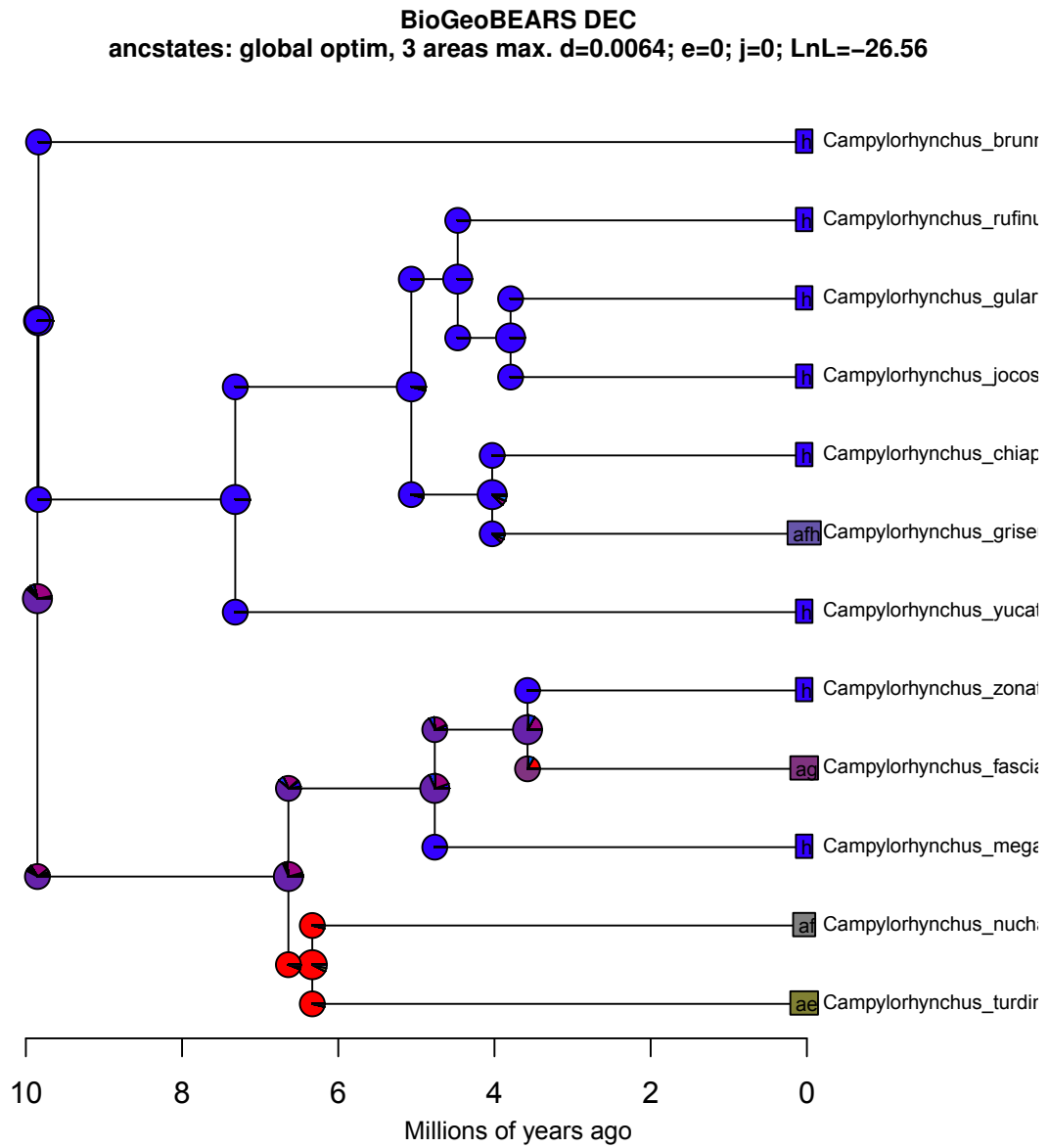


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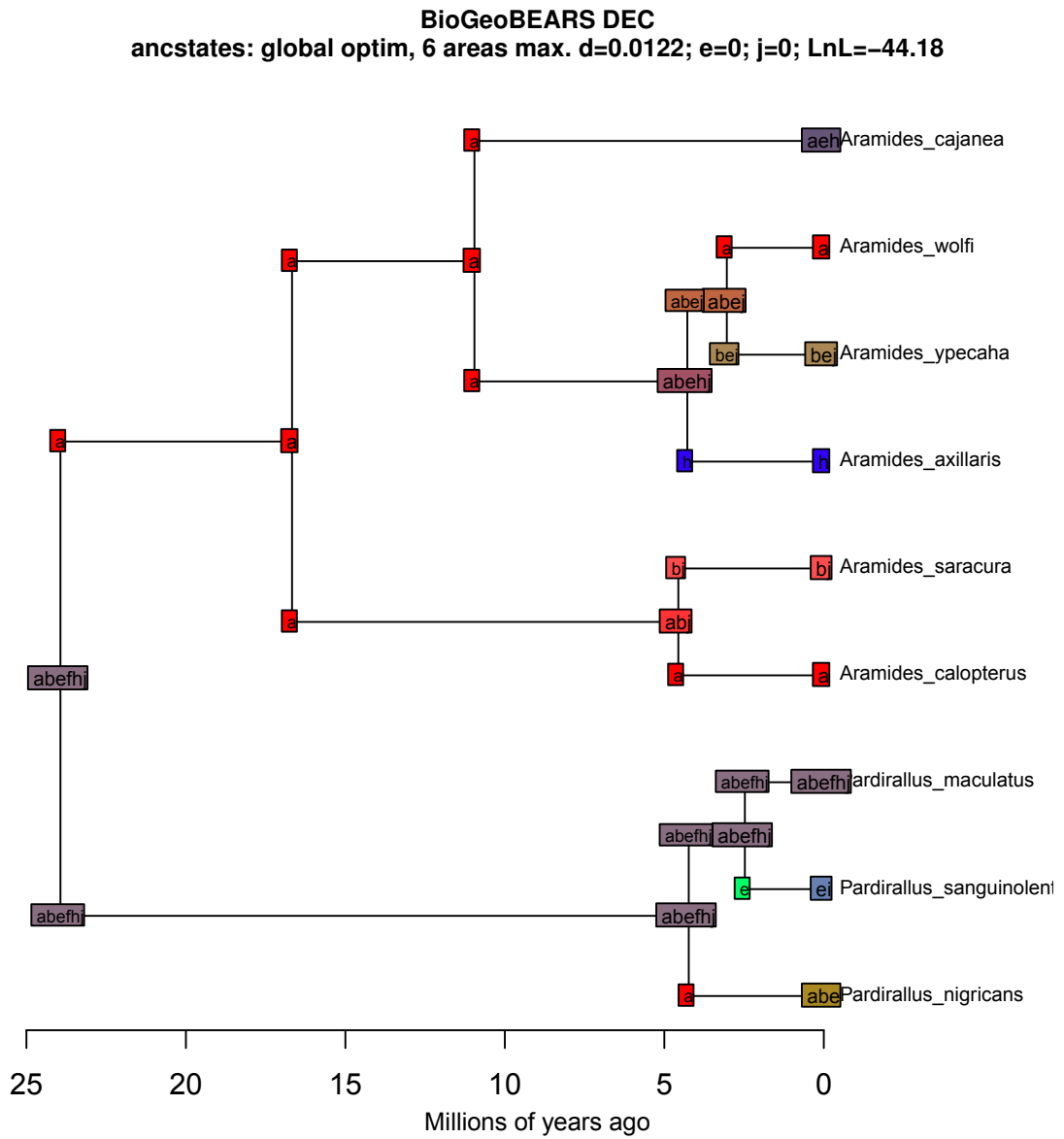


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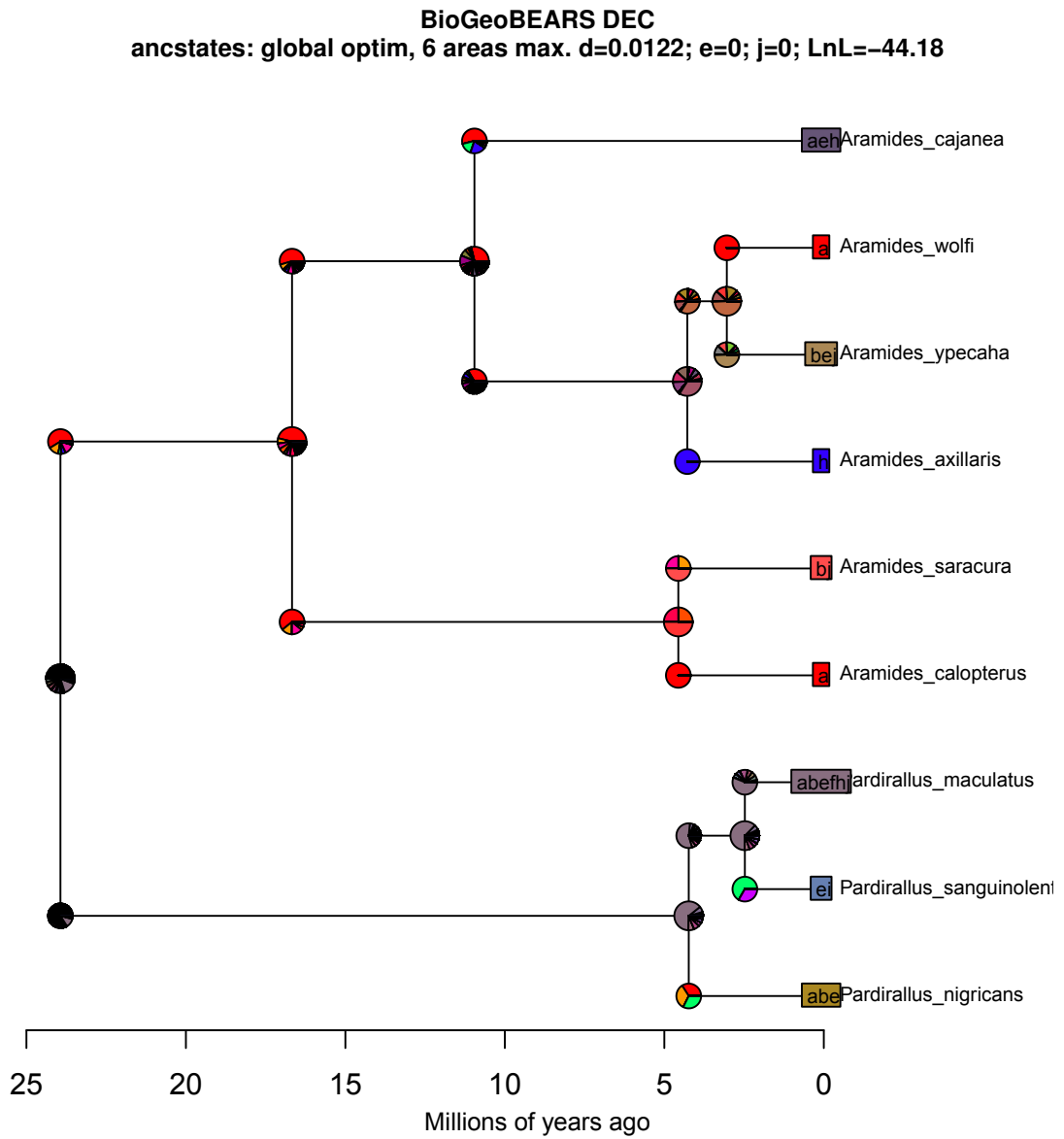


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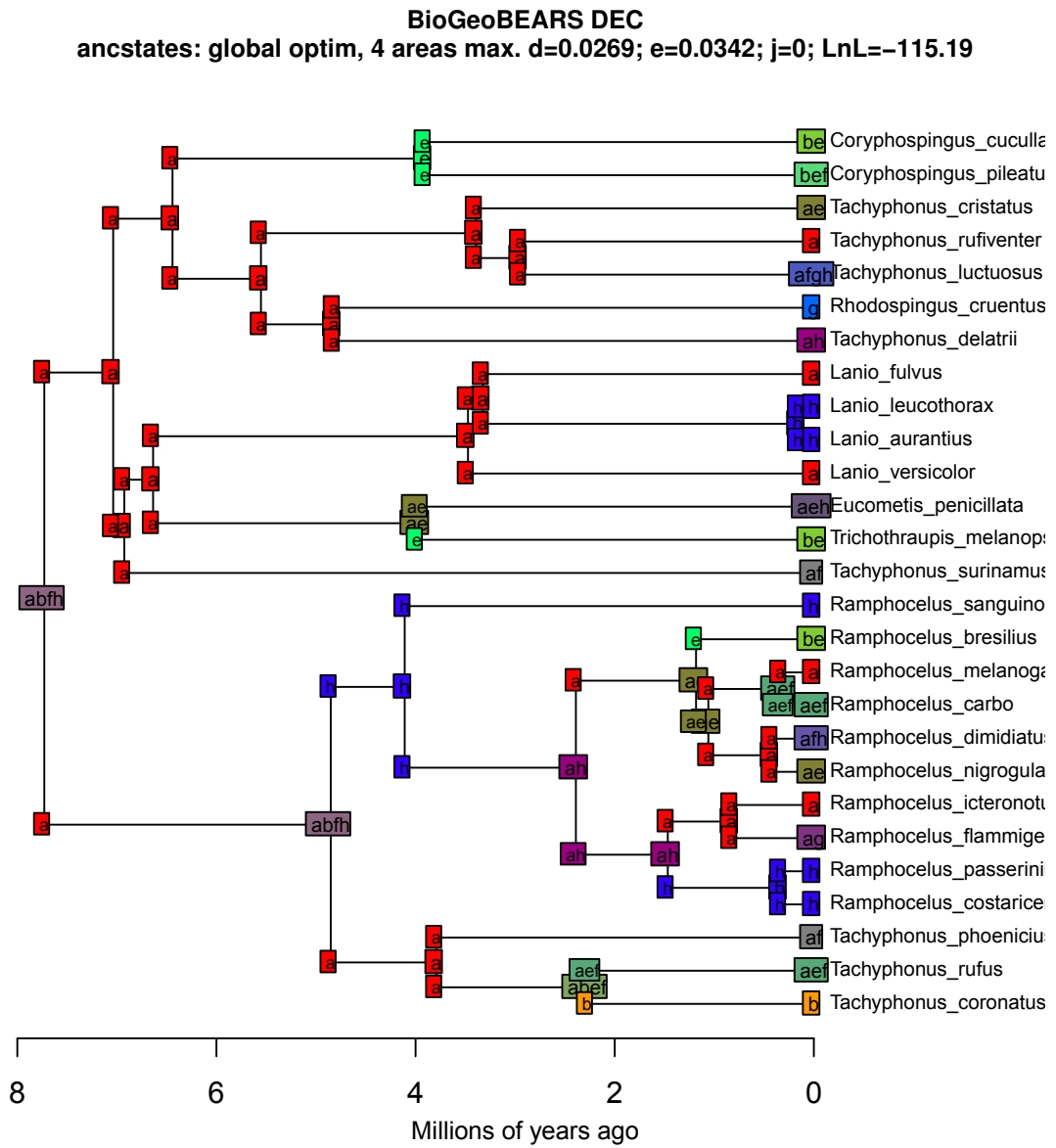


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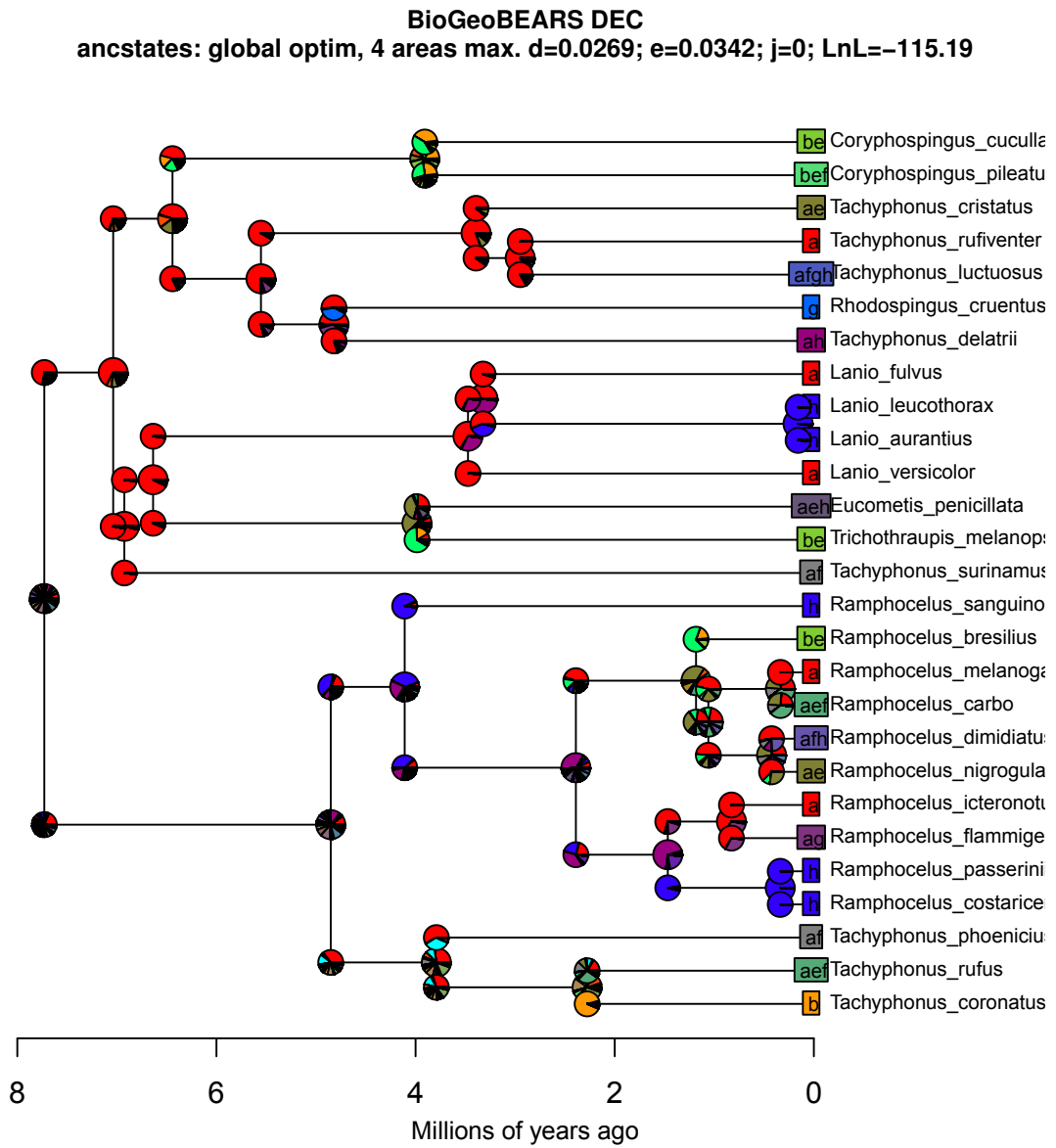


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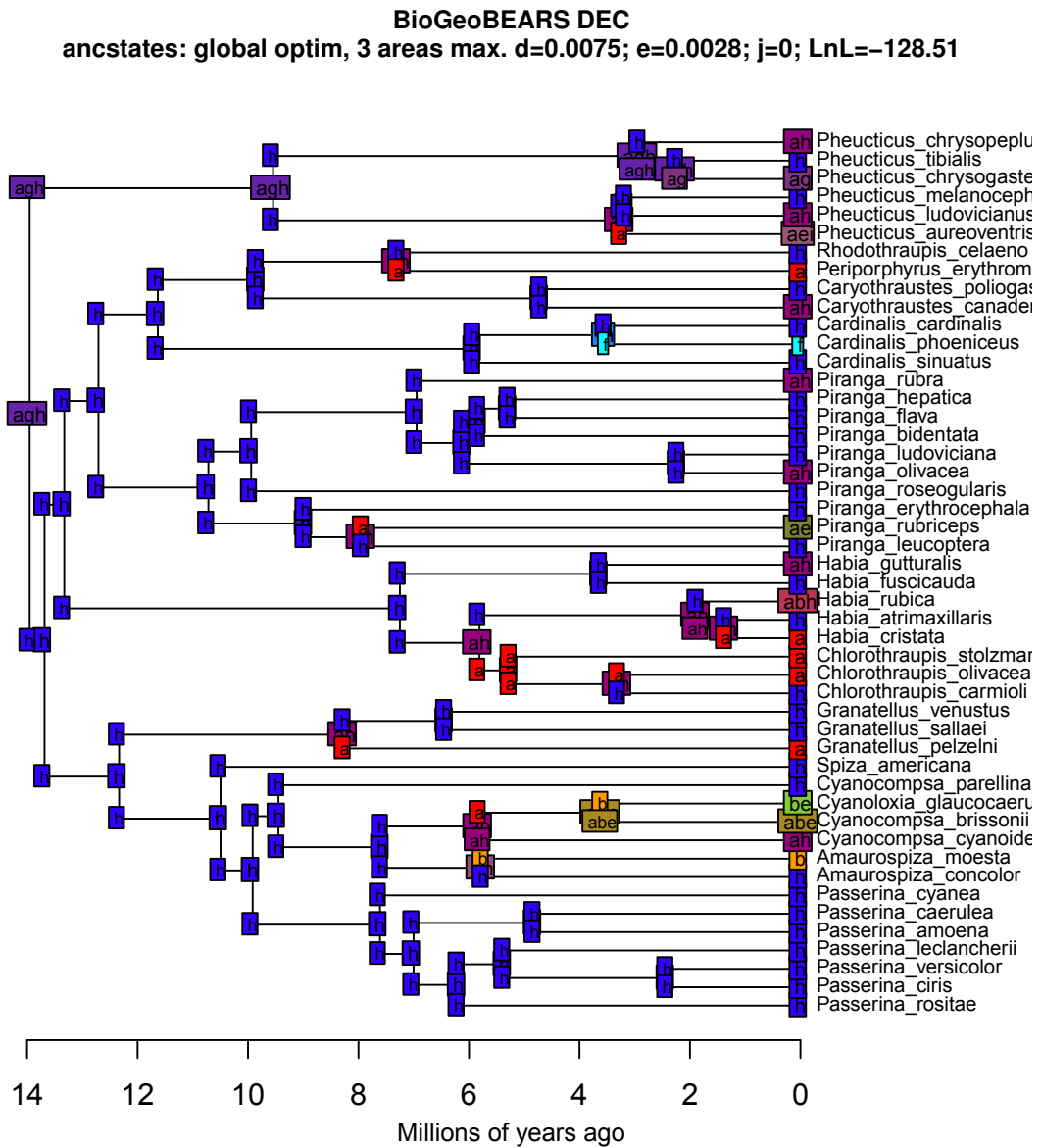


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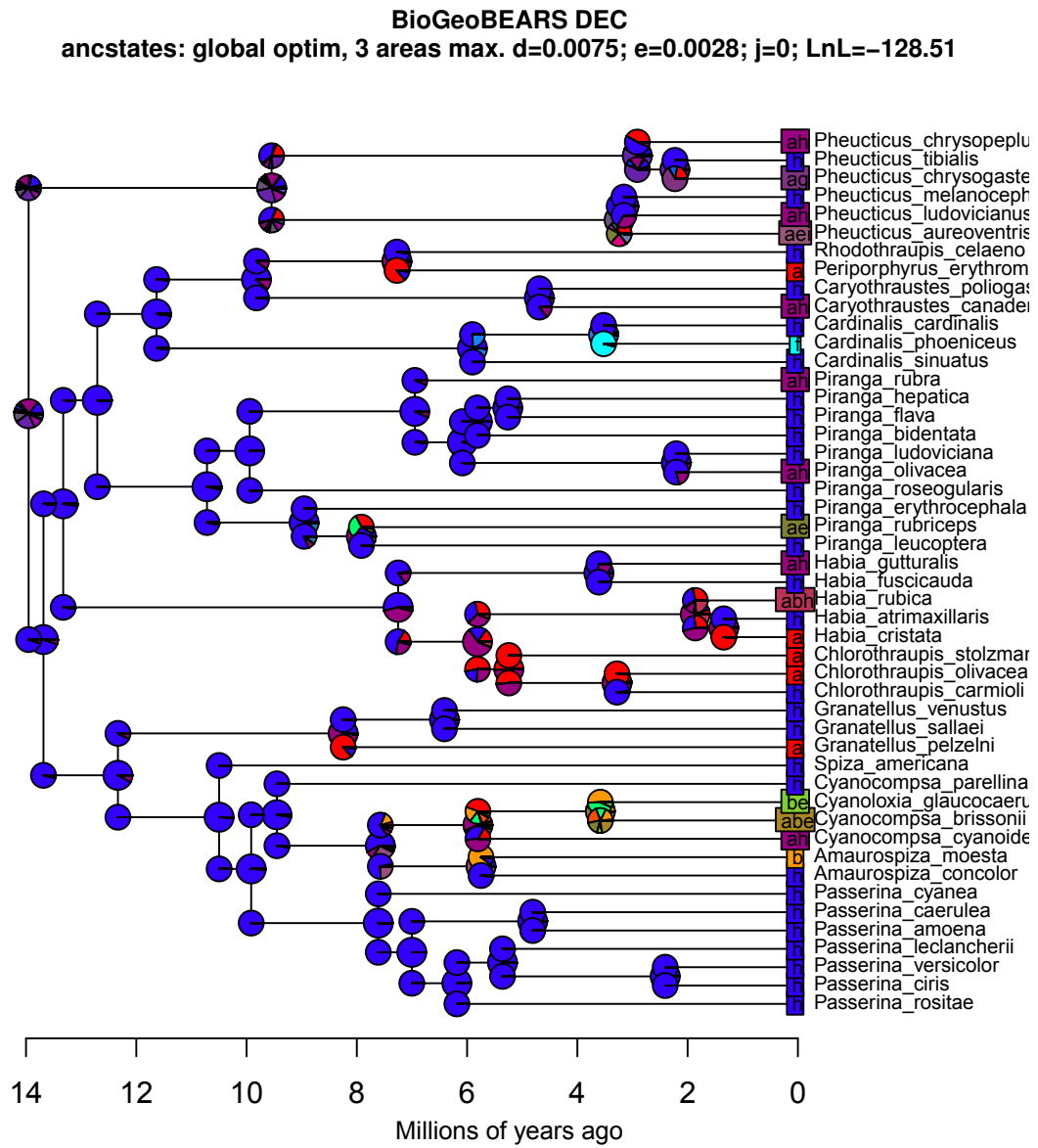


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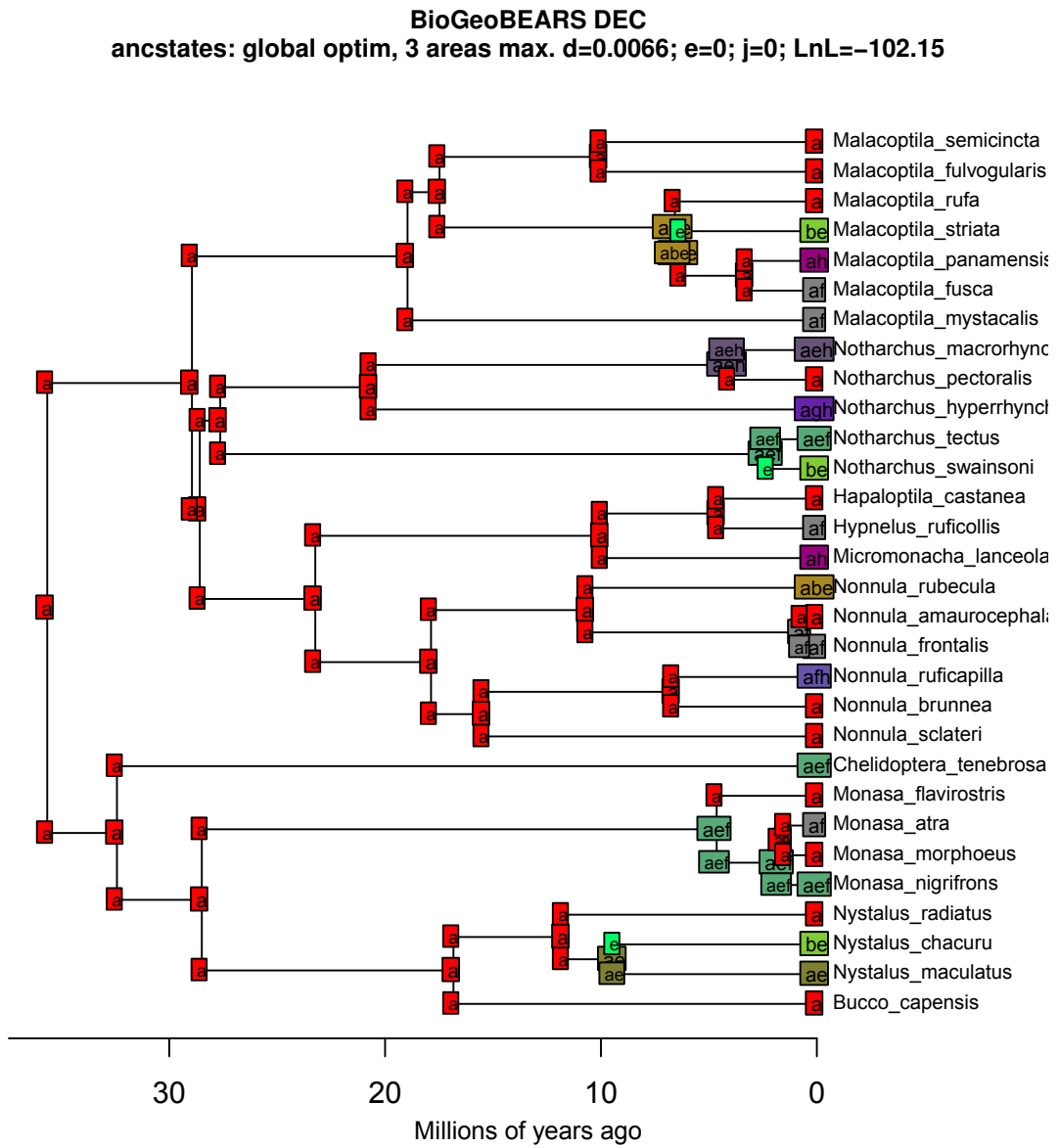


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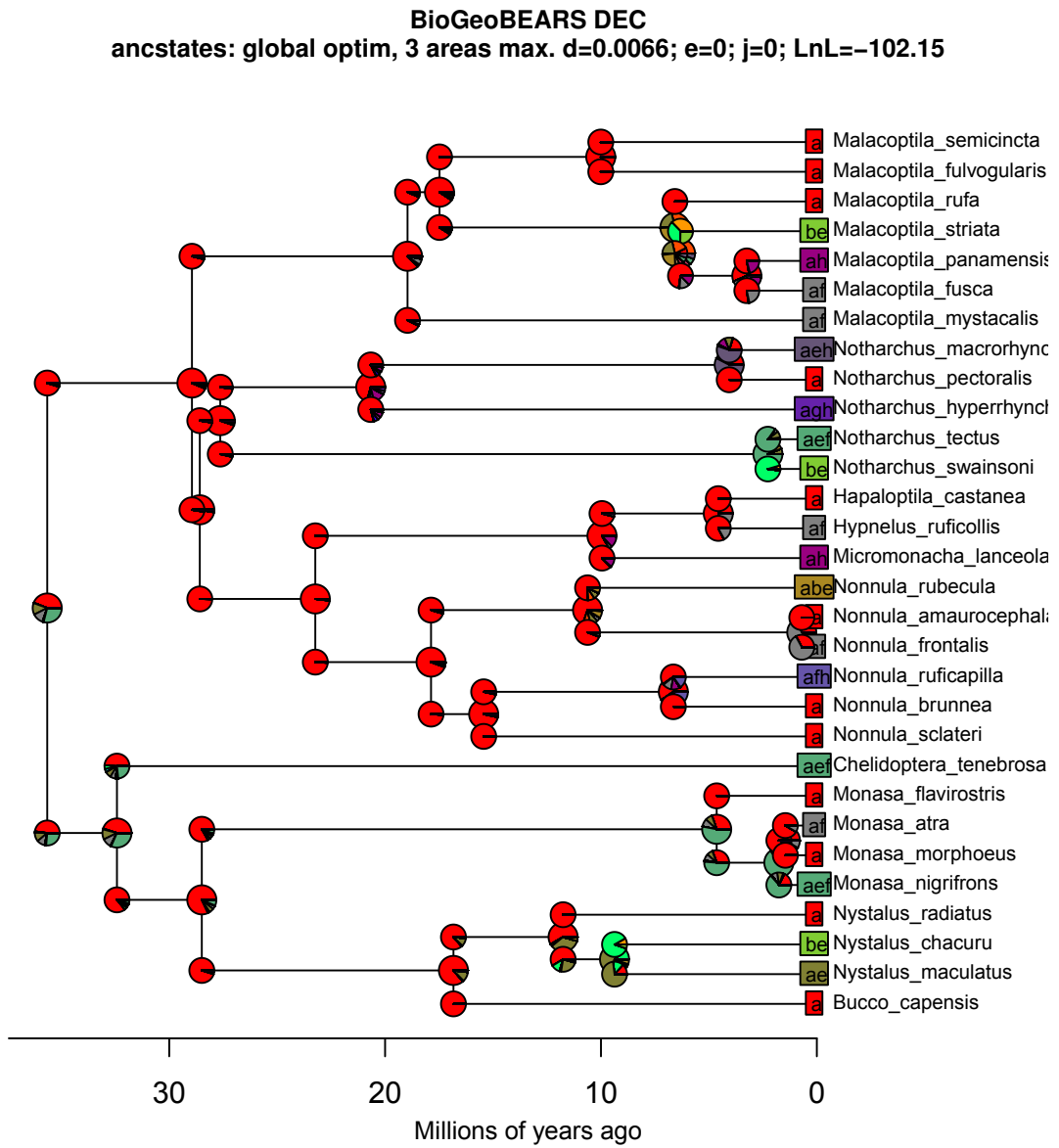


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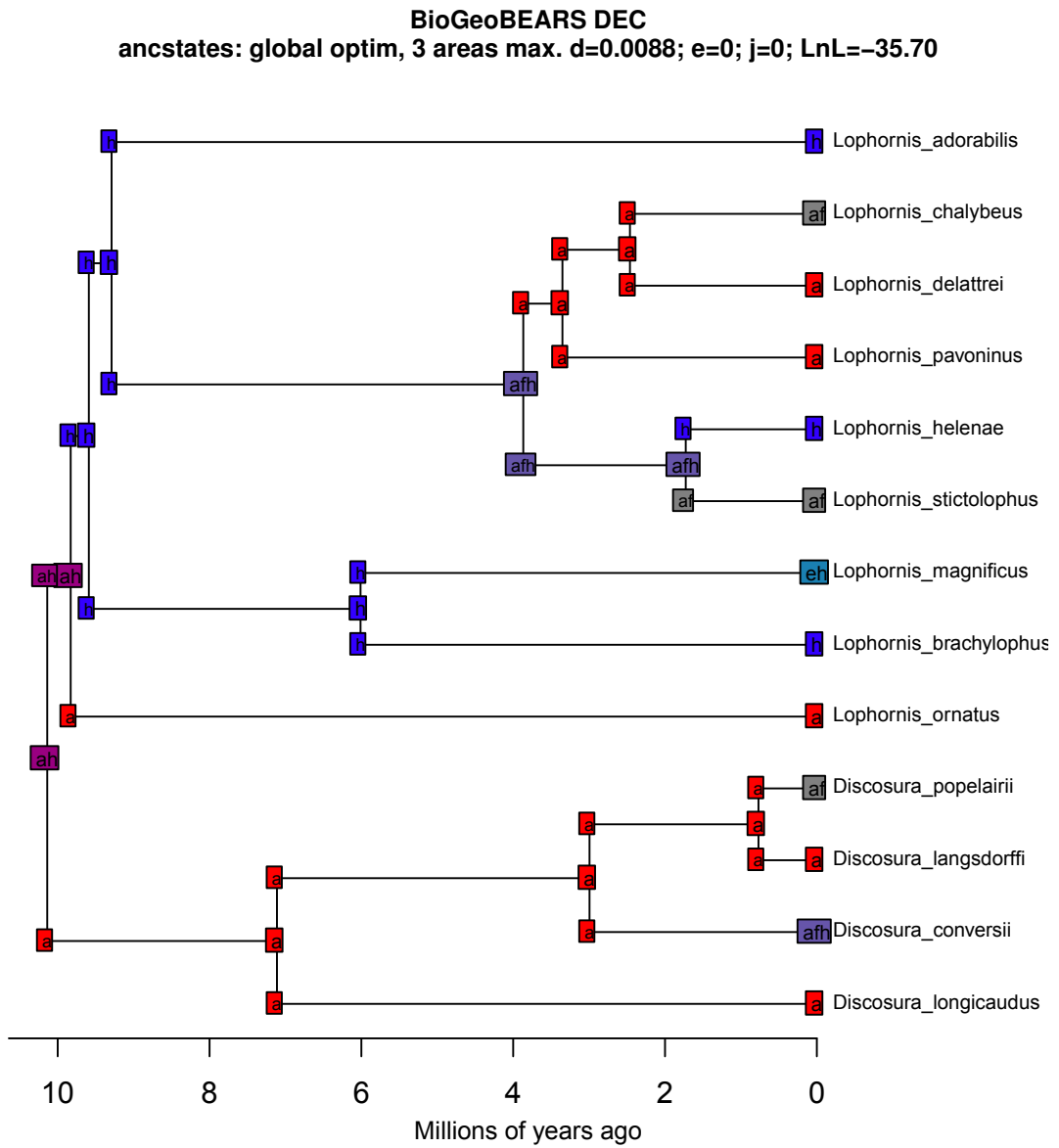


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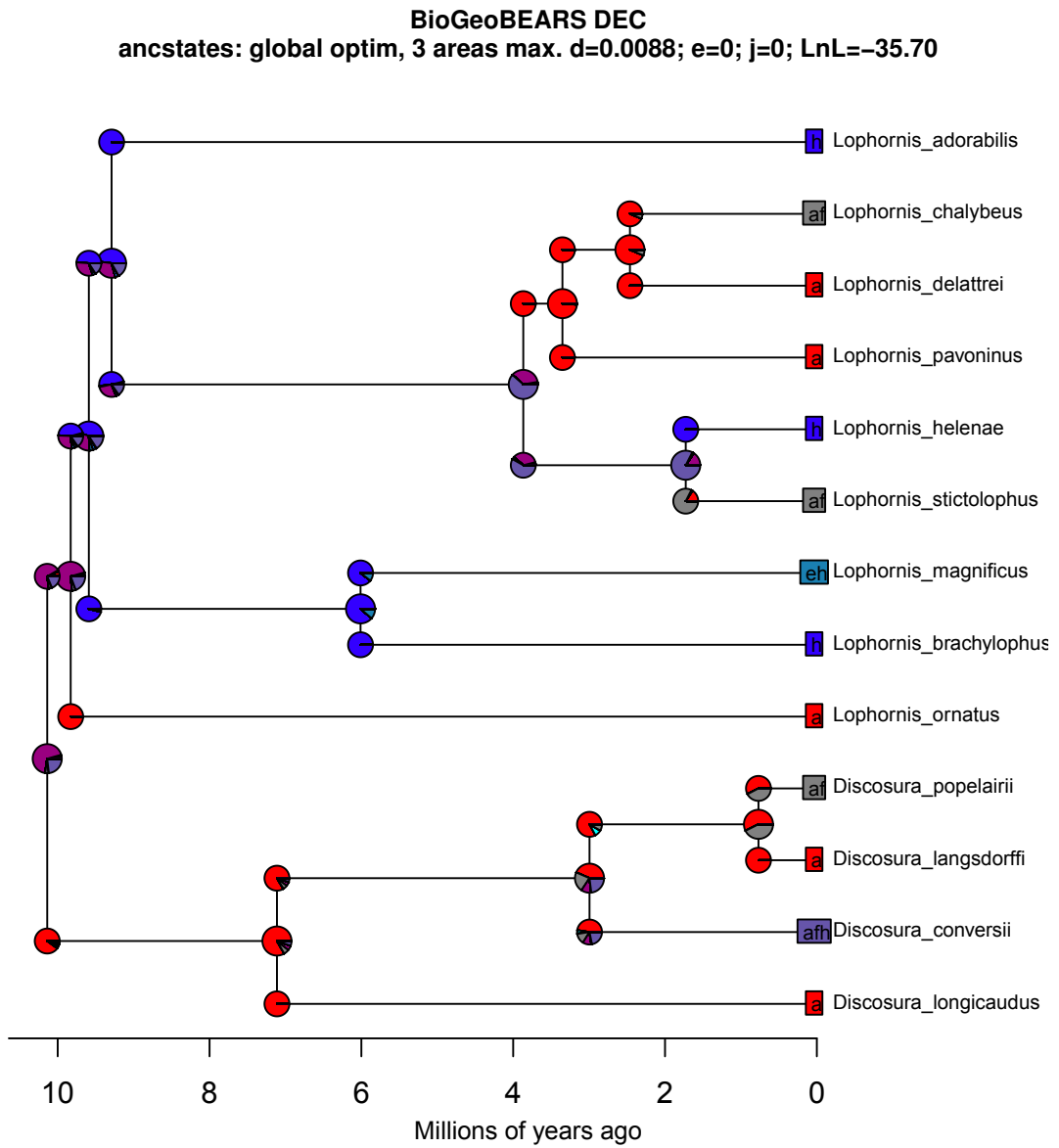


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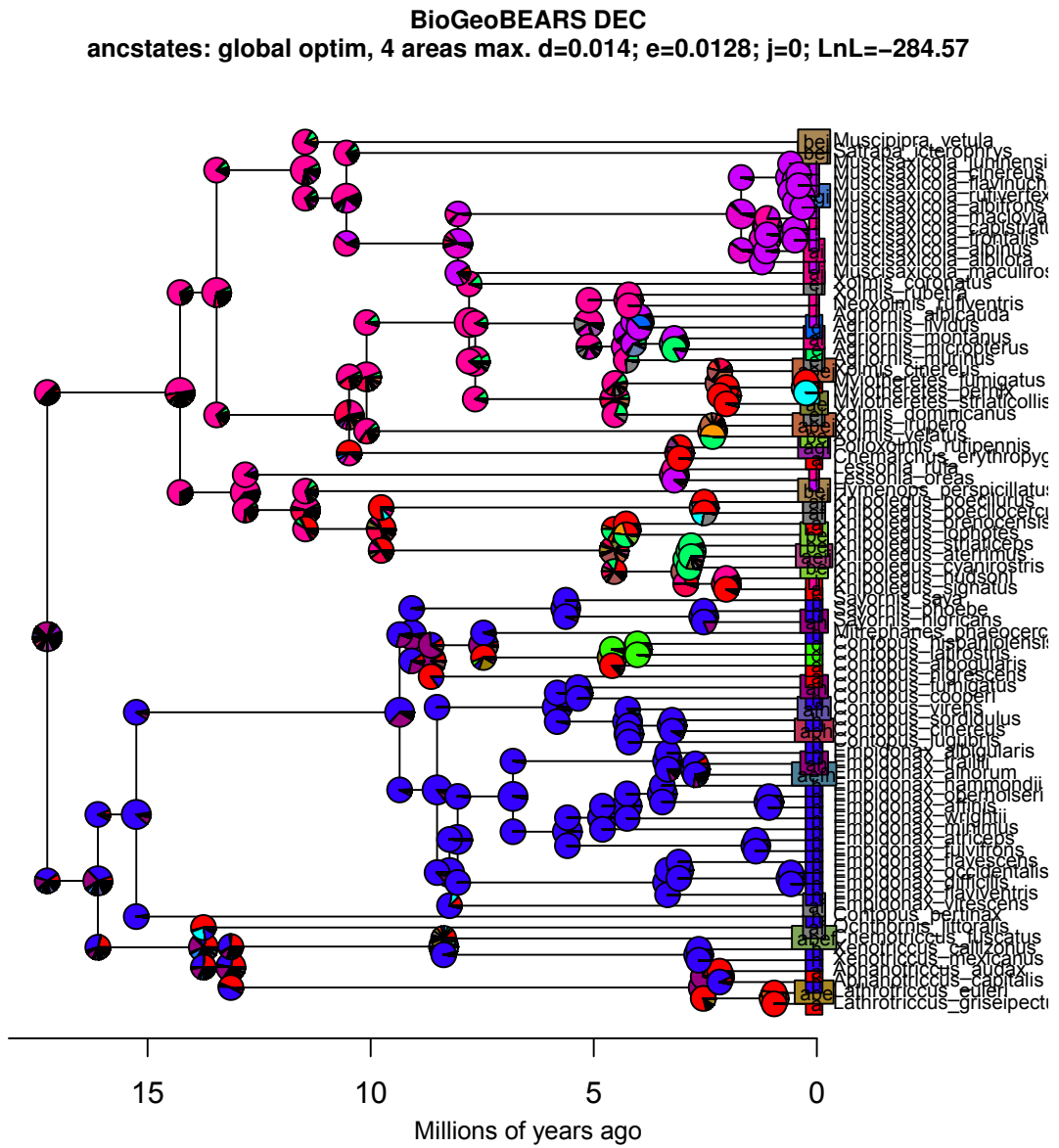


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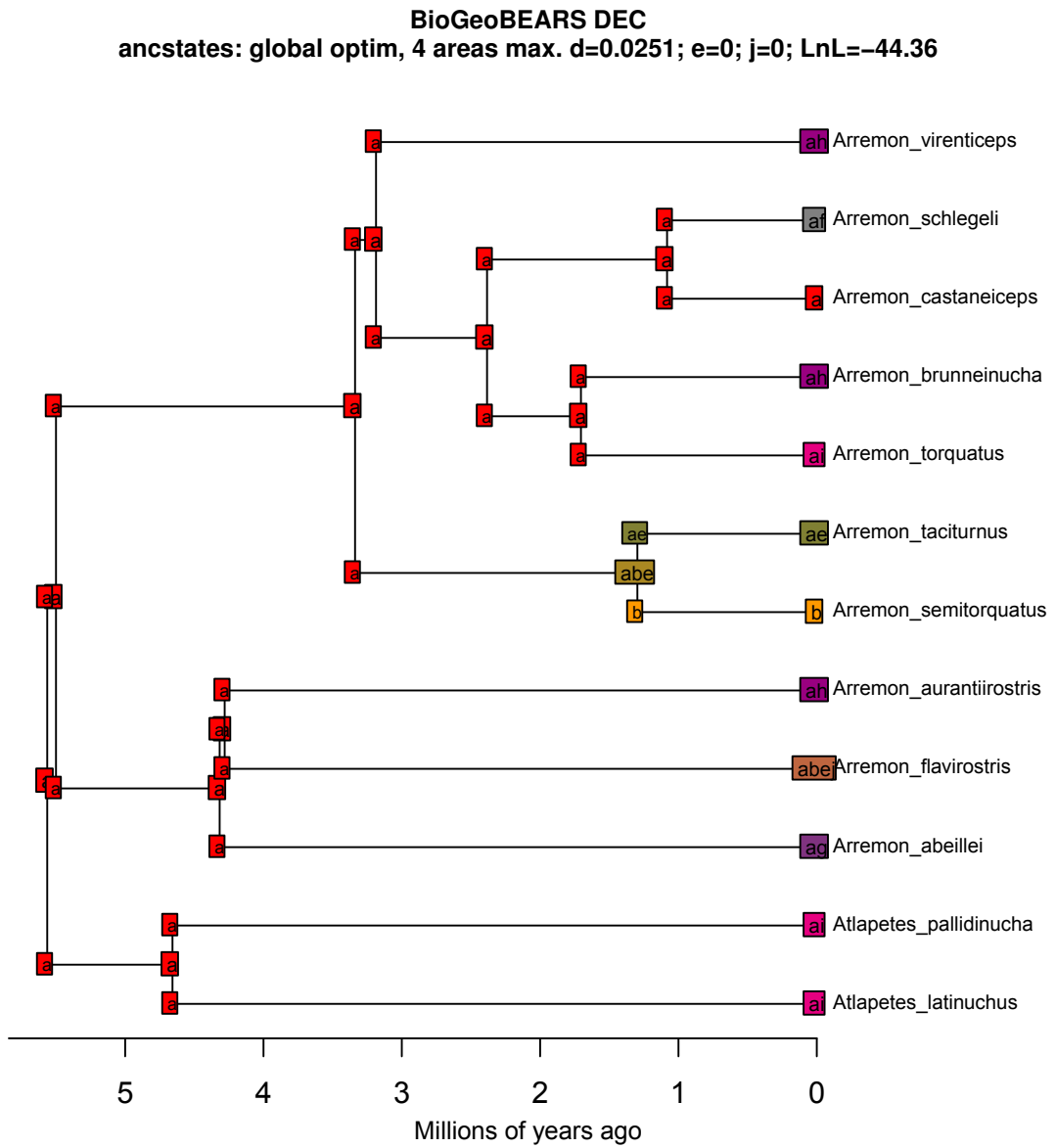


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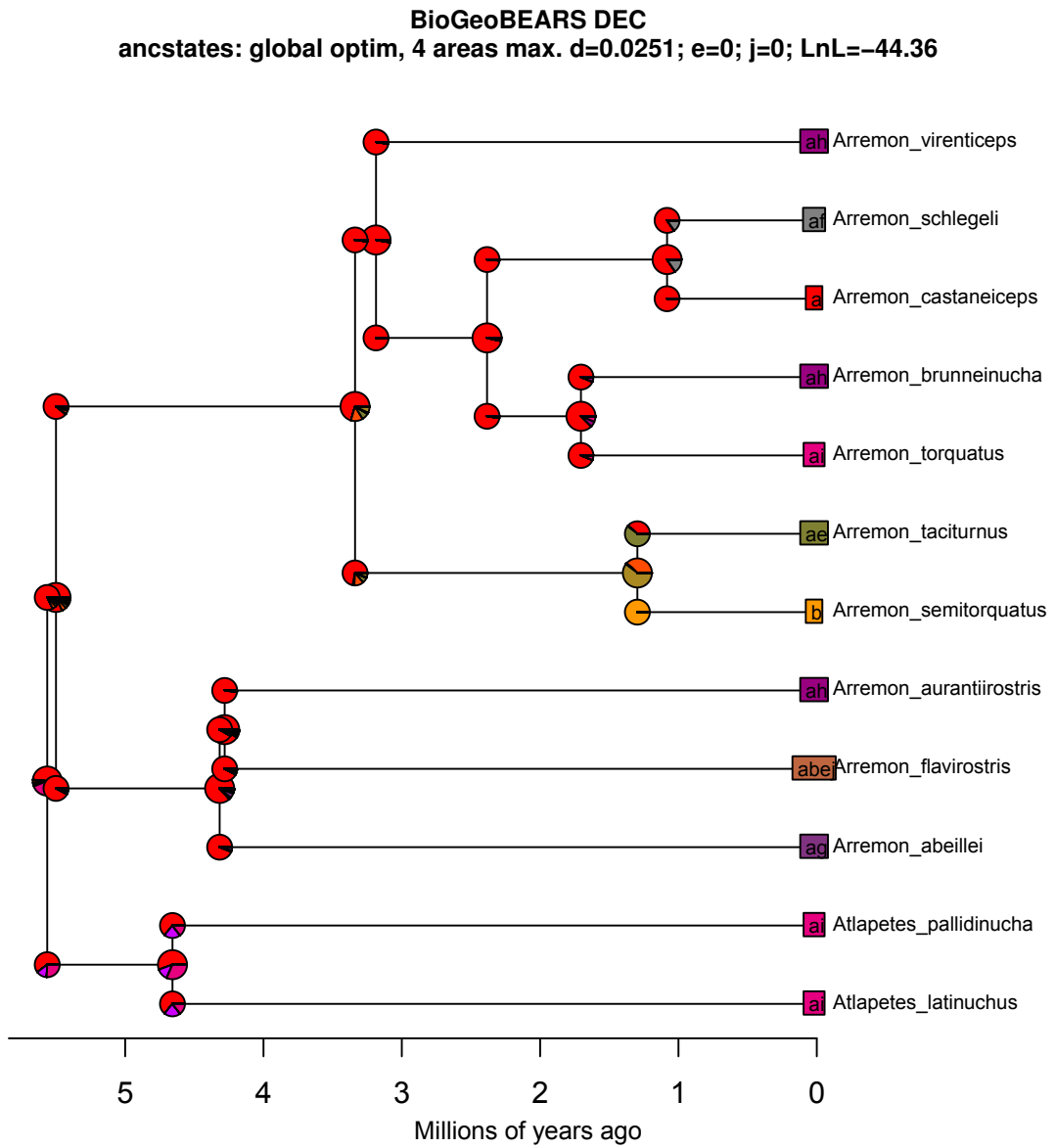


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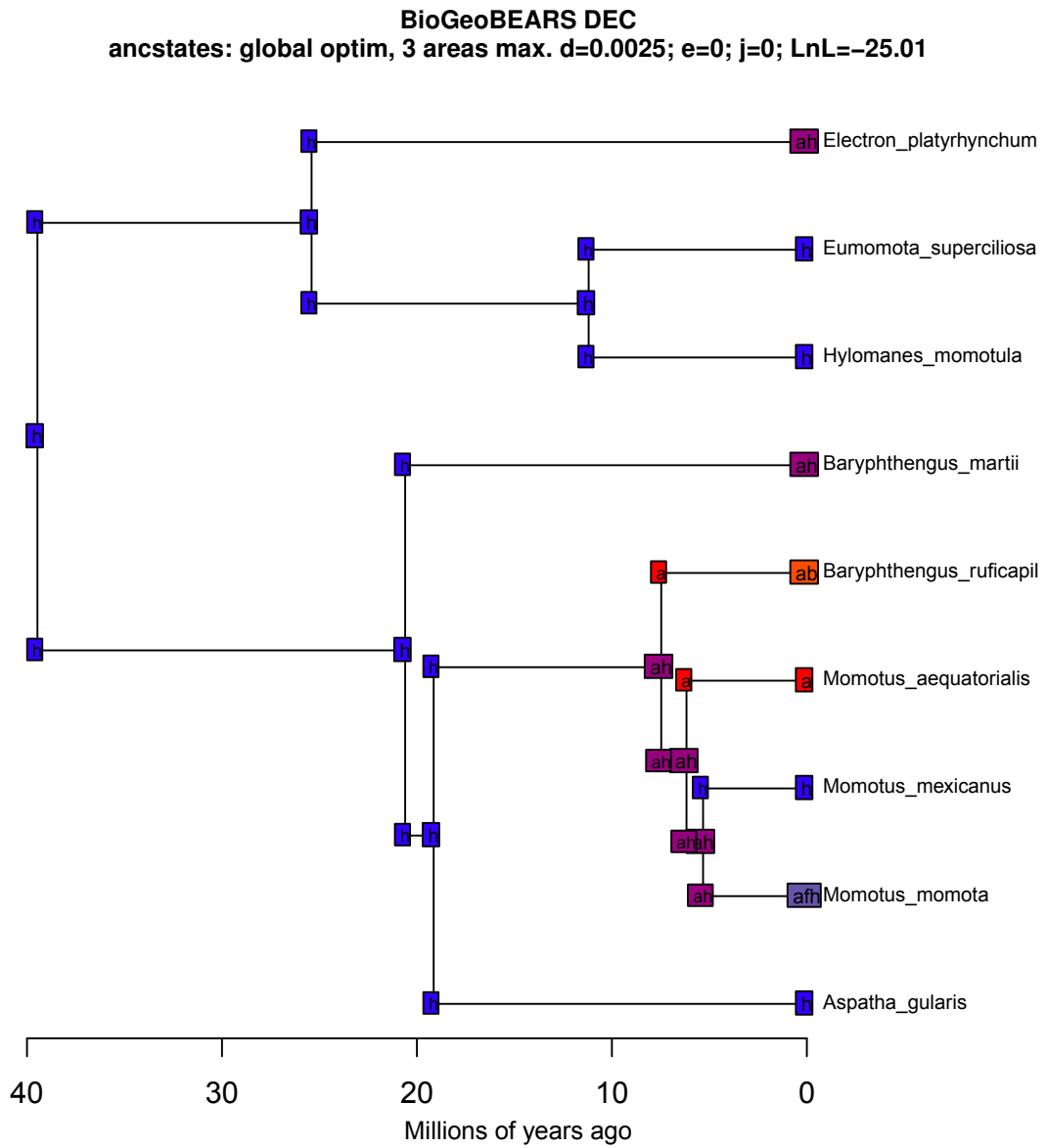


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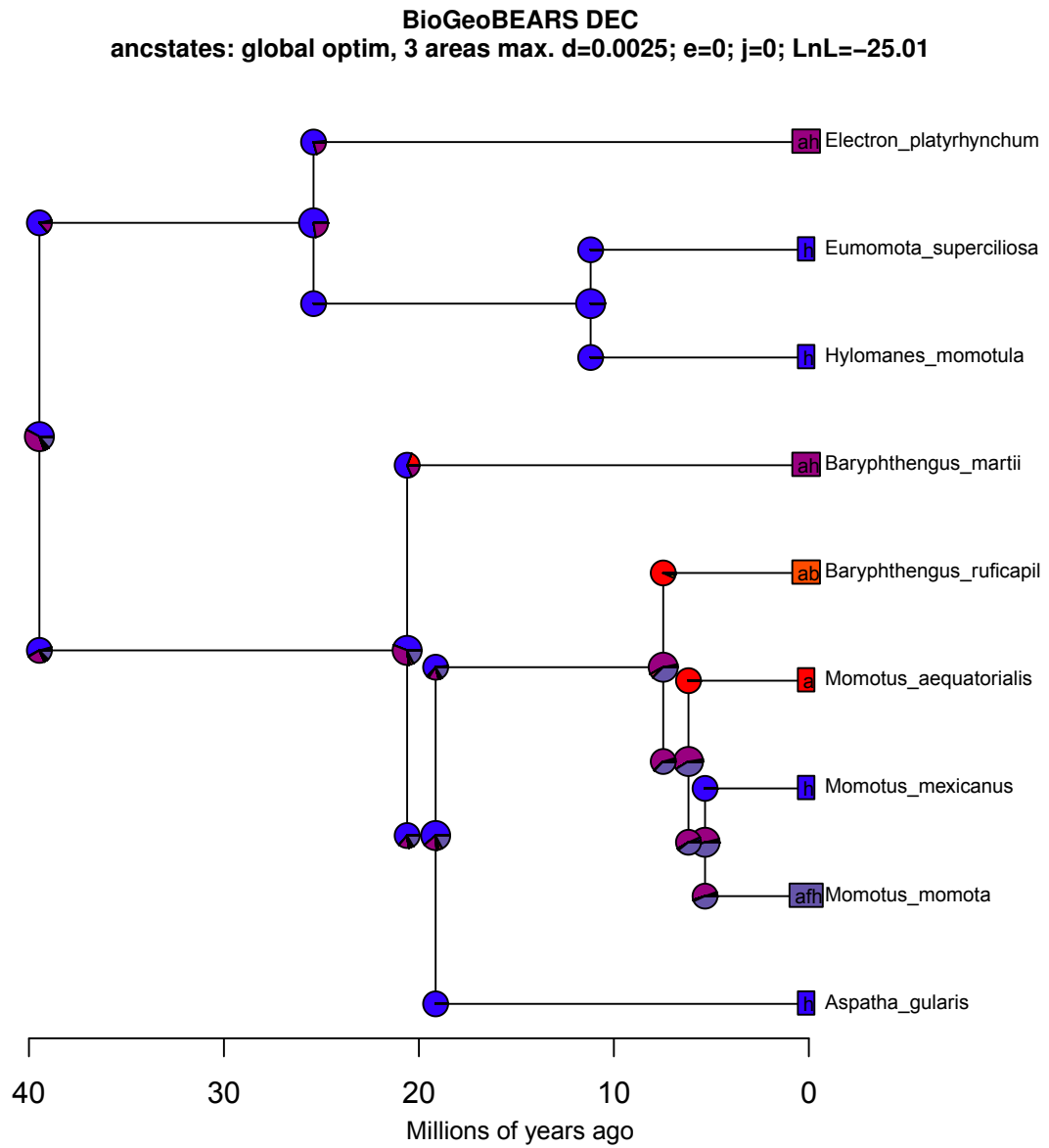


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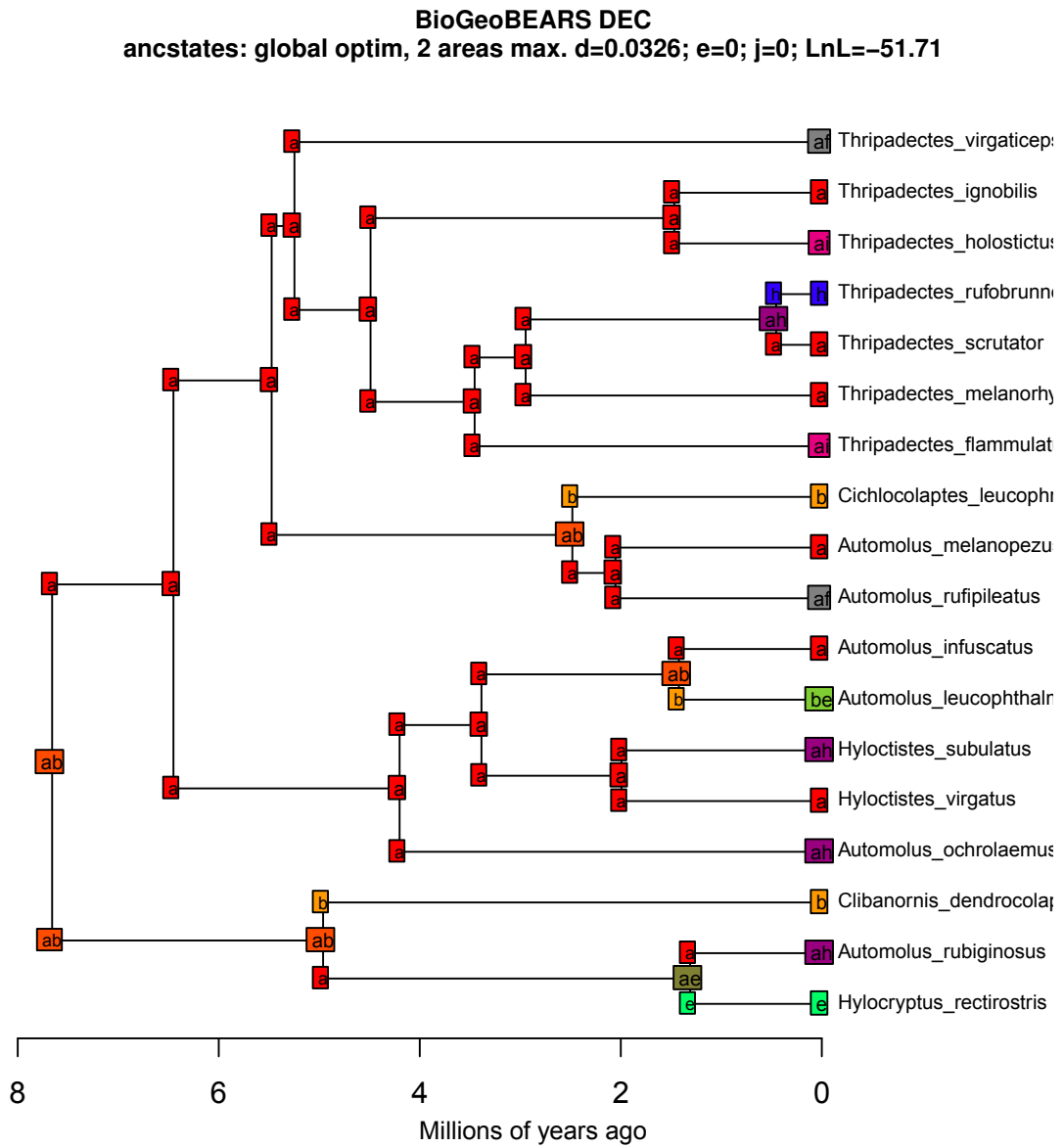


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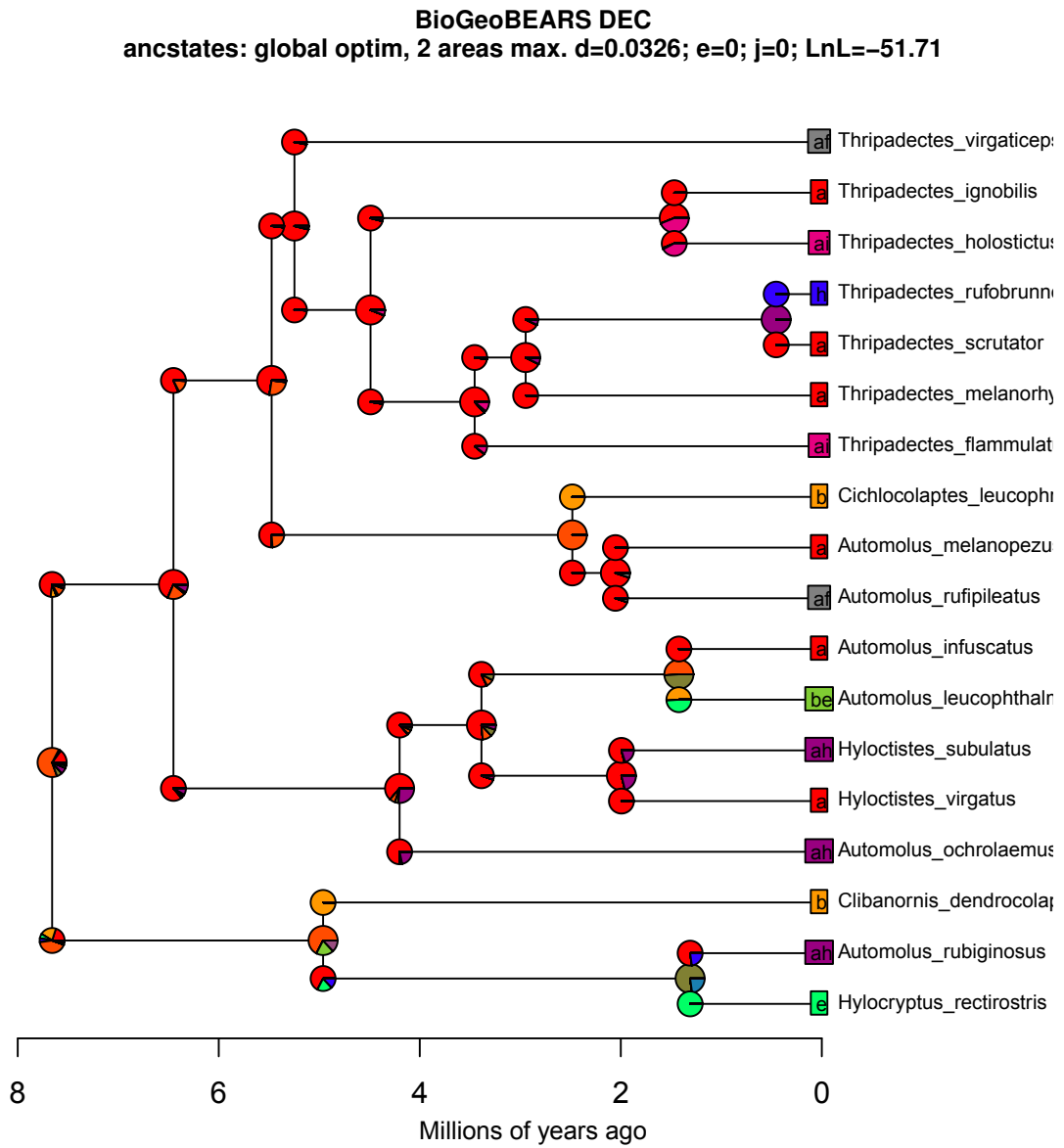


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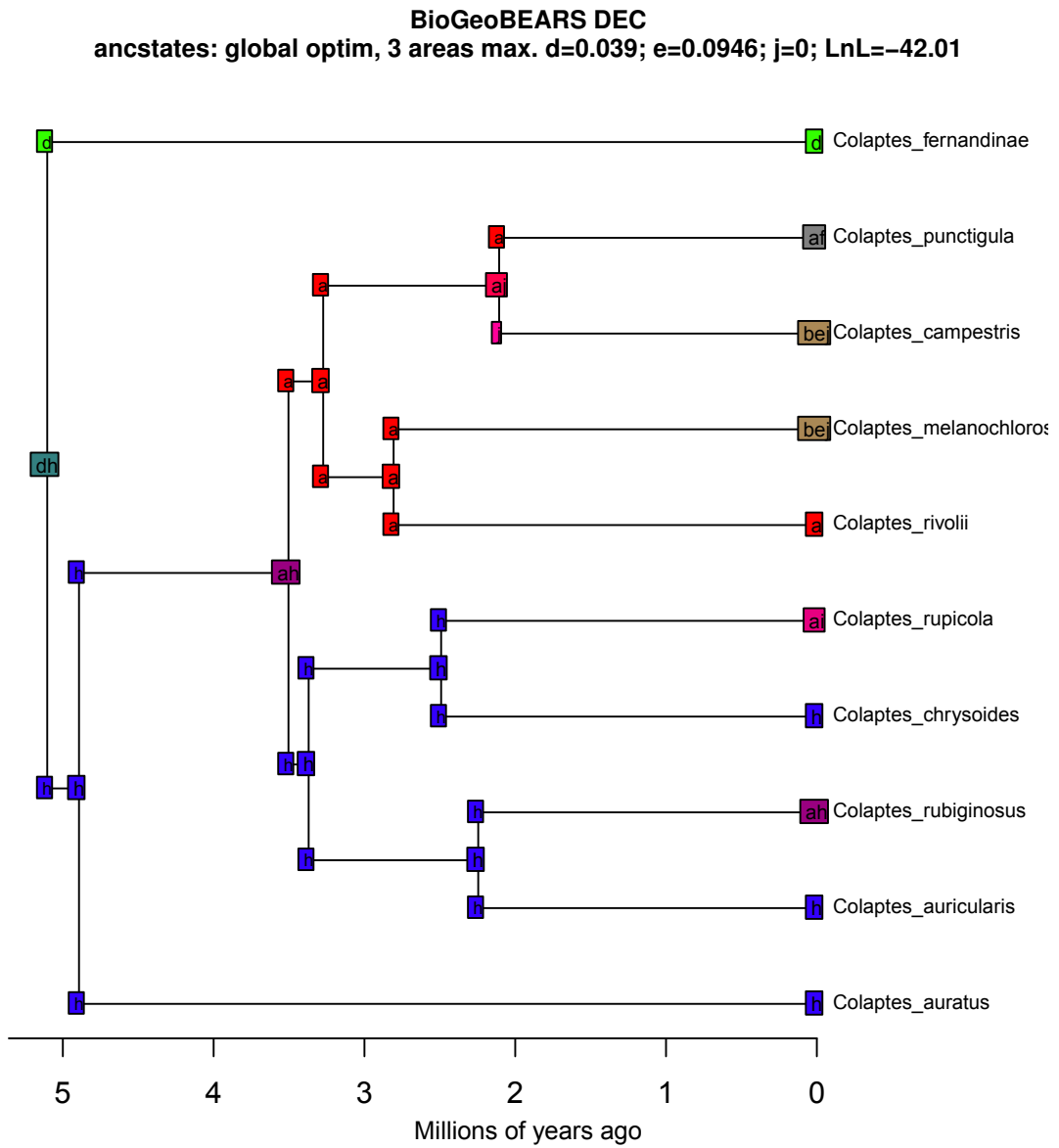


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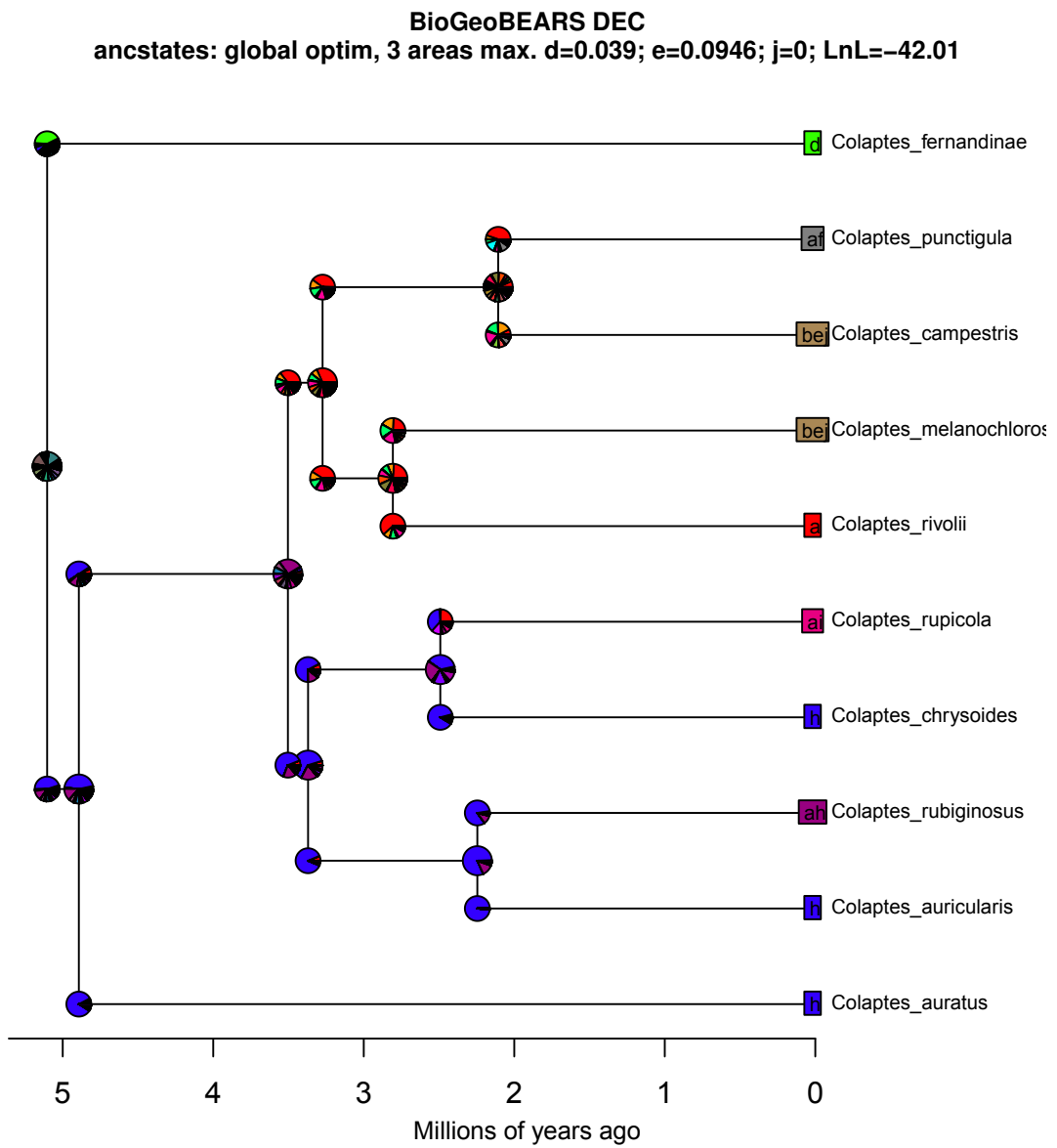


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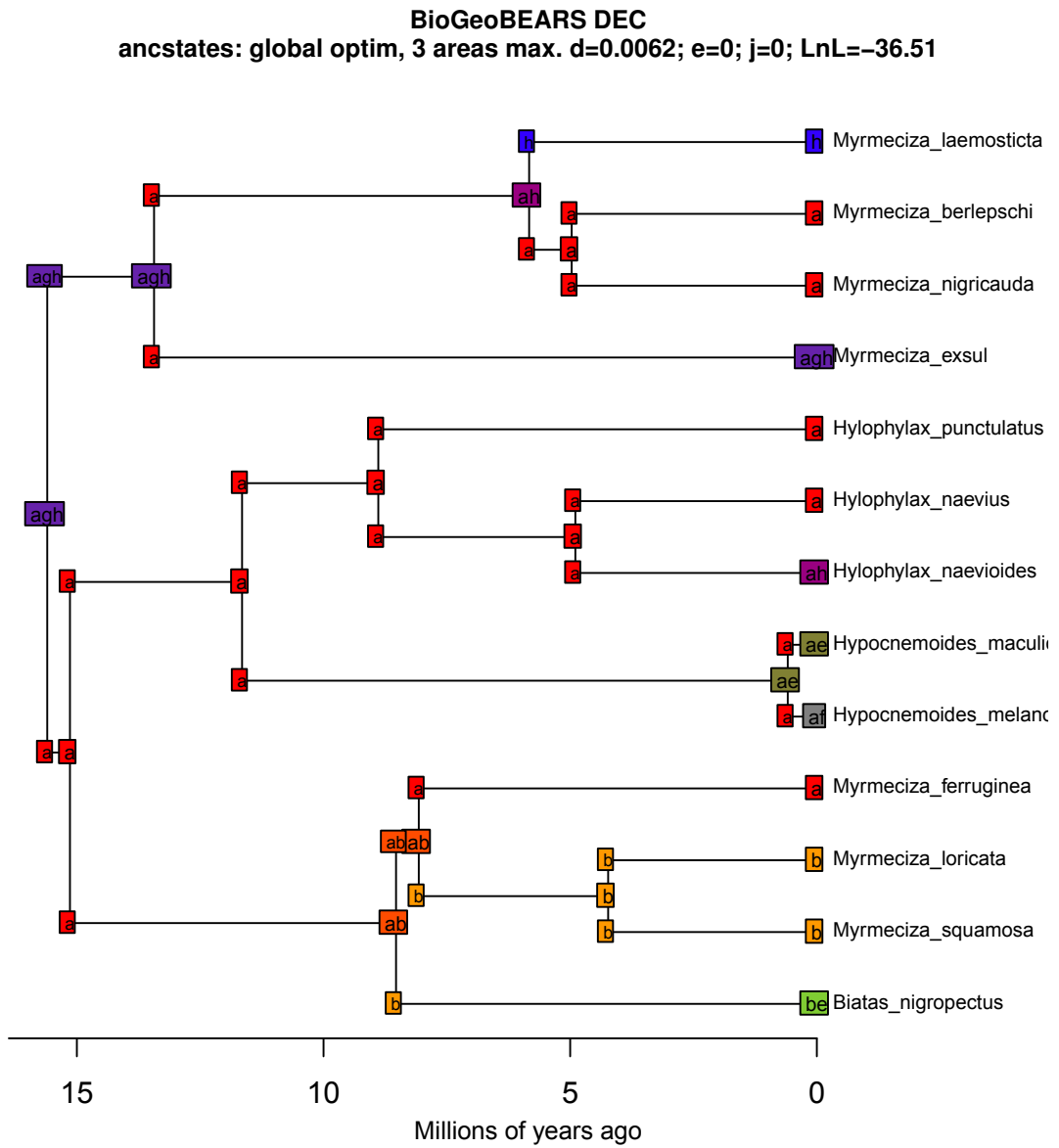


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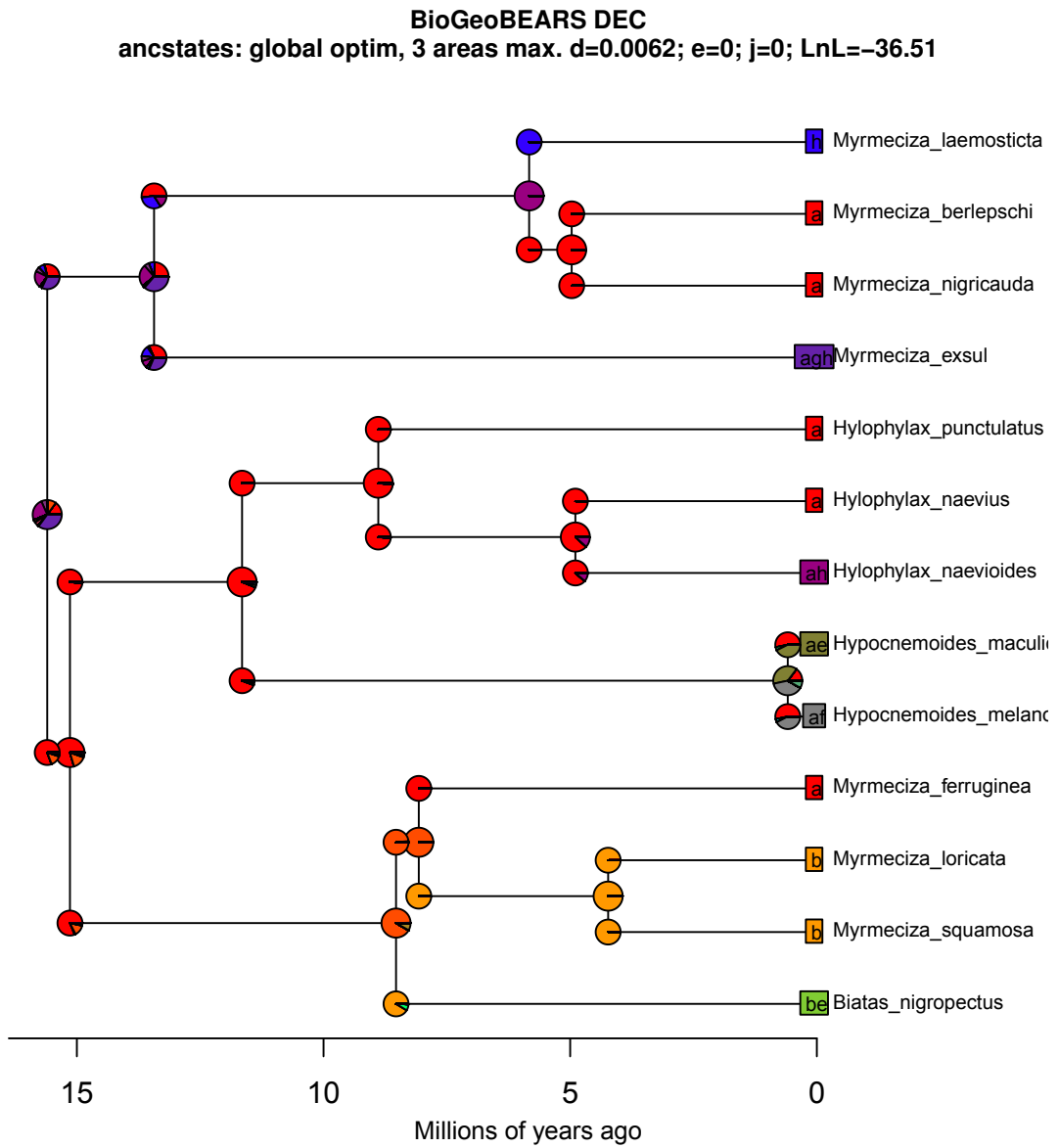


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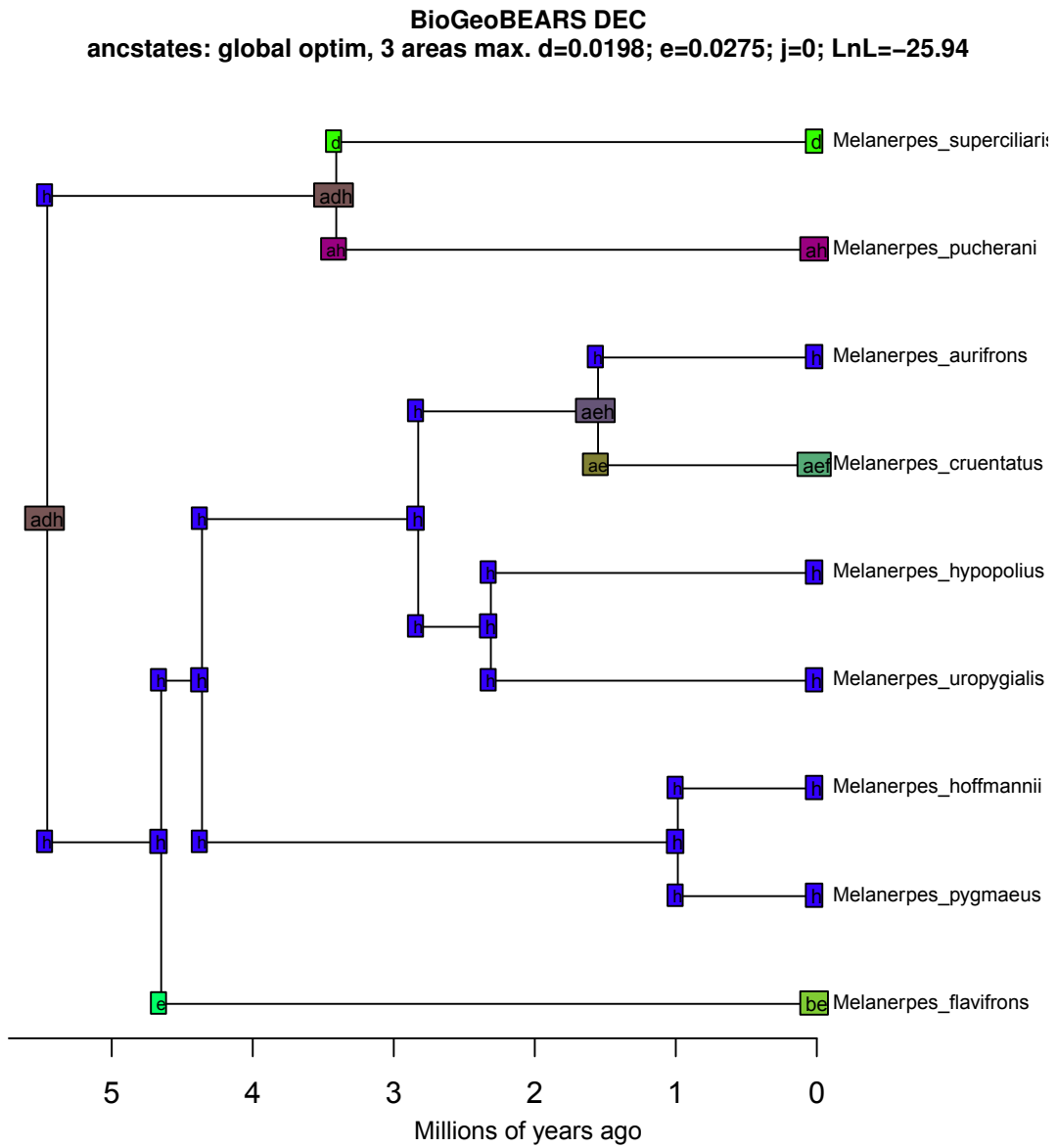


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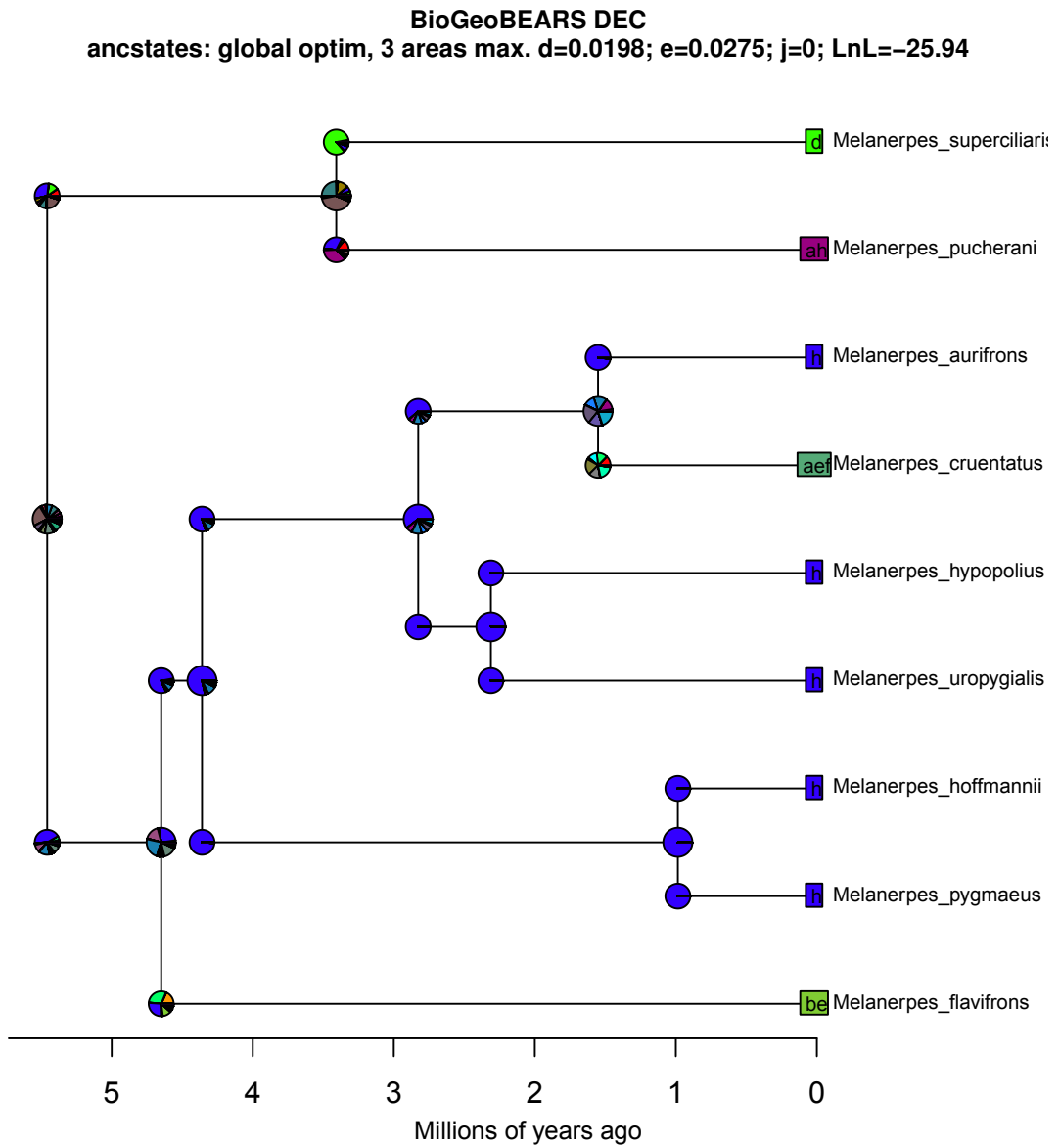


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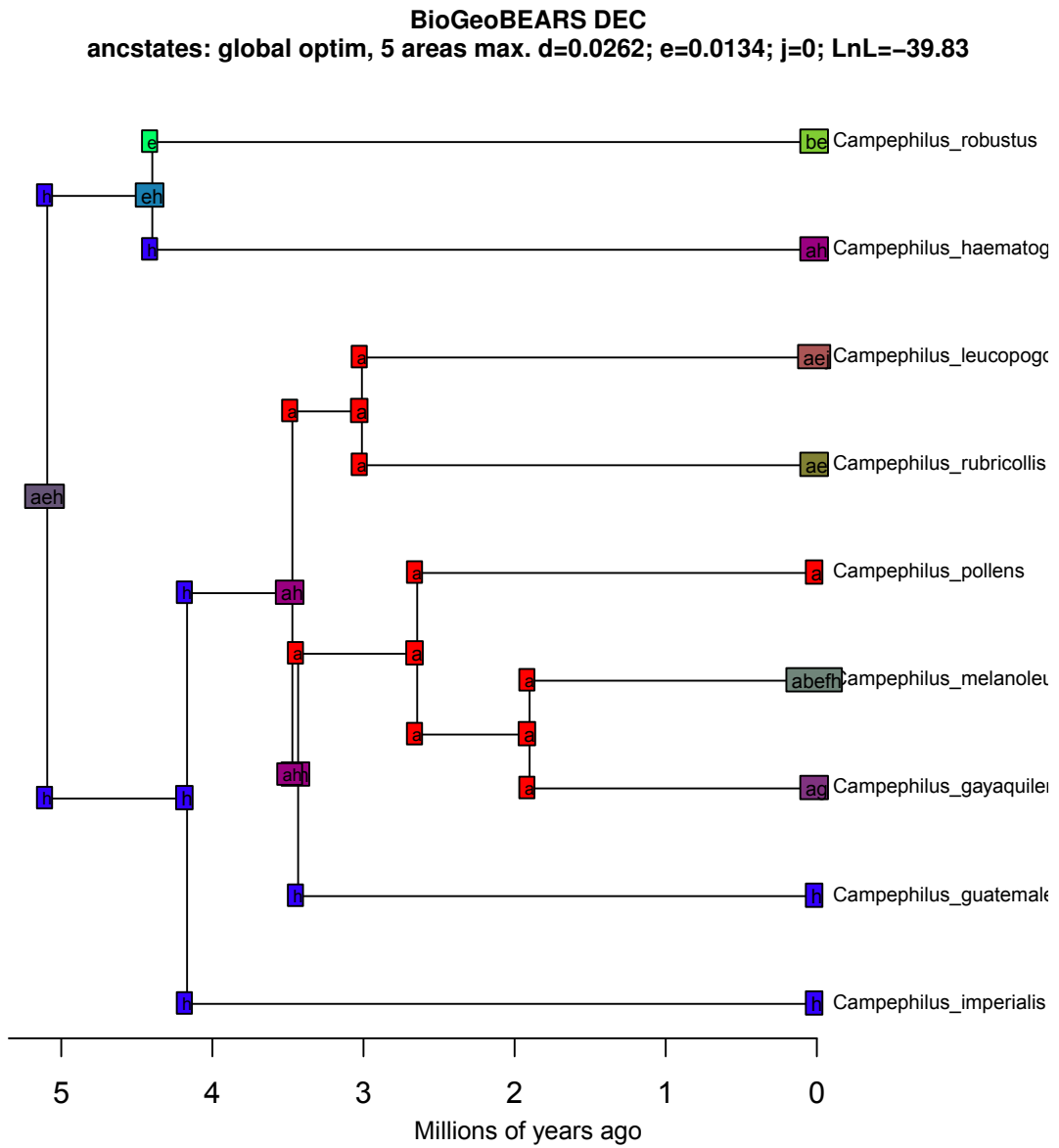


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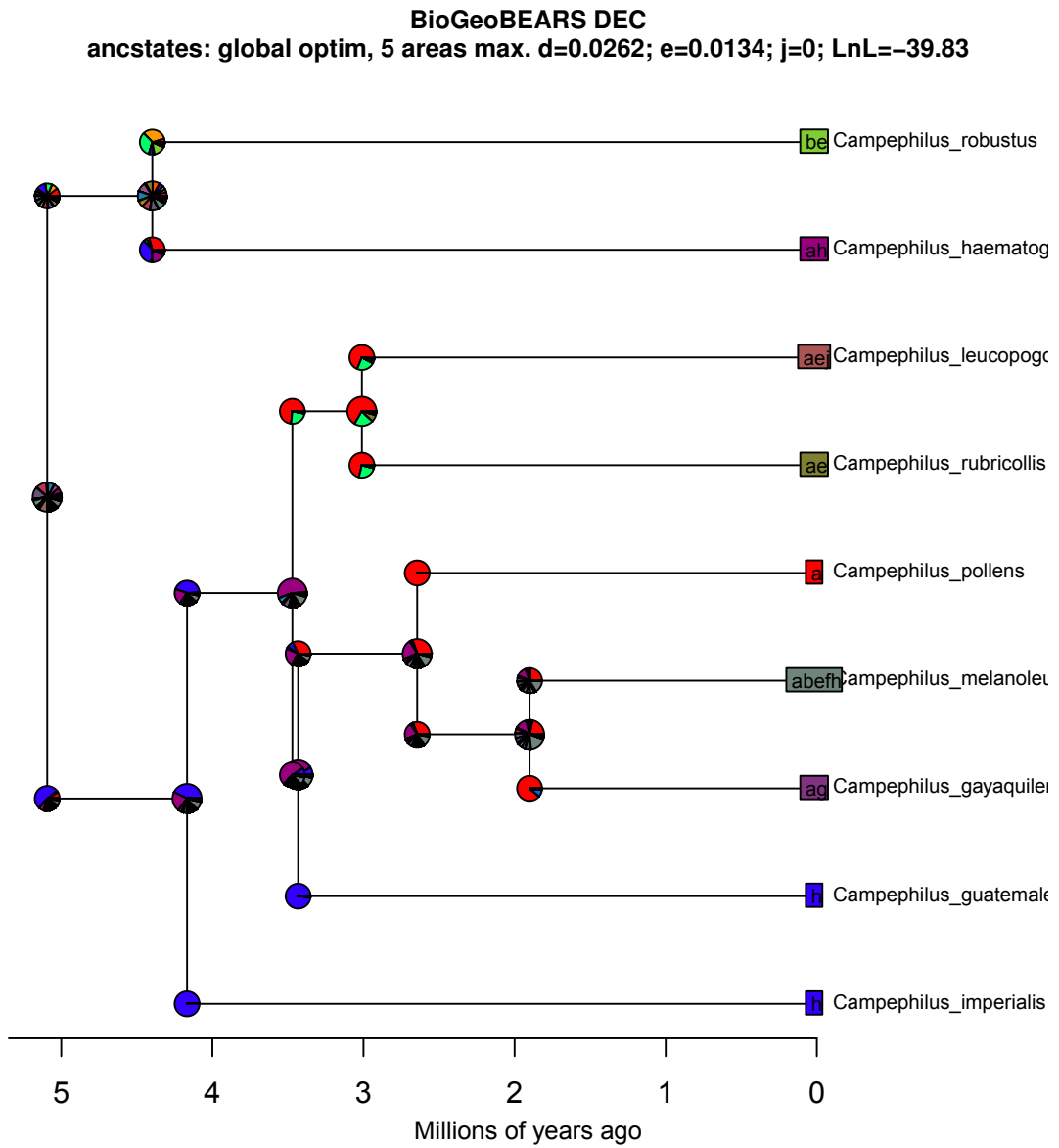


Figure S6: Clades of ferns

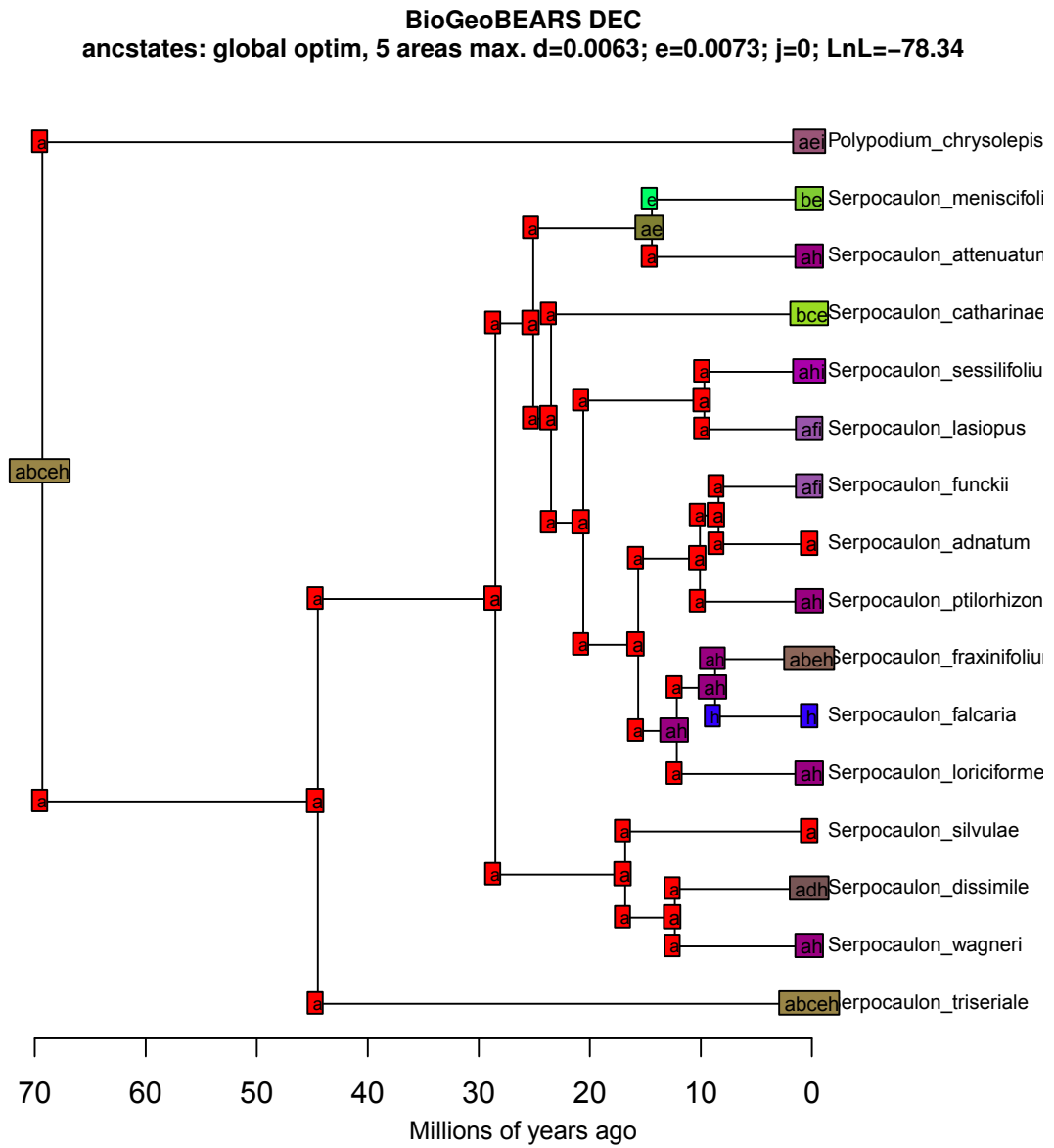


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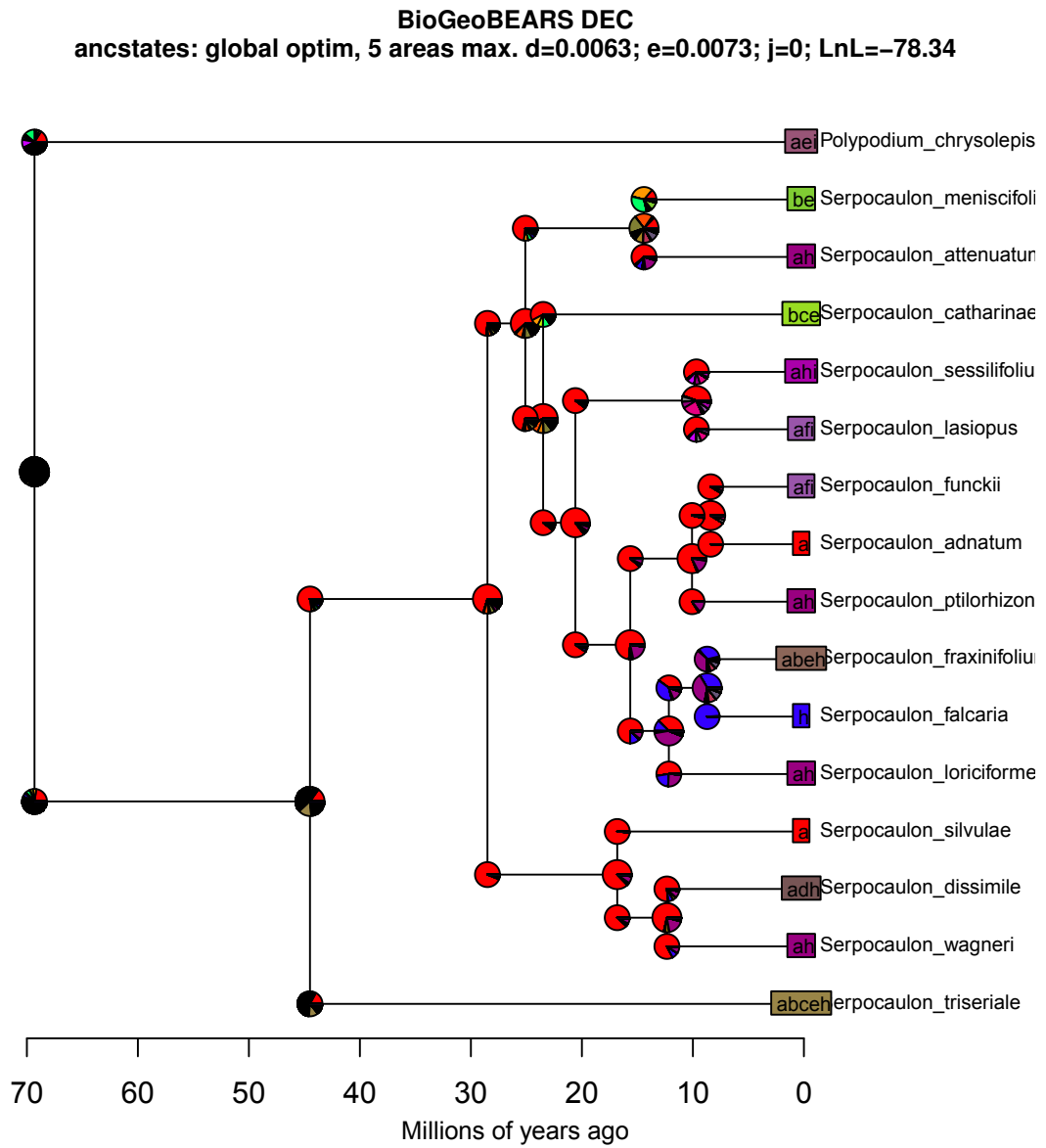


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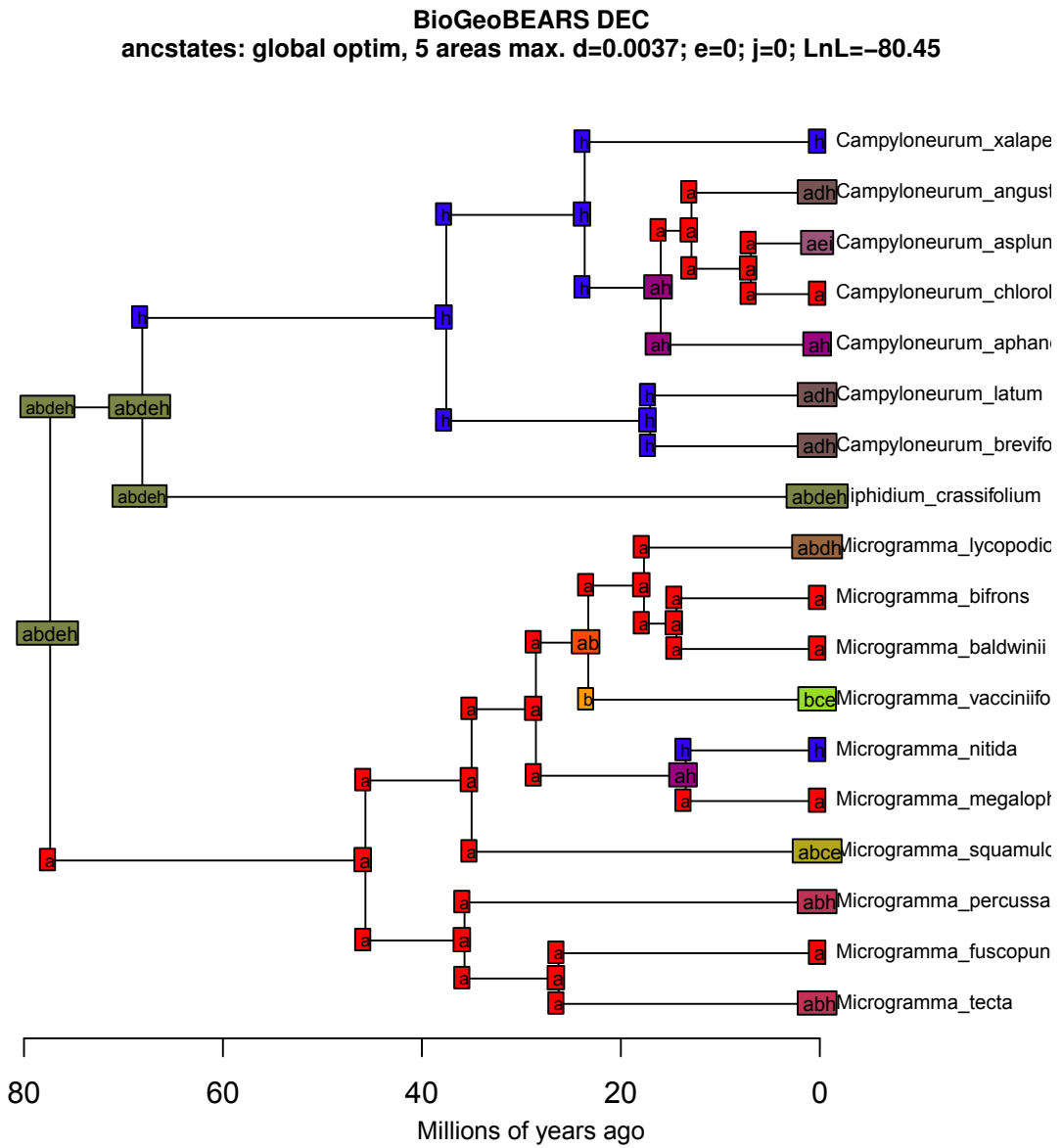


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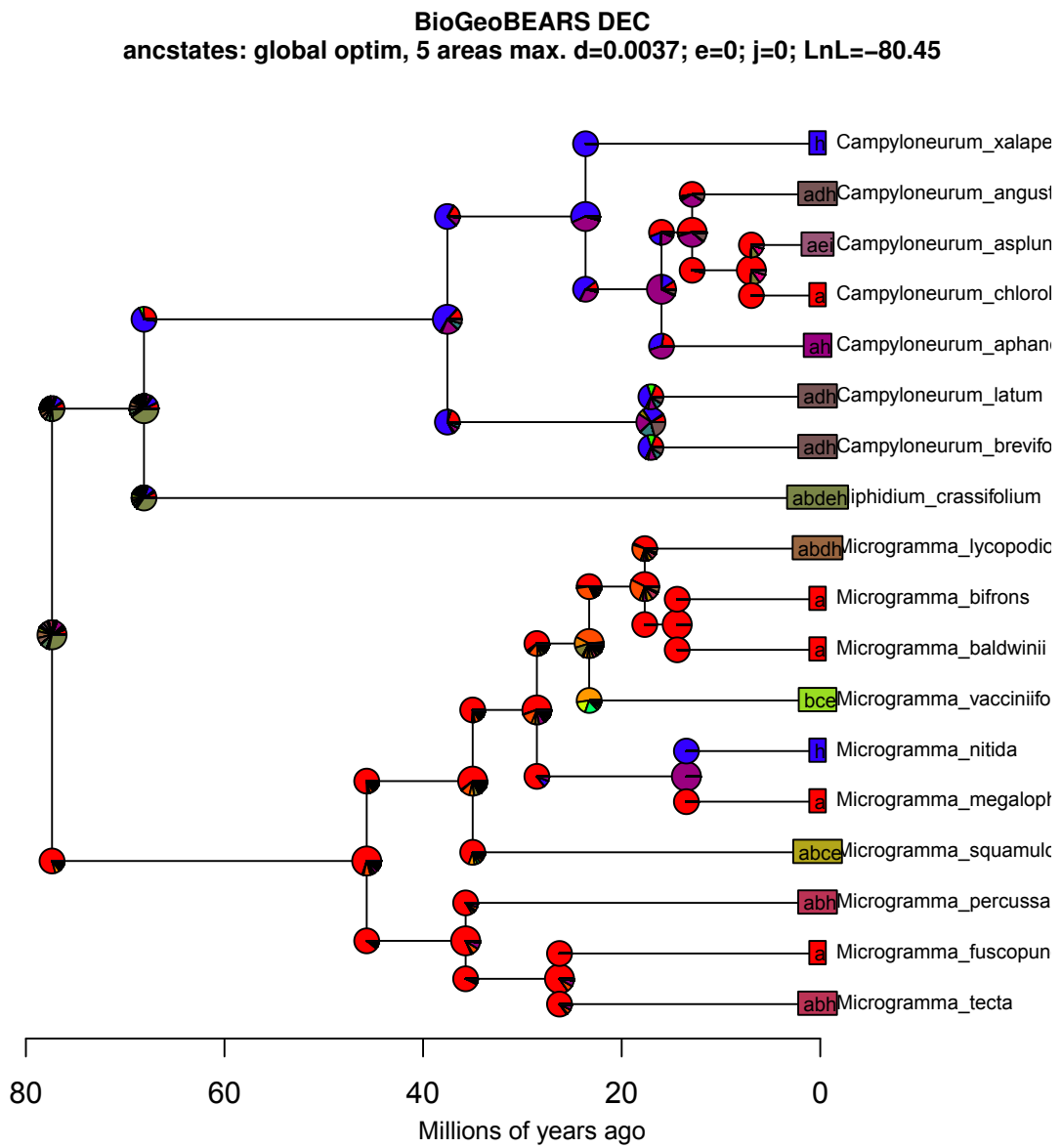


Figure S6: Clades of ferns

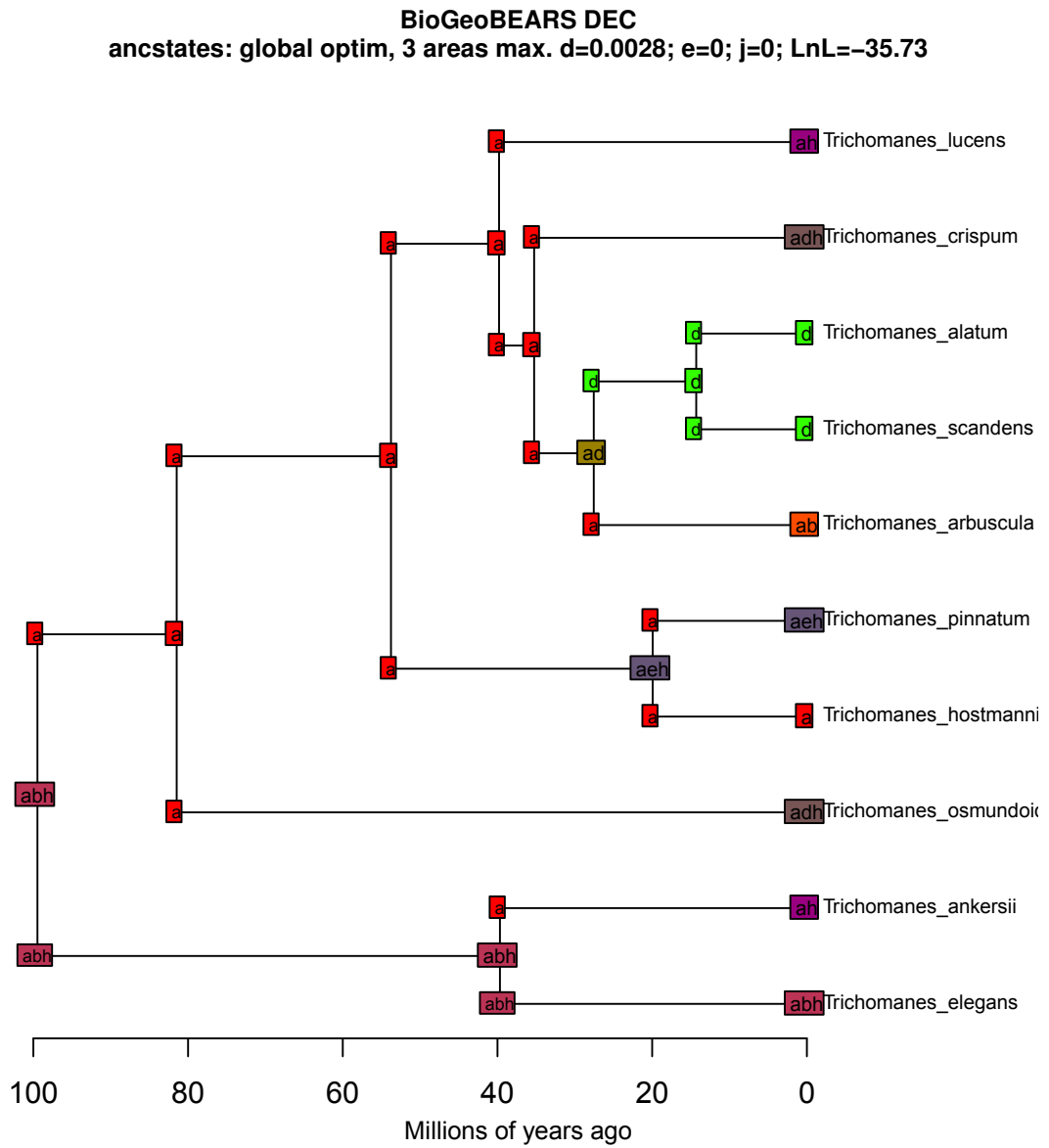


Figure S6: Clades of ferns

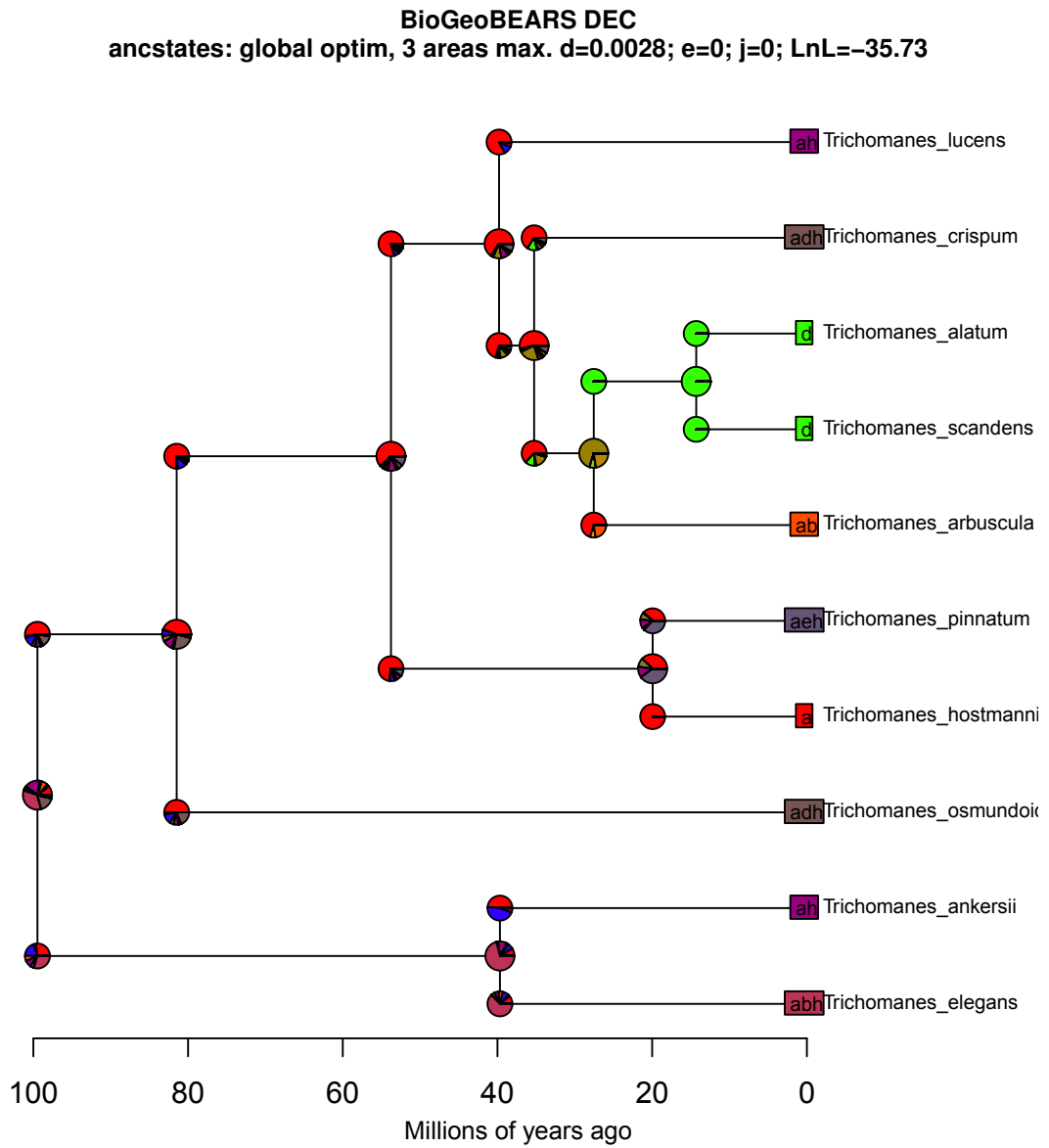


Figure S6: Clades of ferns

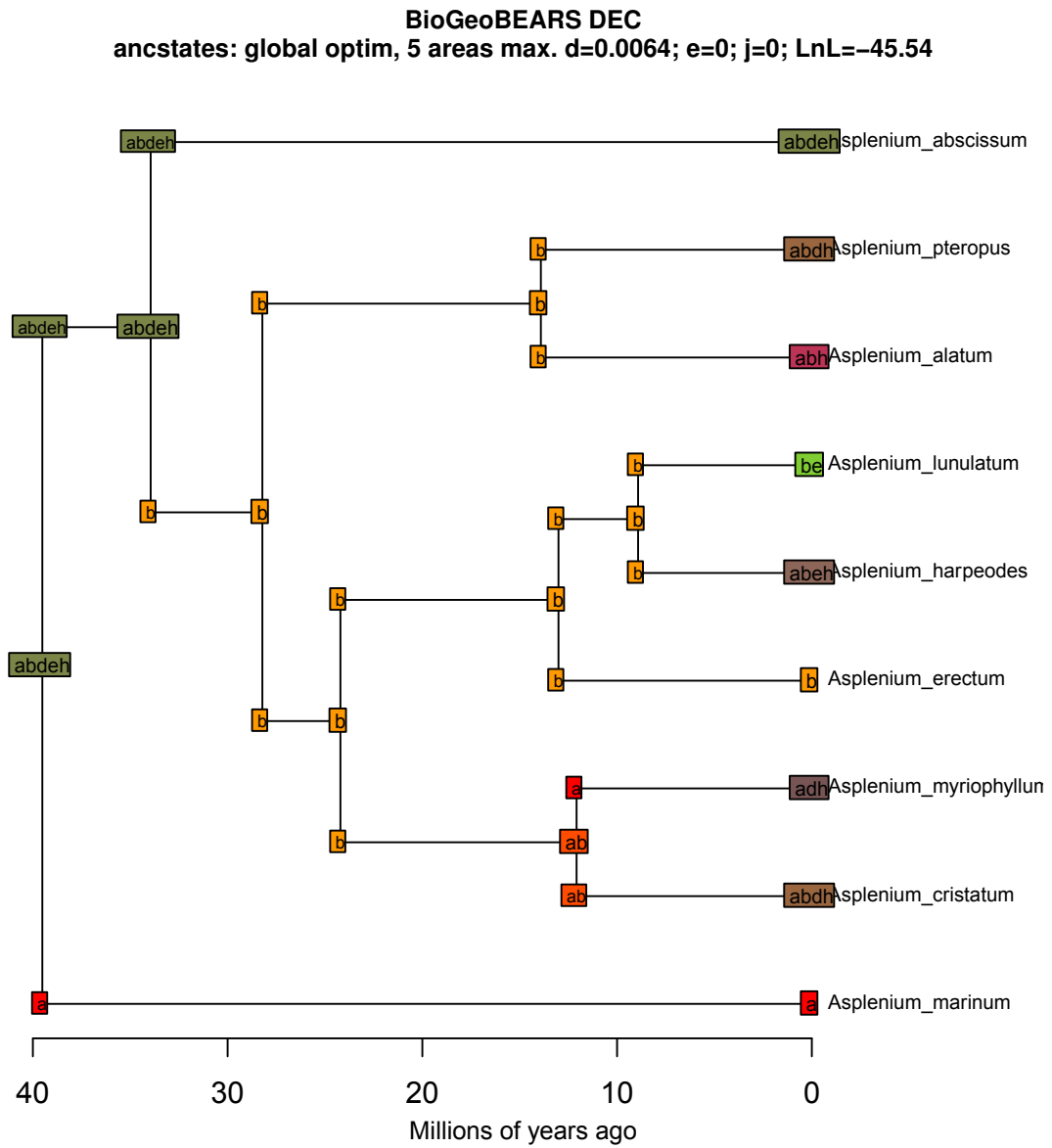


Figure S6: Clades of ferns

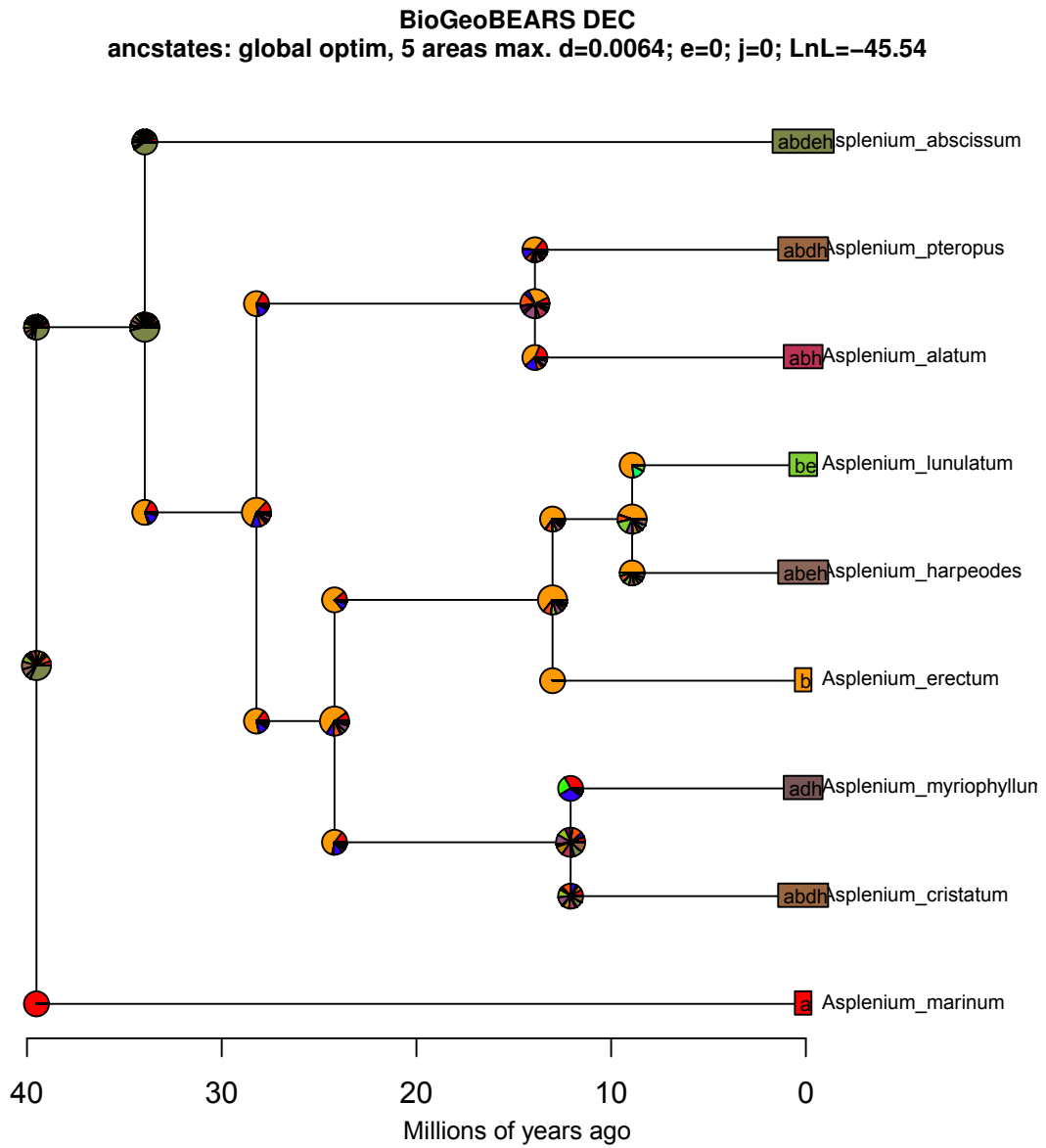


Figure S7: Clades of mammals

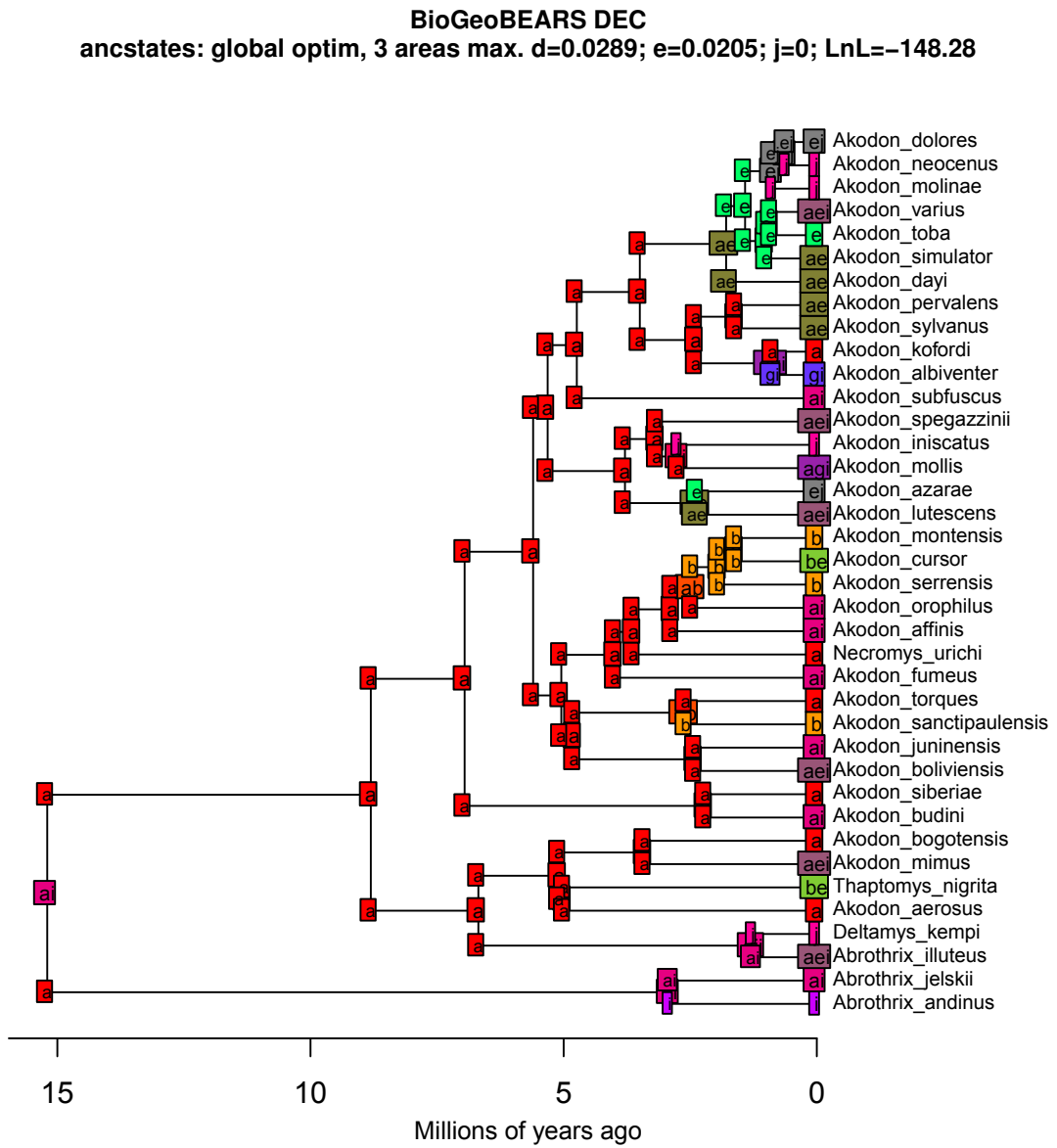


Figure S7: Clades of mammals

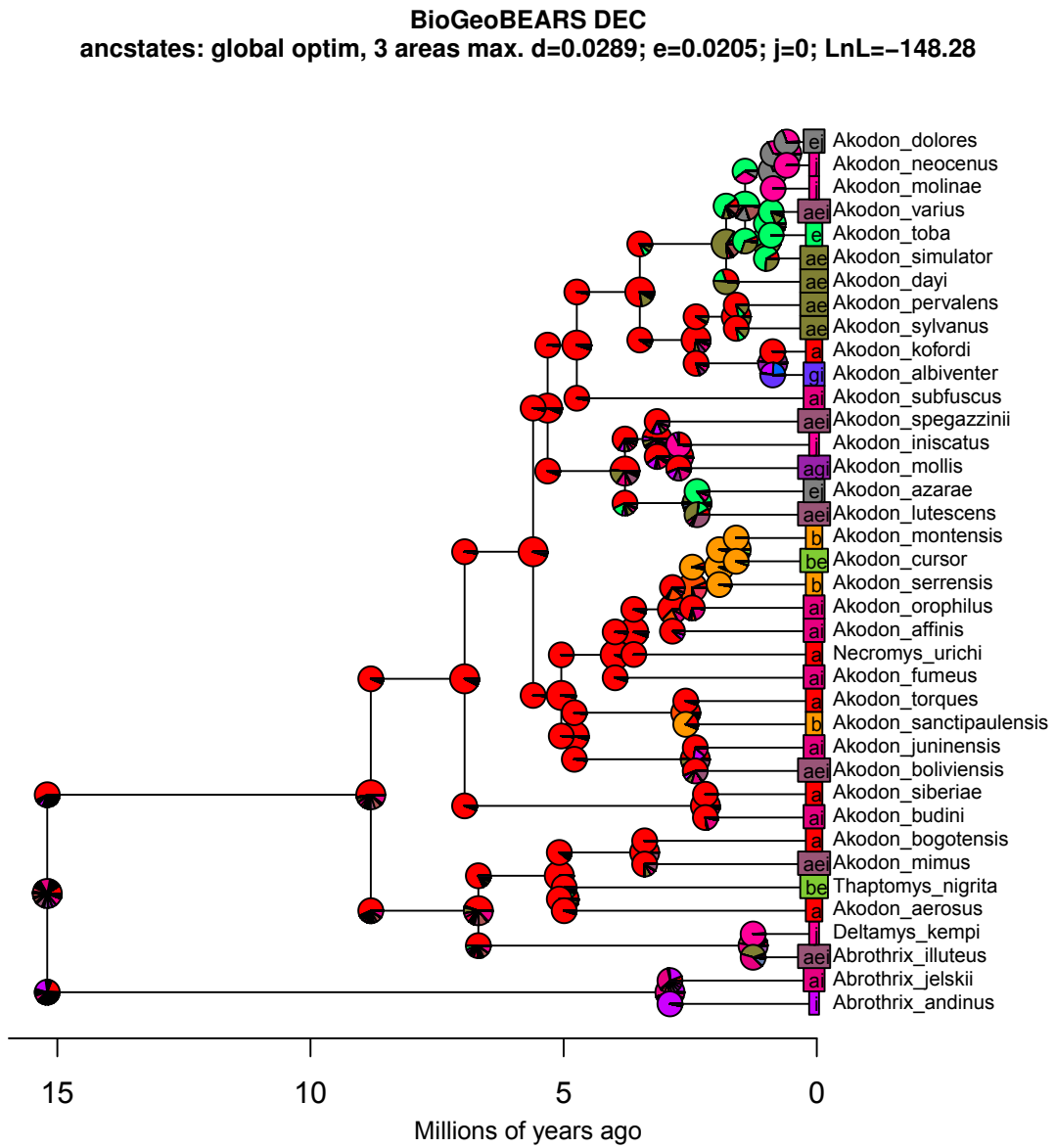


Figure S7: Clades of mammals

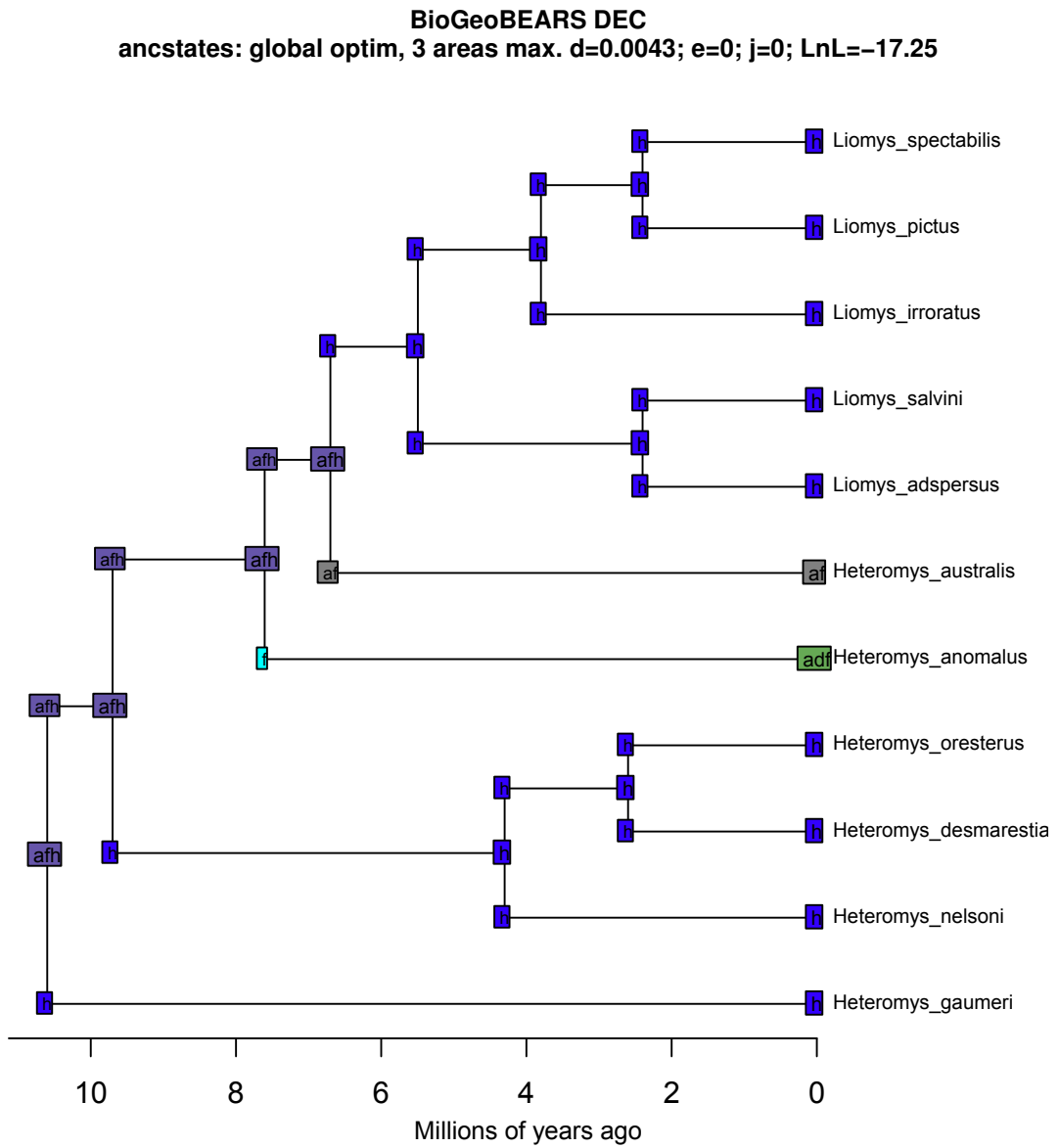


Figure S7: Clades of mammals

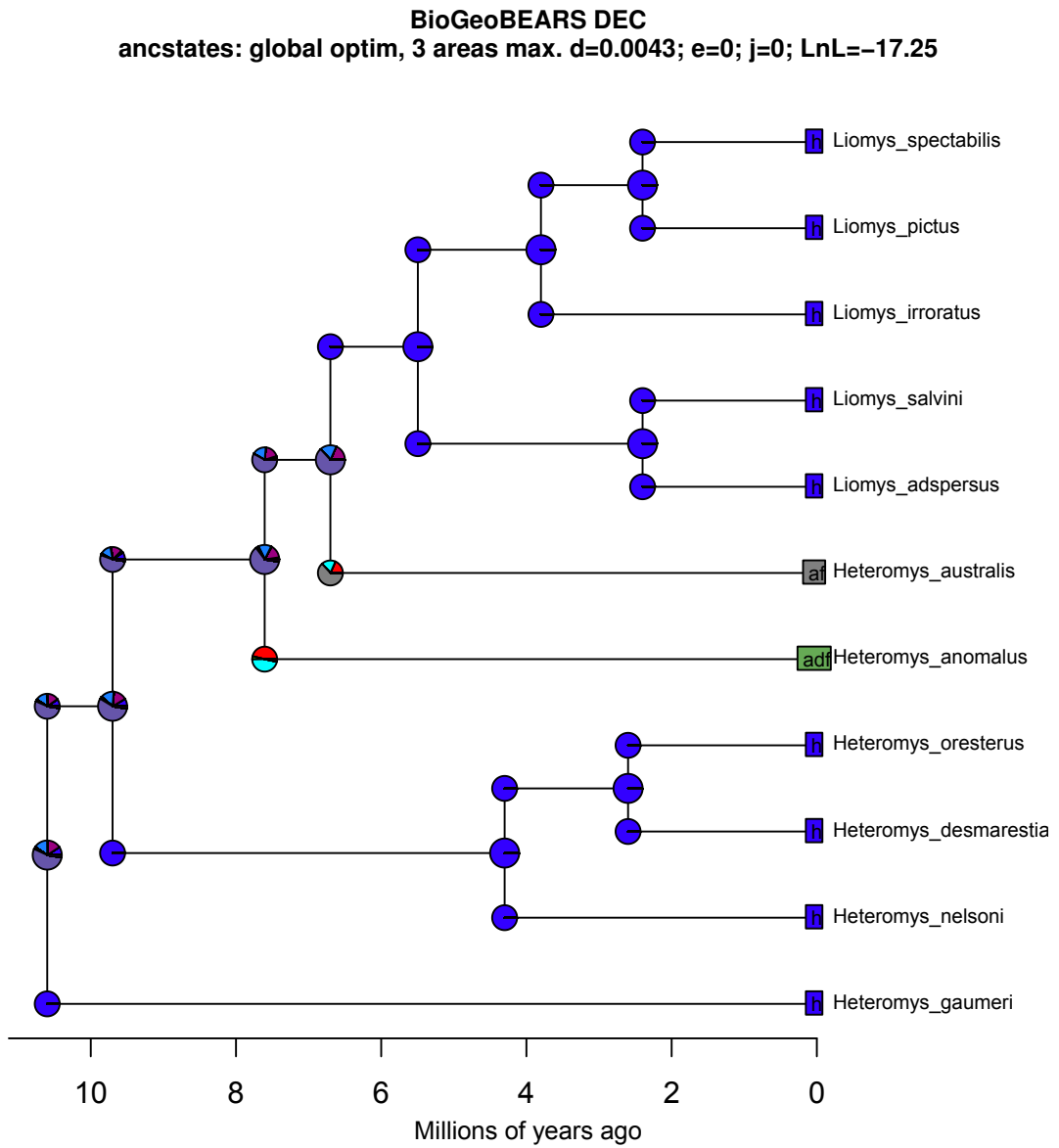


Figure S7: Clades of mammals

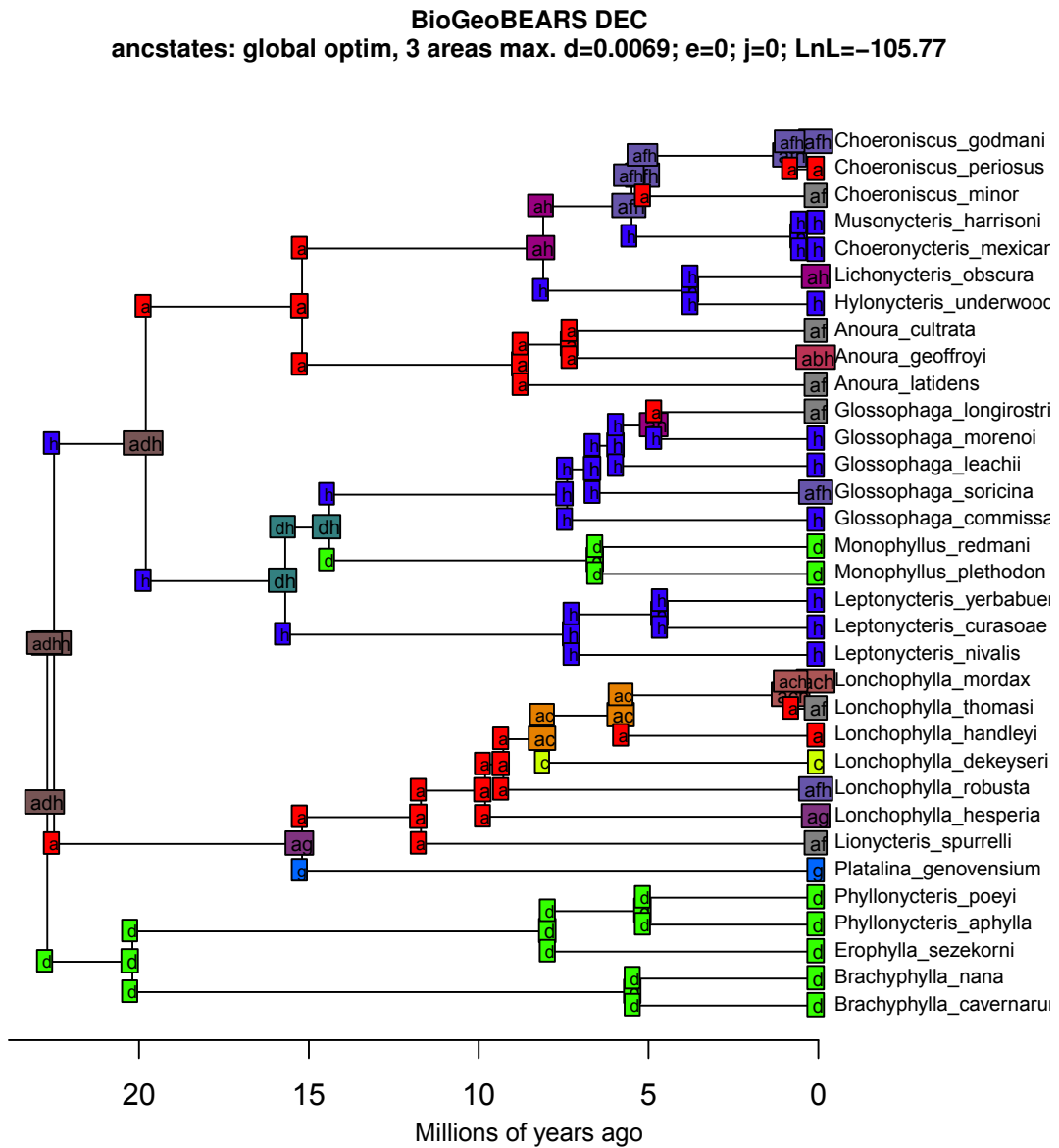


Figure S7: Clades of mammals

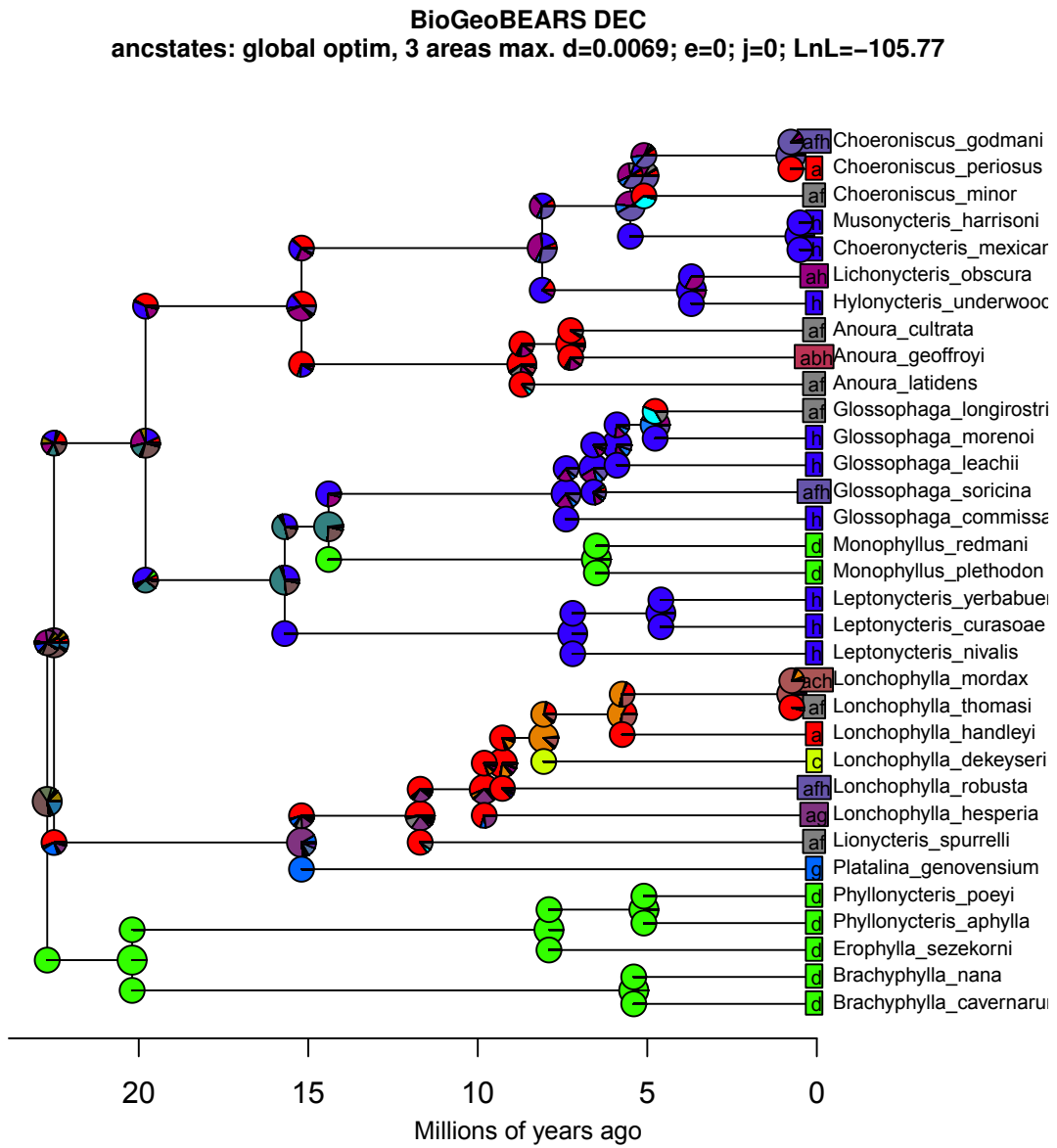


Figure S7: Clades of mammals

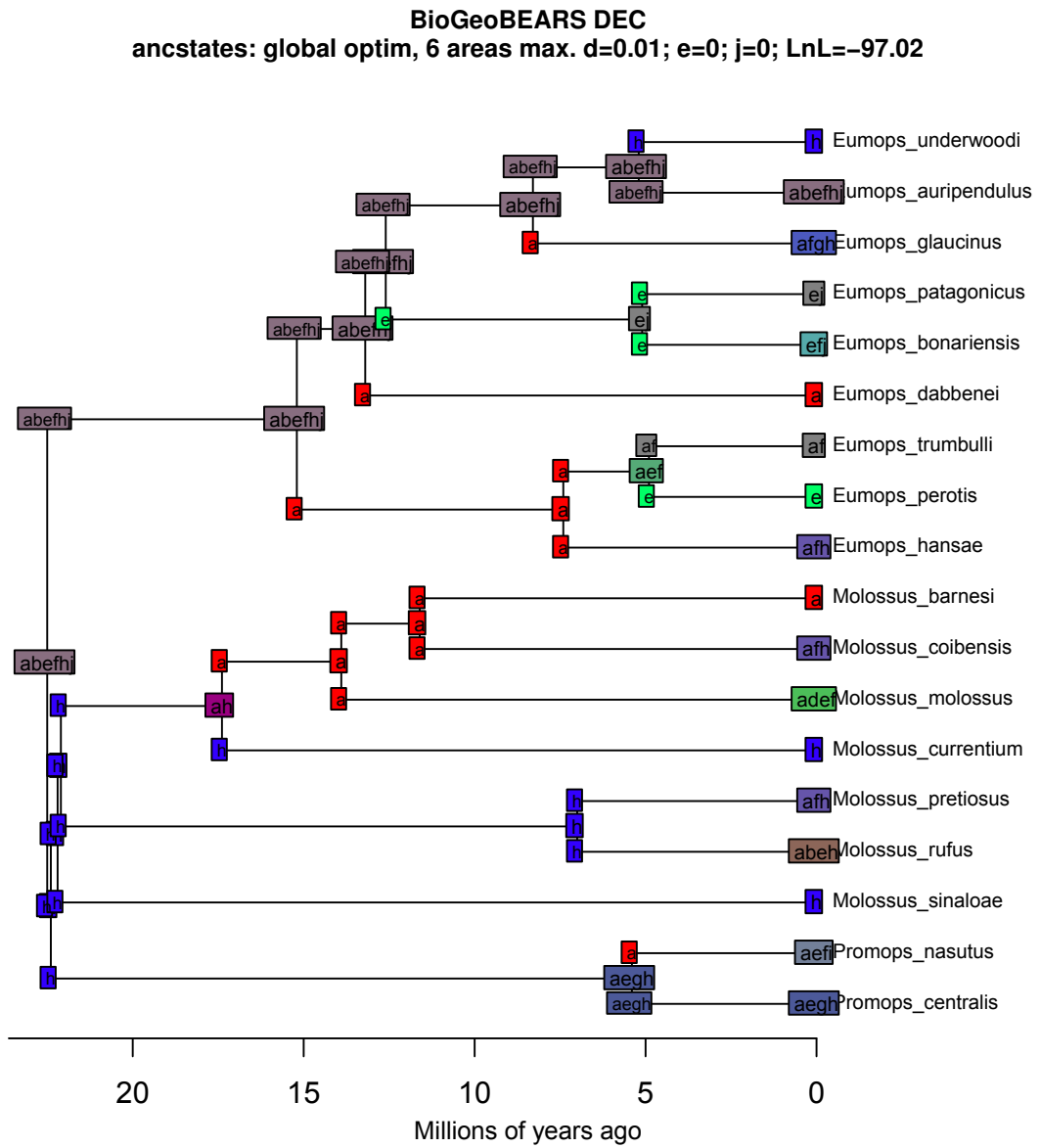


Figure S7: Clades of mammals

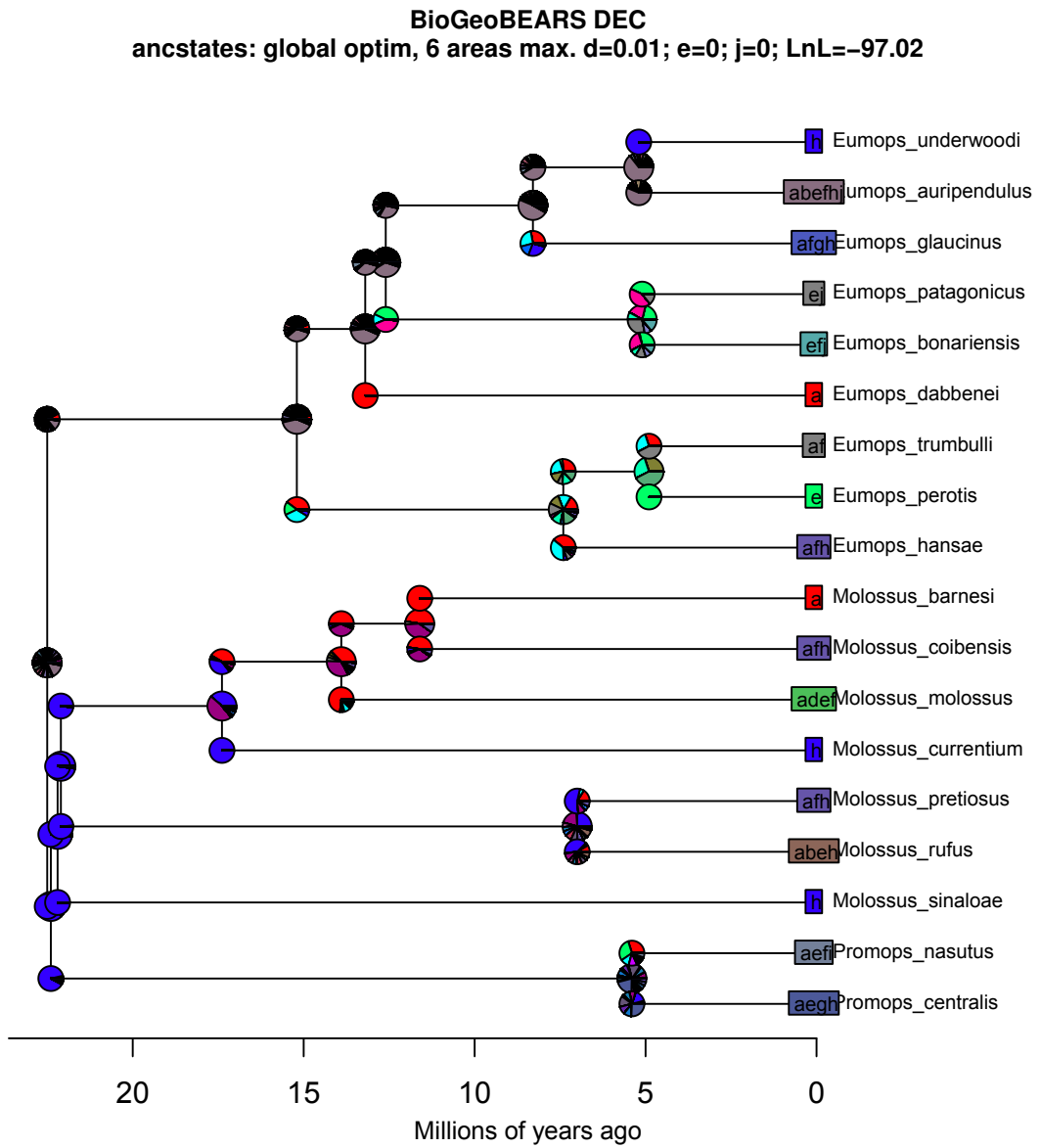


Figure S7: Clades of mammals

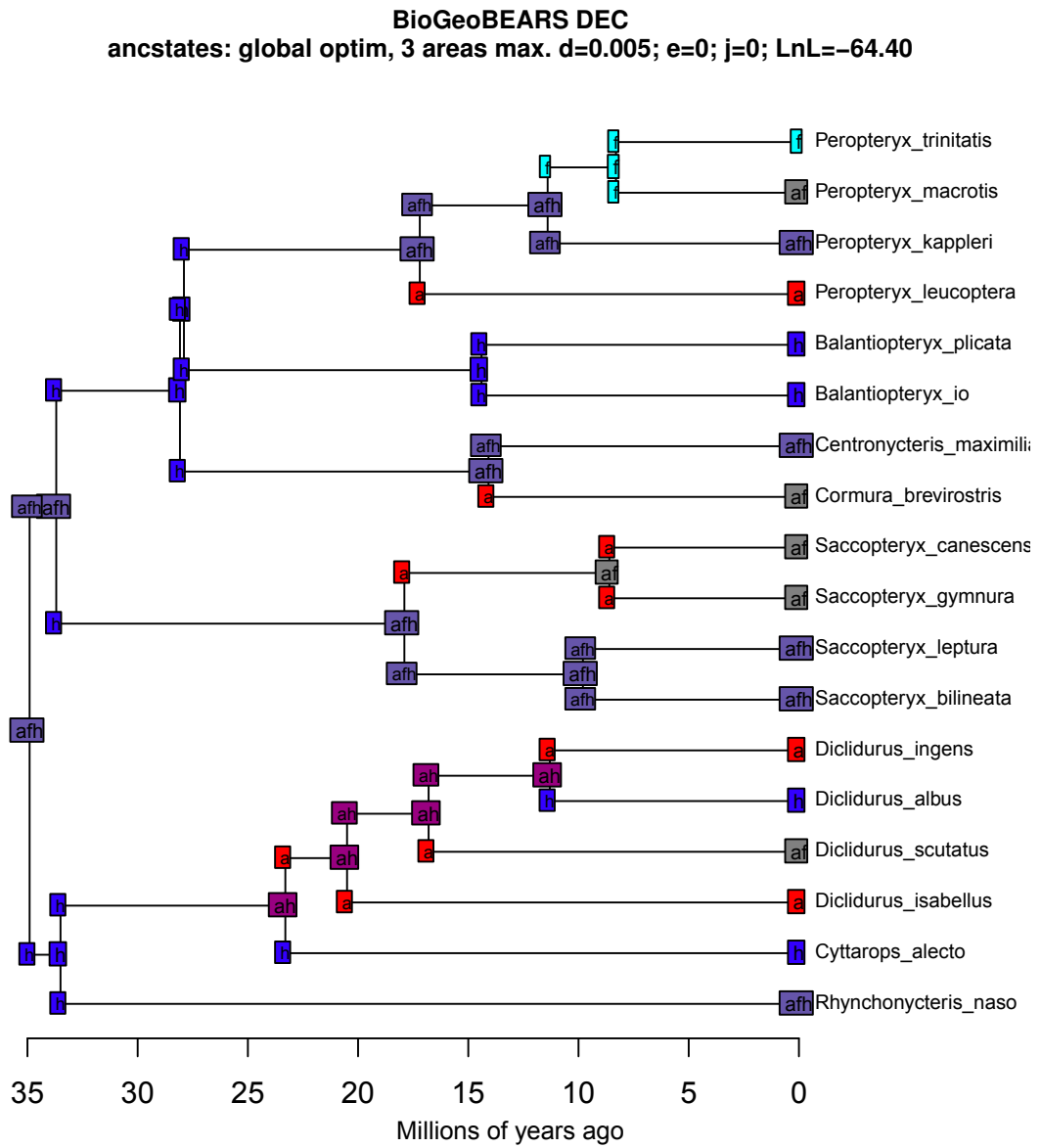


Figure S7: Clades of mammals

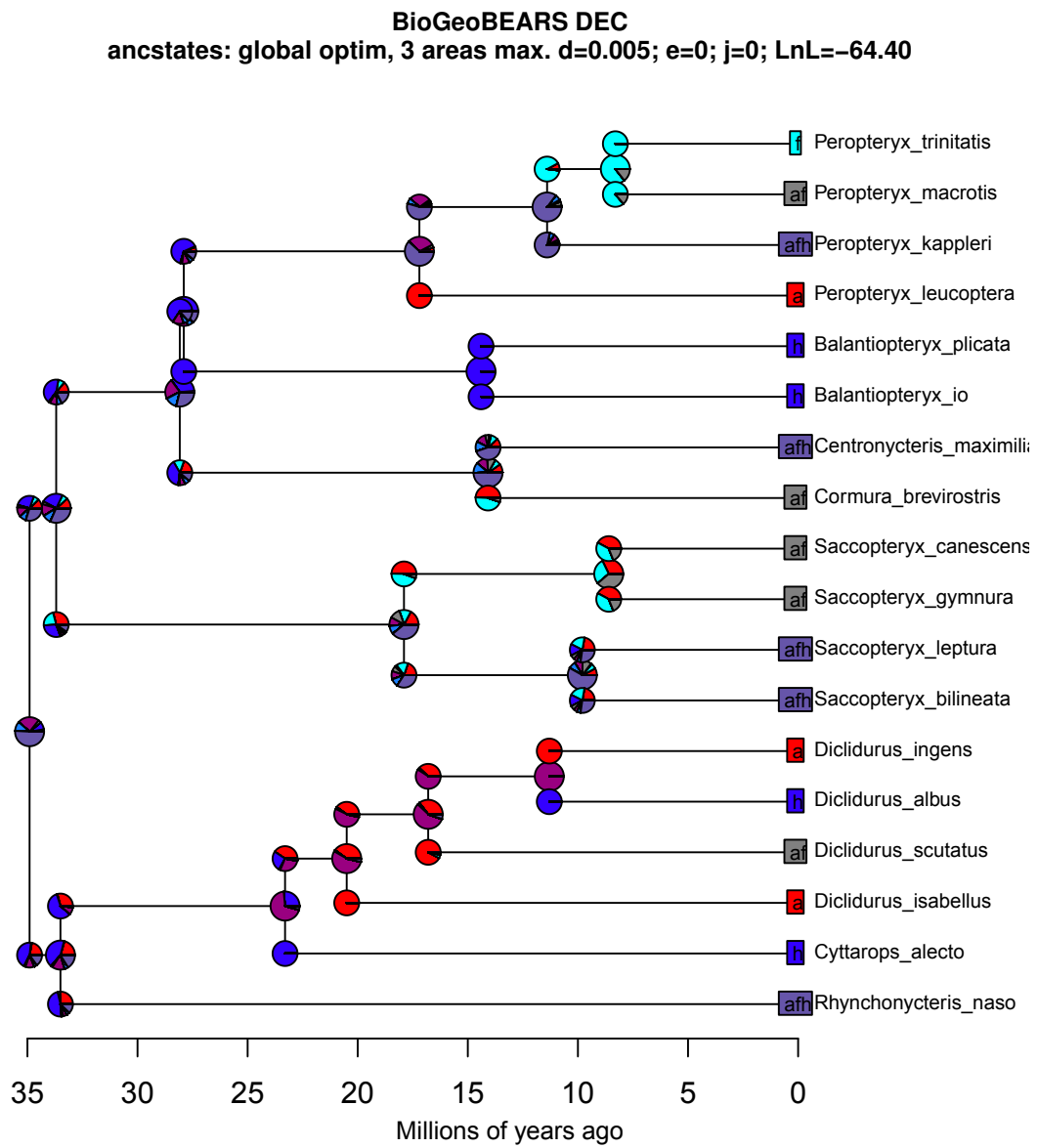


Figure S7: Clades of mammals

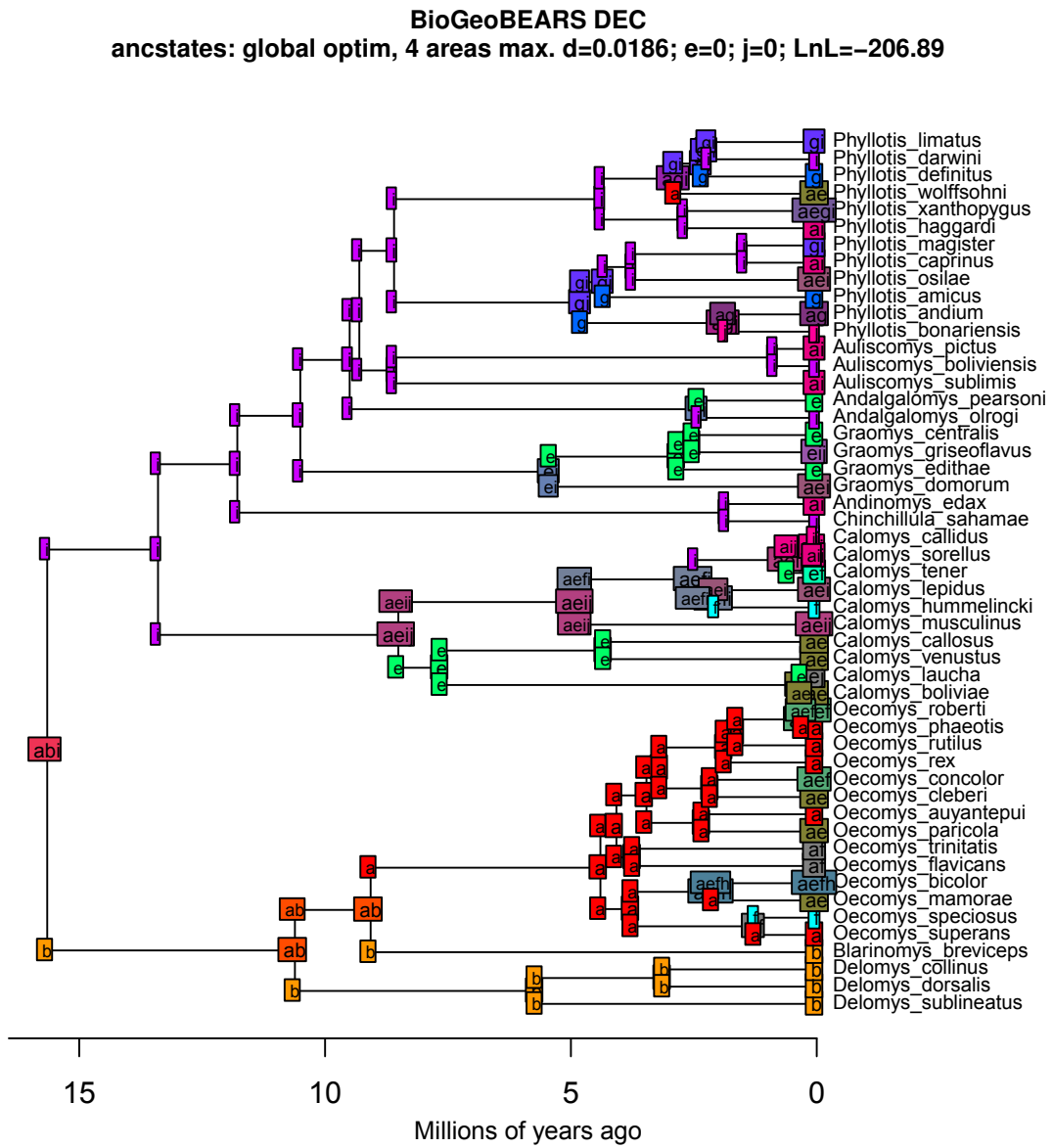


Figure S7: Clades of mammals

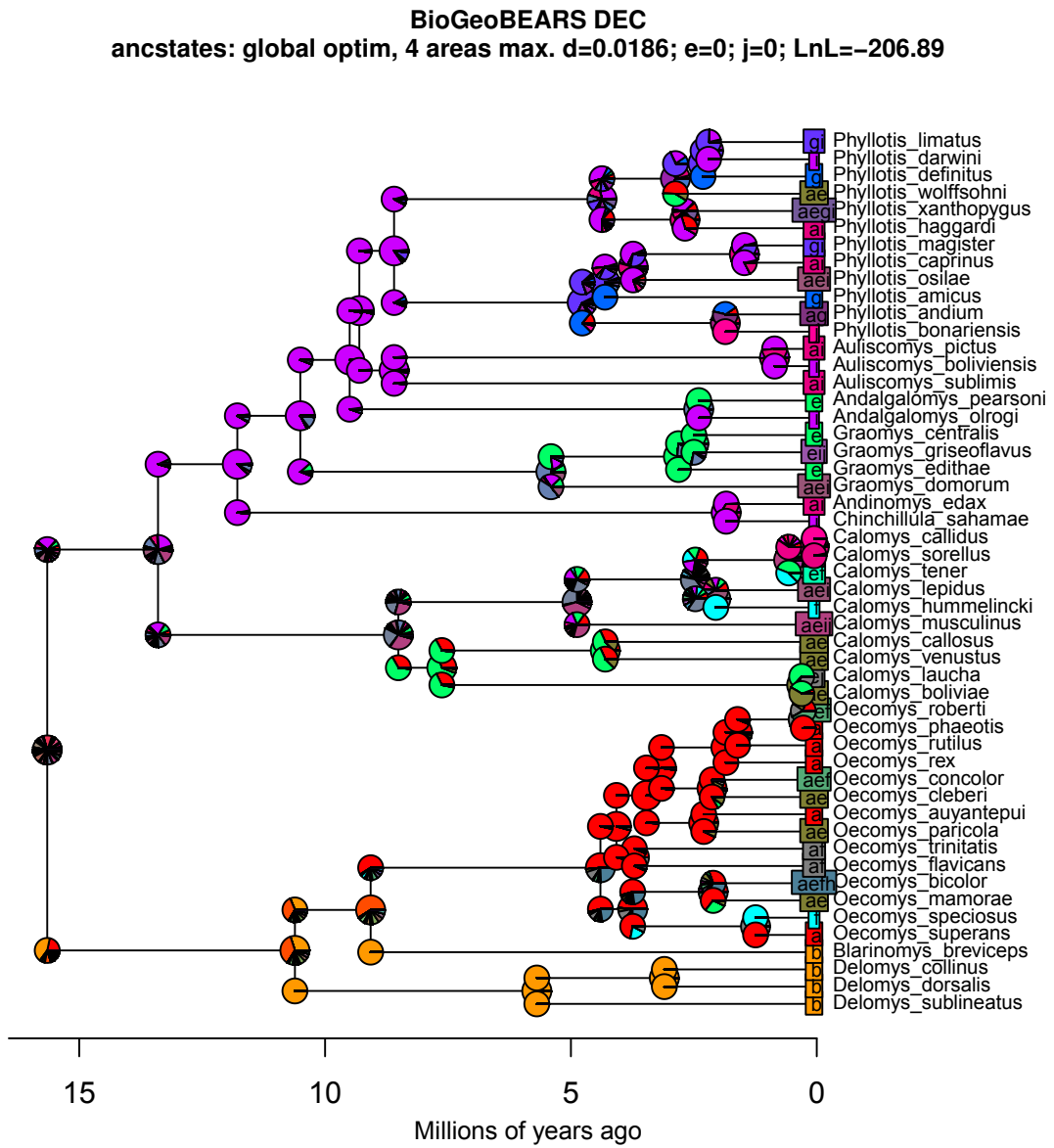


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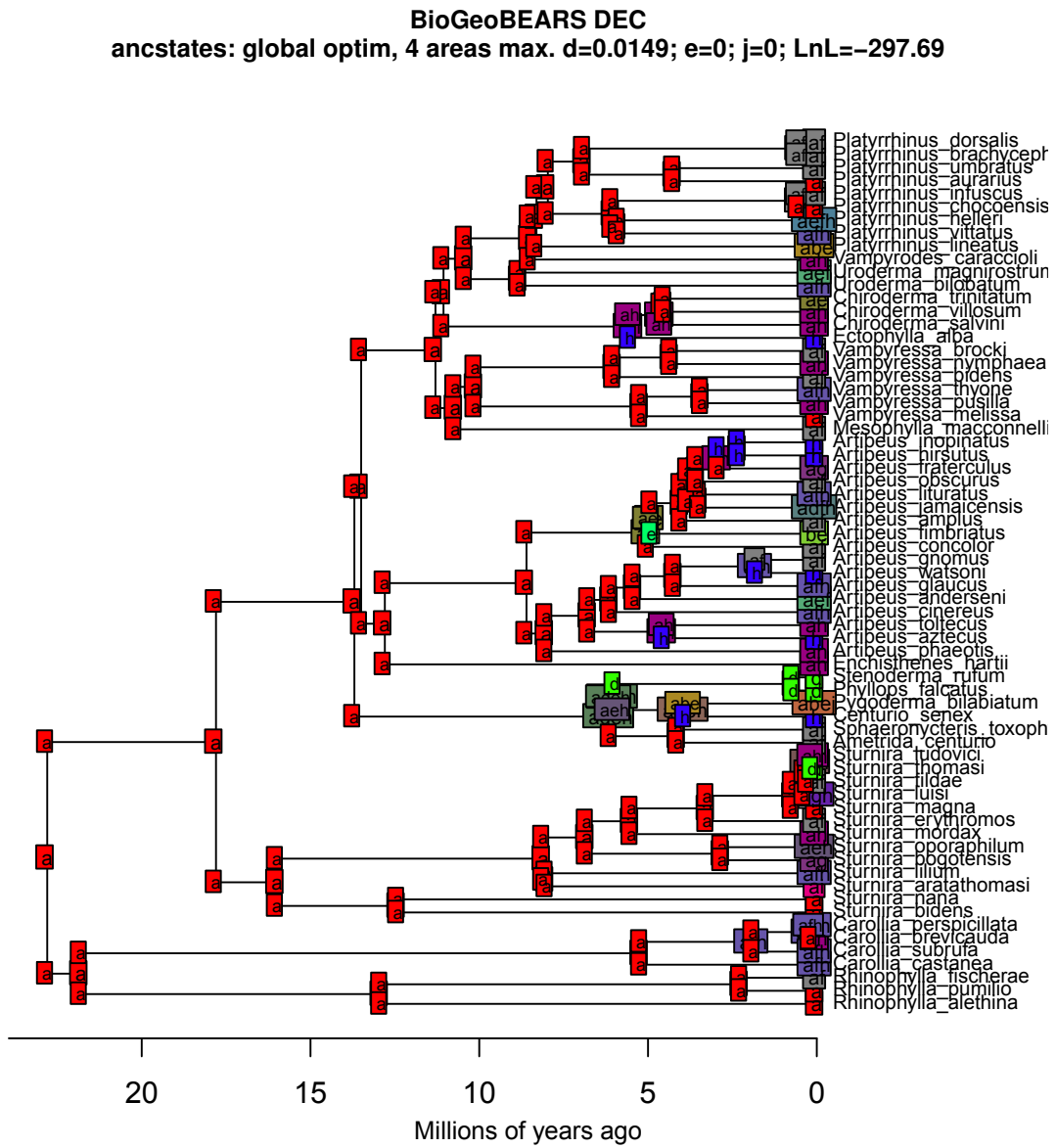


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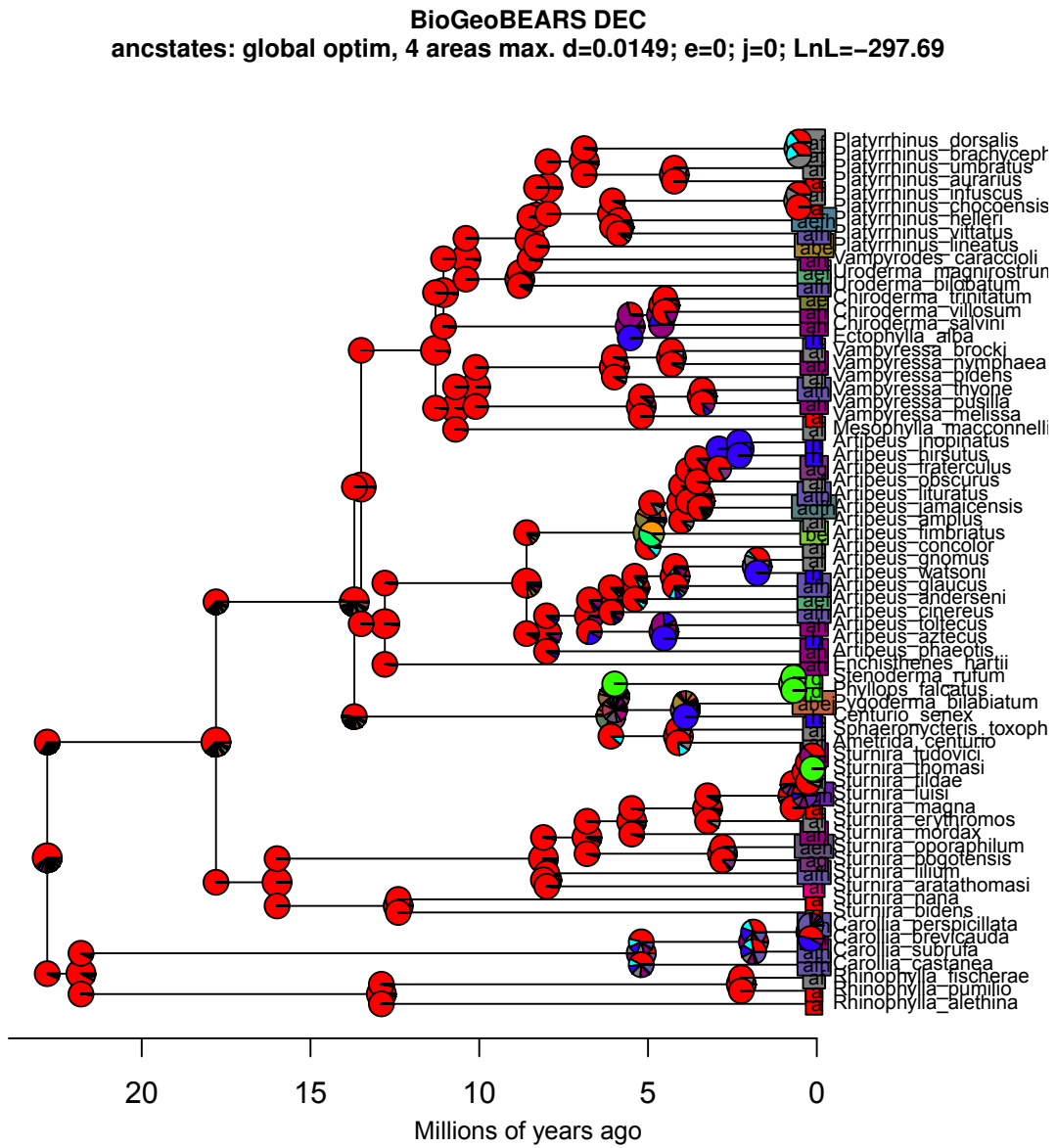


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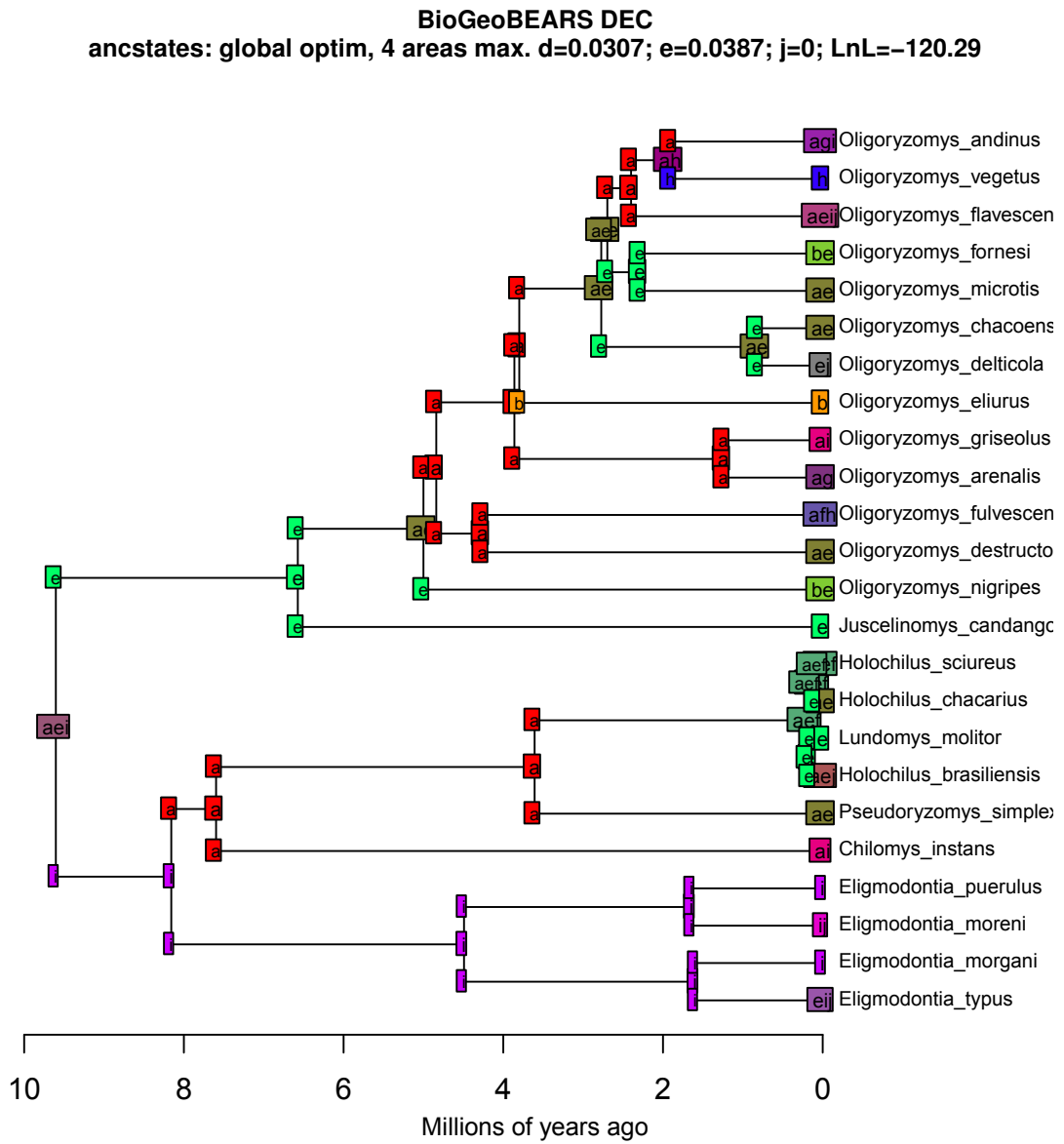


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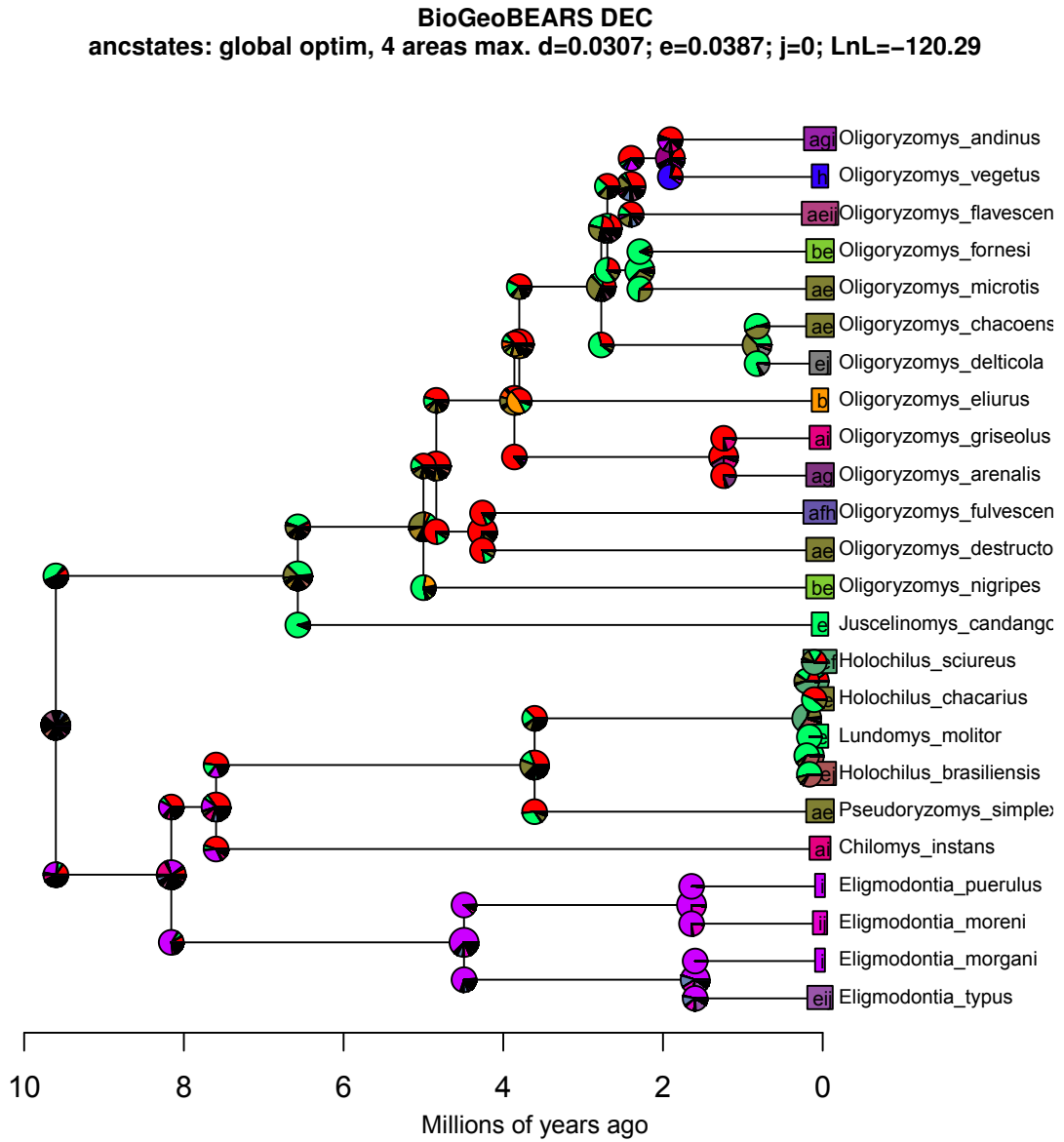


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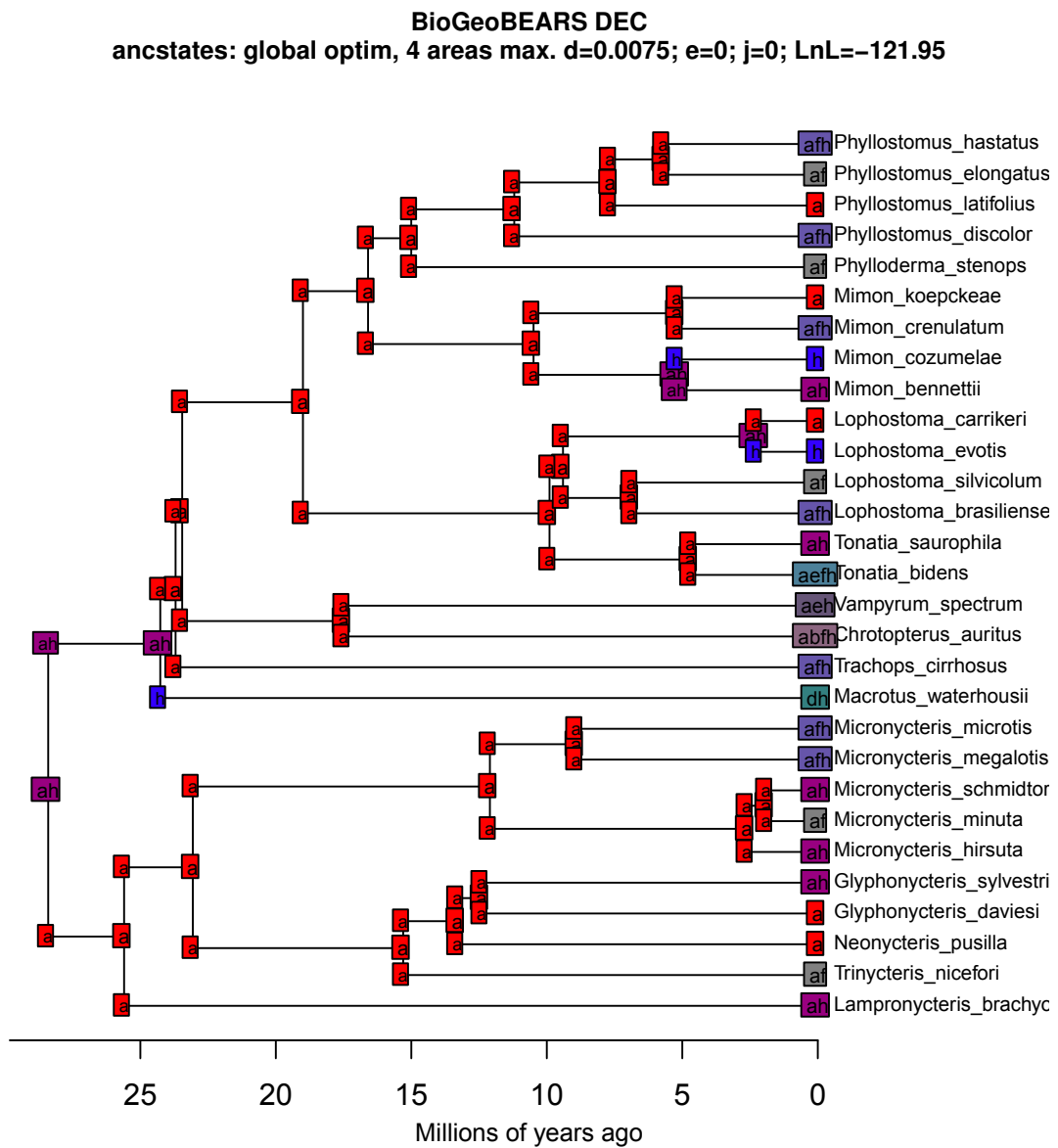


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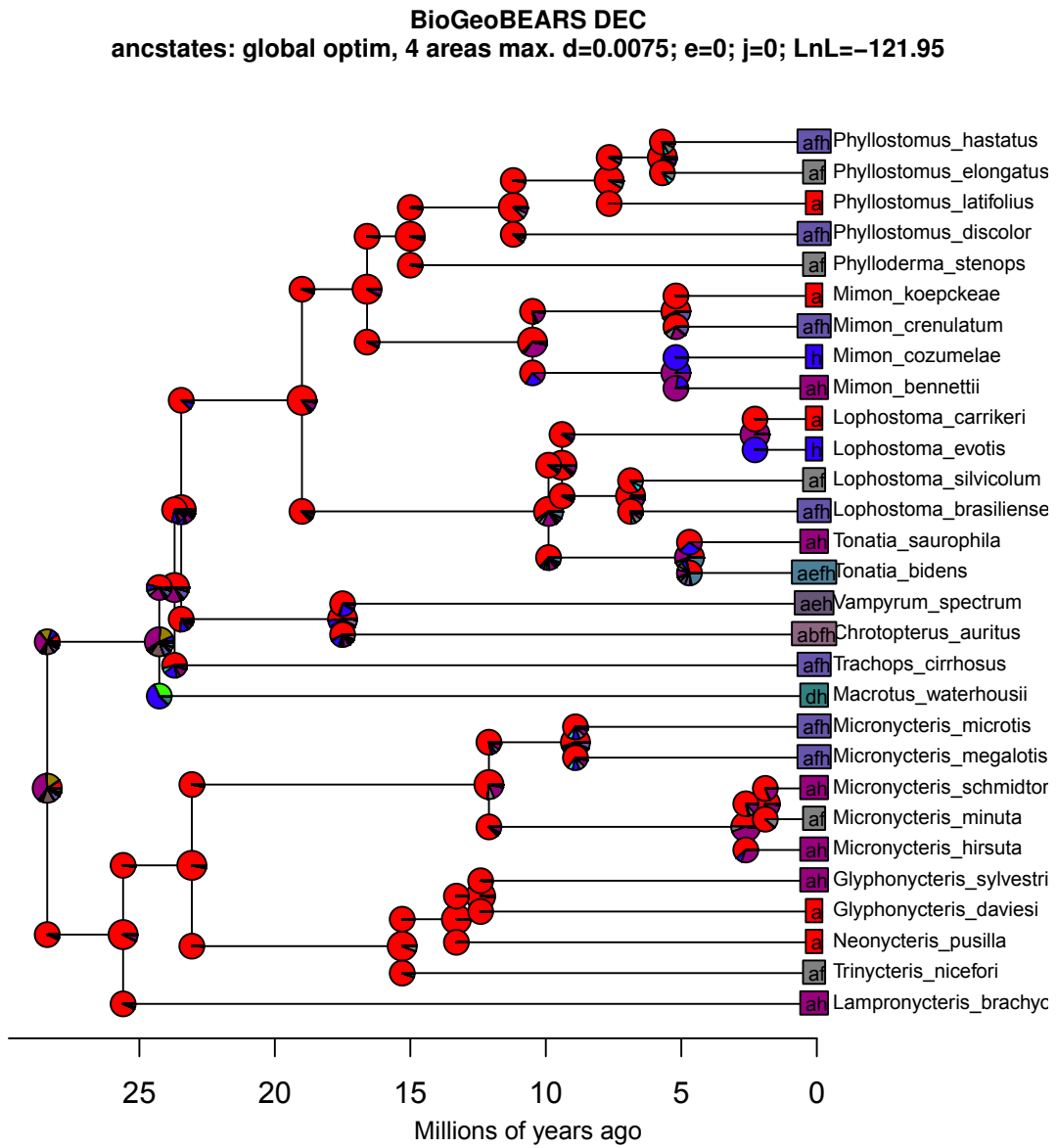


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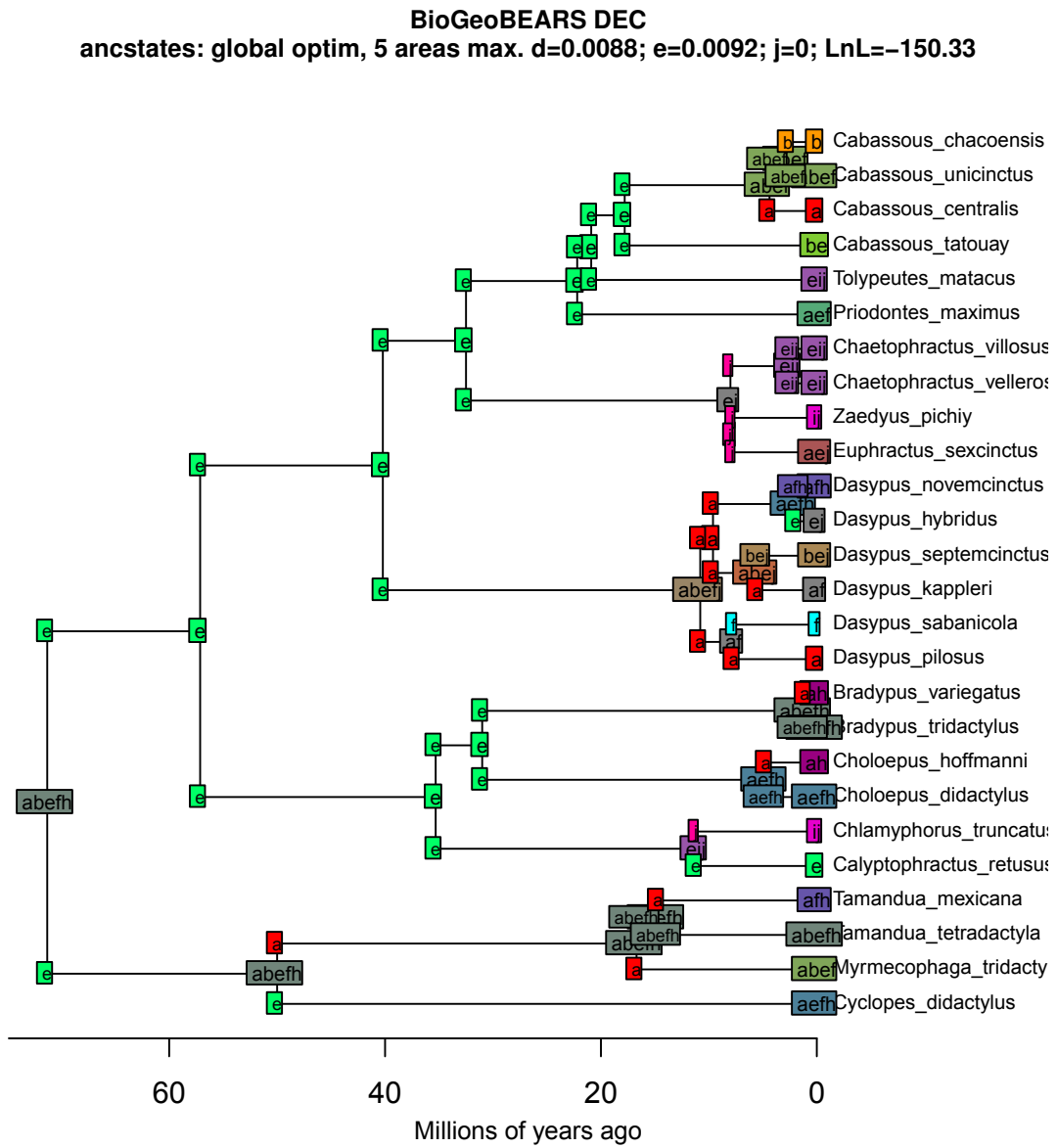


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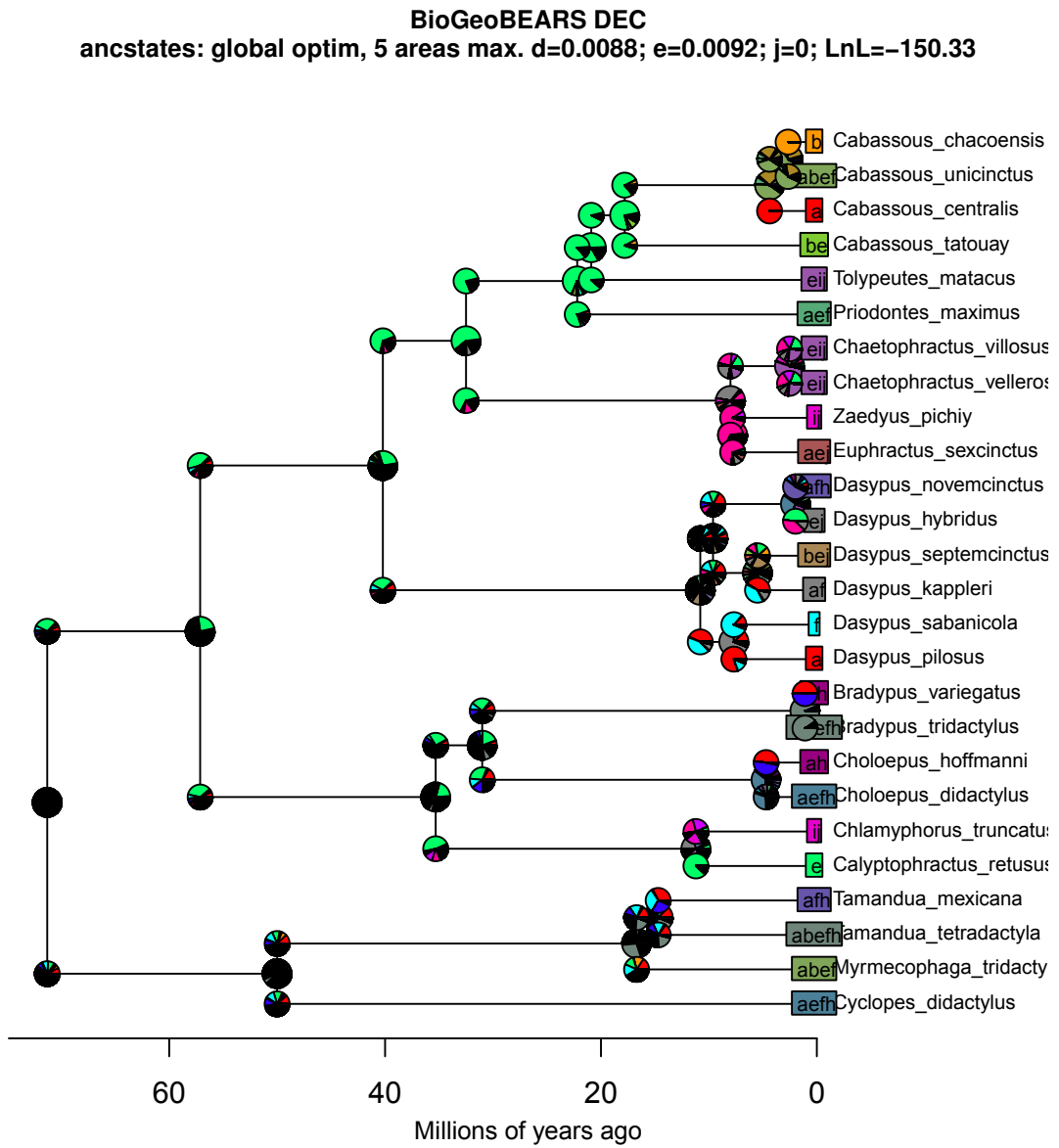


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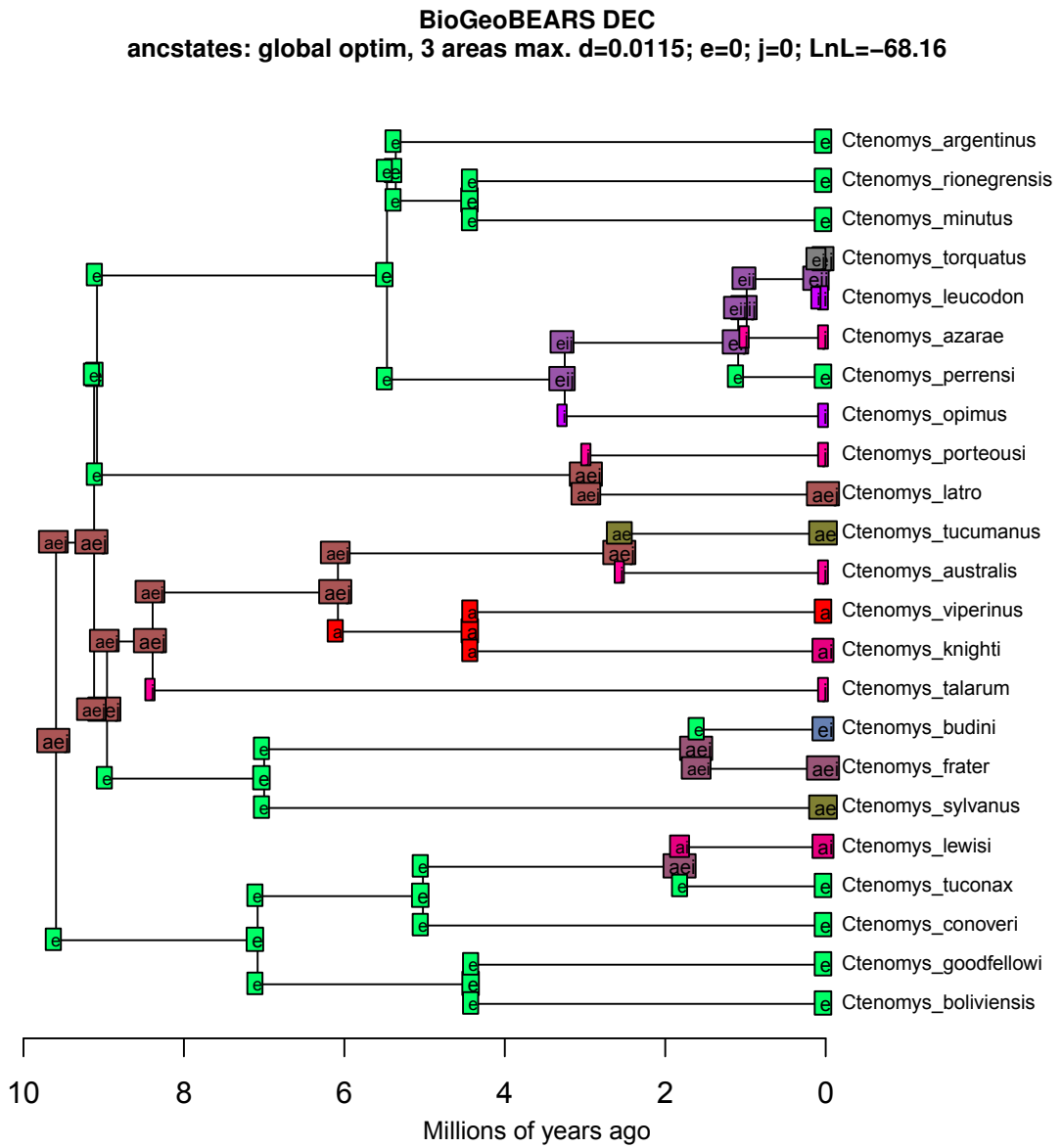


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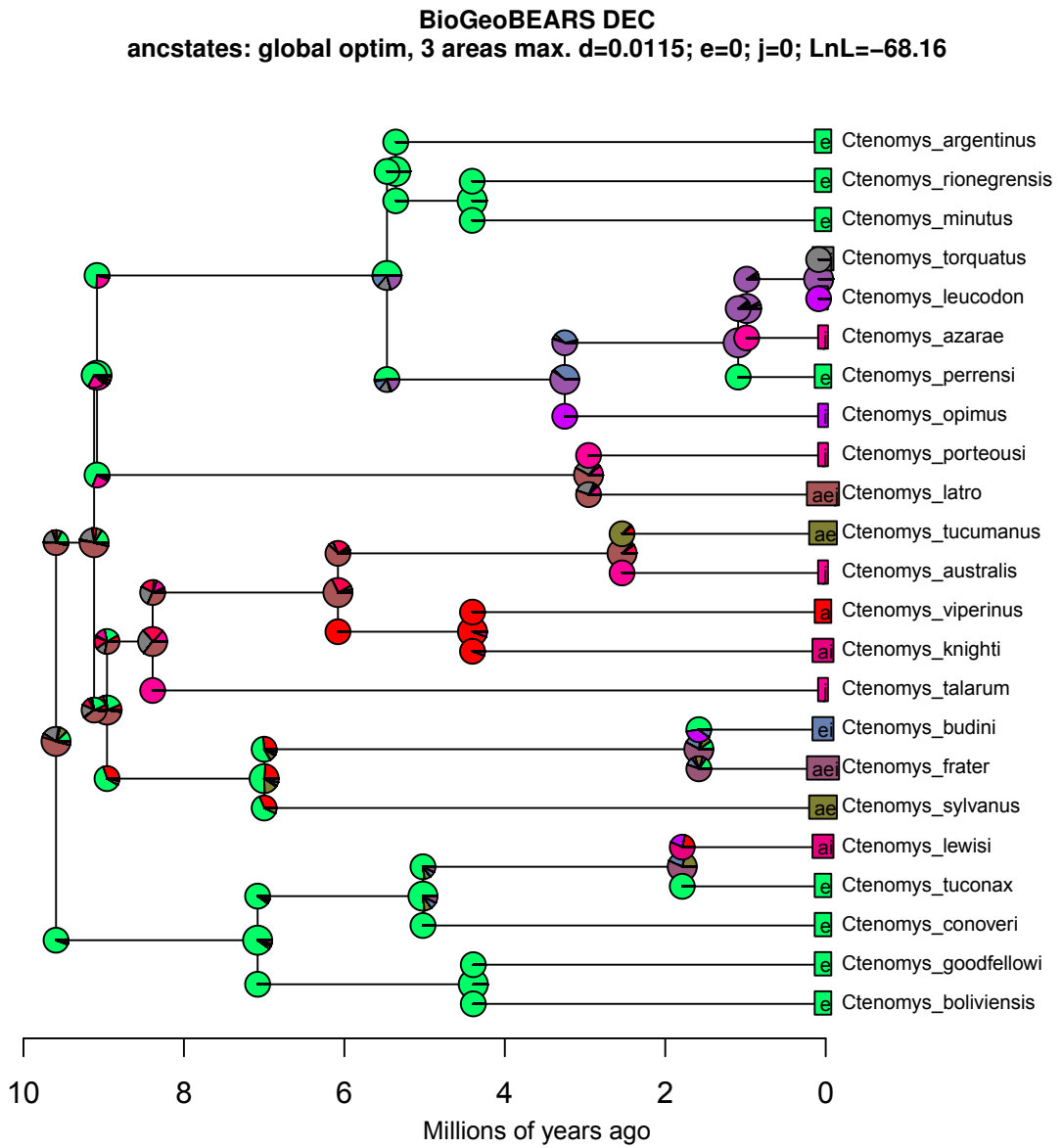


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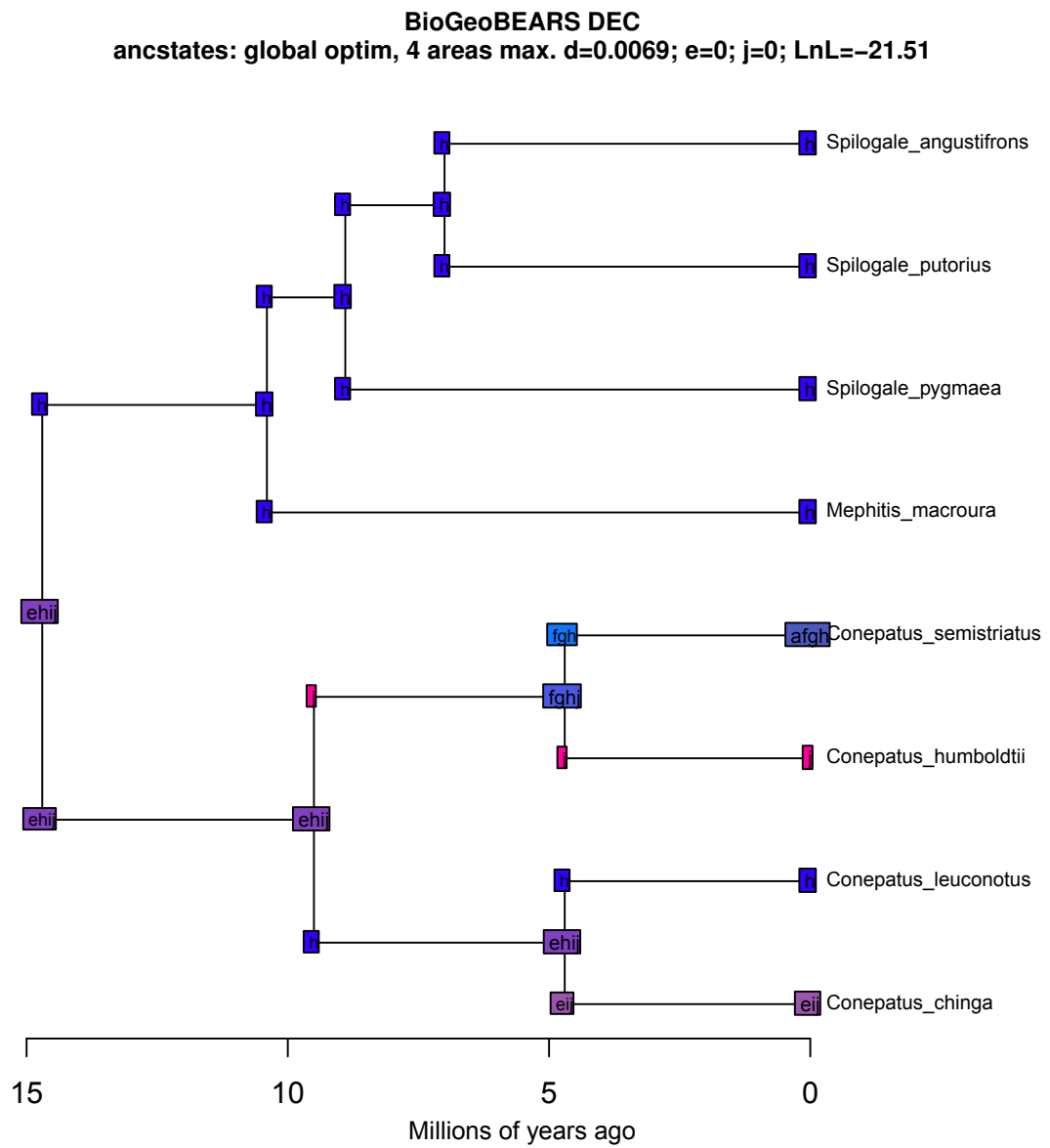


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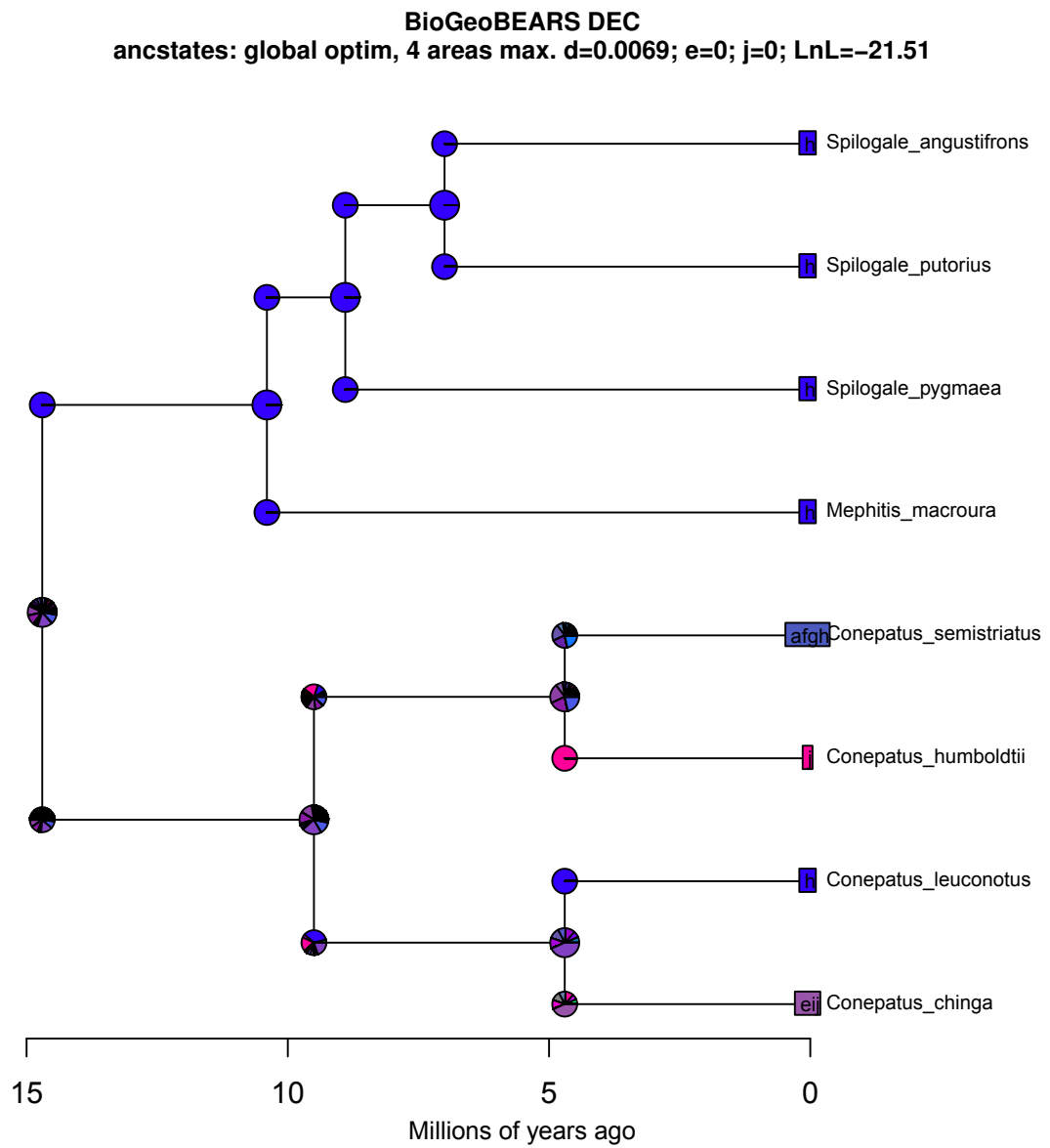


Figure S8: Clades of squamates

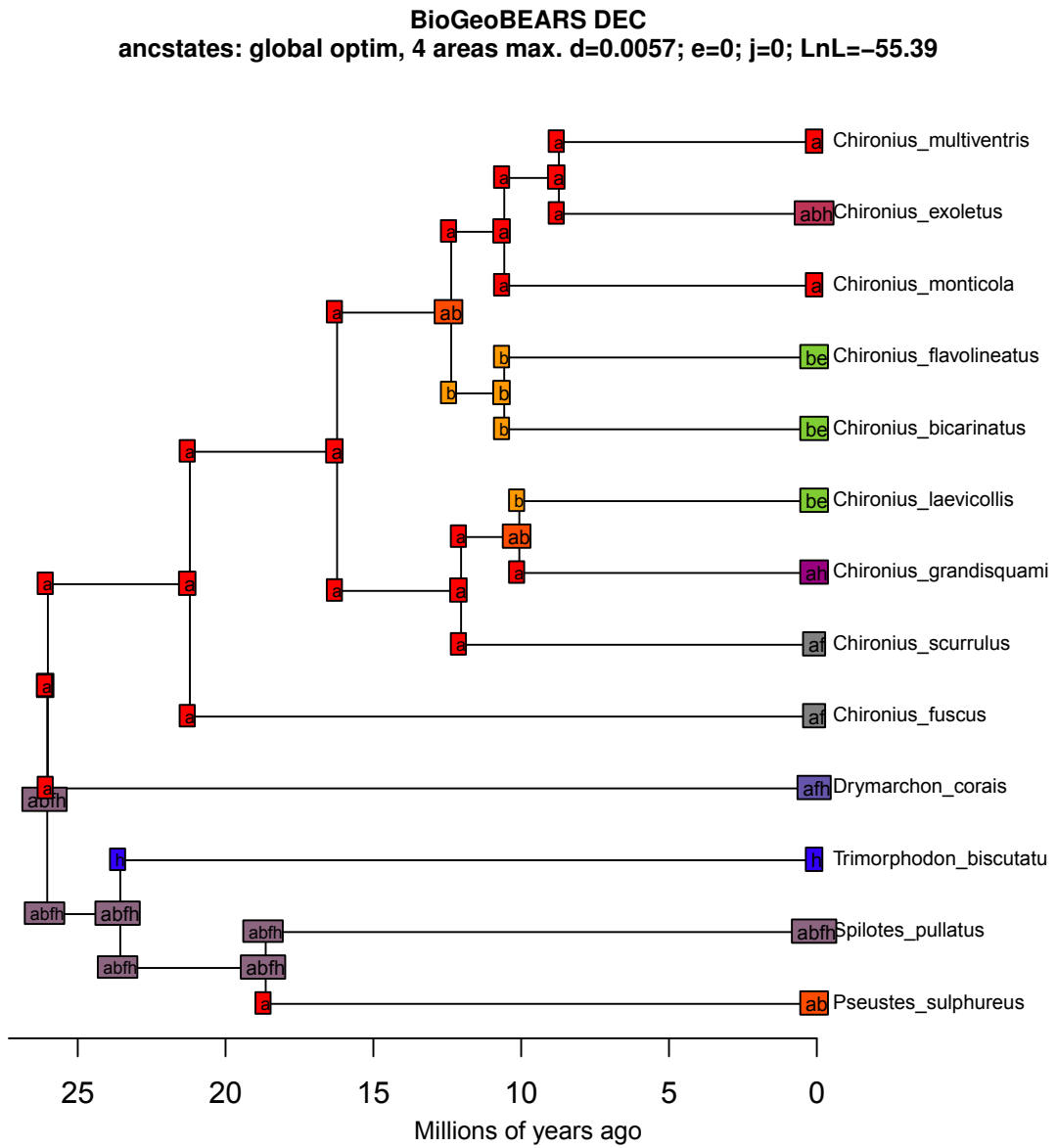


Figure S8: Clades of squamates

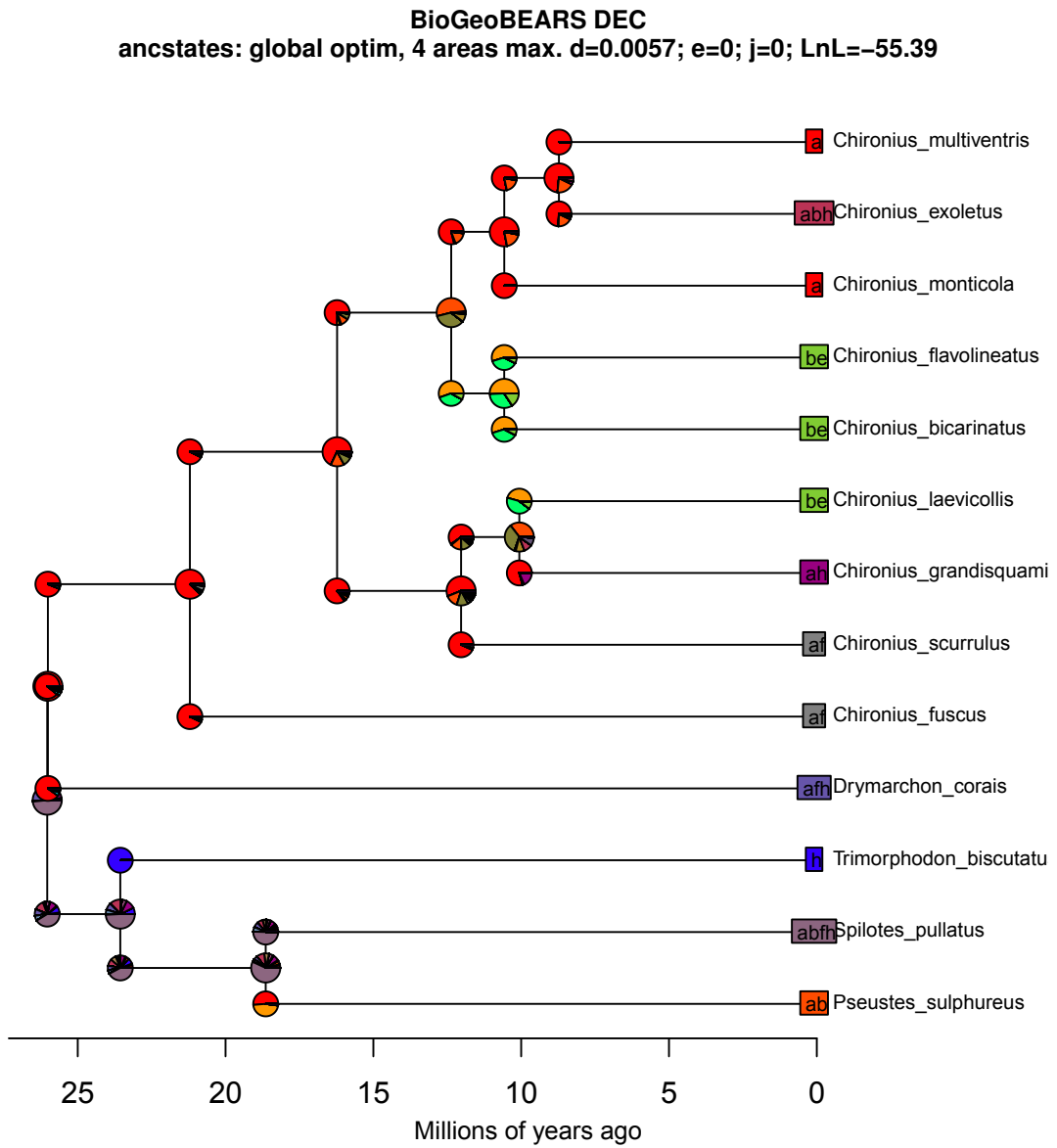


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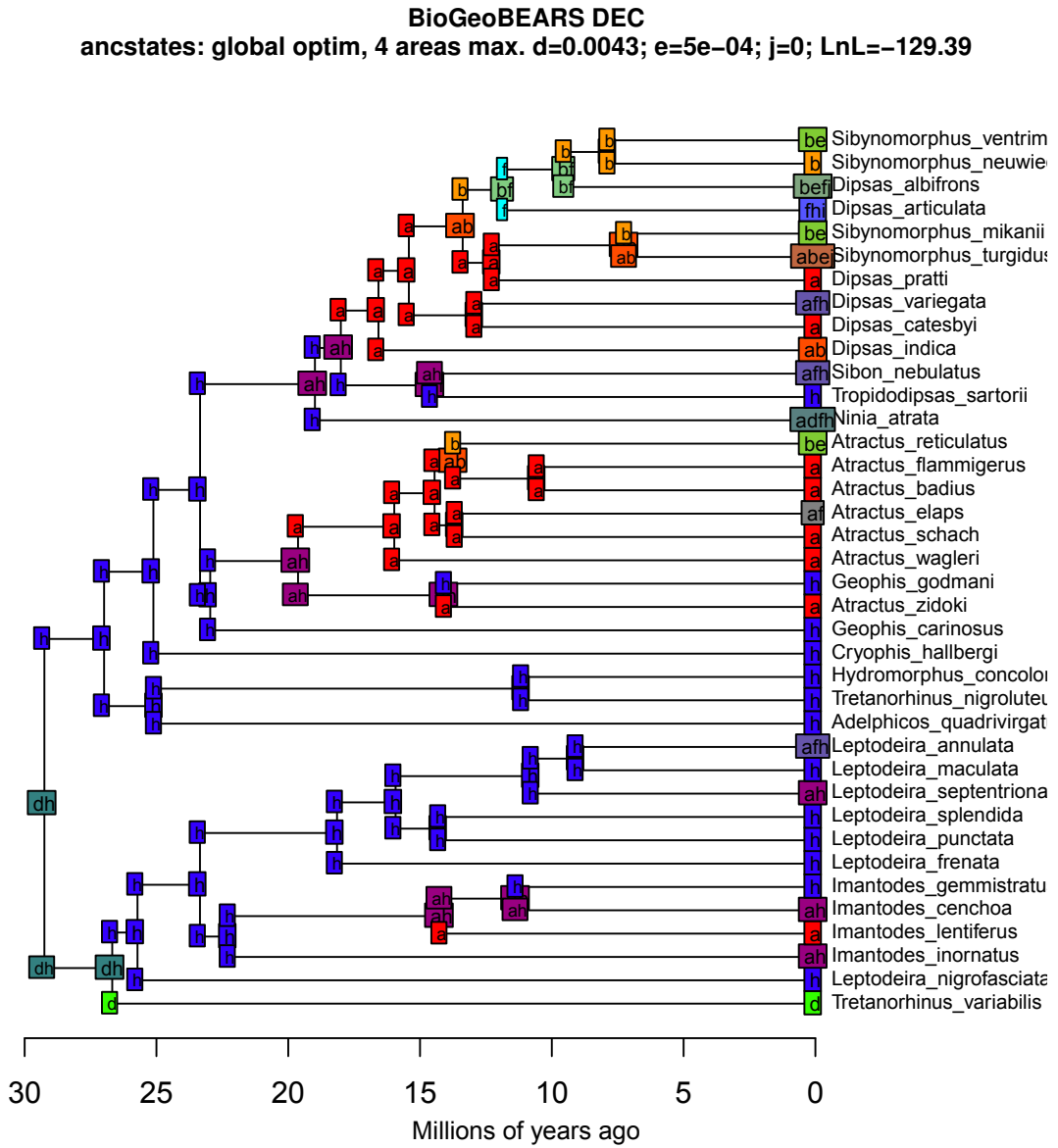


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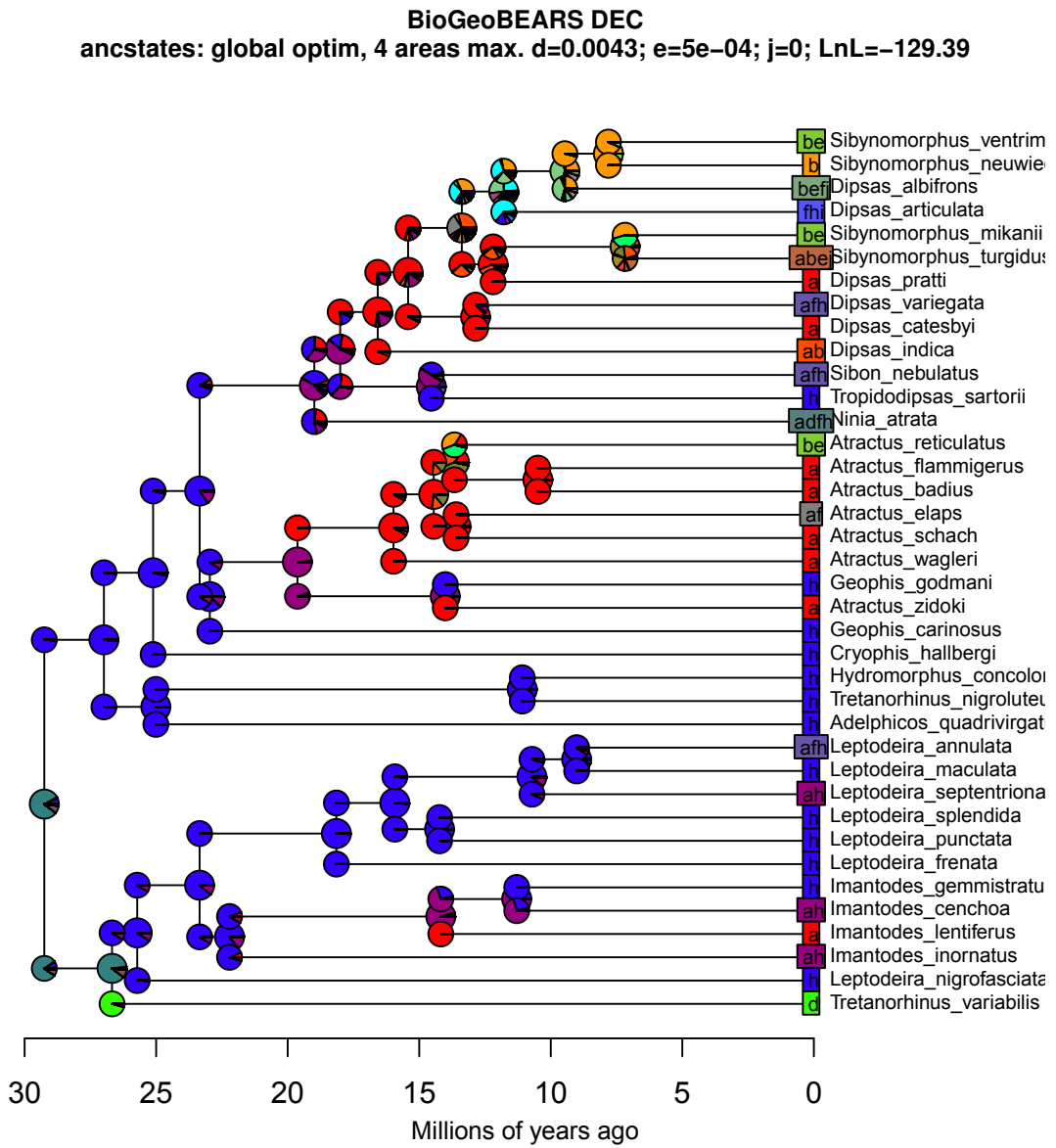


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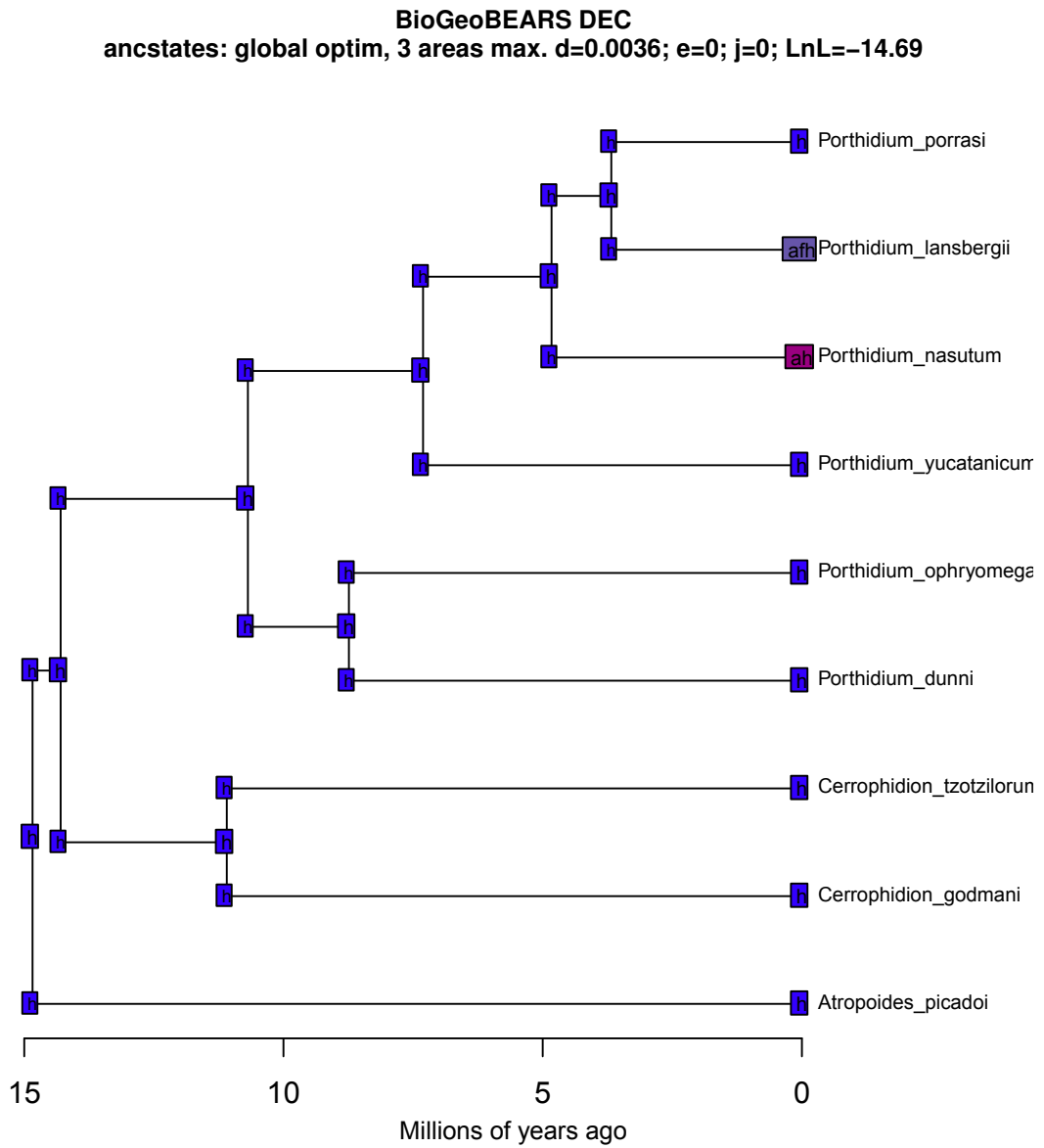


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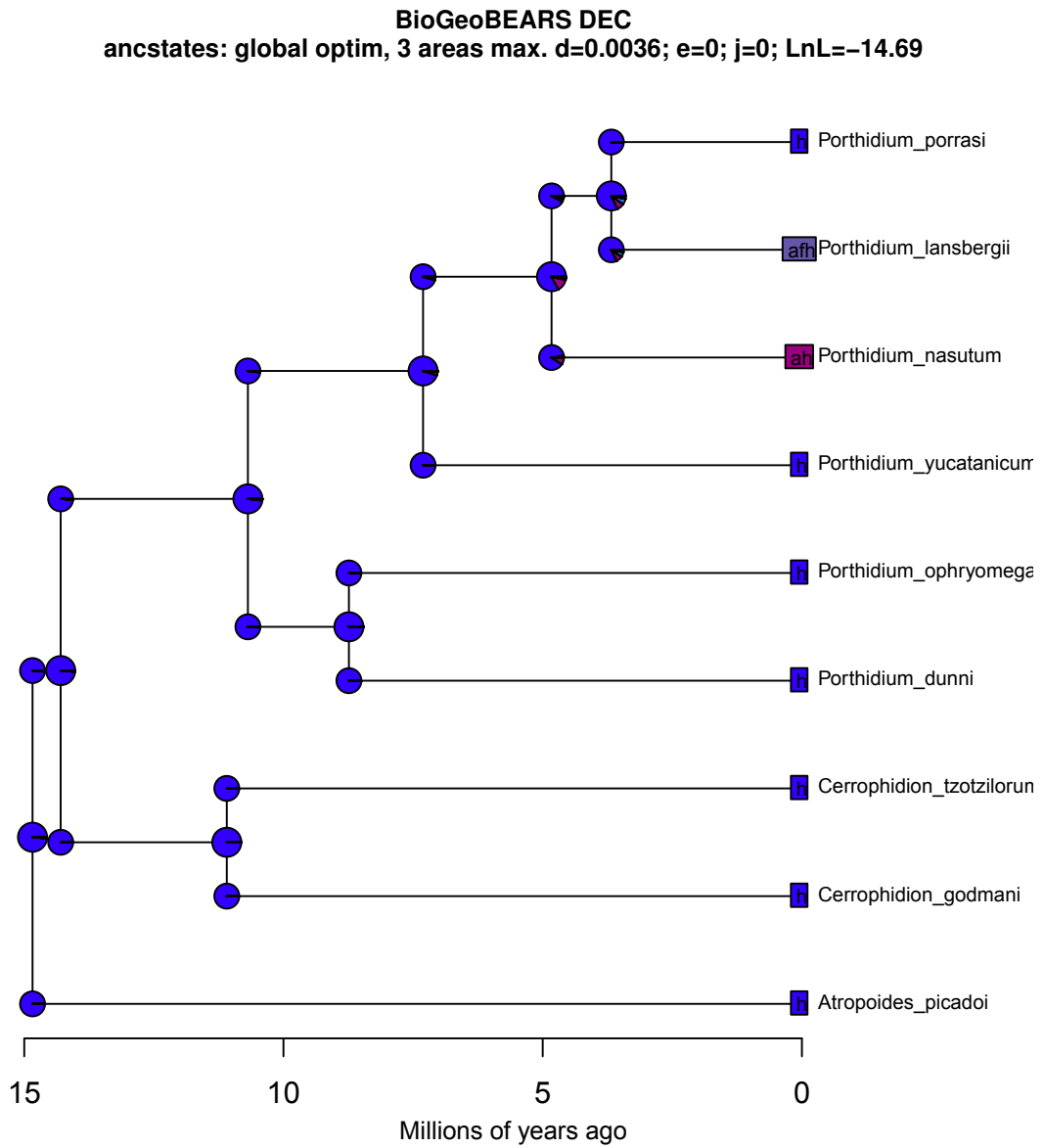


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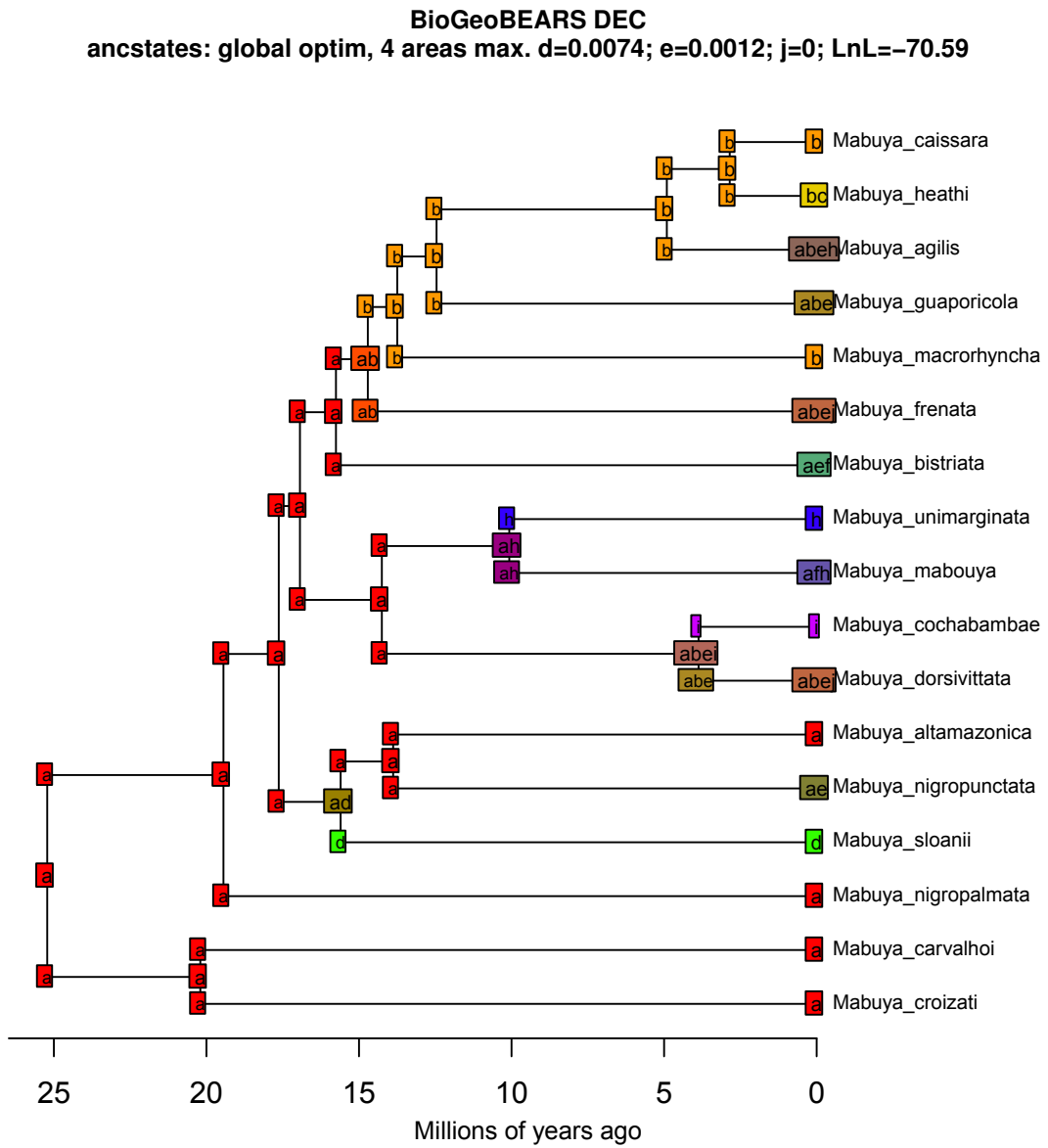


Figure S8: Clades of squamates

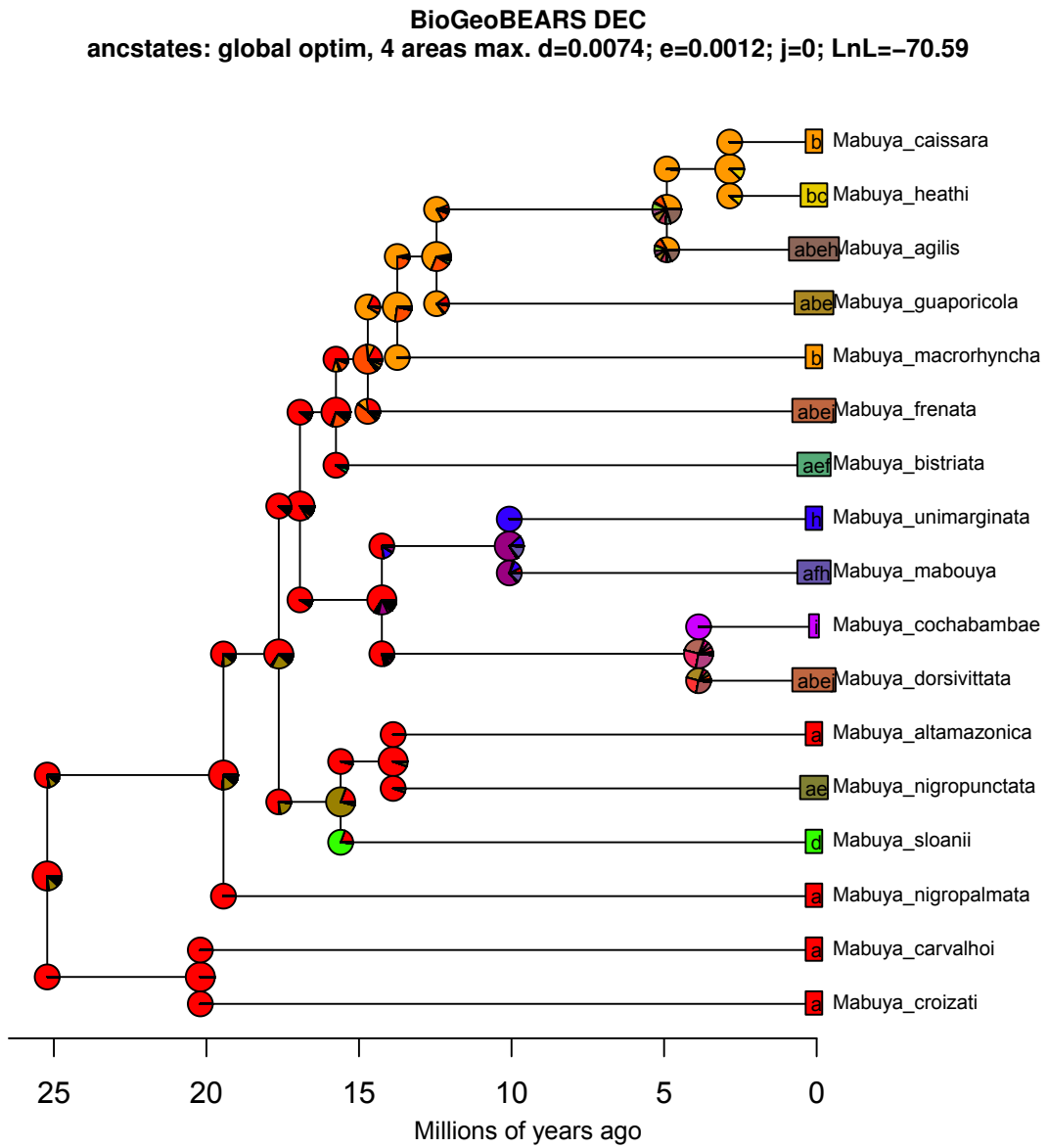


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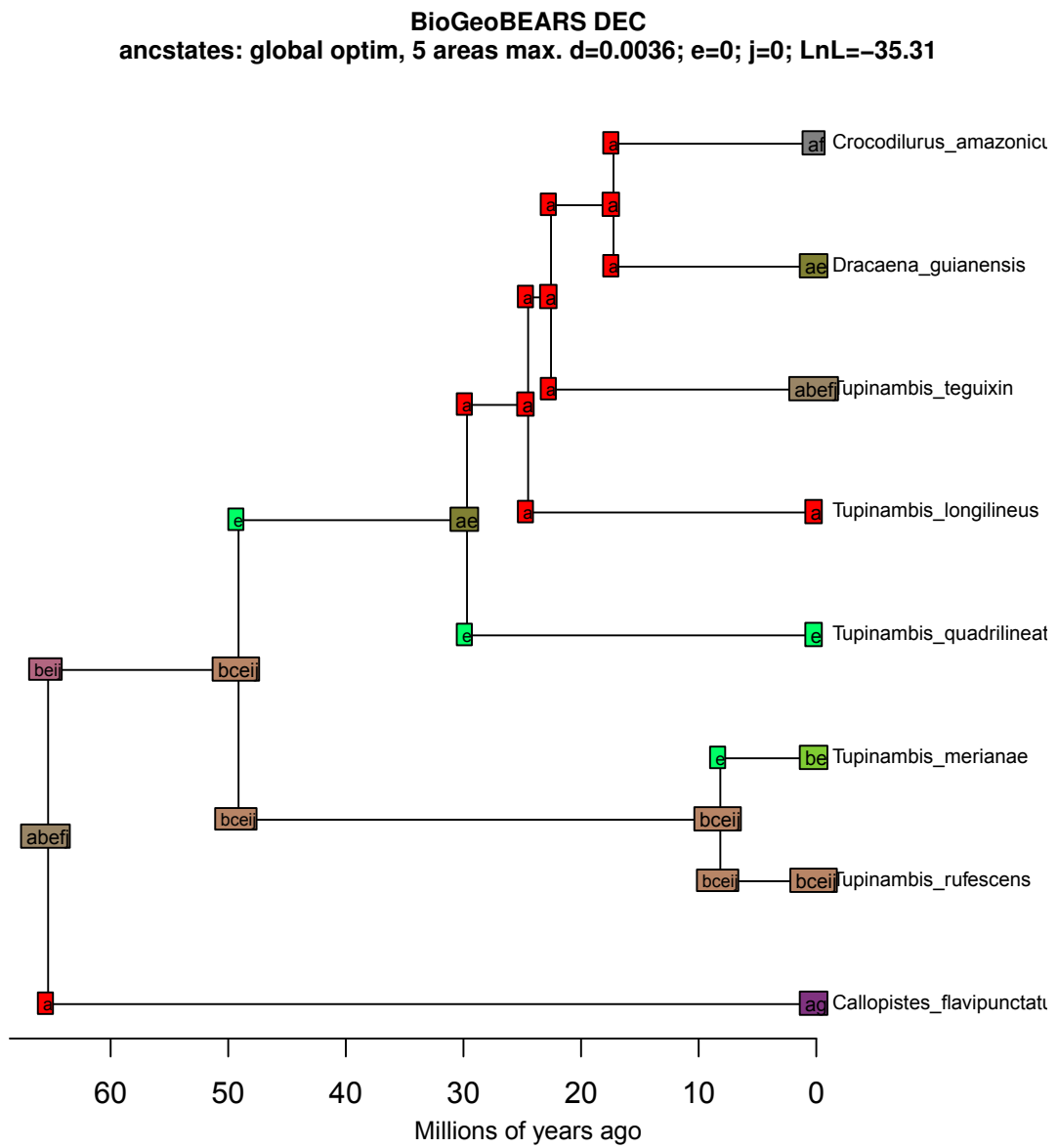


Figure S8: Clades of squamates

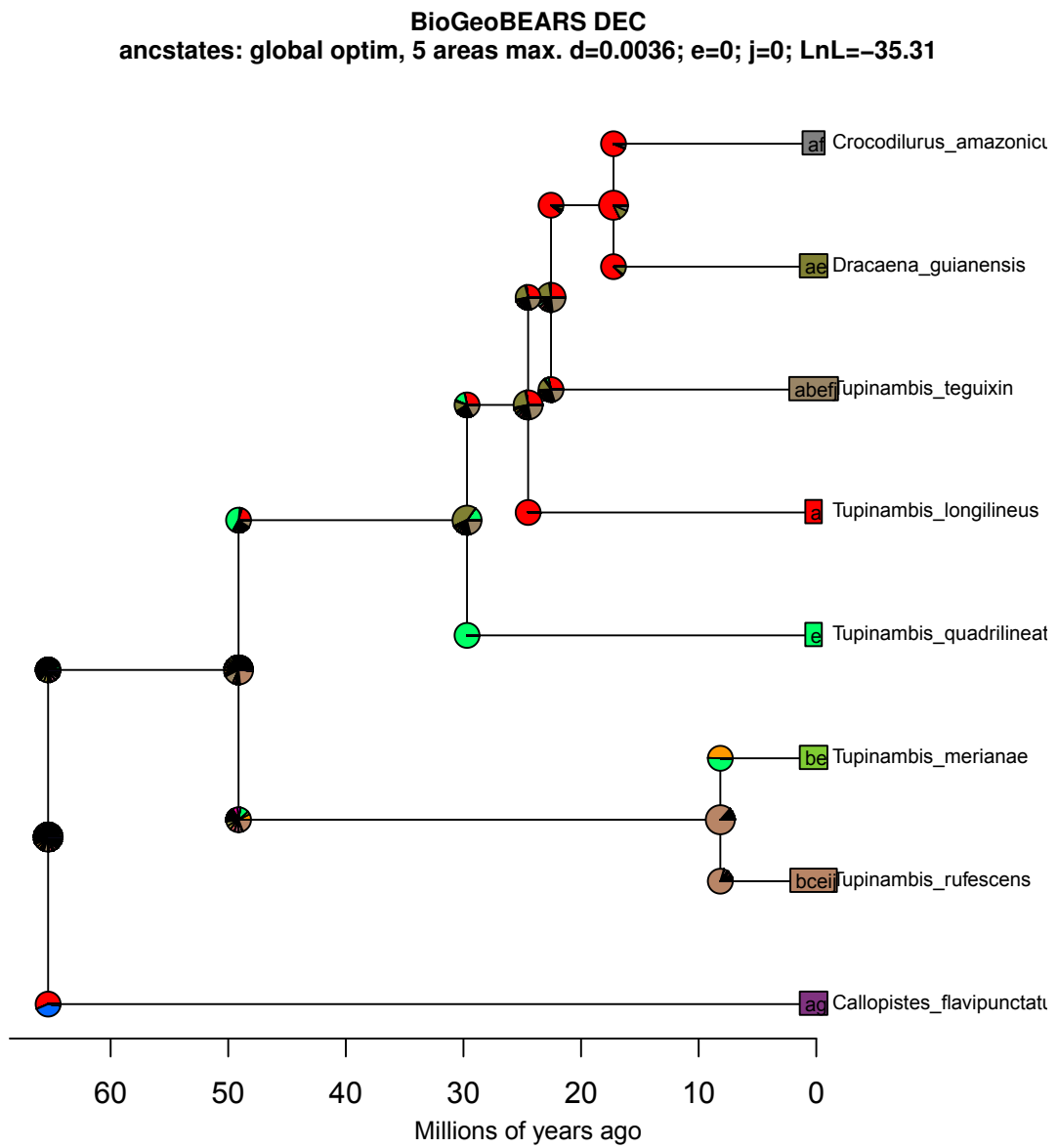


Figure S8: Clades of squamates

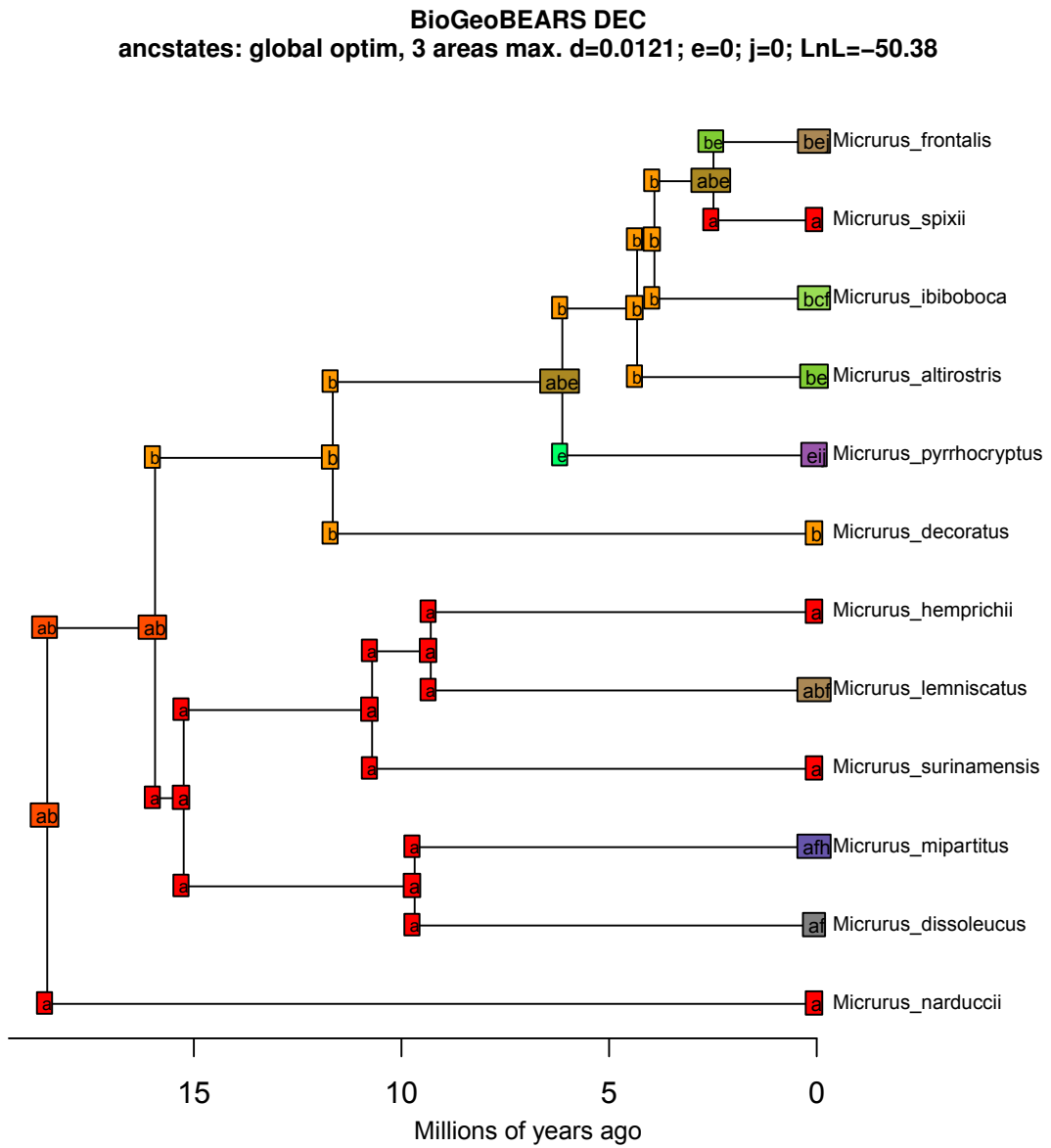


Figure S8: Clades of squamates

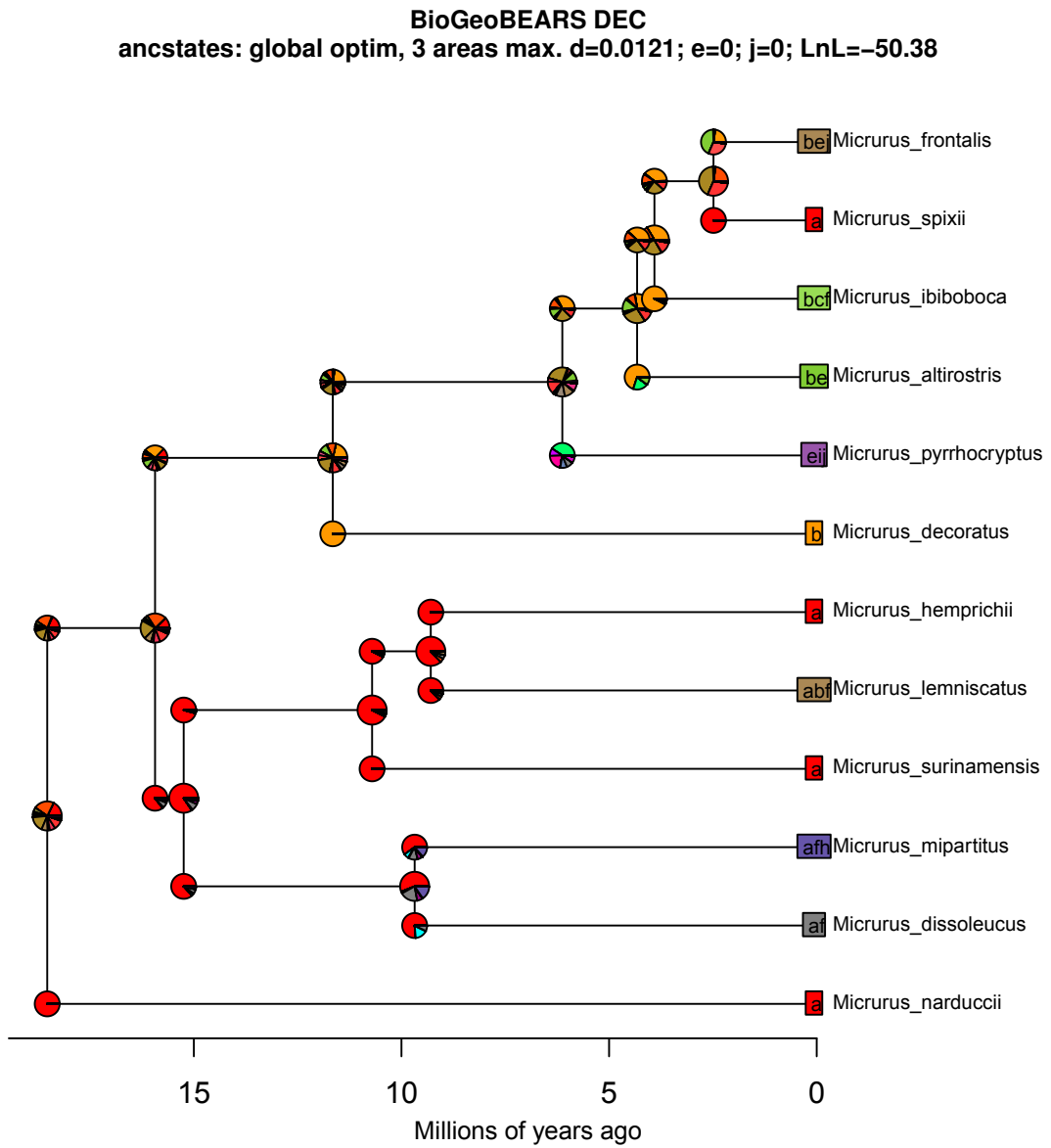


Figure S8: Clades of squamates

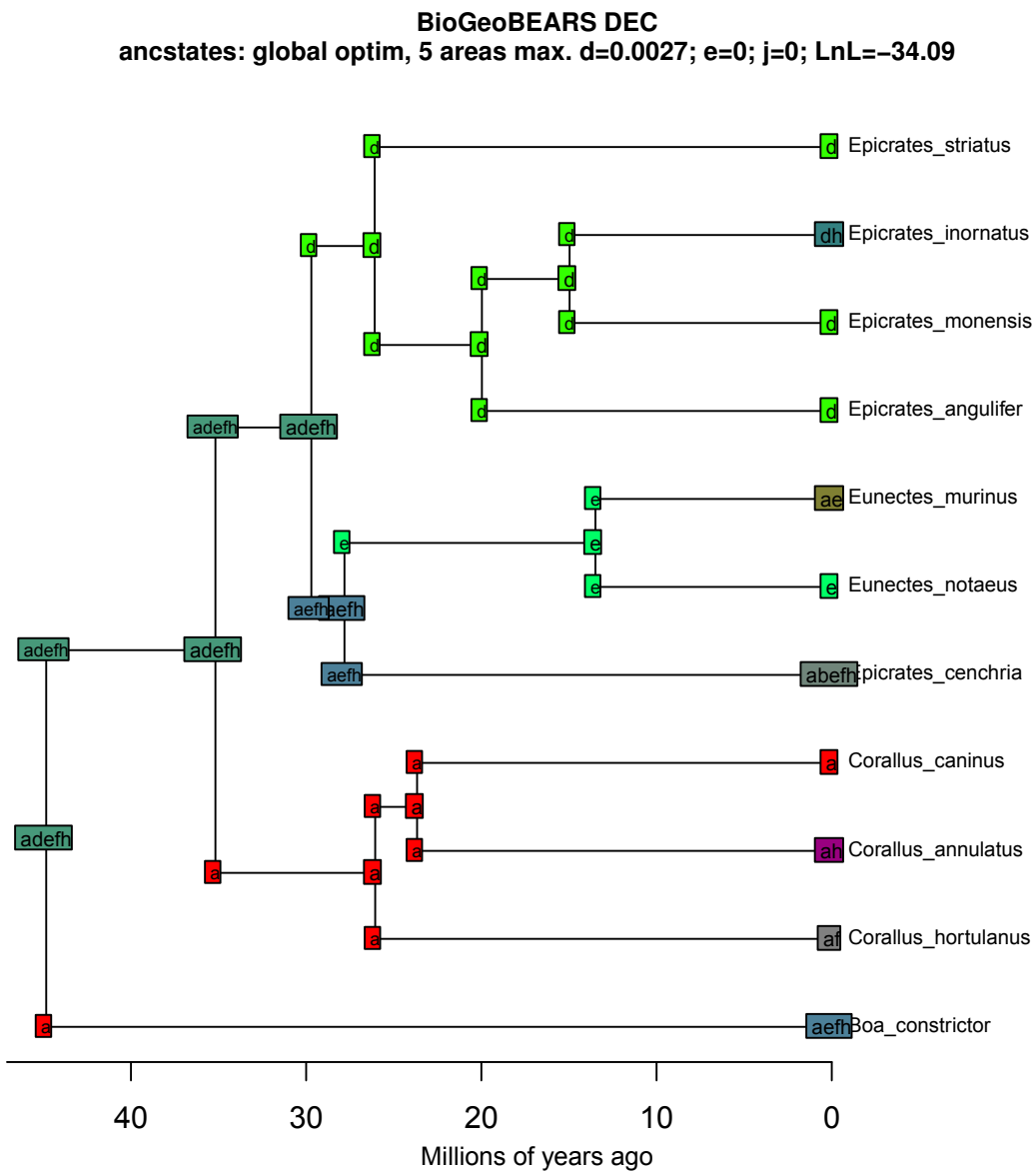


Figure S8: Clades of squamates

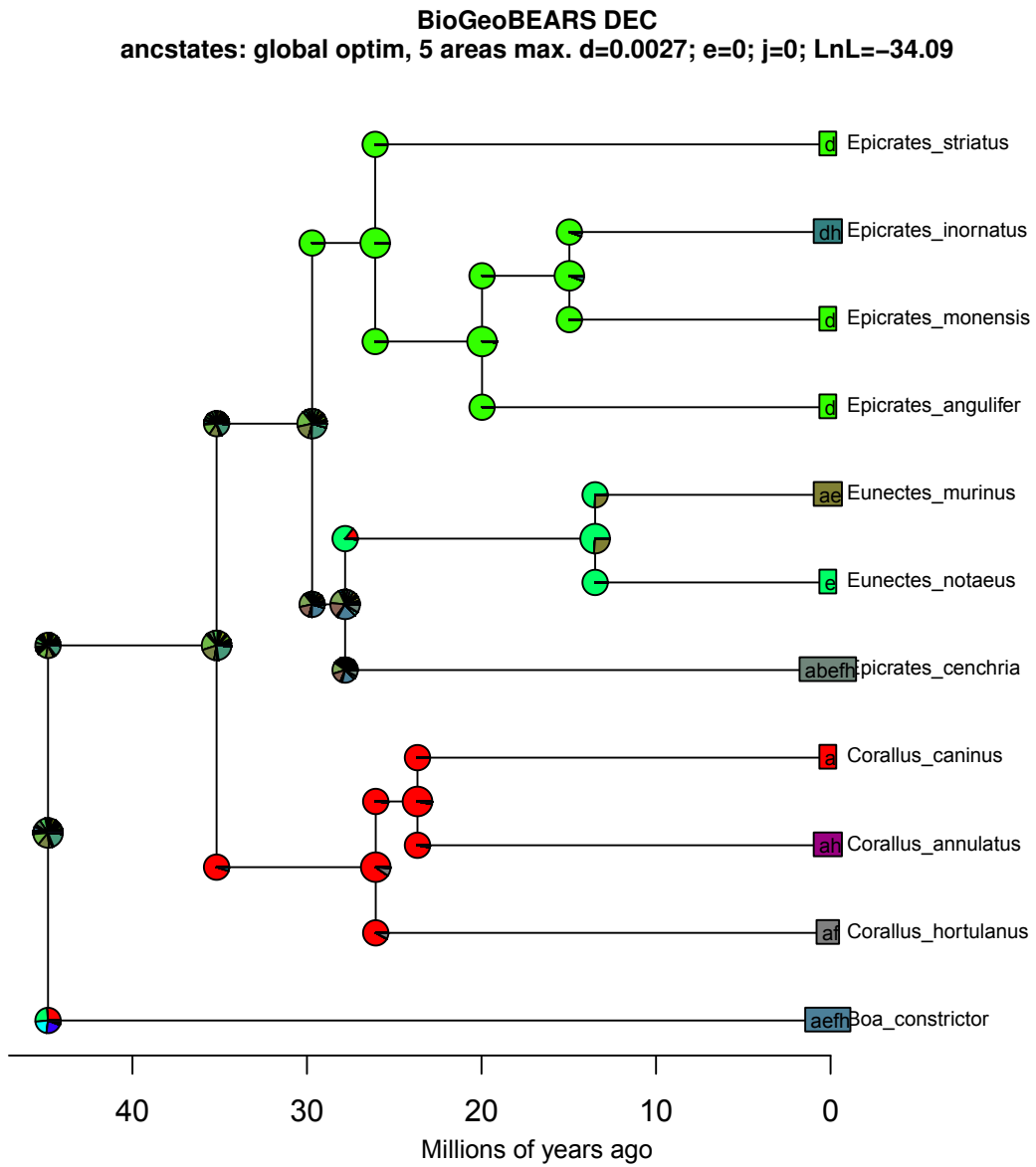


Figure S8: Clades of squamates

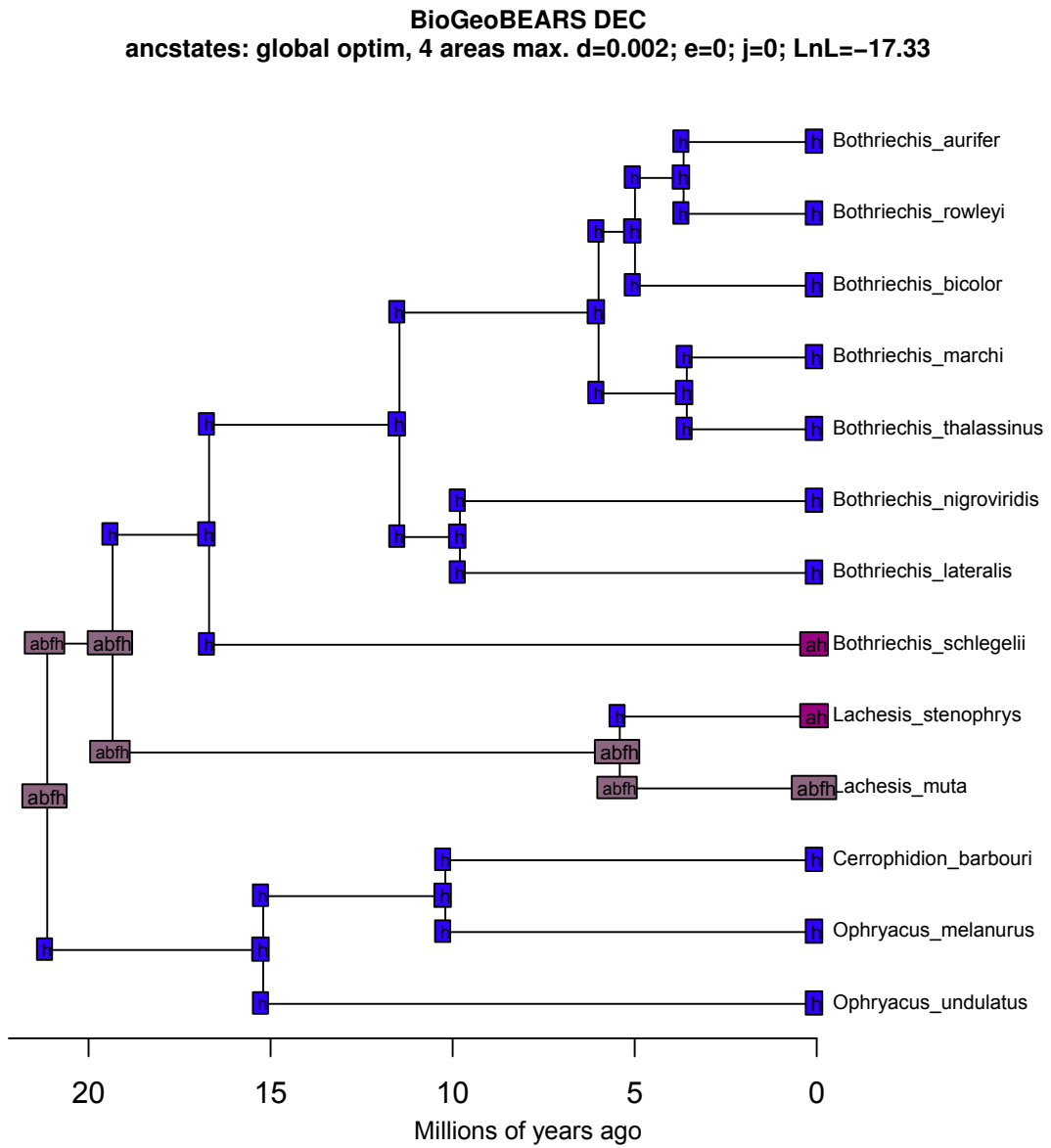


Figure S8: Clades of squamates

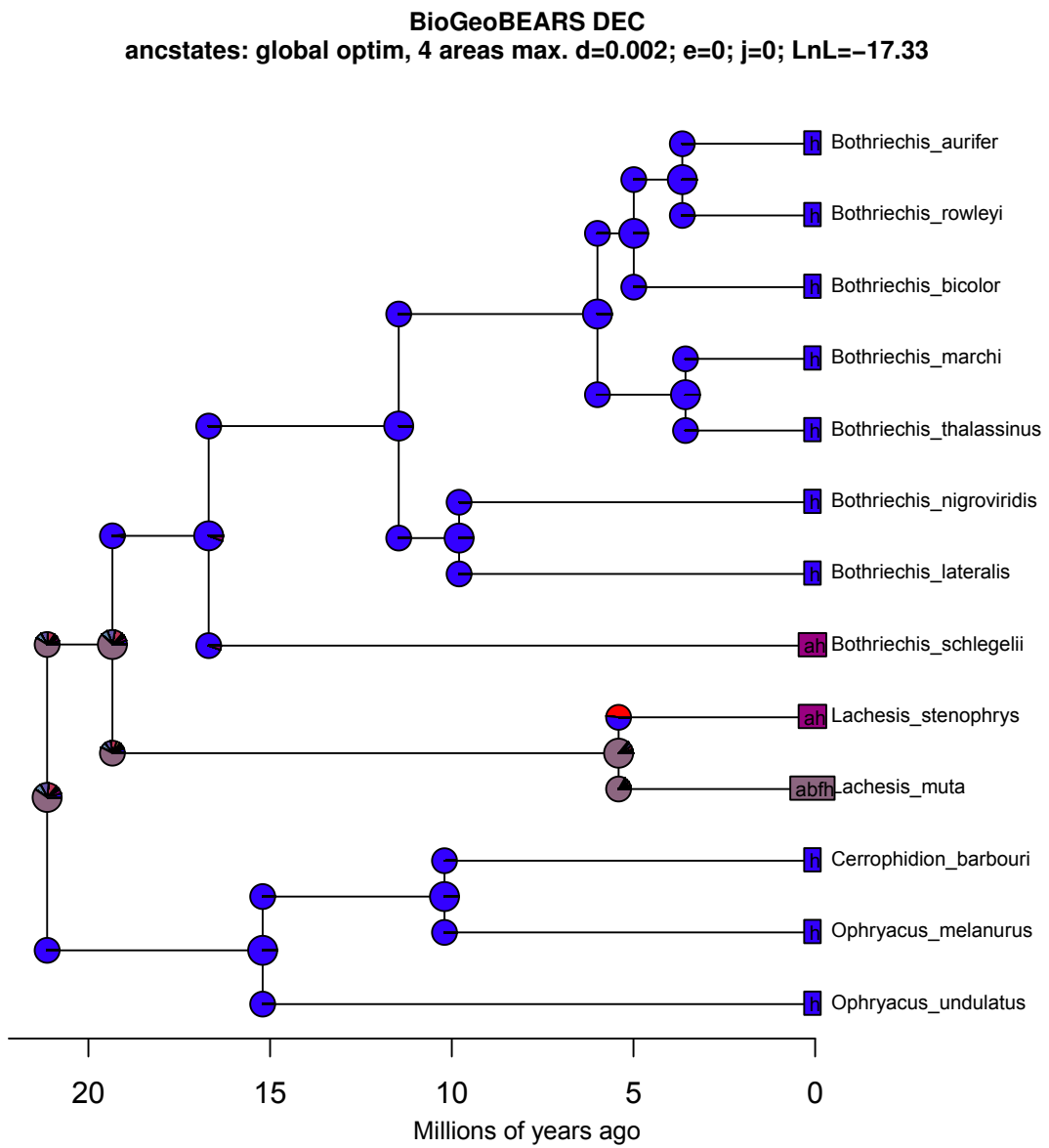


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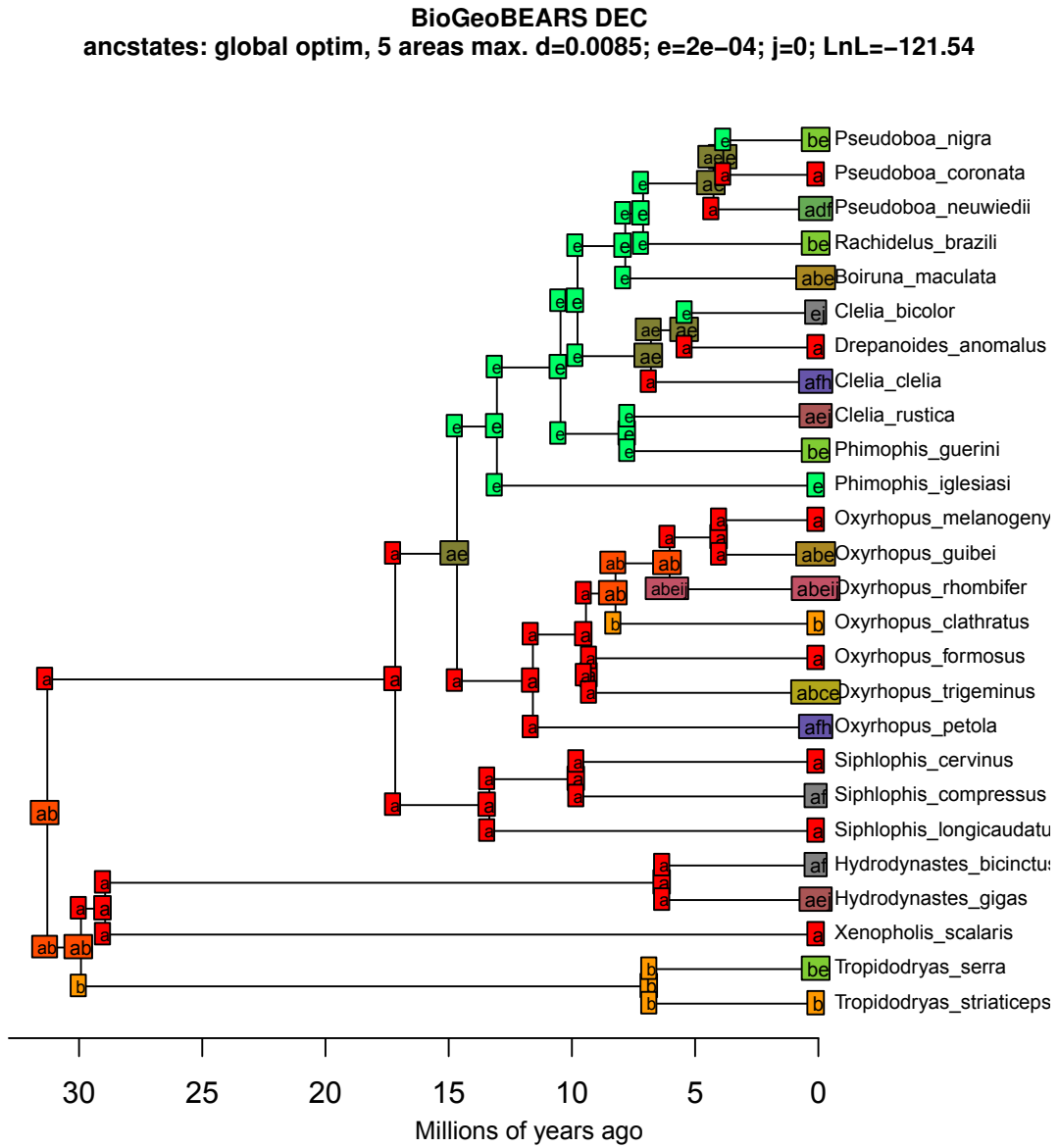


Figure S8: Clades of squamates

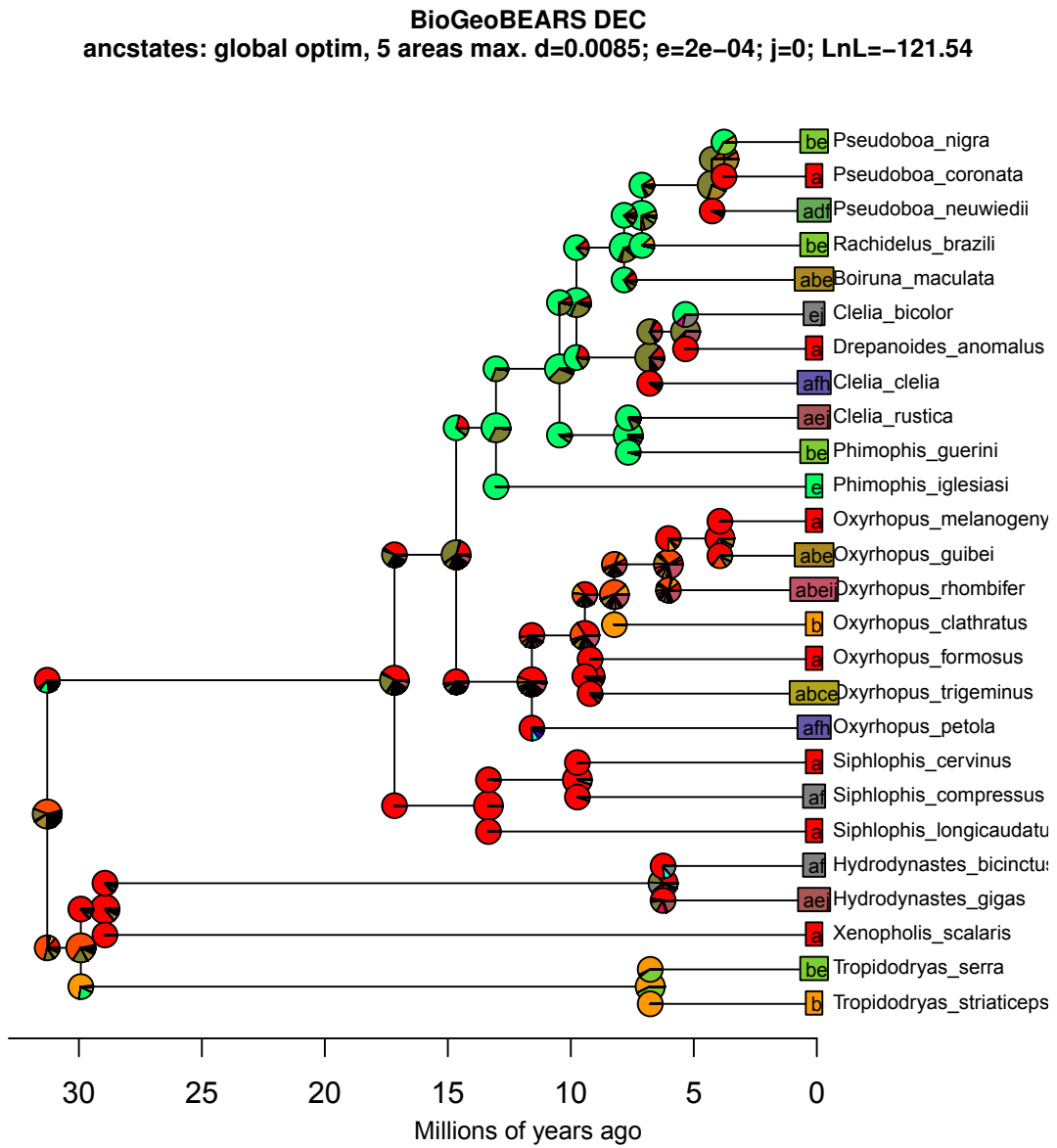


Figure S8: Clades of squamates

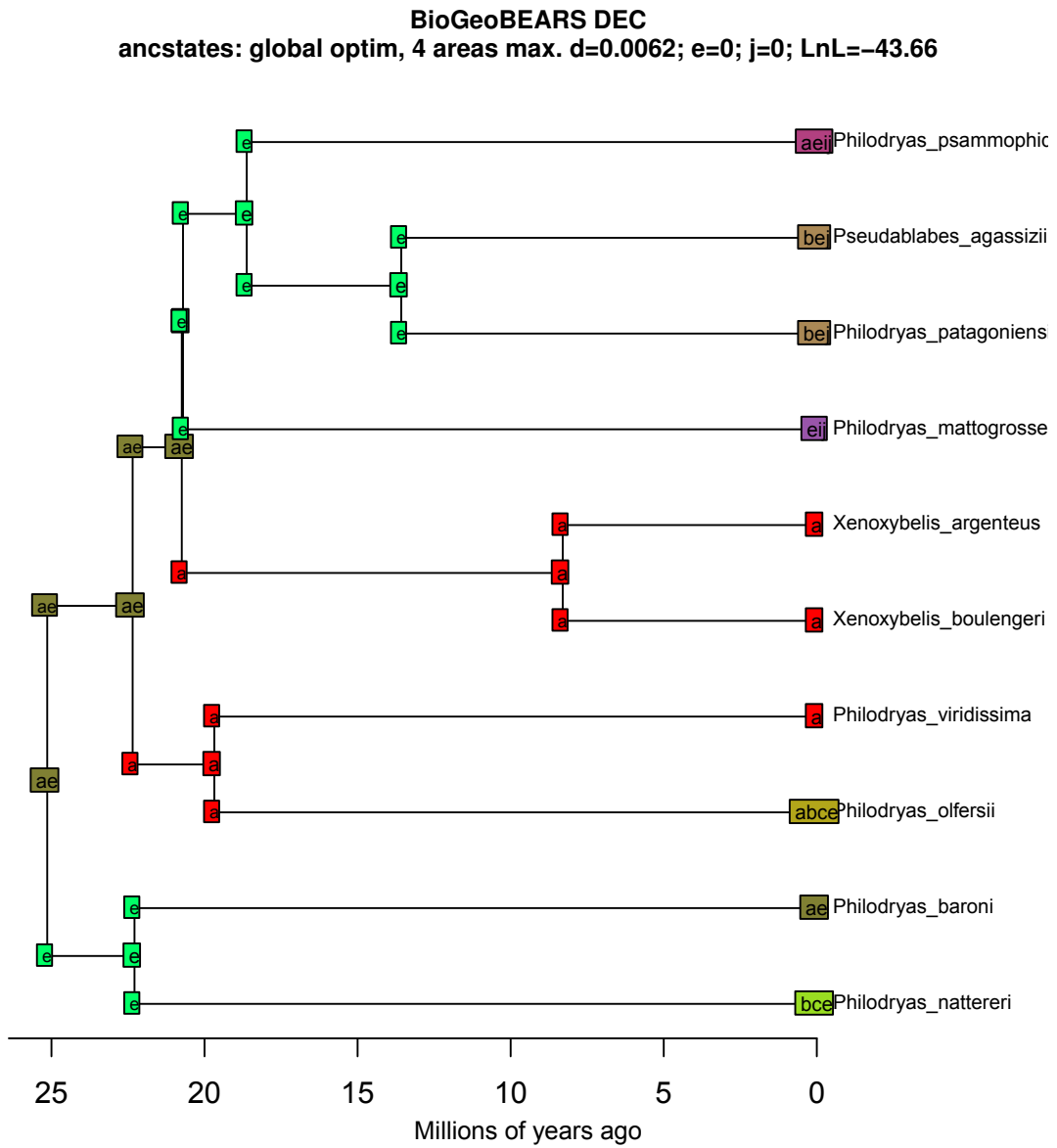


Figure S8: Clades of squamates

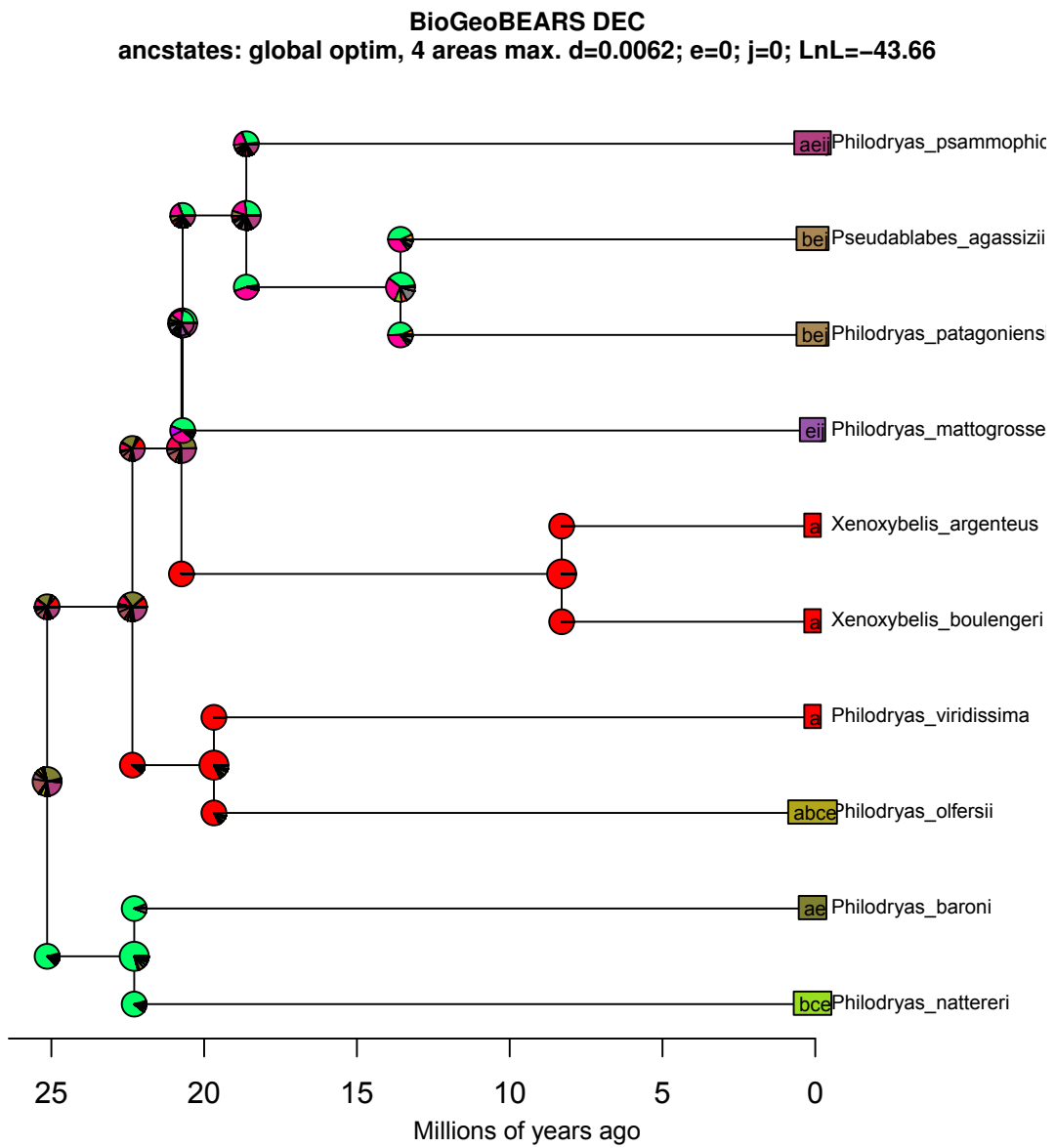


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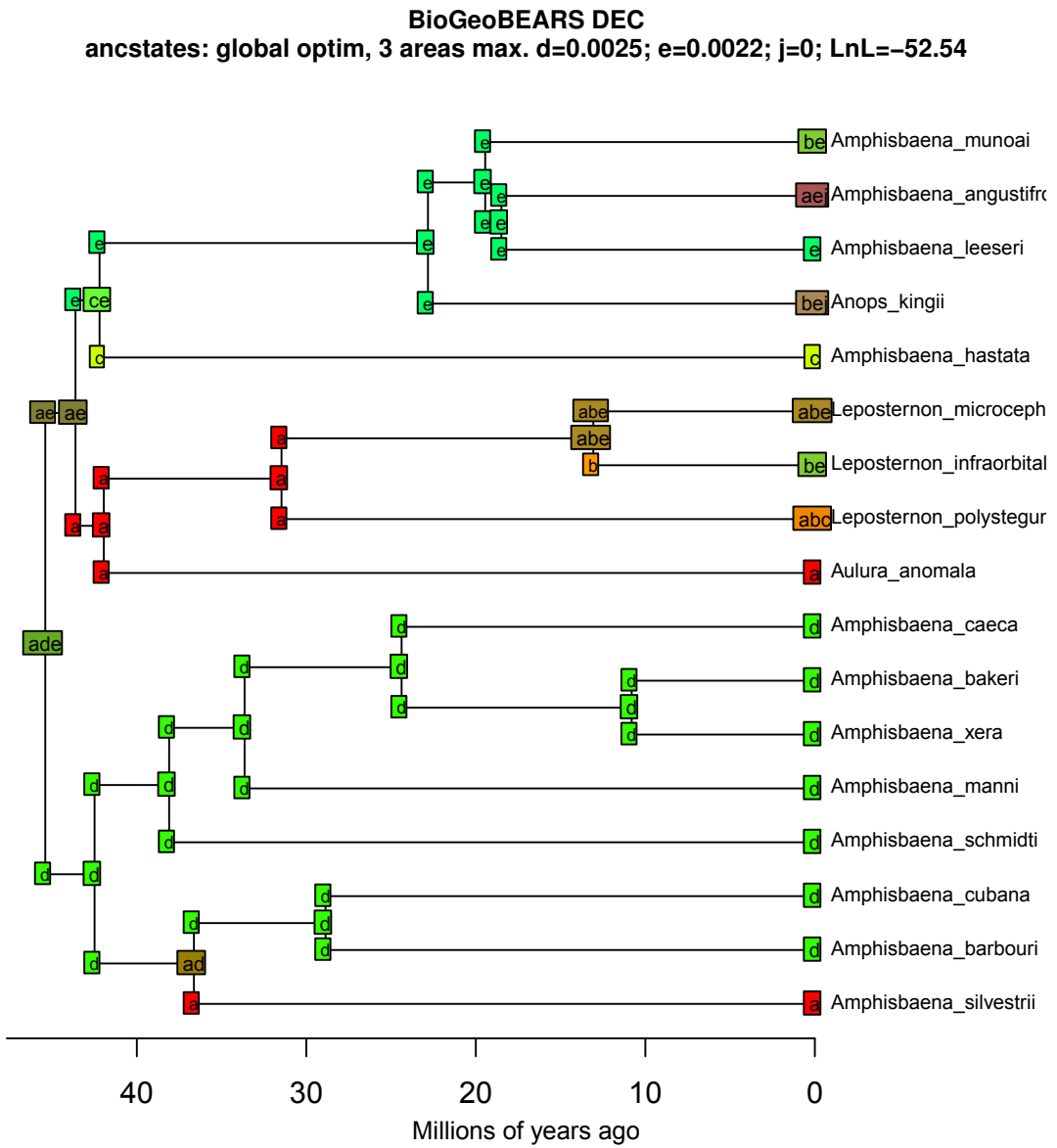


Figure S8: Clades of squamates

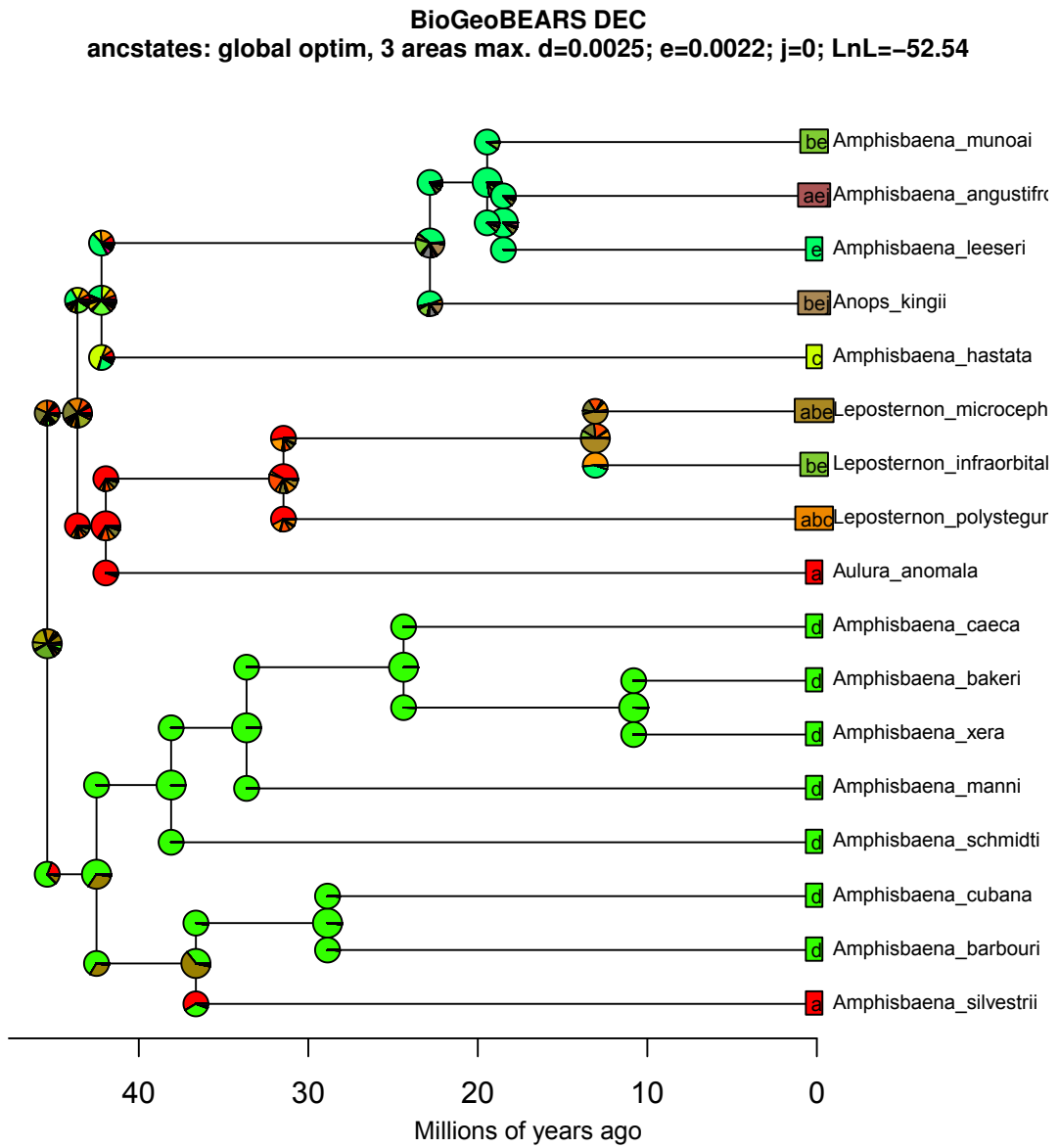


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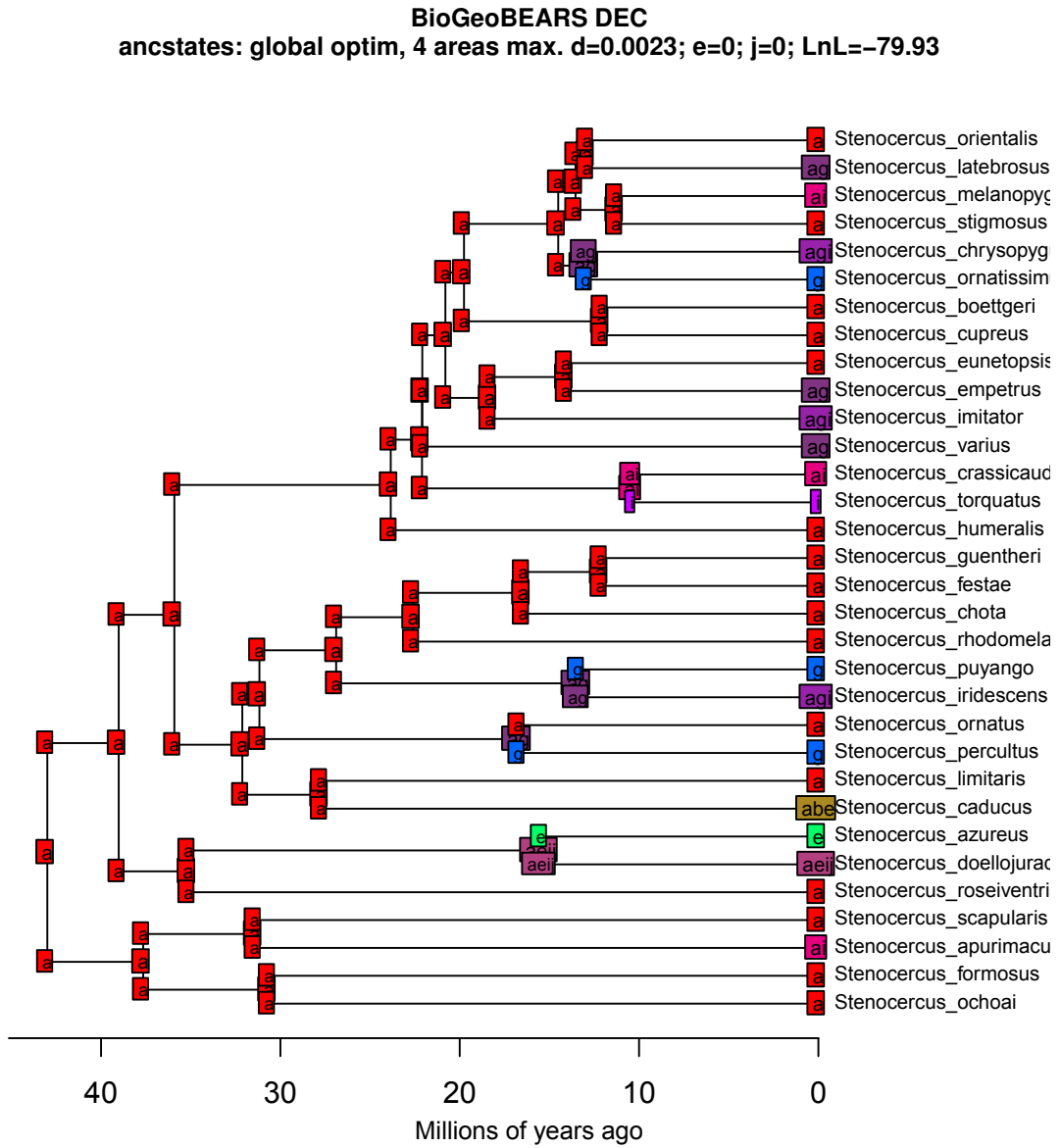


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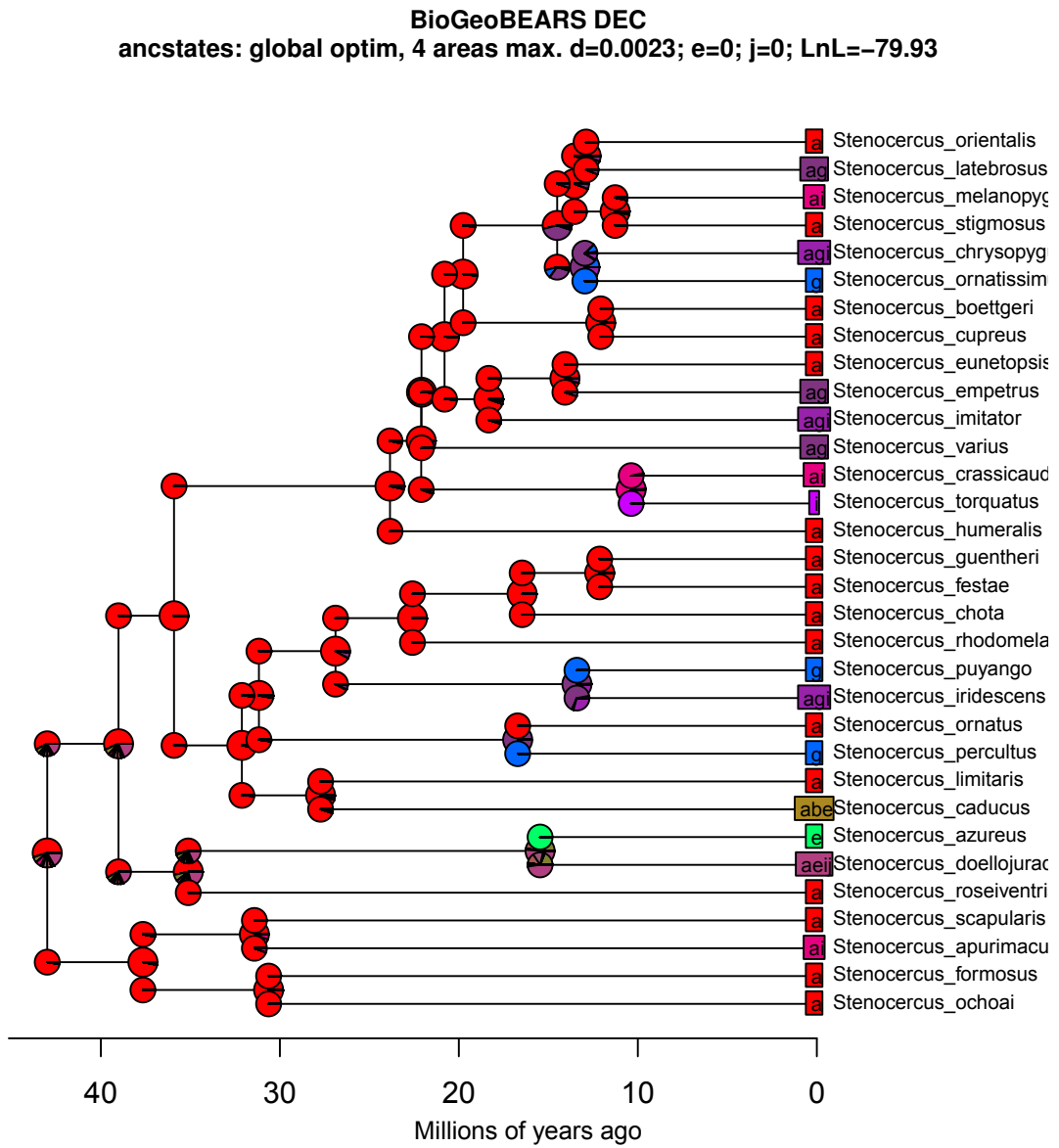


Figure S8: Clades of squamates

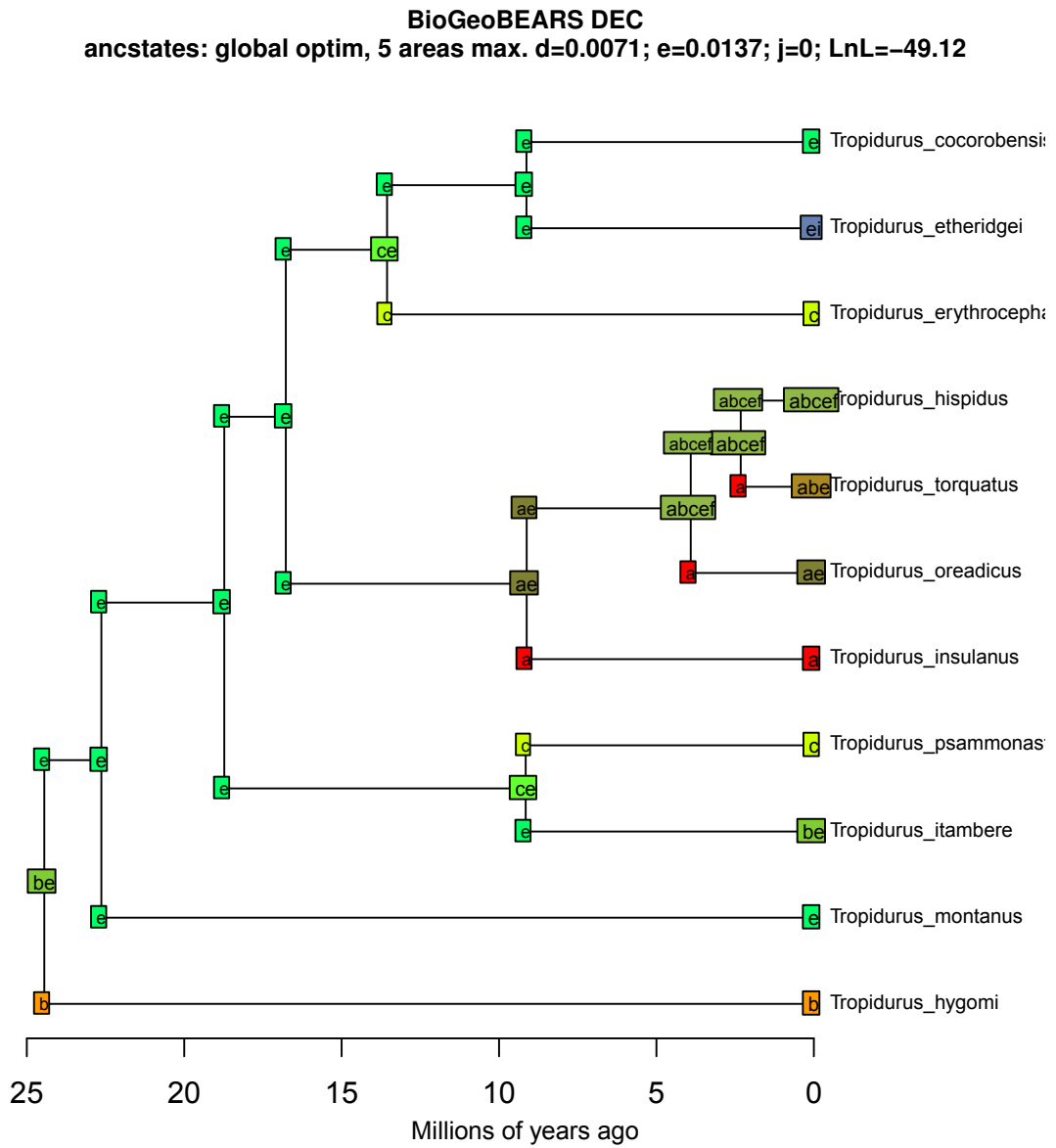


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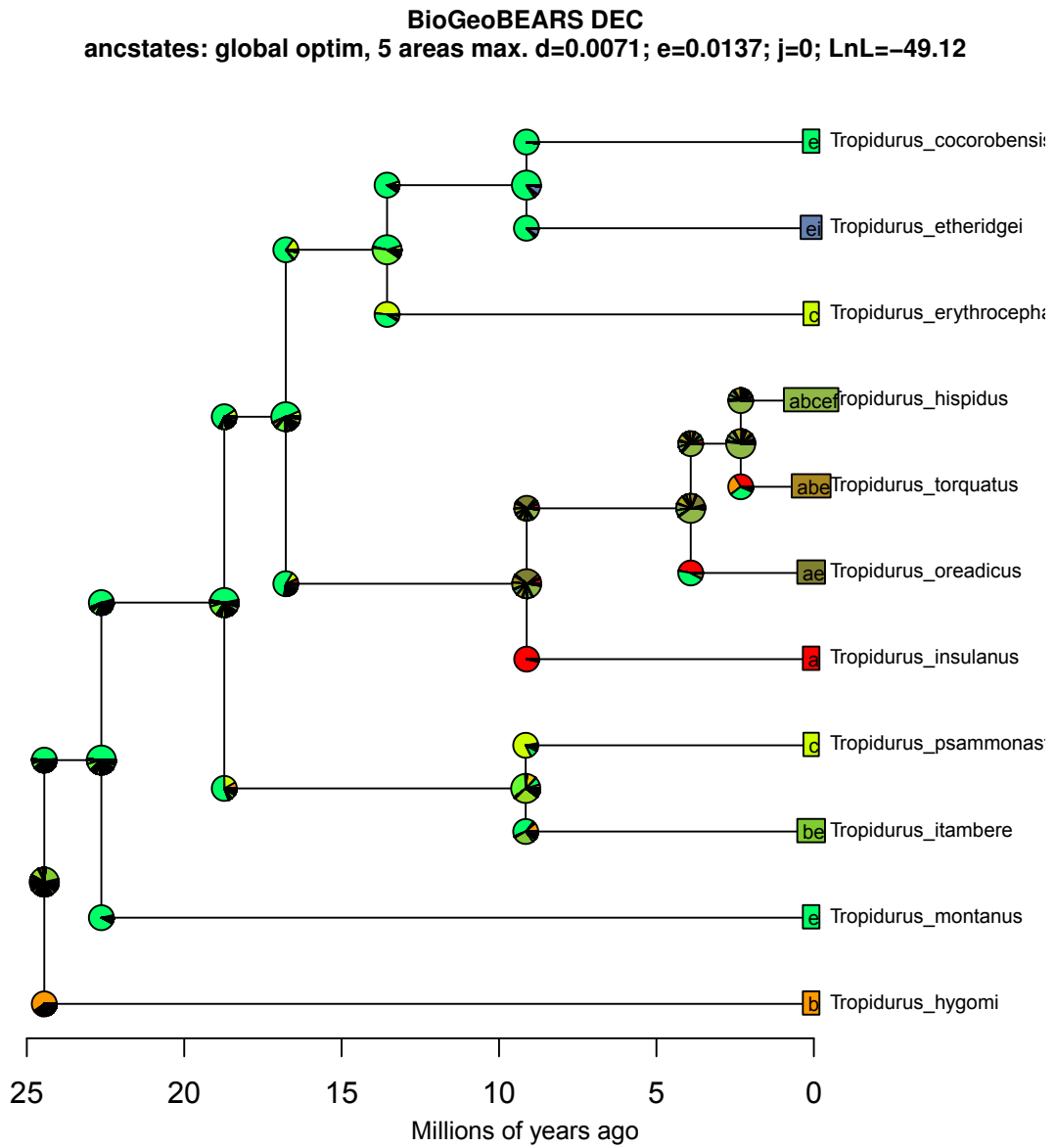


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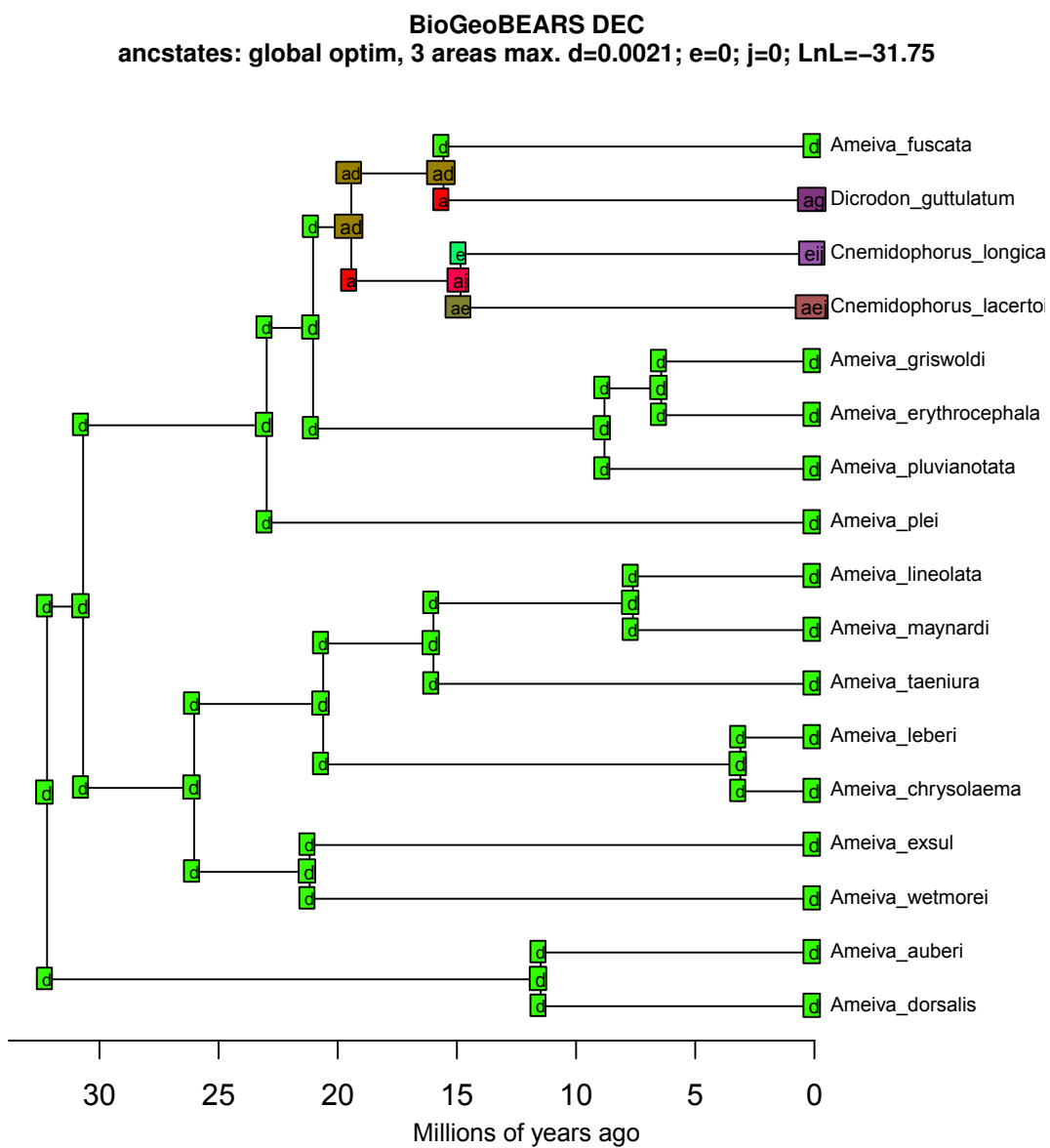


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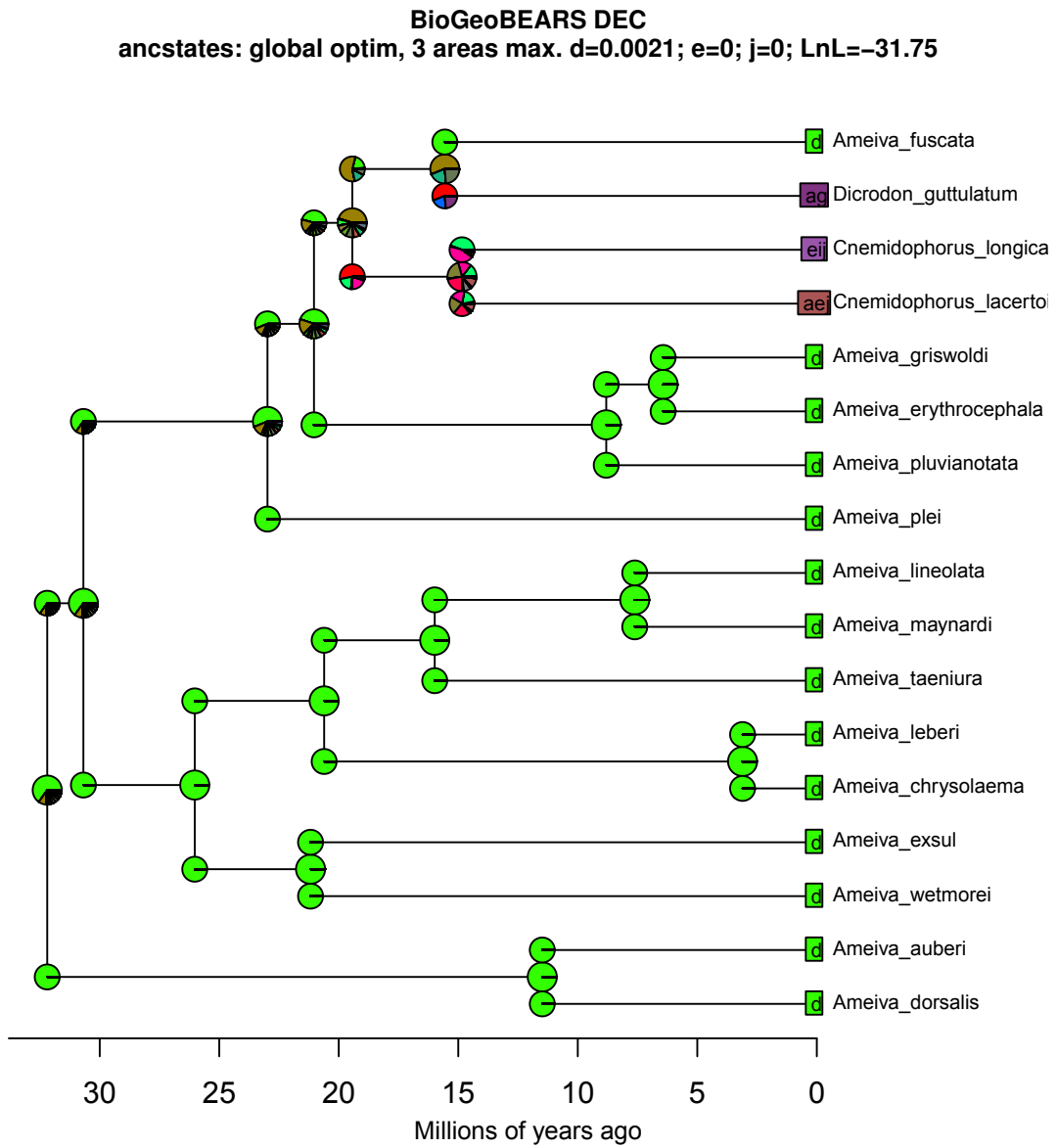


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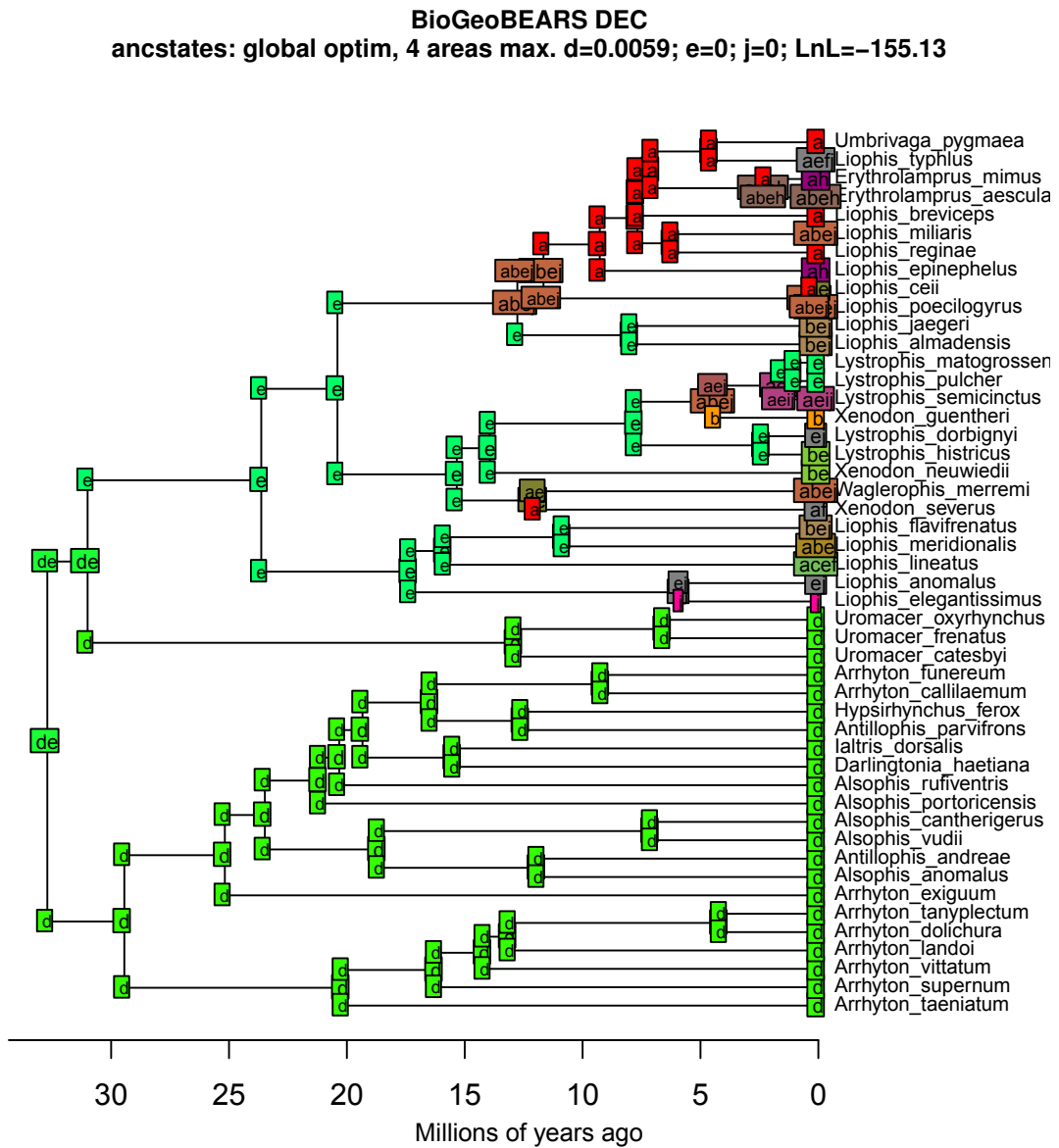


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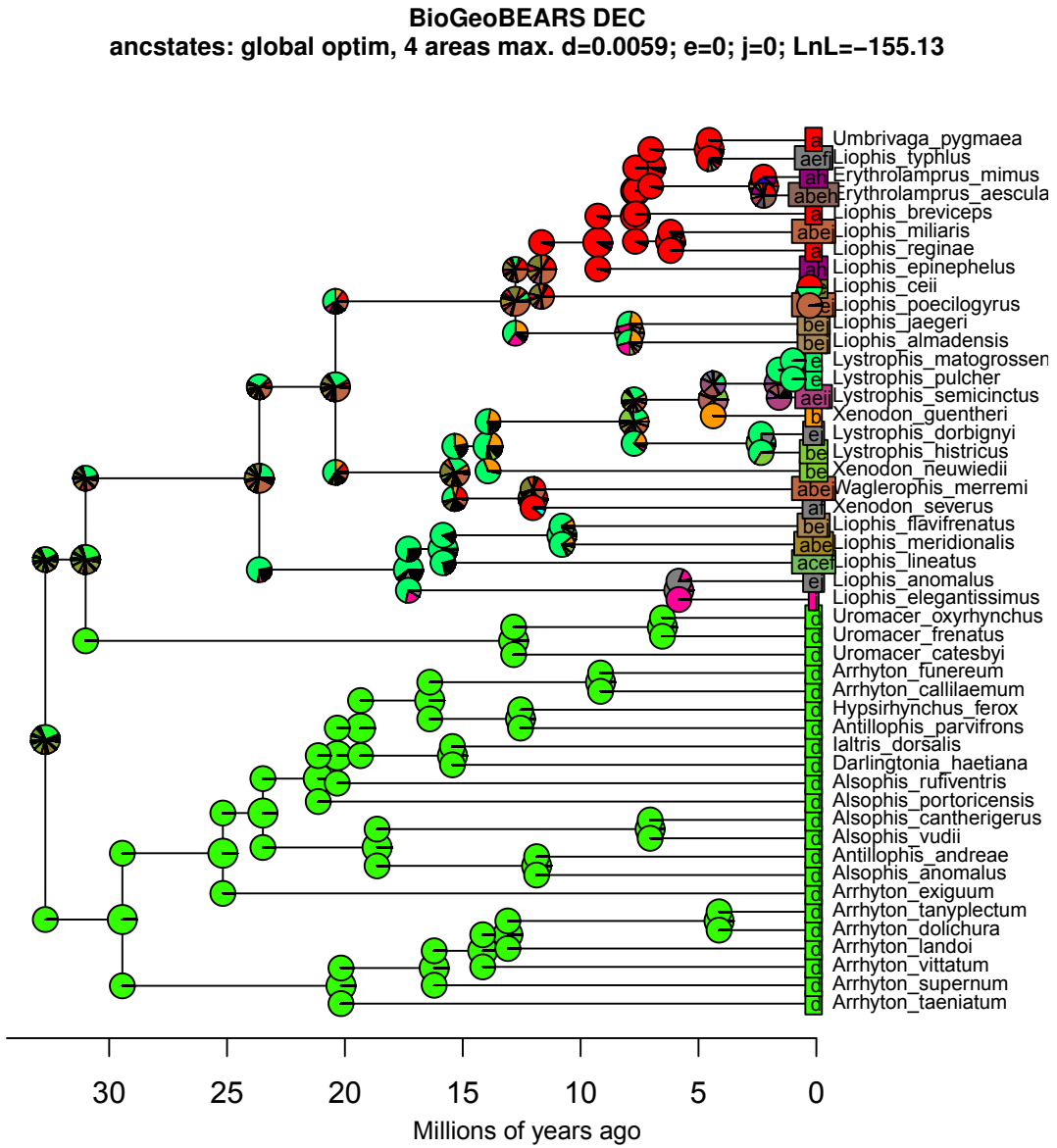


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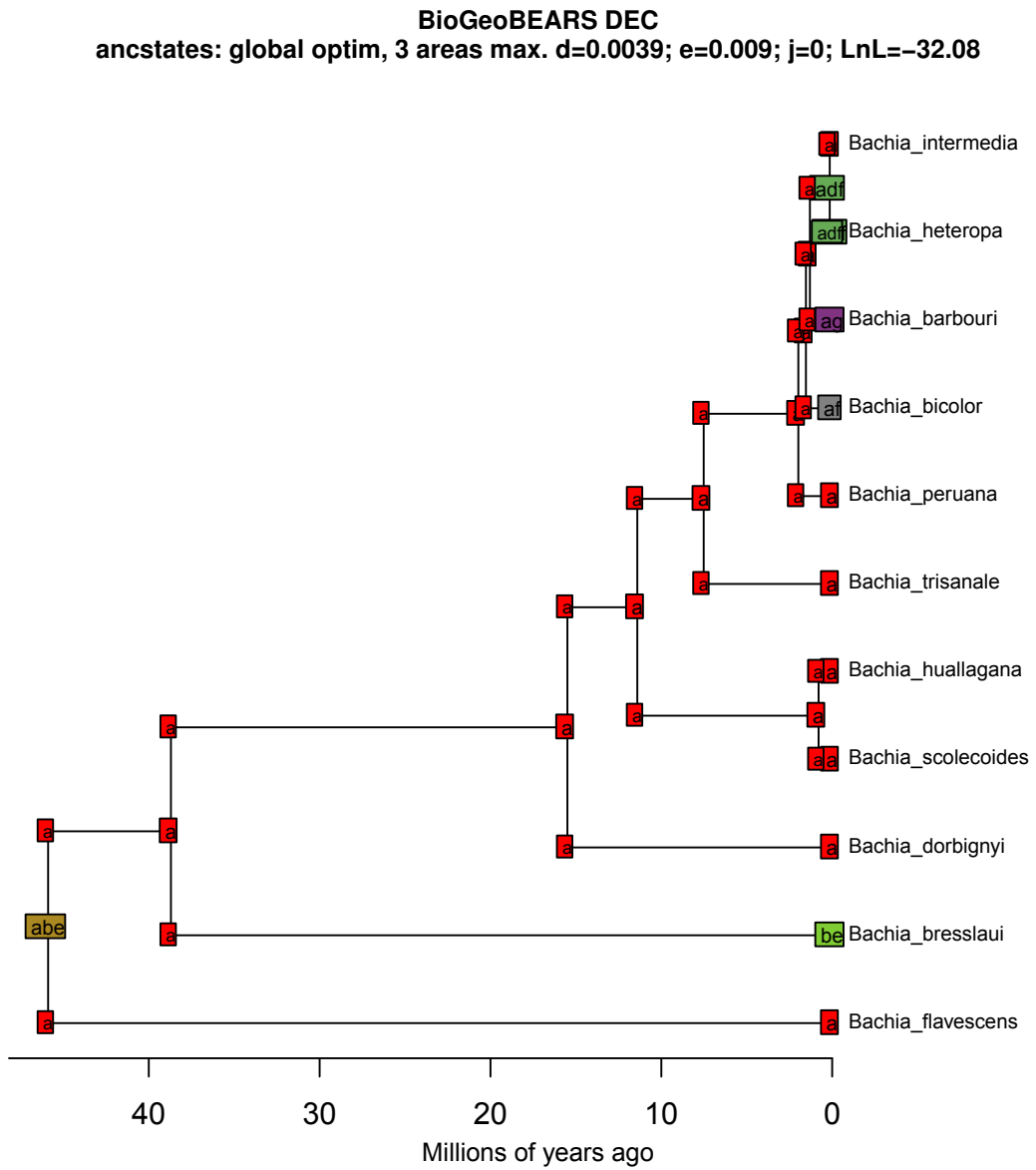


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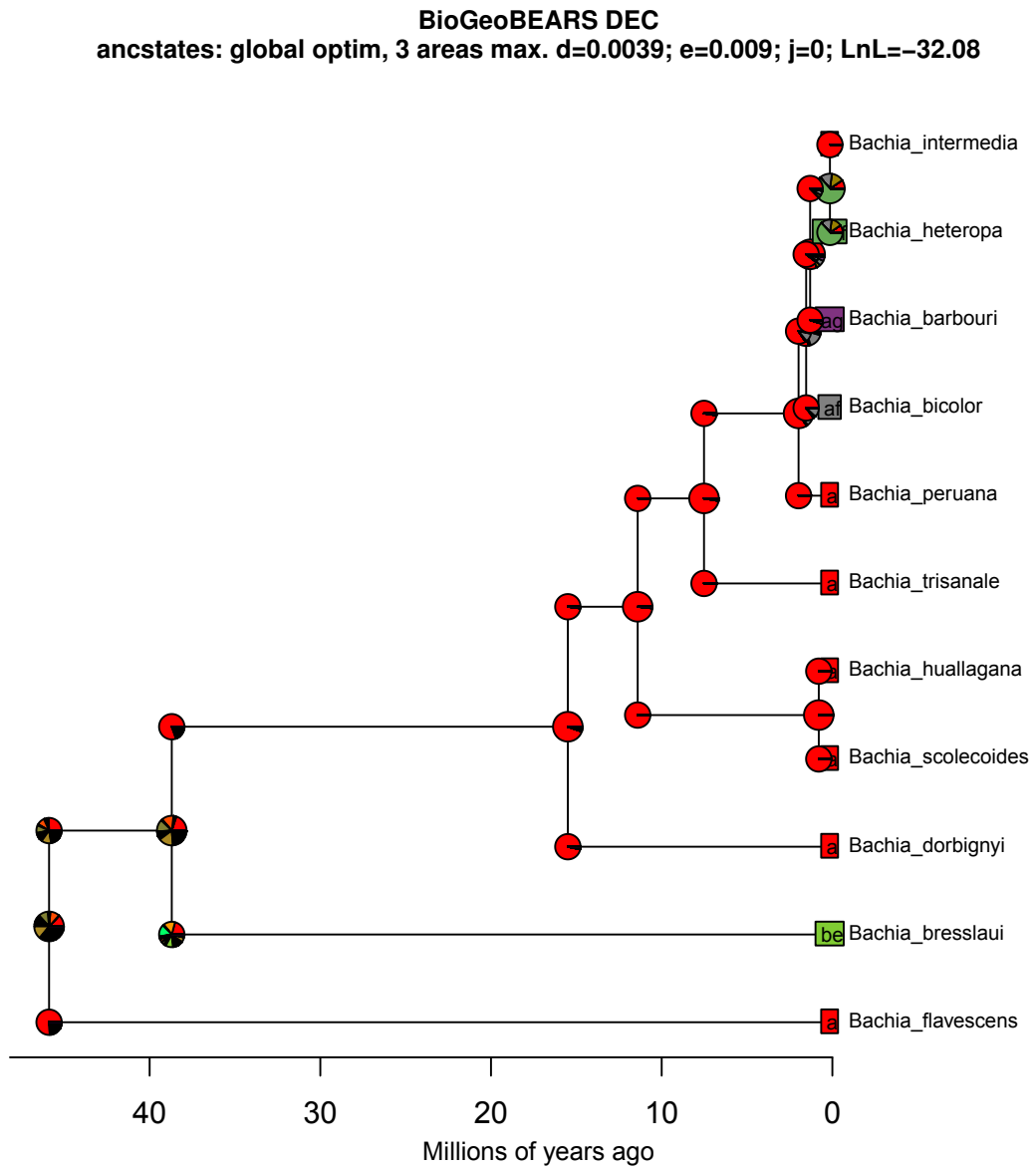


Figure S8: Clades of squamates

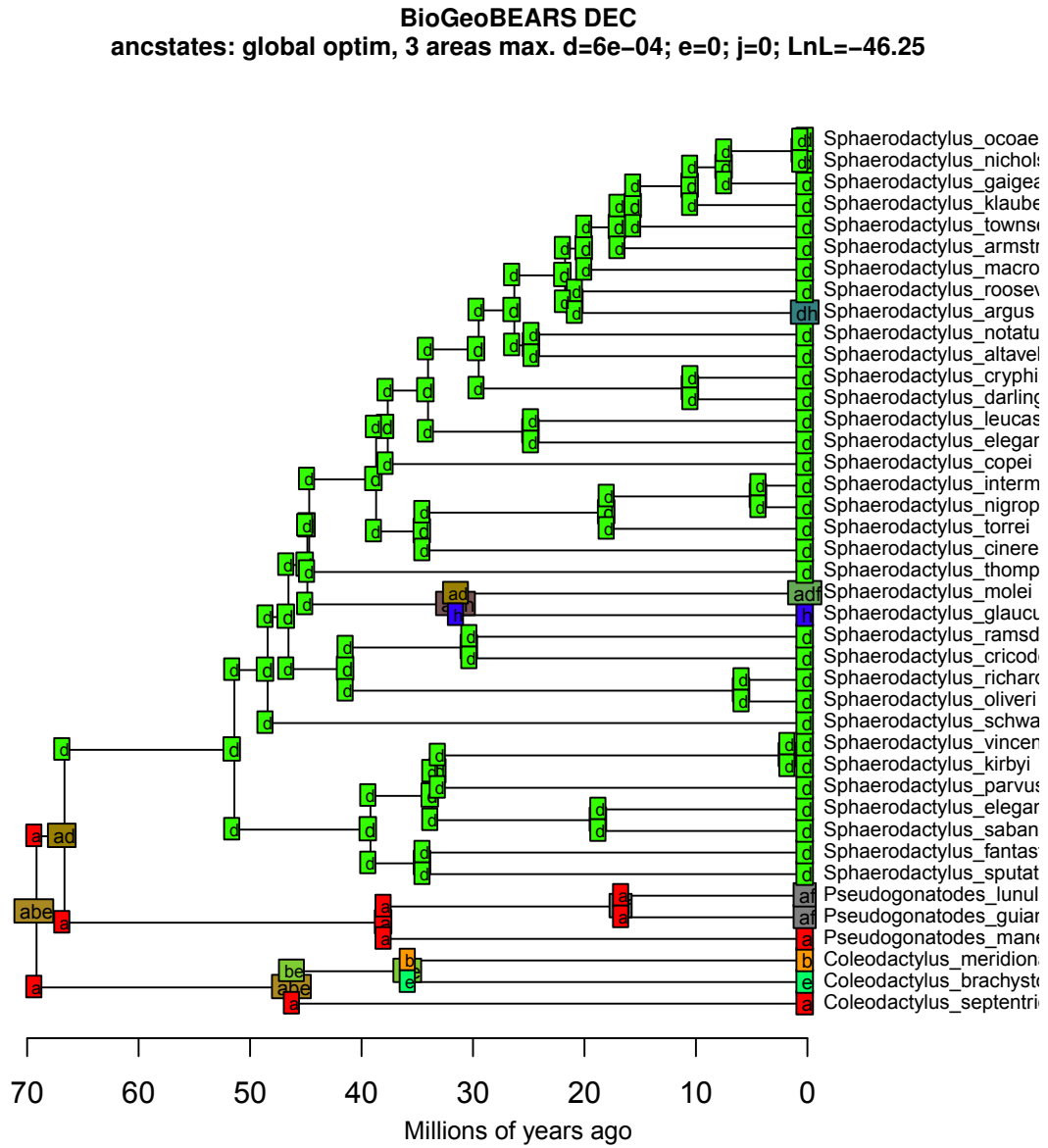


Figure S8: Clades of squamates

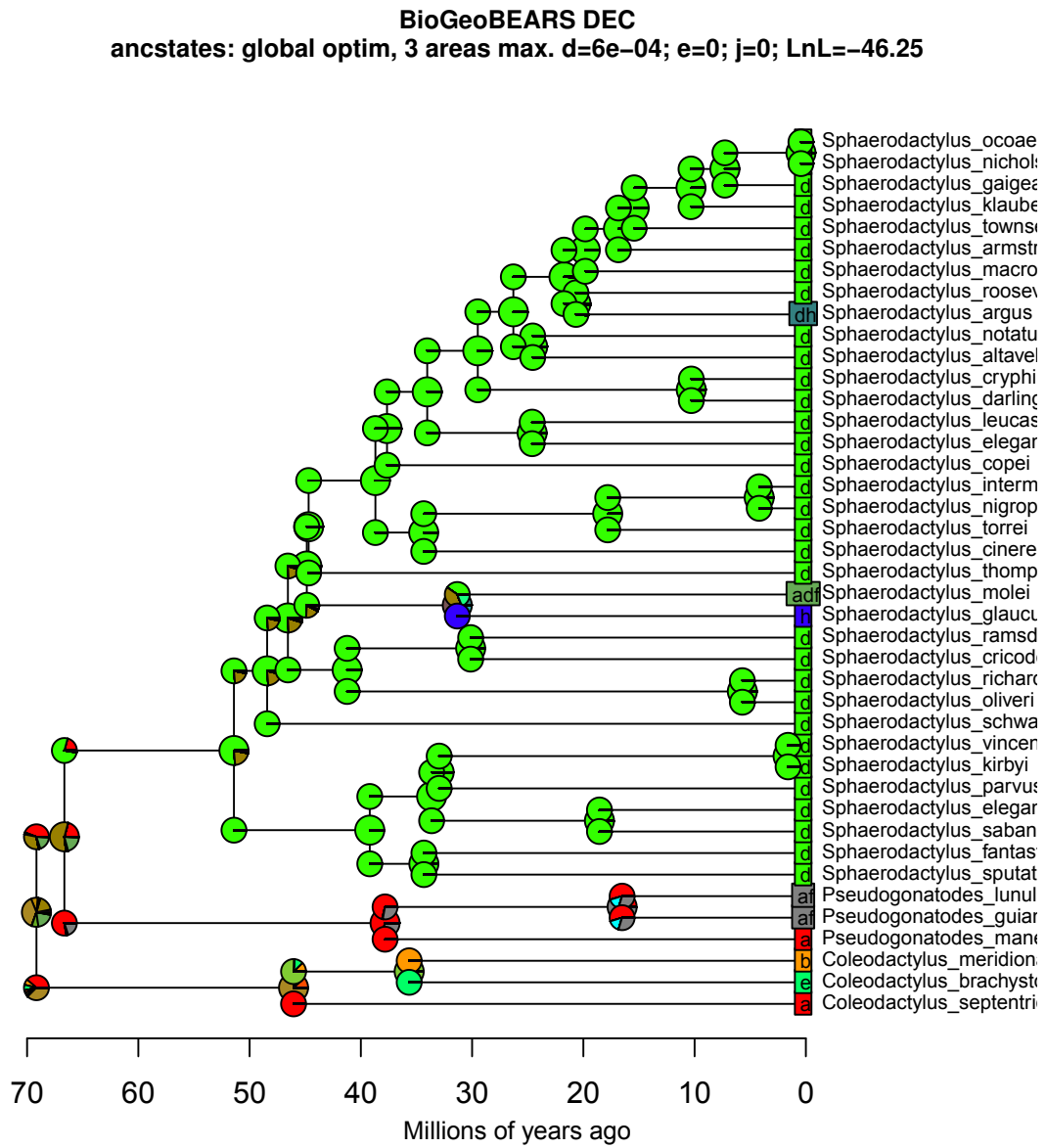


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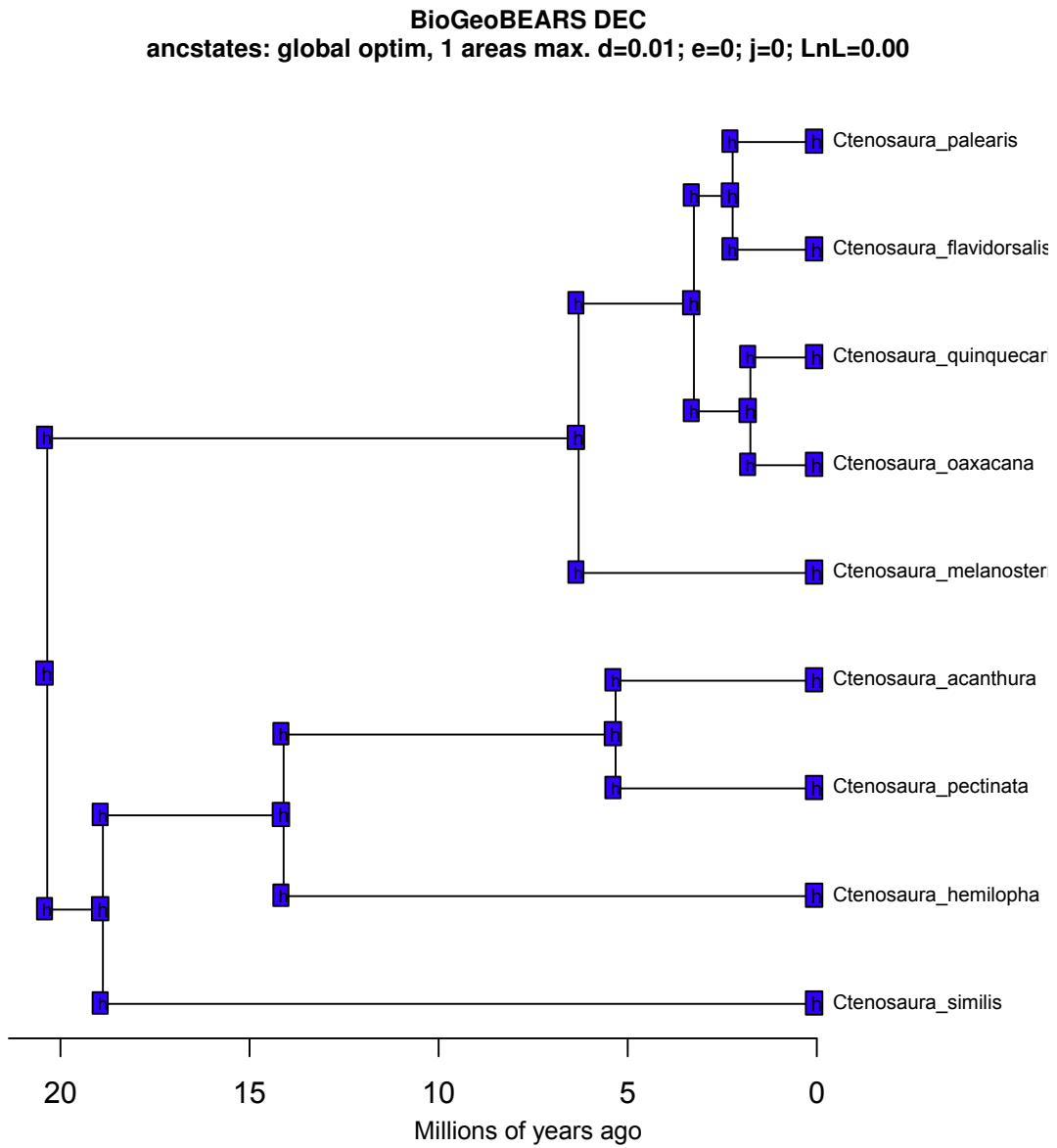


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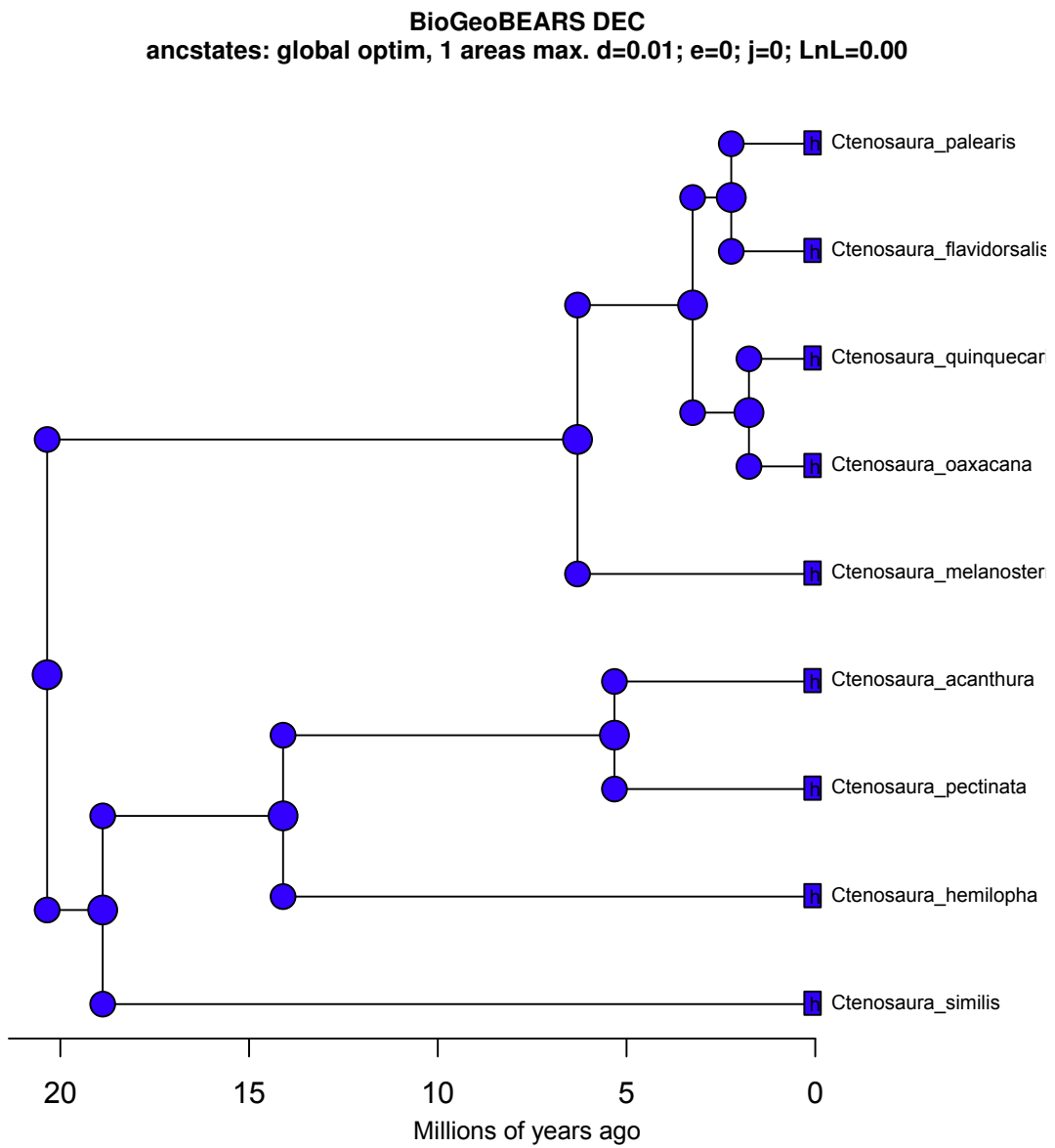


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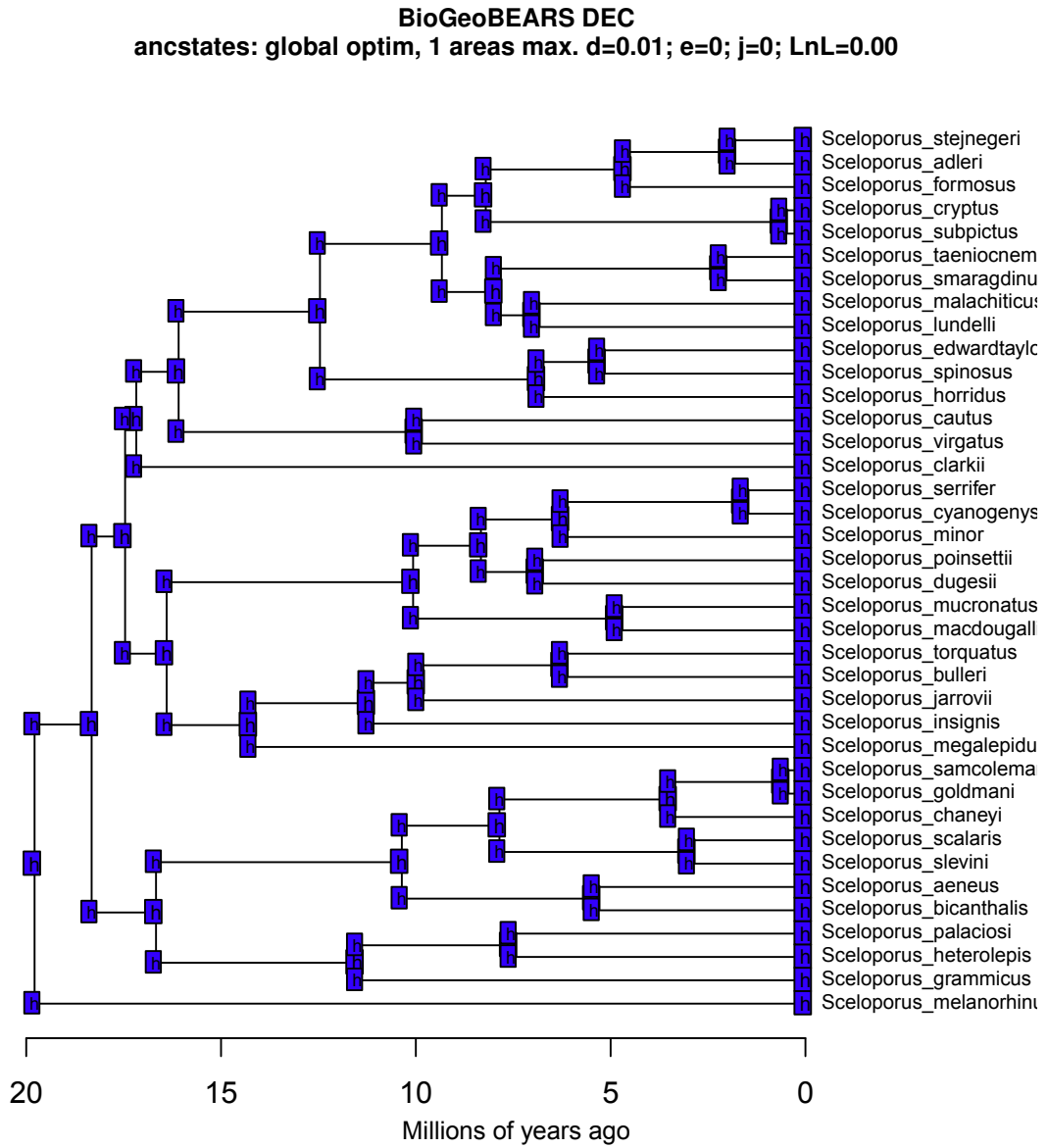


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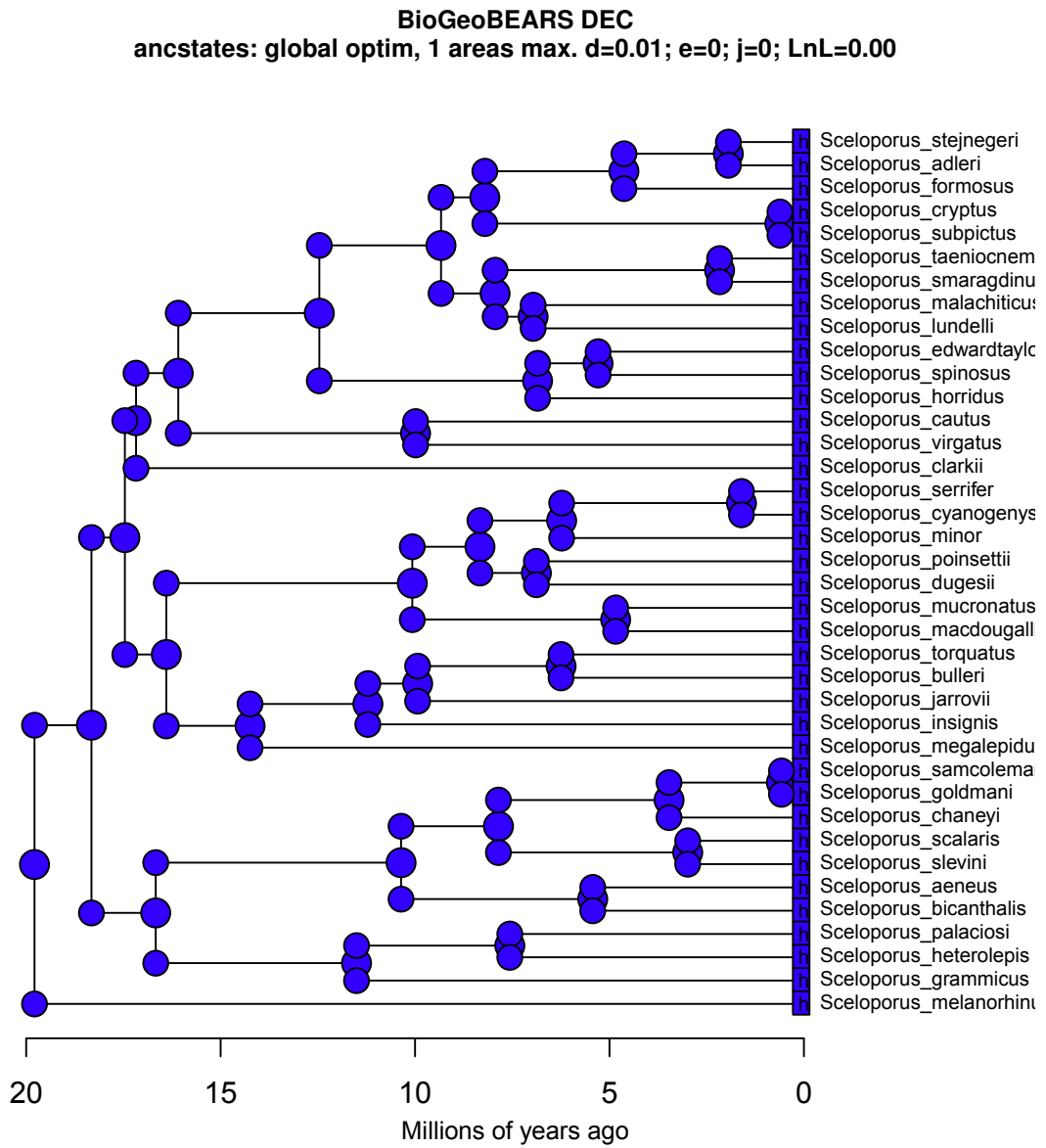


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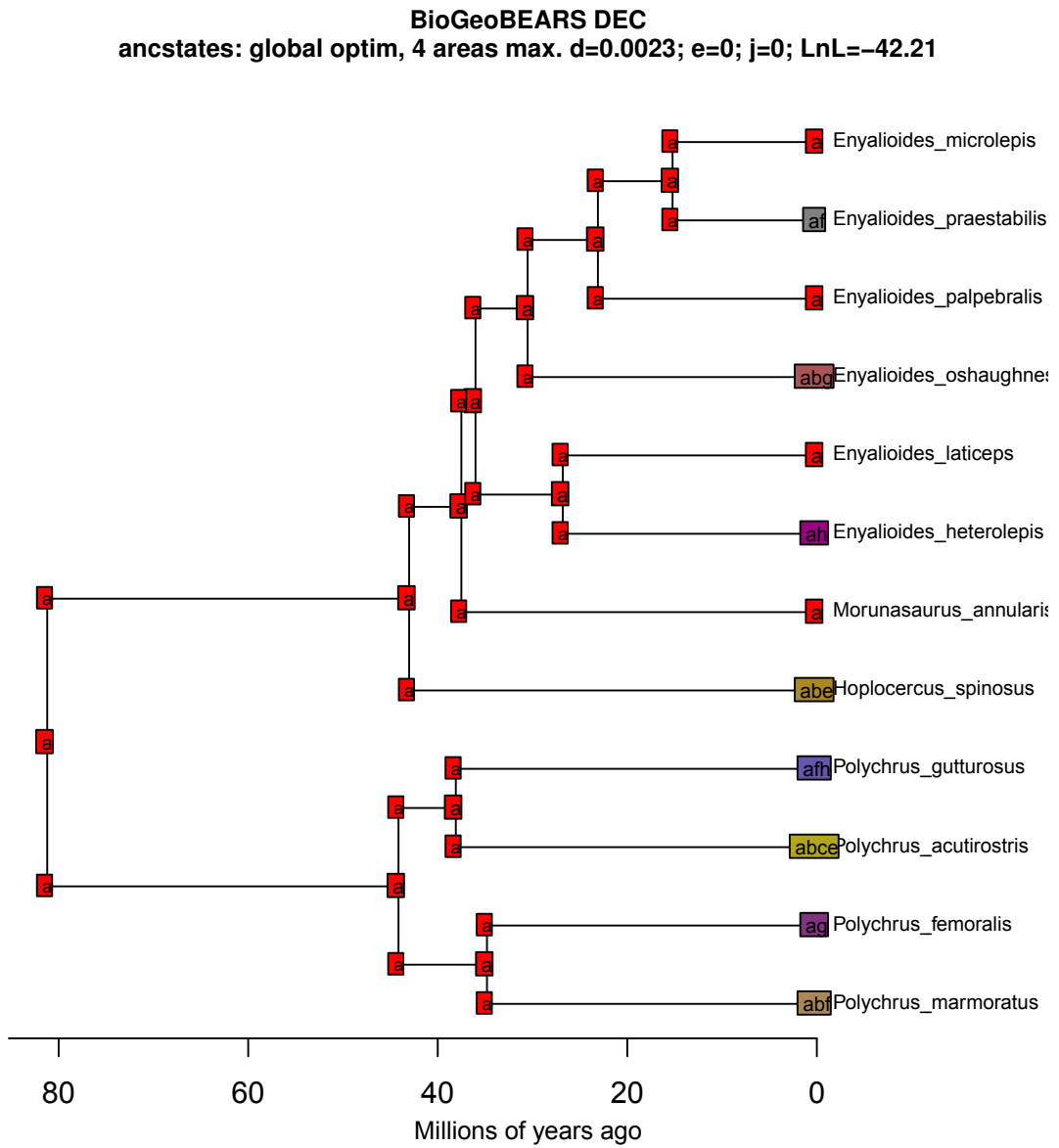


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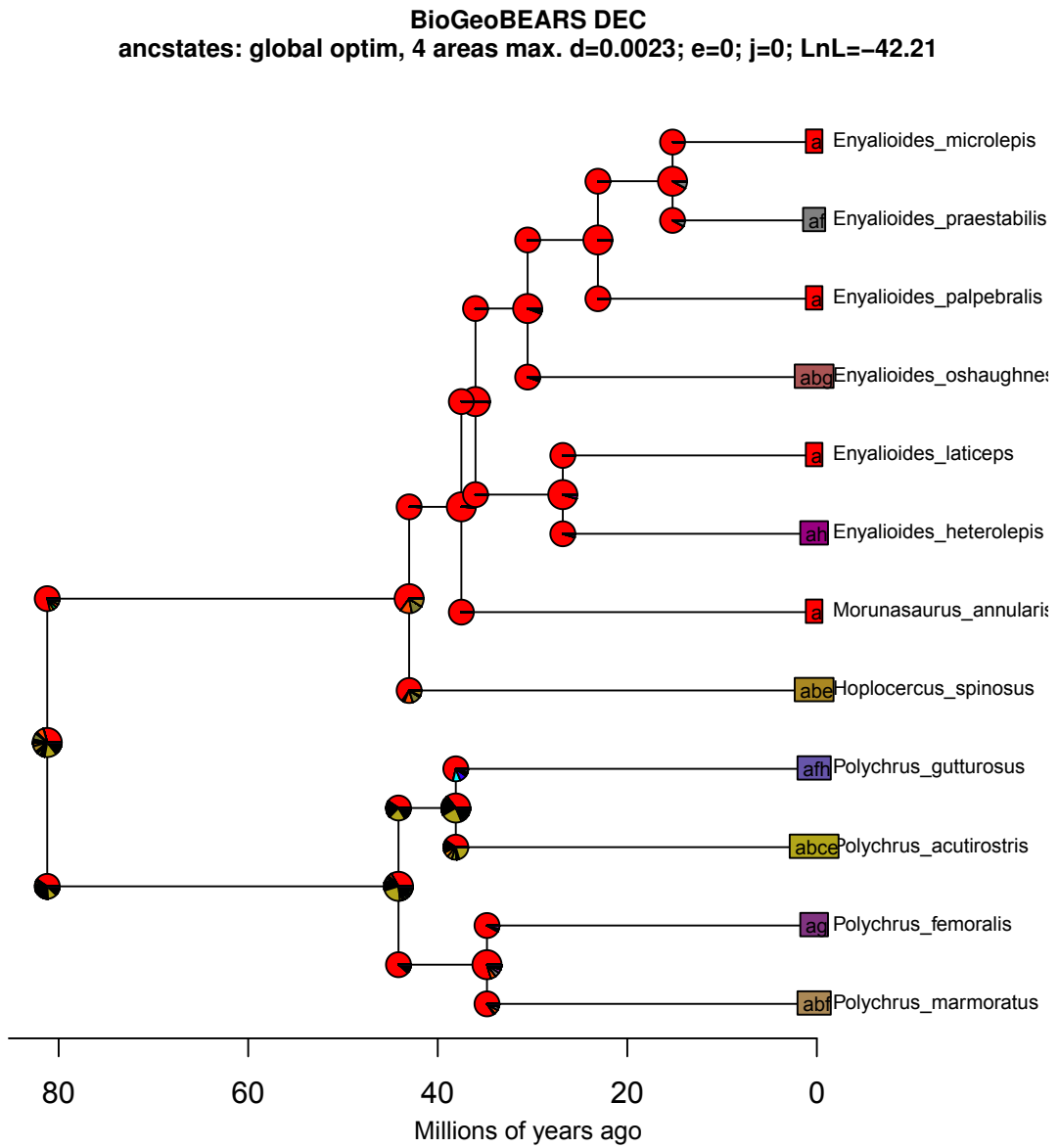


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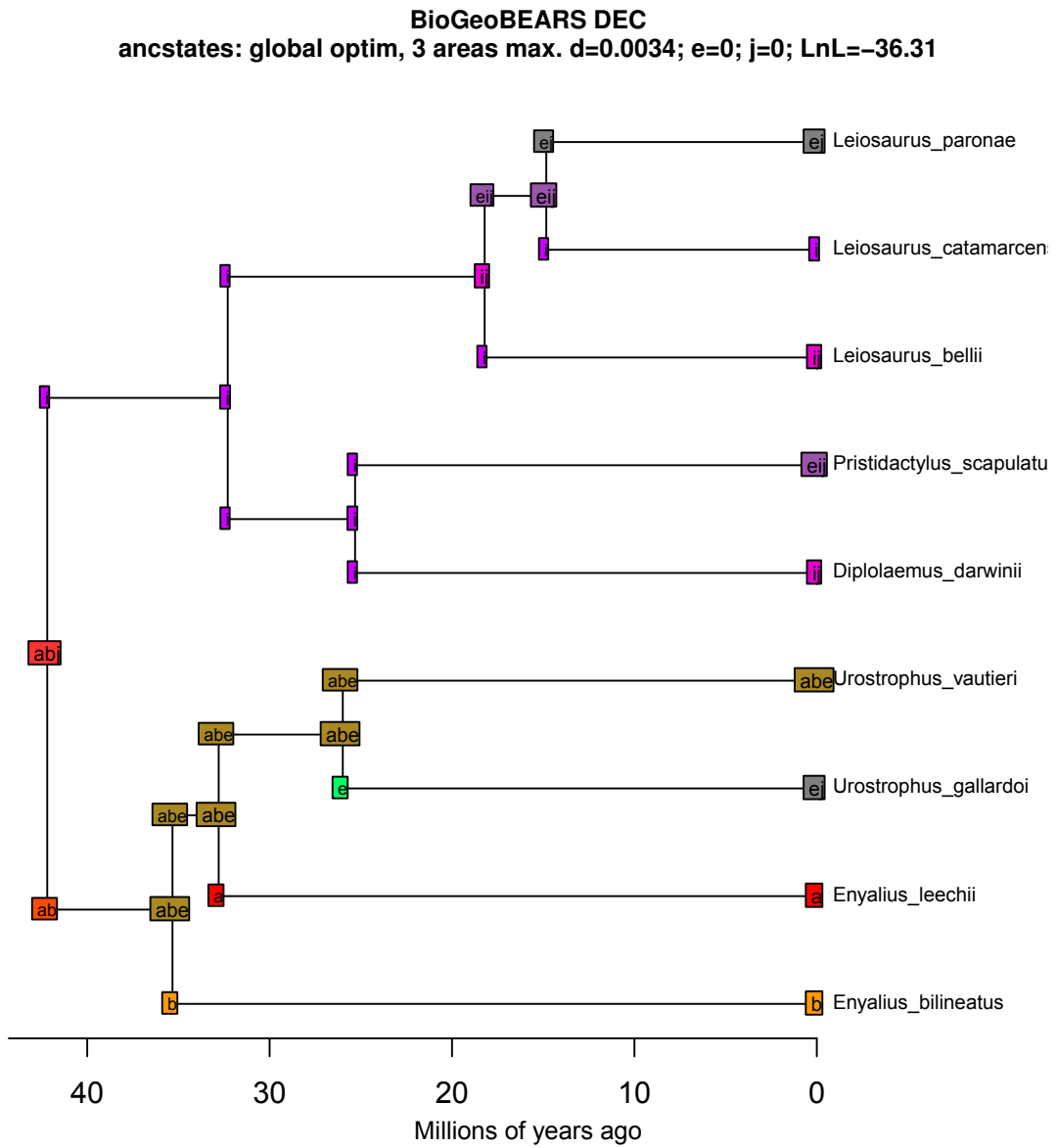


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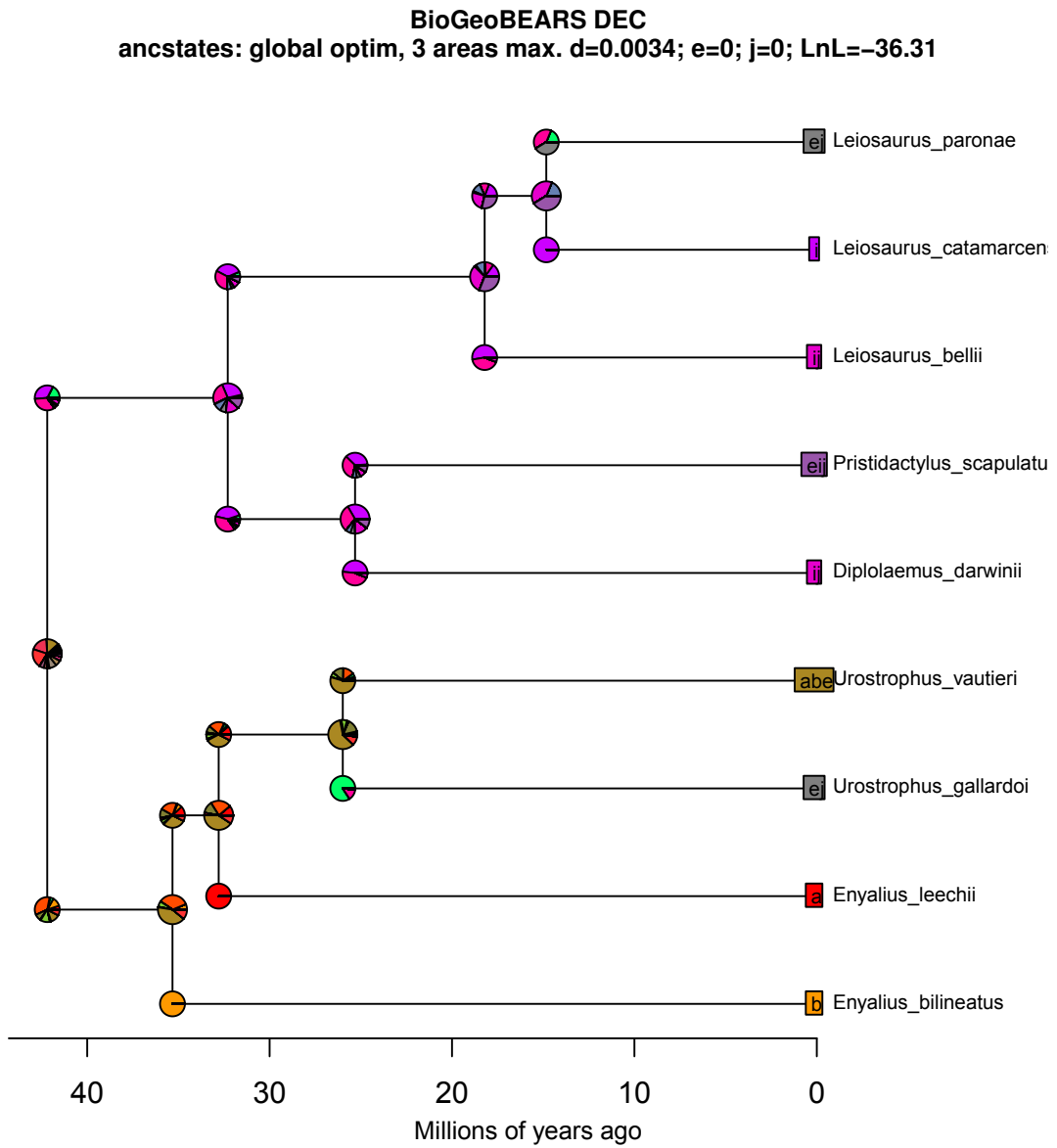


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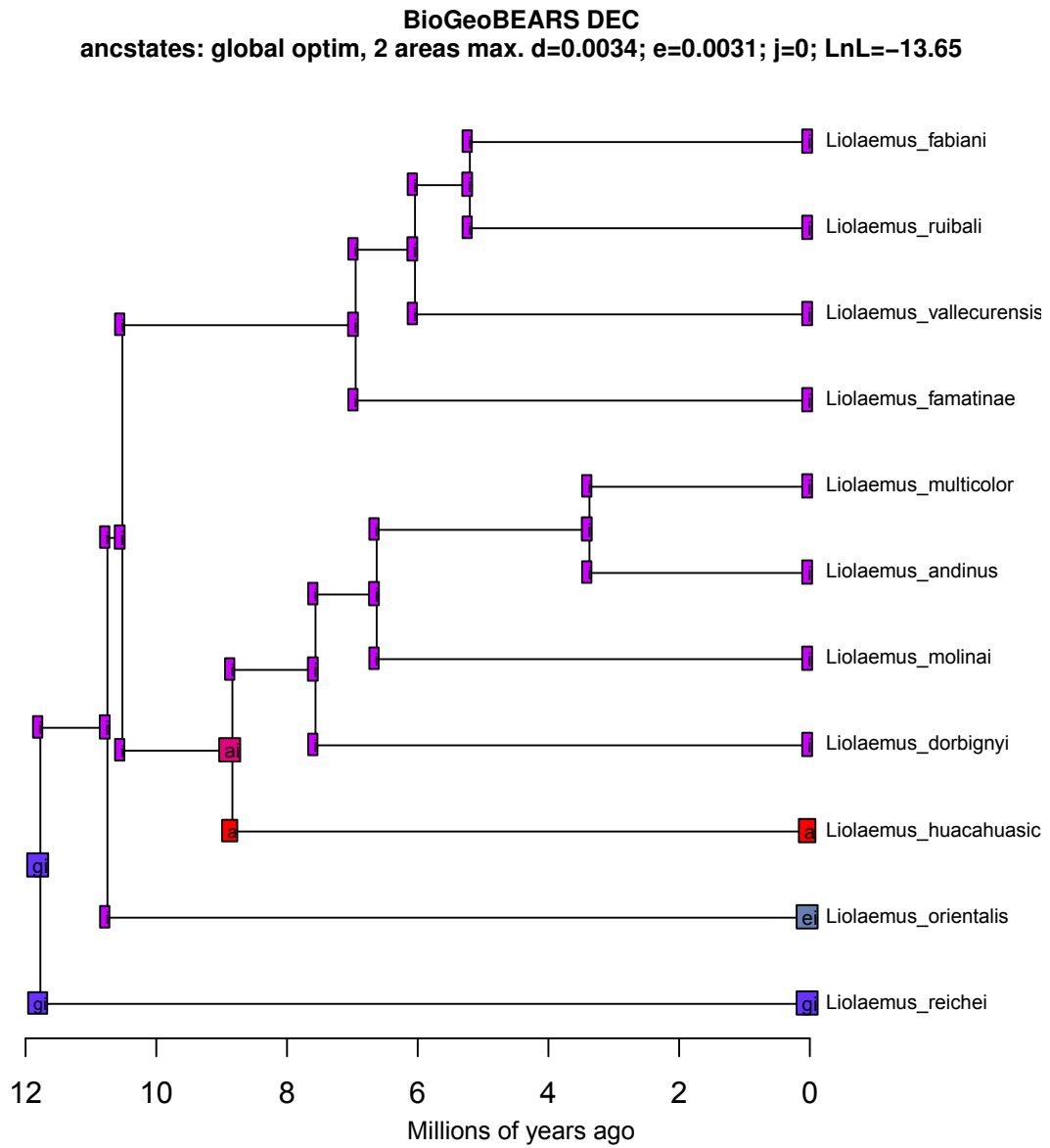


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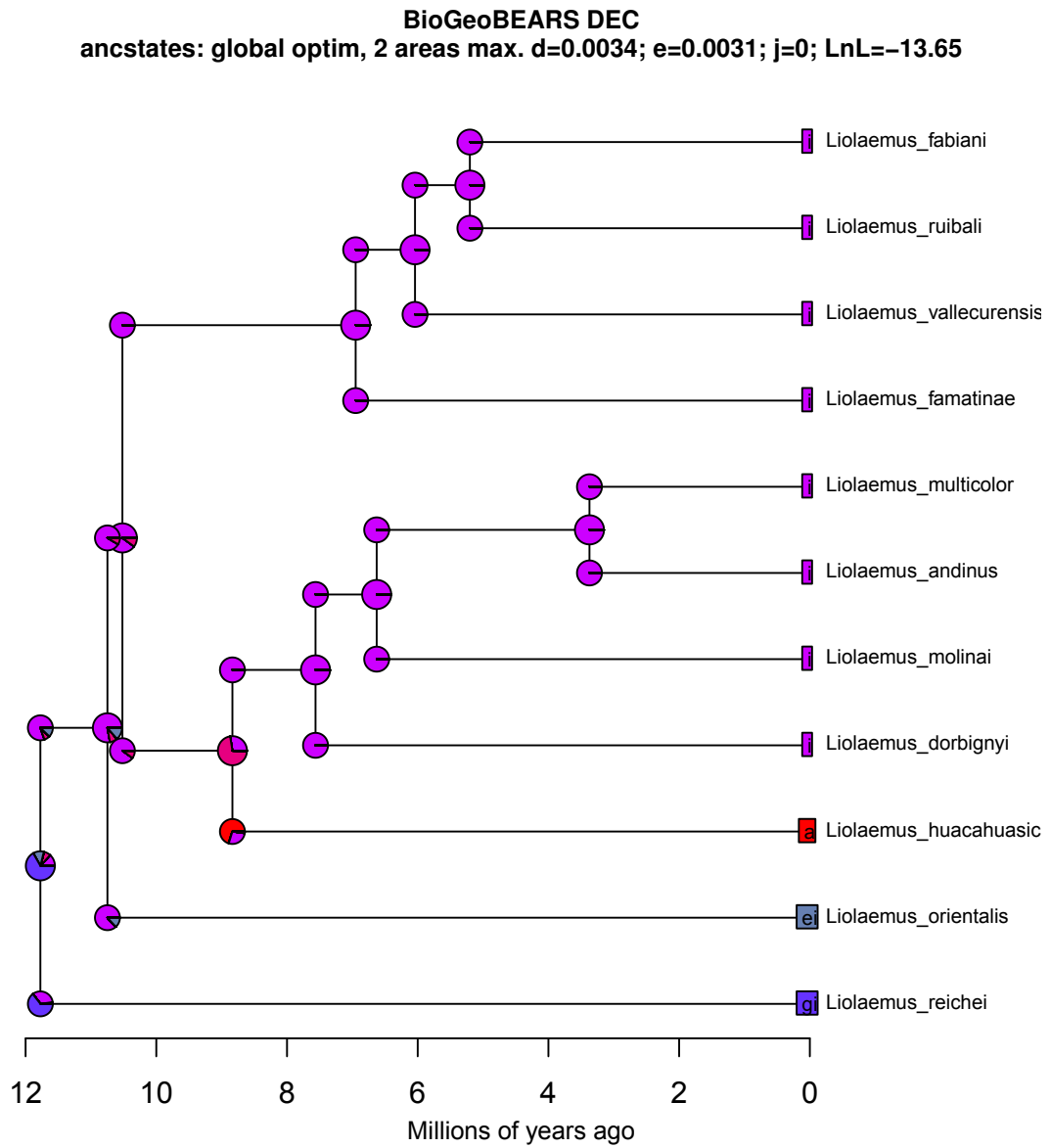


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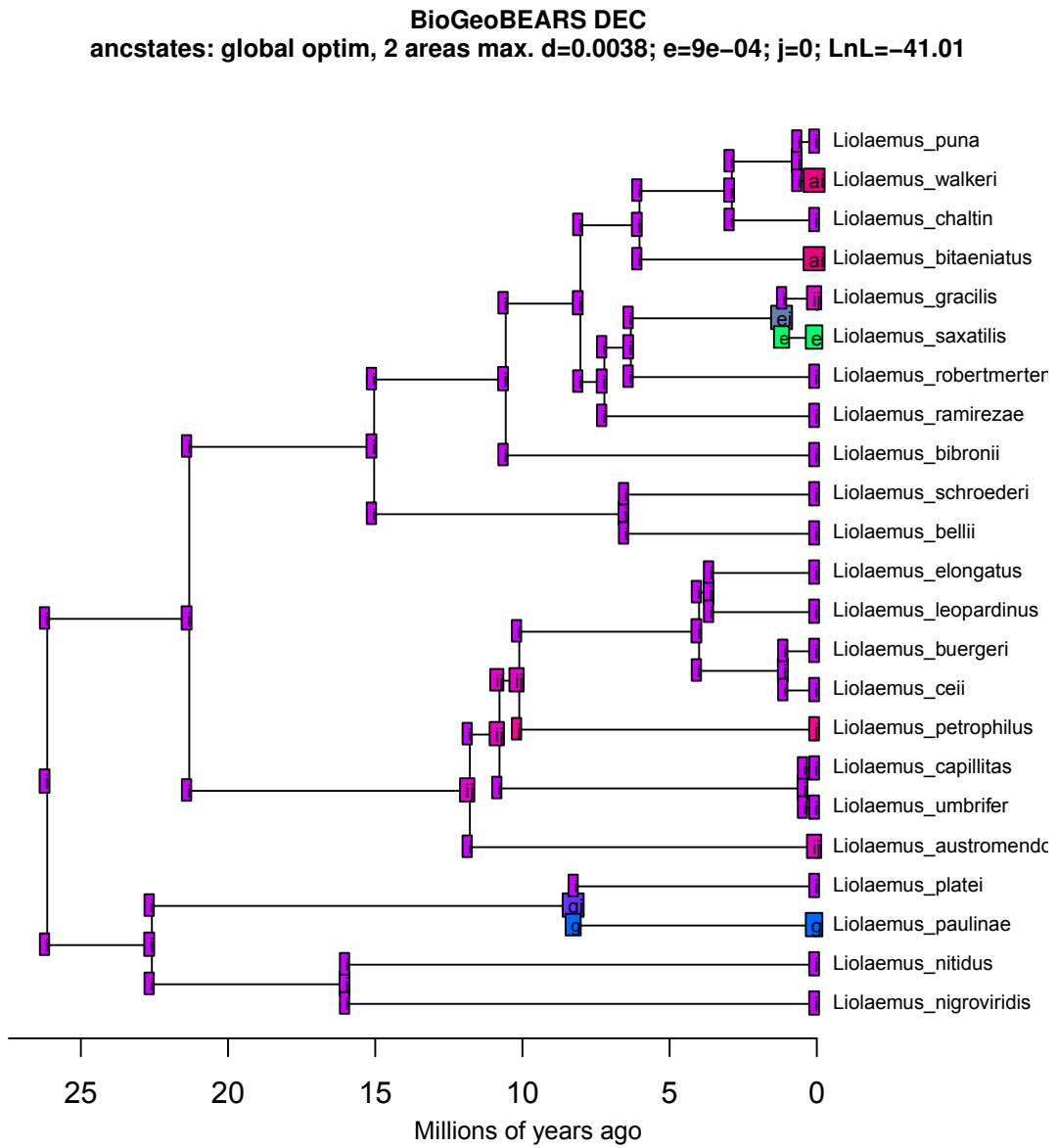


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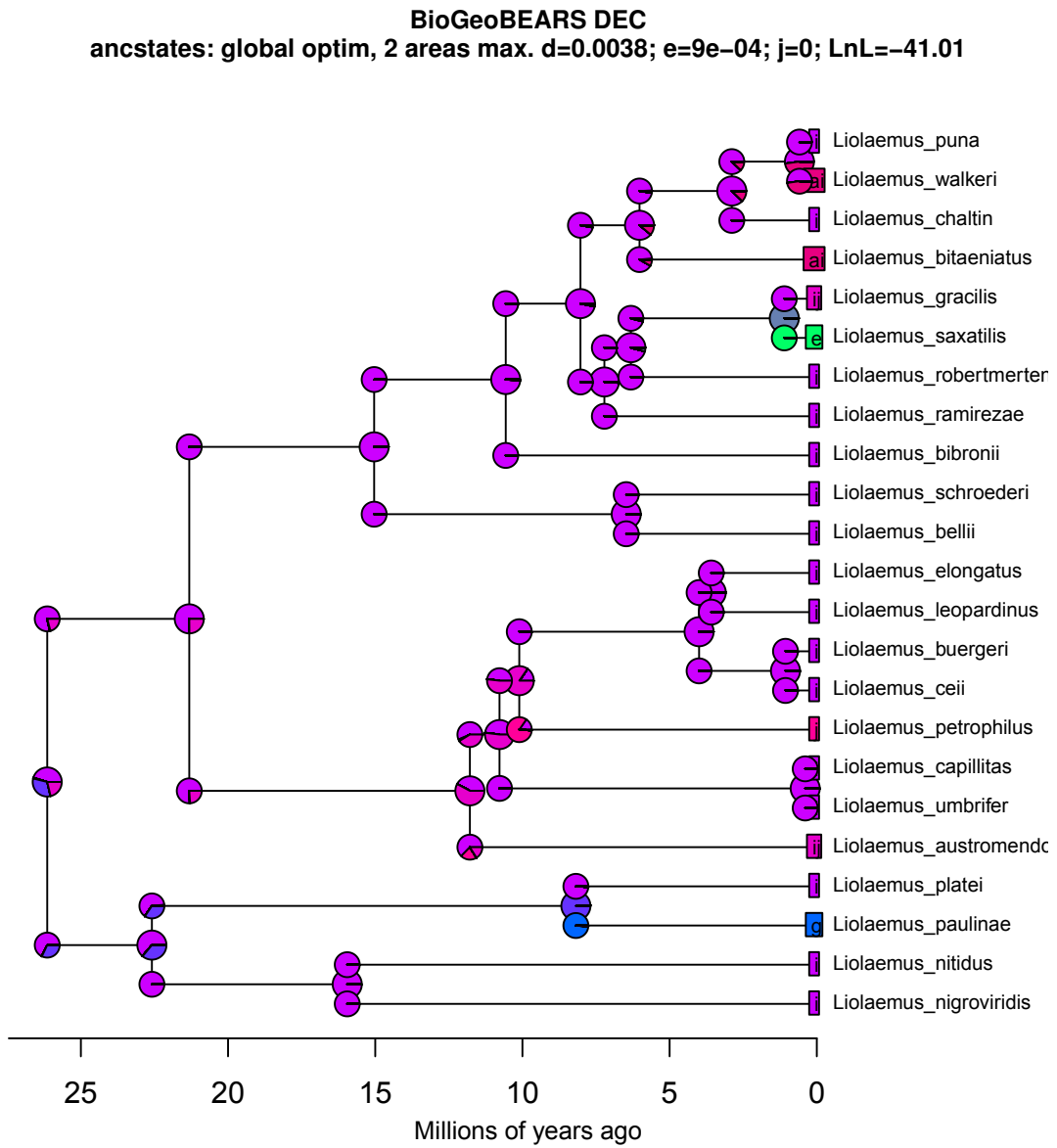


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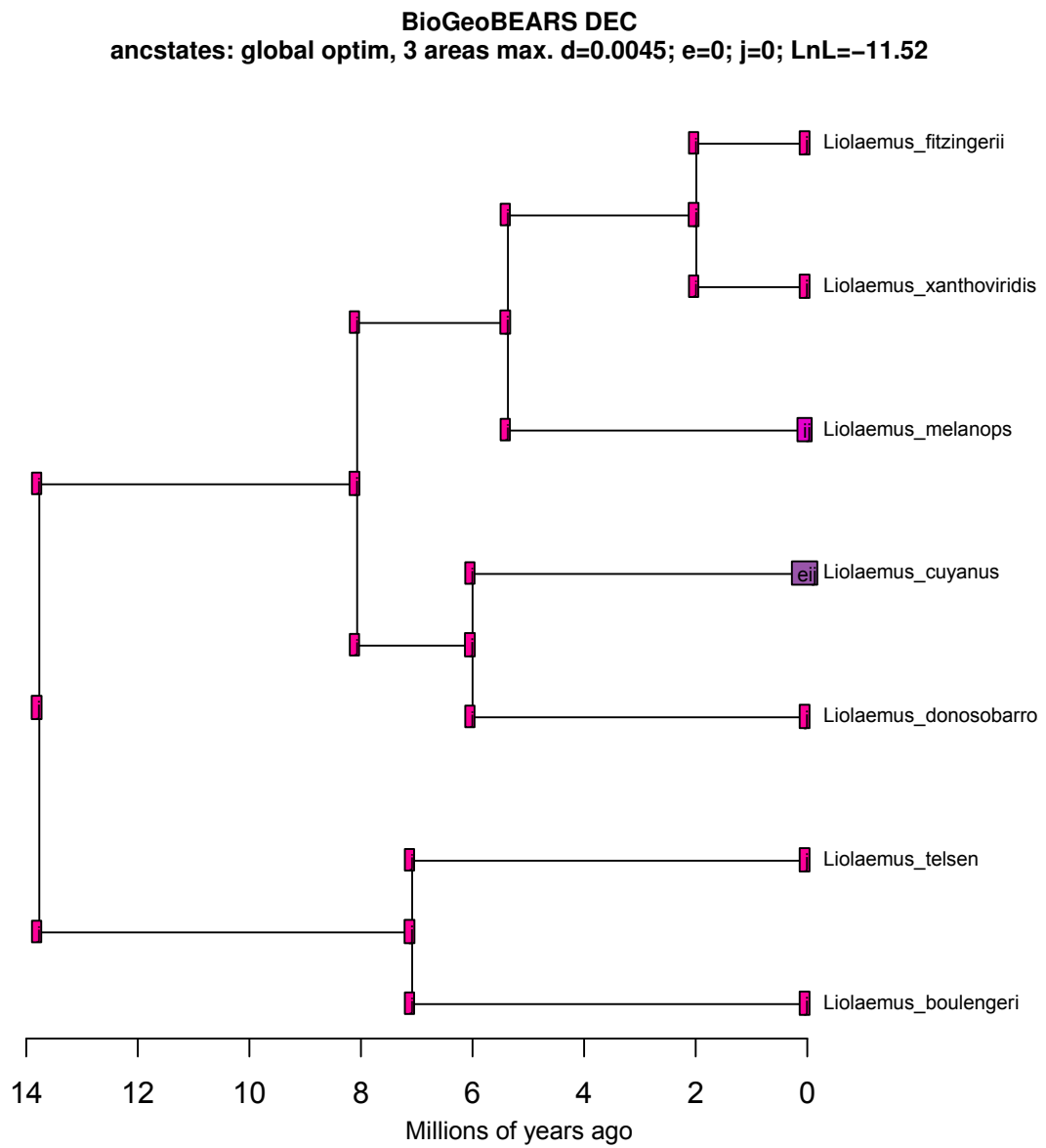


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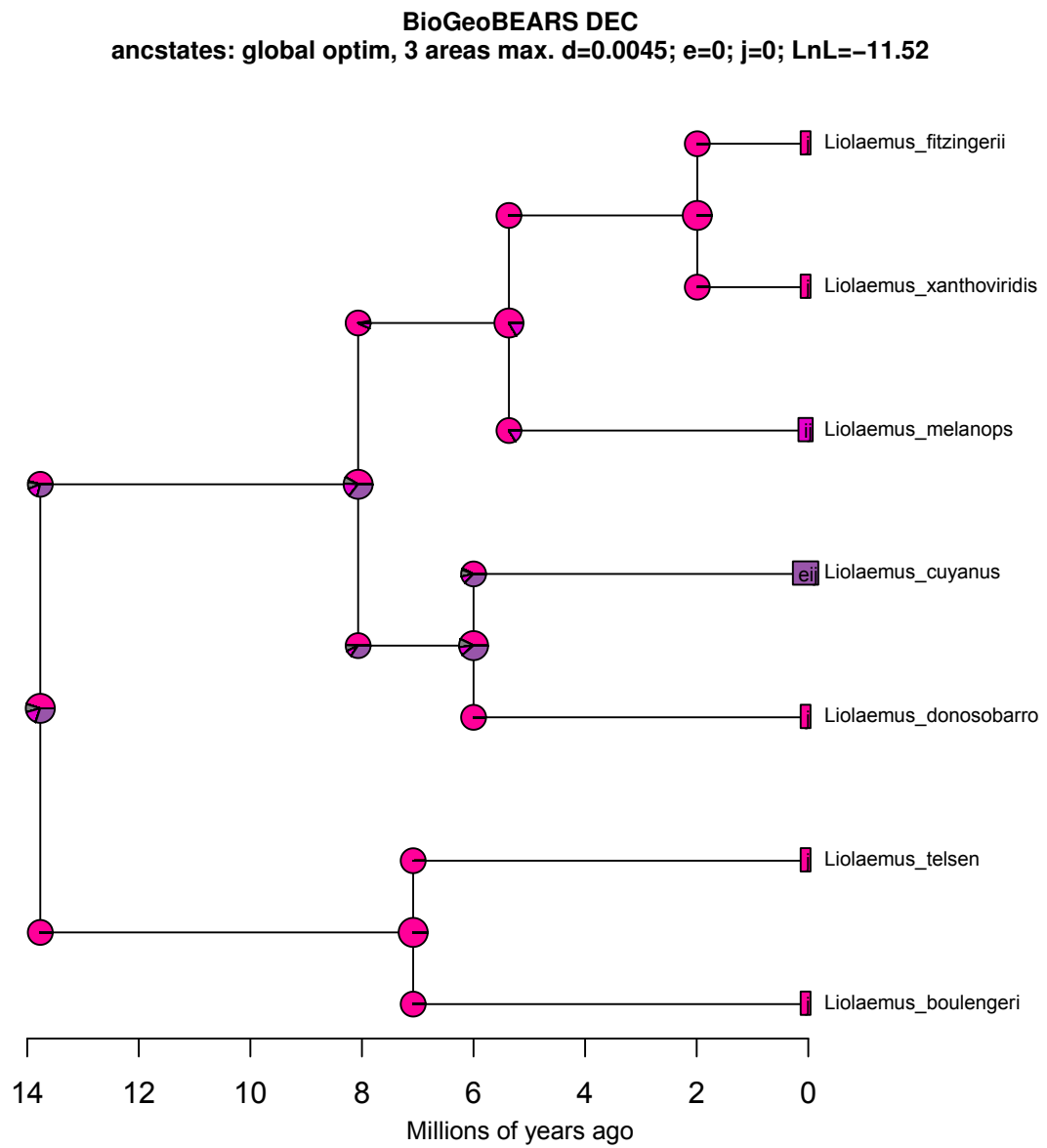


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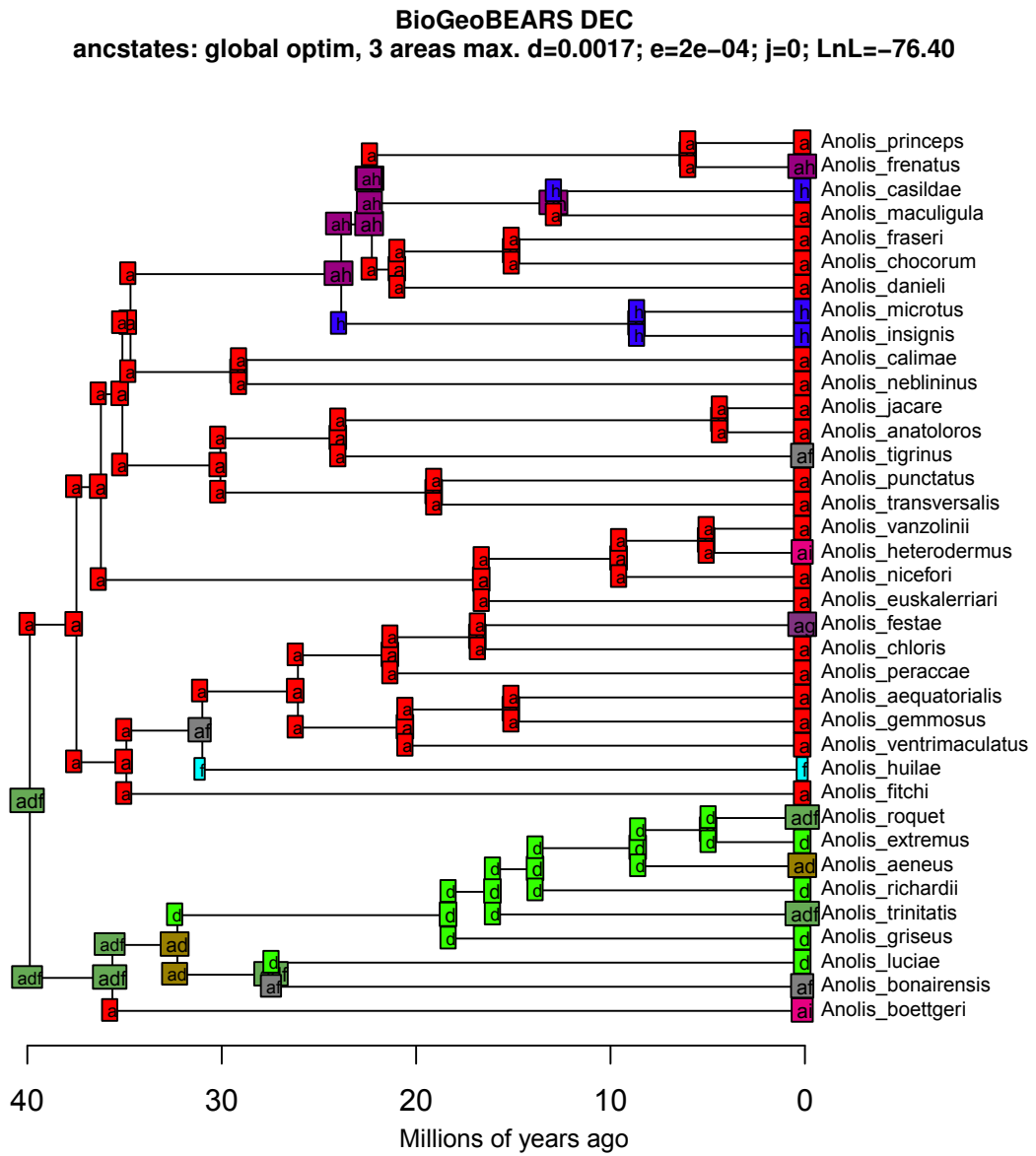


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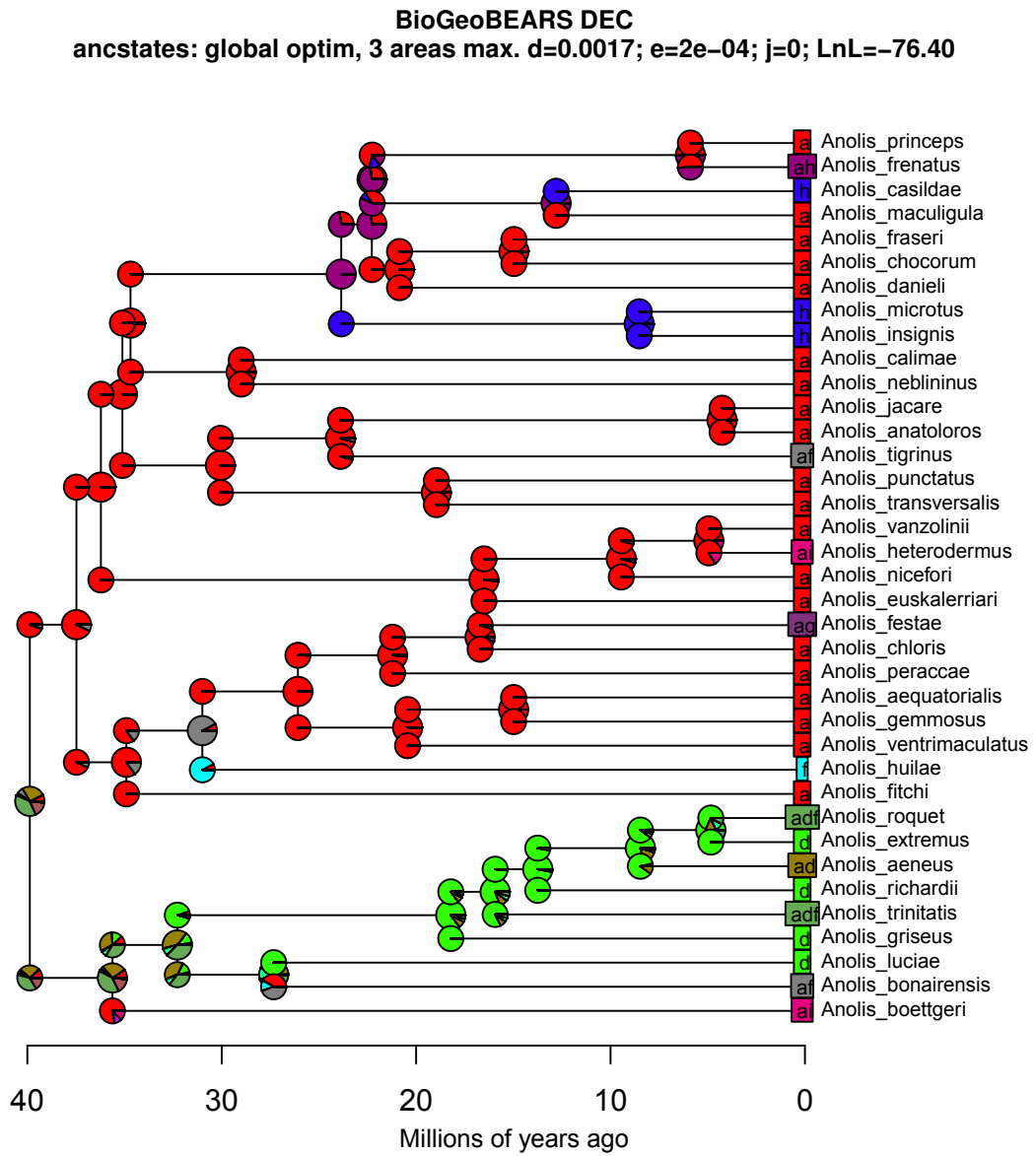


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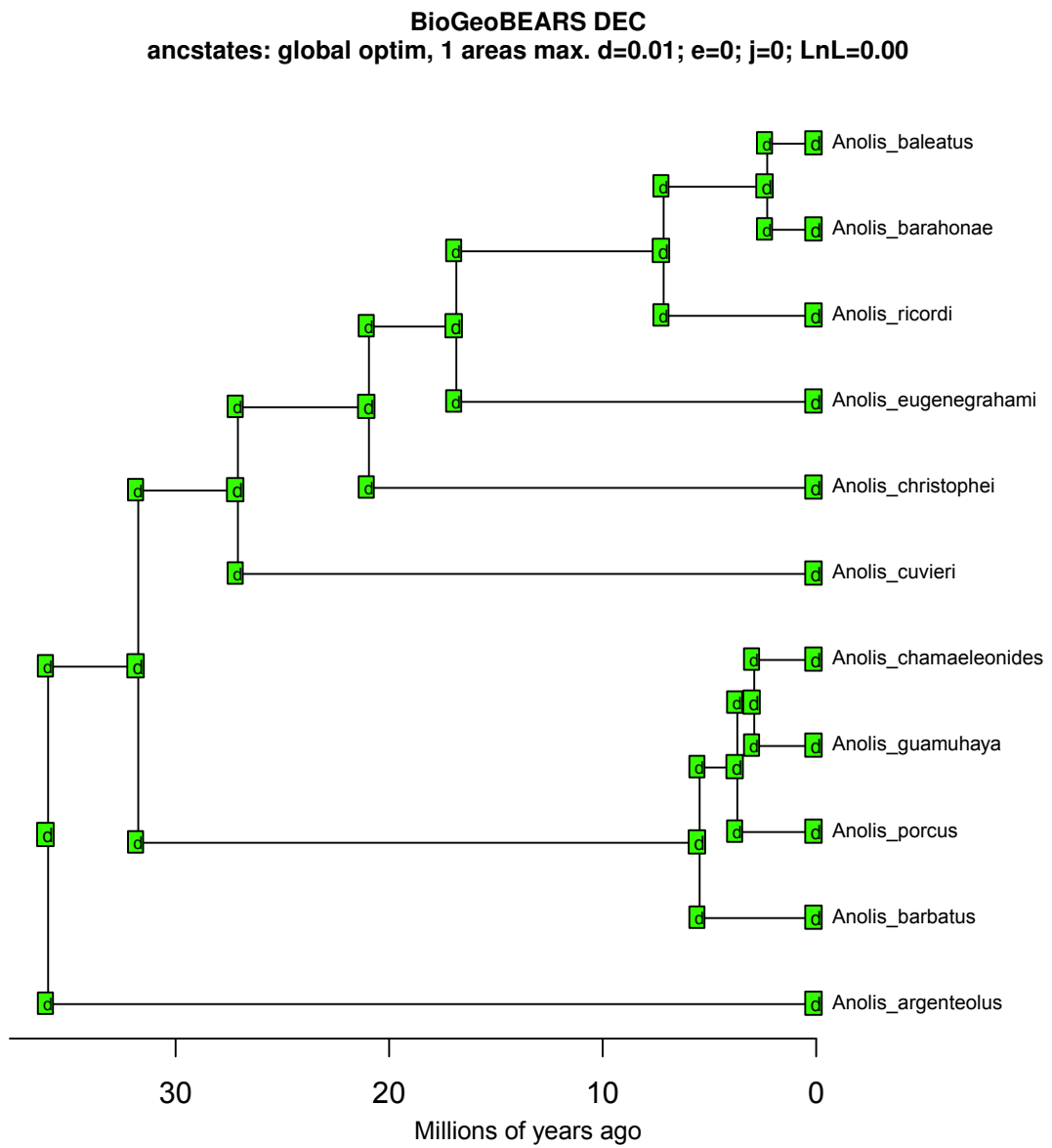


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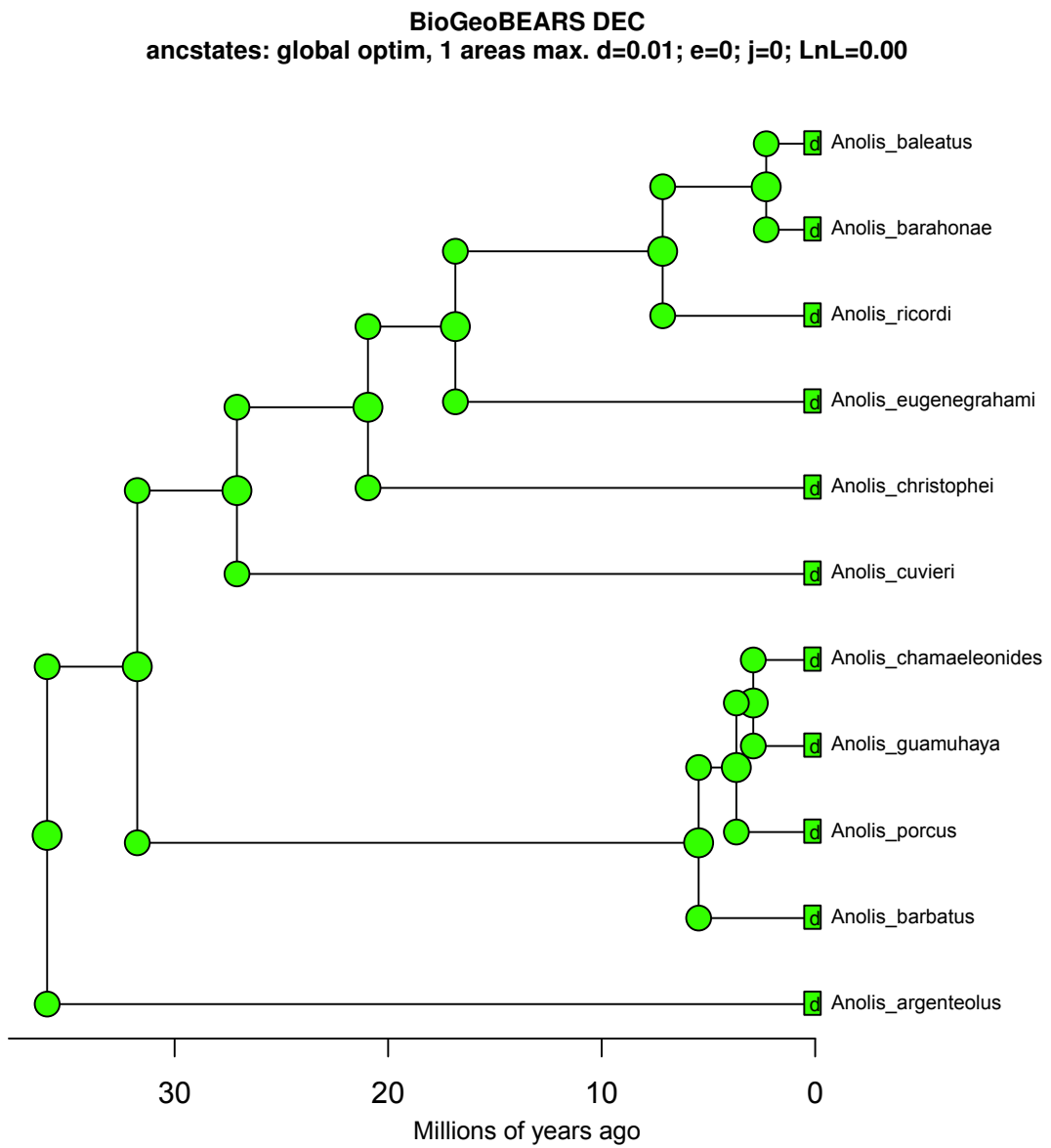


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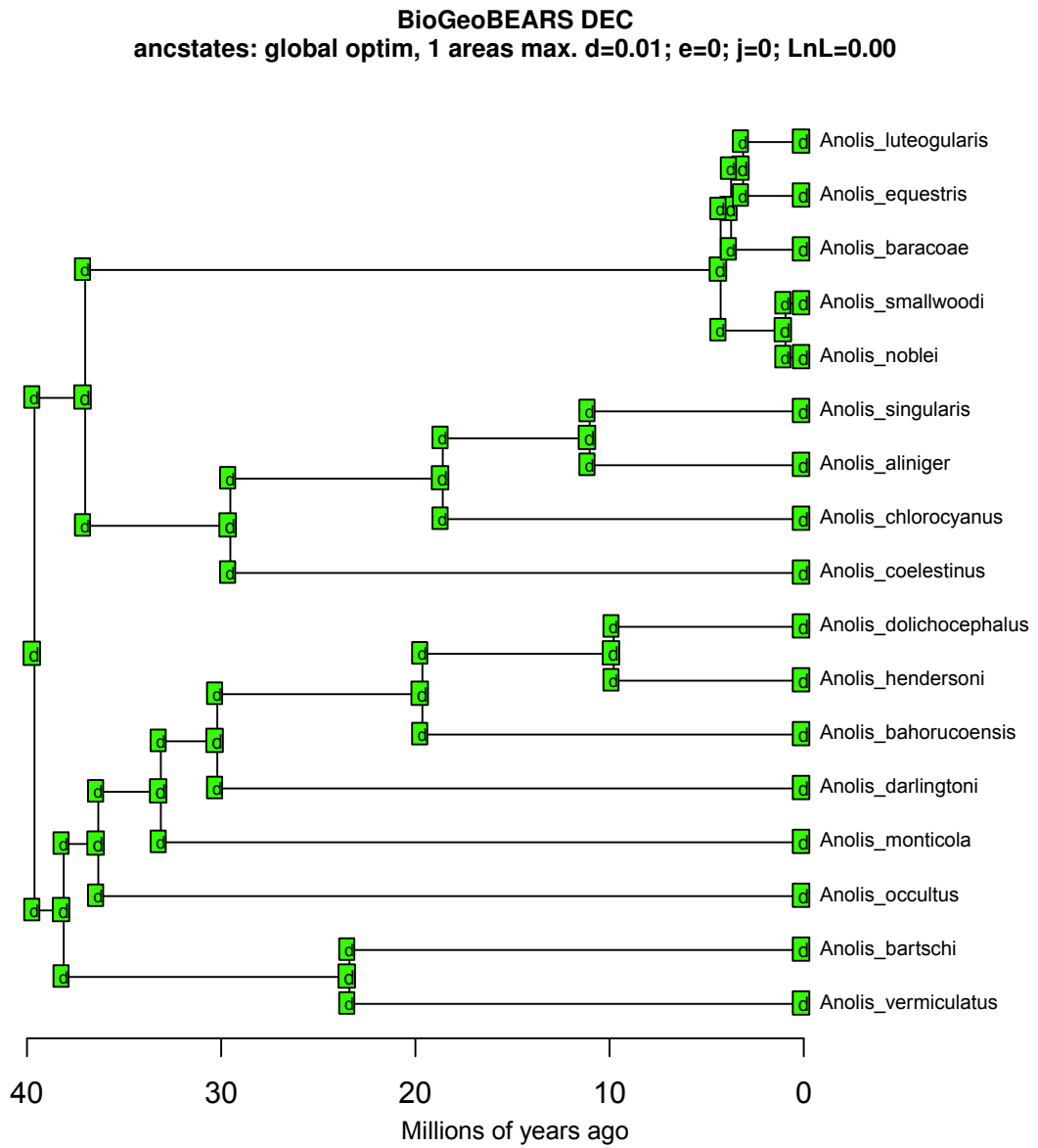


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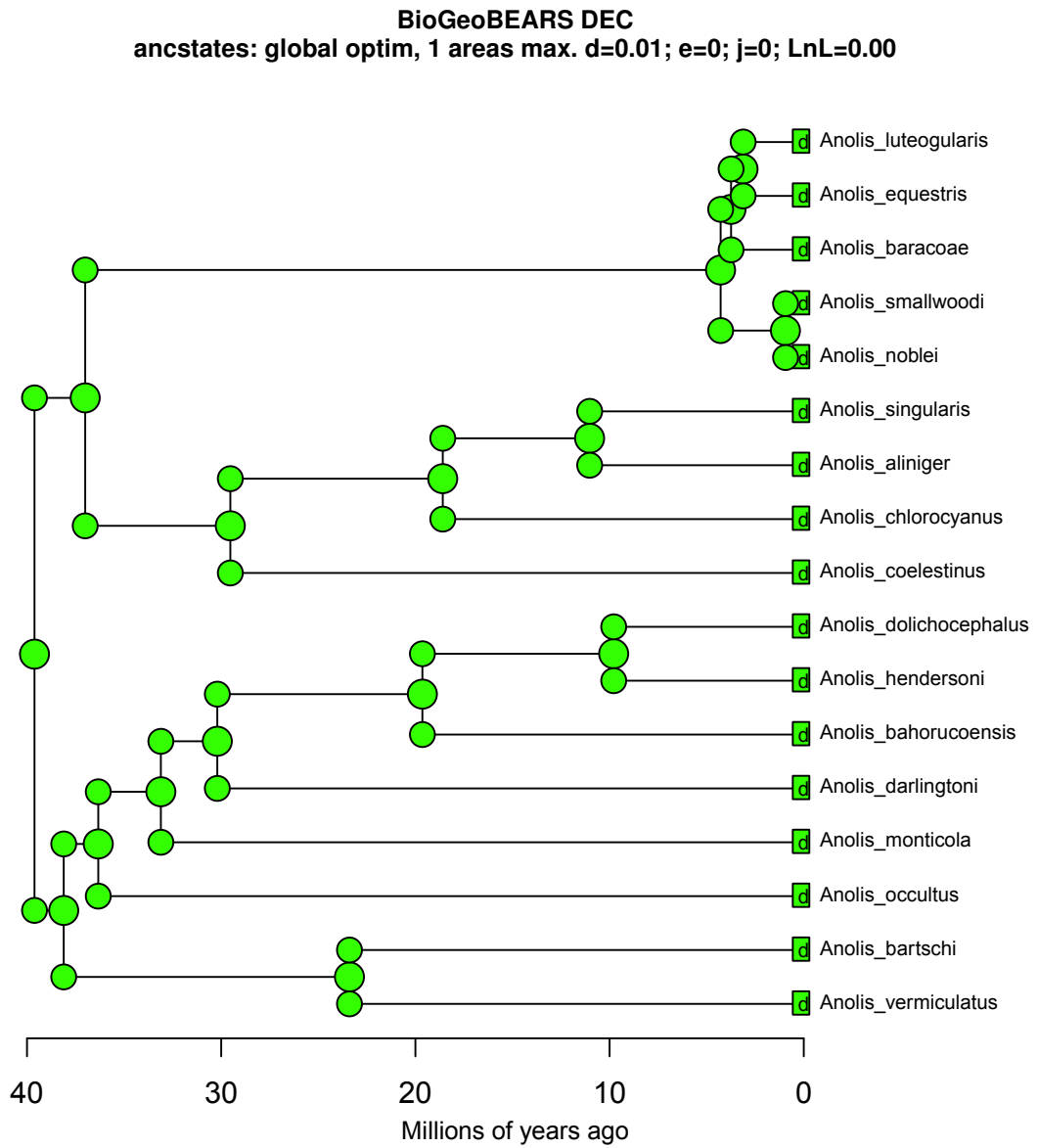


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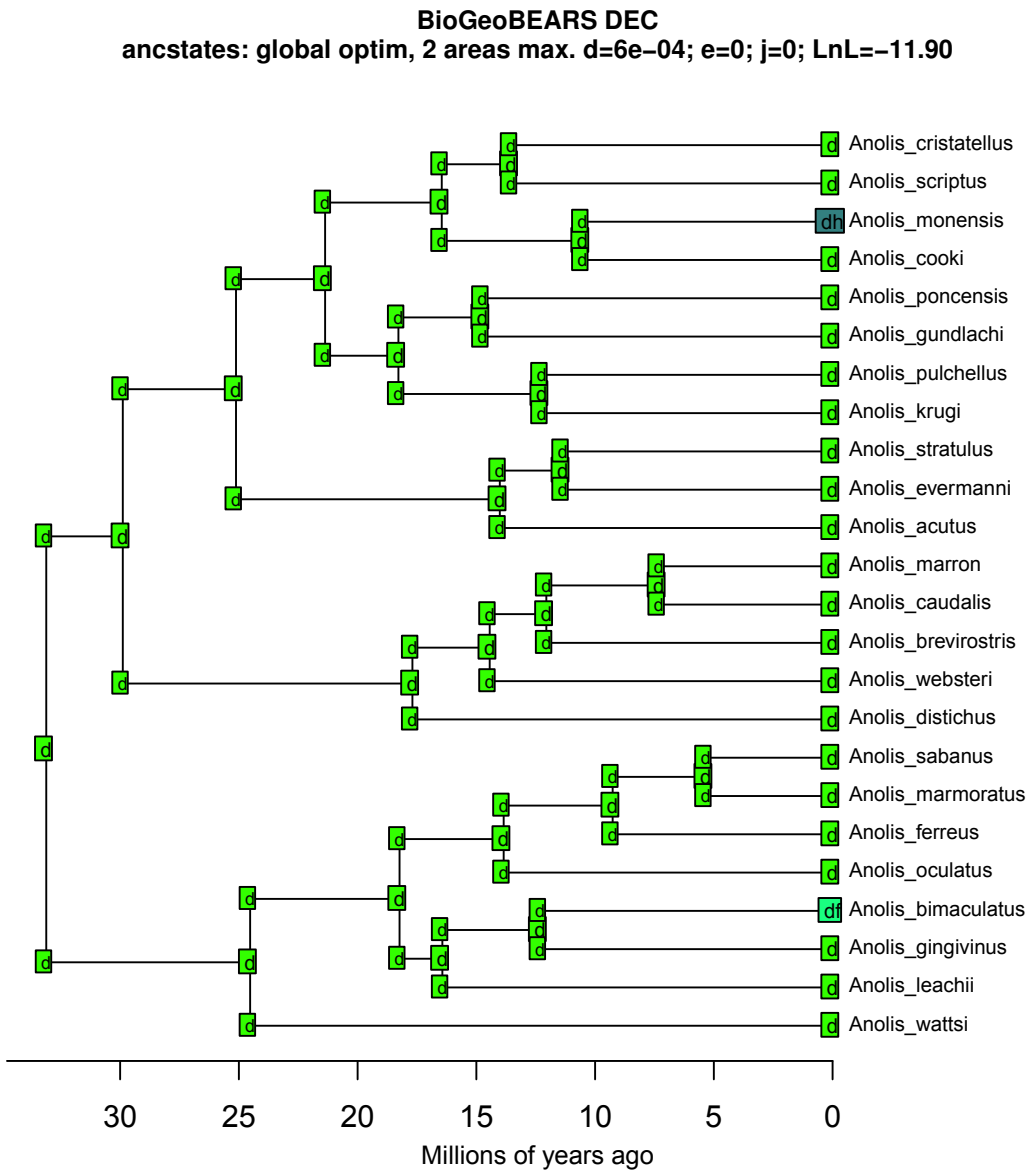


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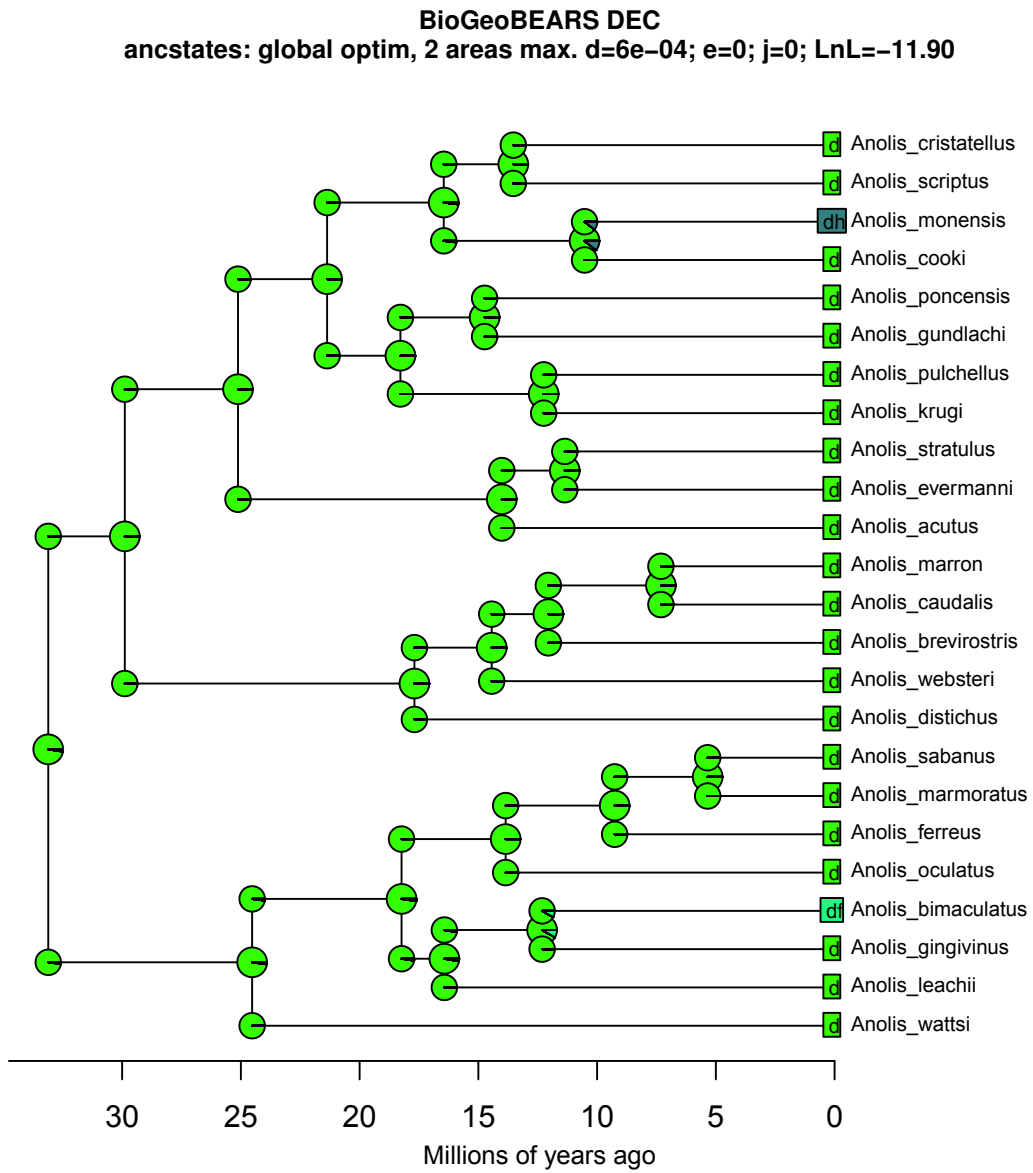


Fig. S9: Summary of biotic interchange (Time-stratified model)

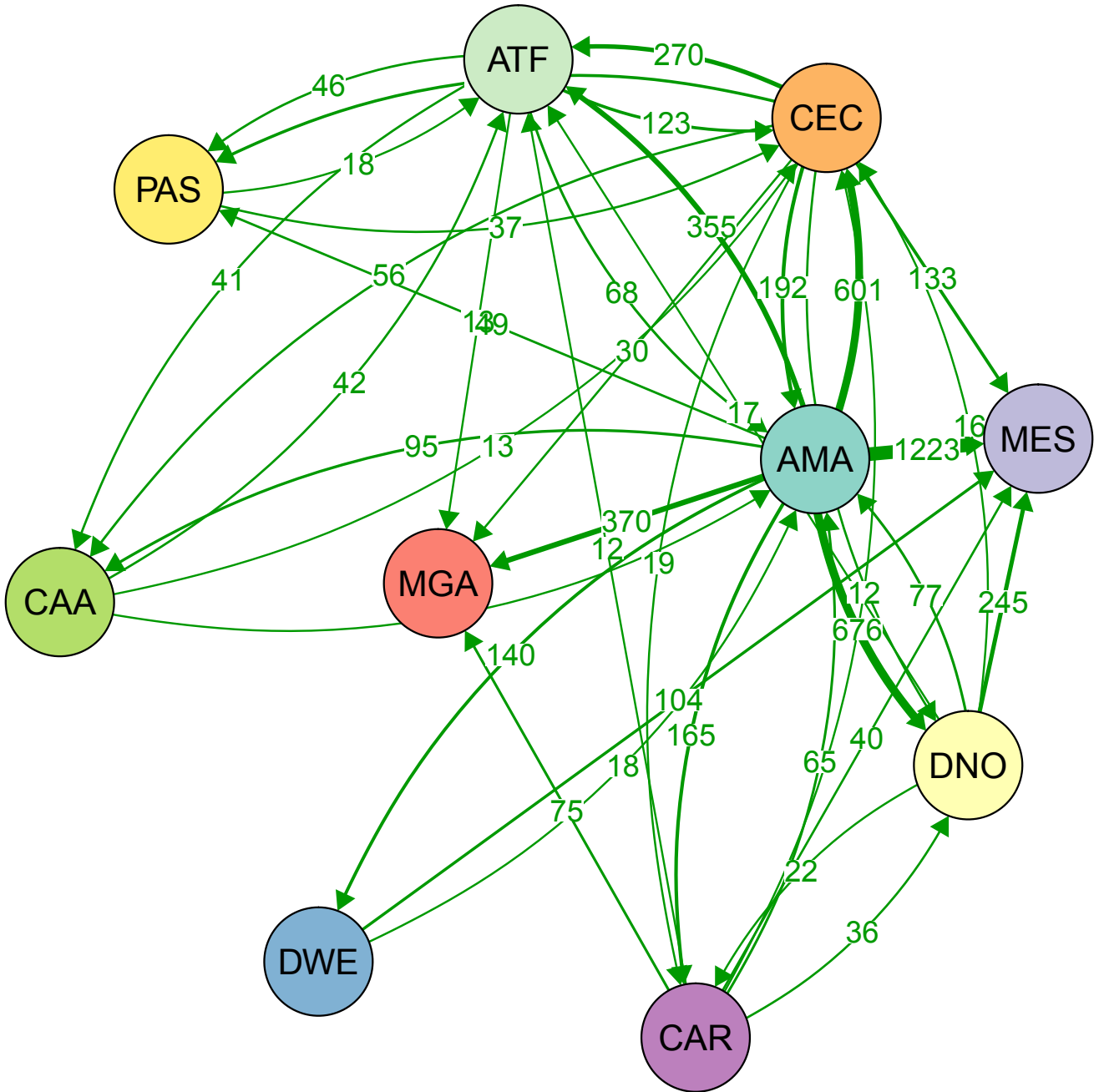
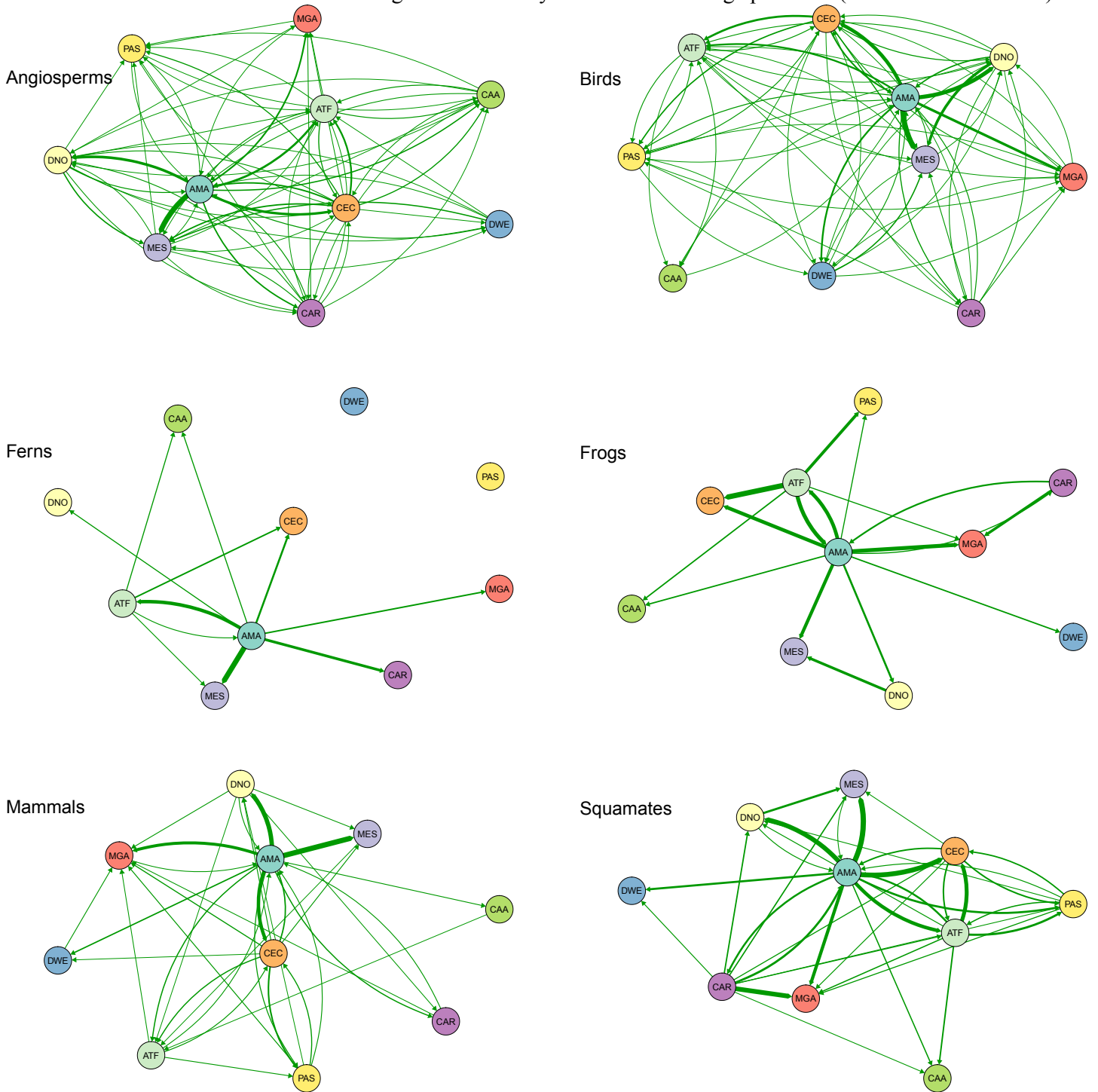
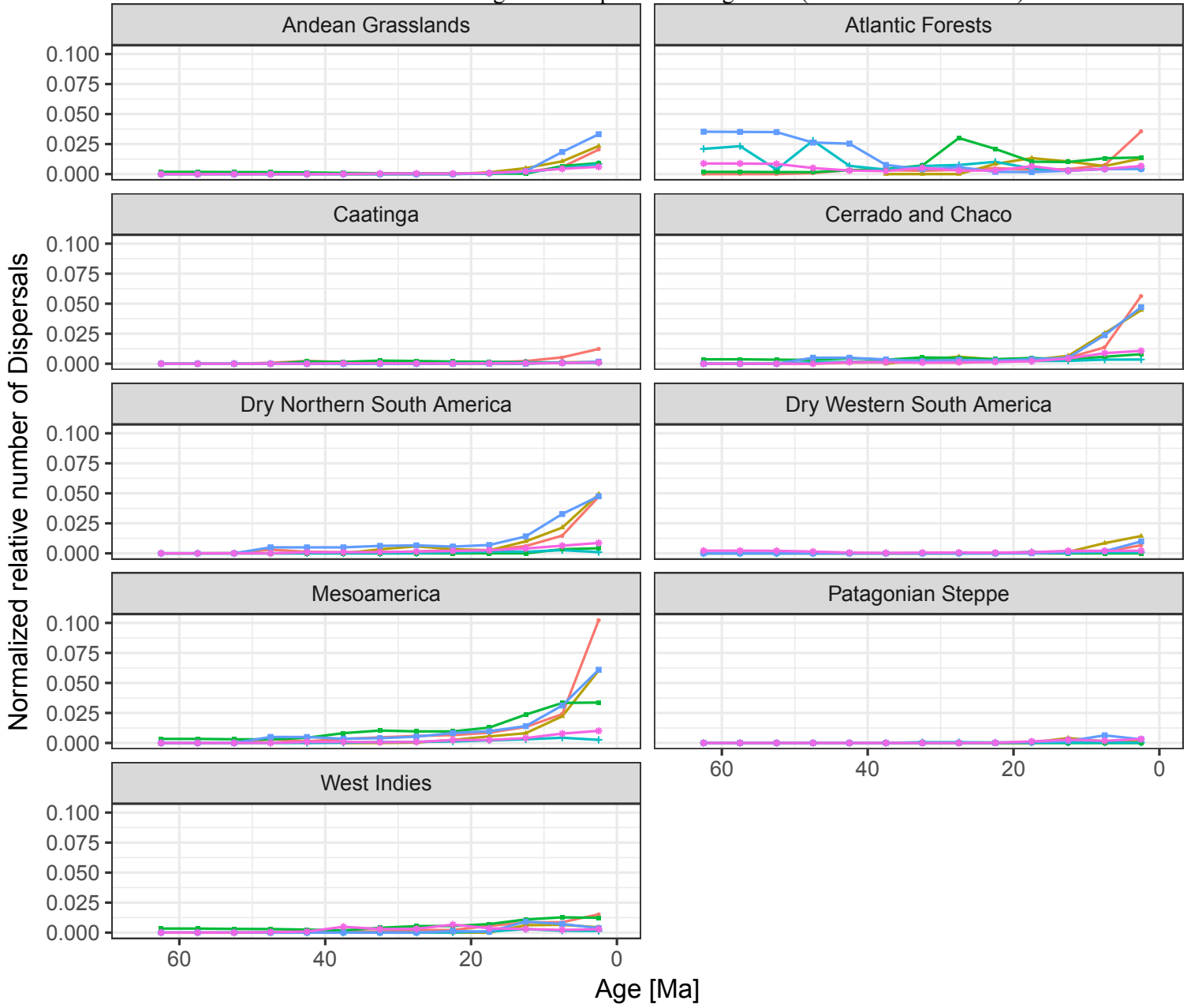


Fig. S10: Summary of biotic interchange per clade (Time-stratified model)



Amazon

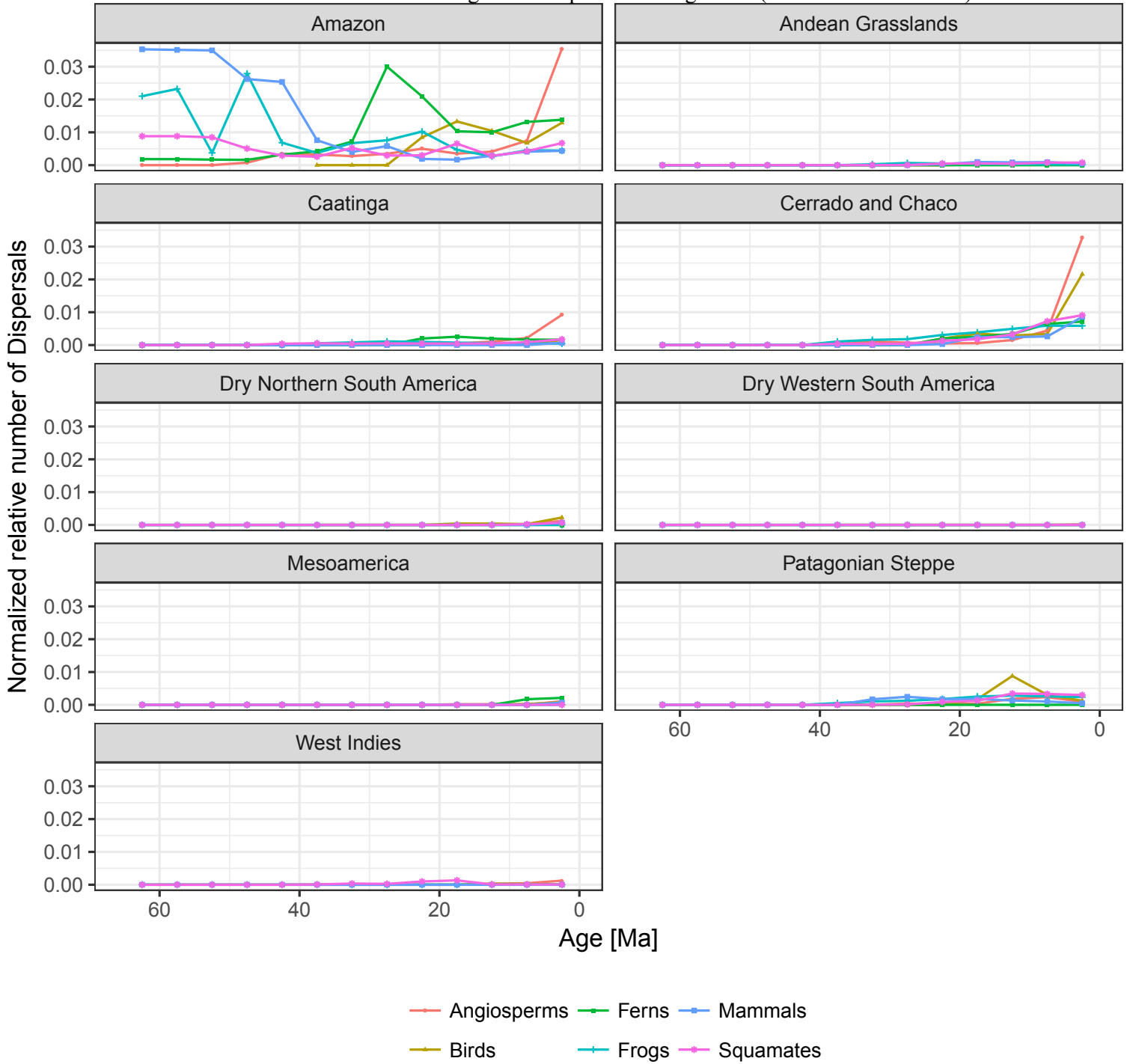
Fig. S11: Dispersals through time (Time-stratified model)



- Angiosperms
- Ferns
- Mammals
- ▲— Birds
- ▲— Frogs
- Squamates

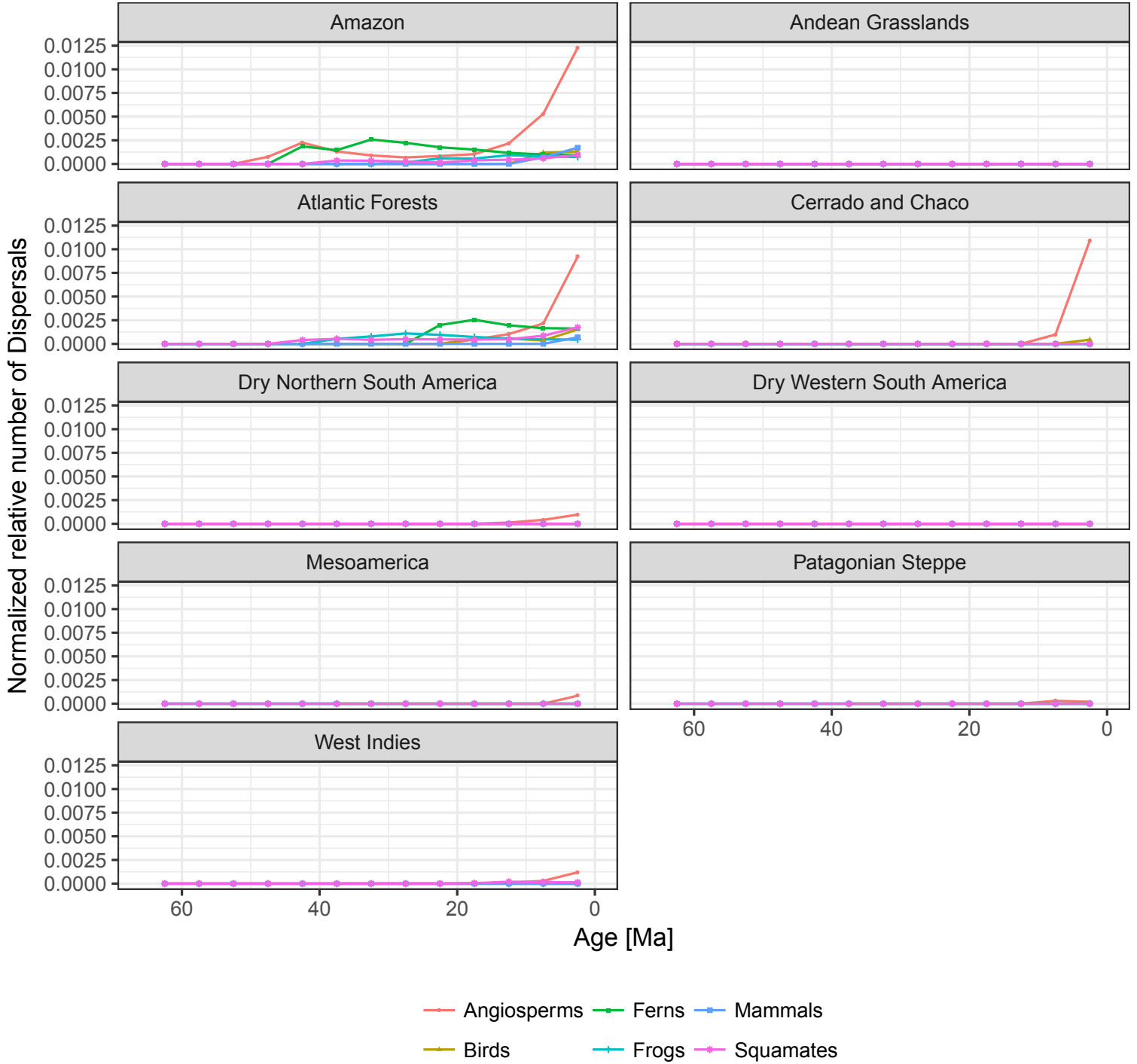
Atlantic Forests

Fig. S11: Dispersals through time (Time-stratified model)



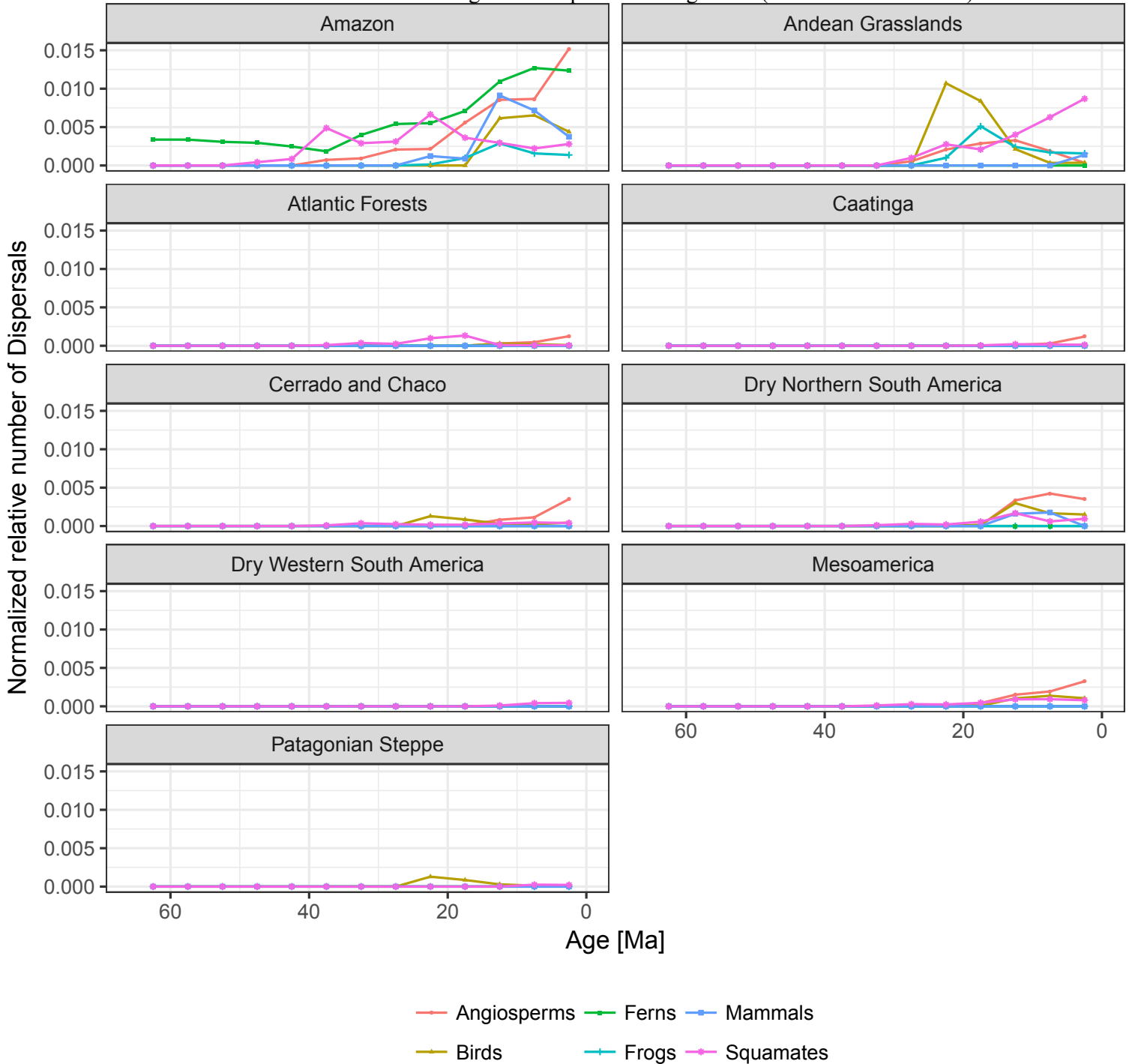
Caatinga

Fig. S11: Dispersals through time (Time-stratified model)



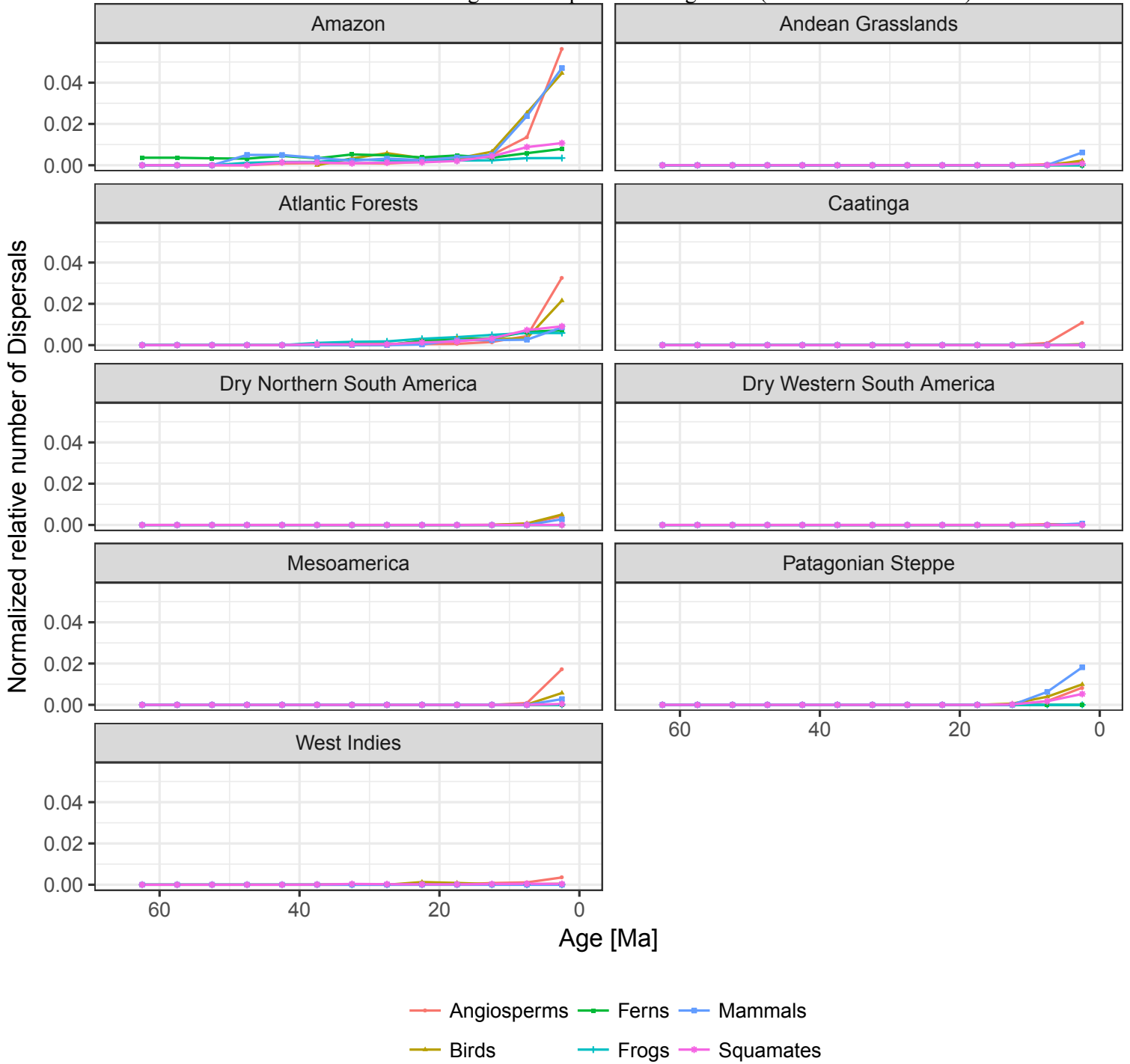
West Indies

Fig. S11: Dispersals through time (Time-stratified model)



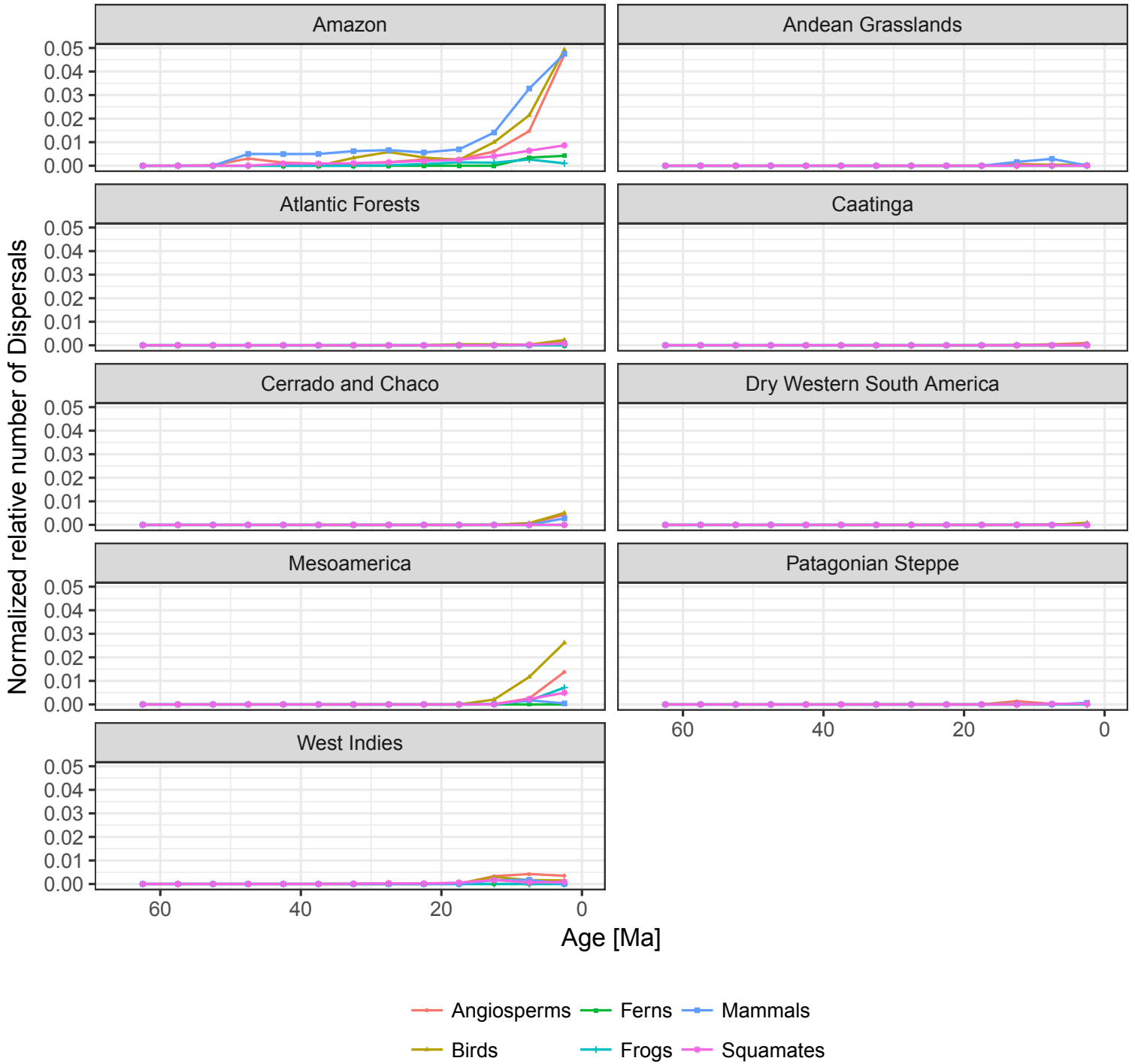
Cerrado and Chaco

Fig. S11: Dispersals through time (Time-stratified model)



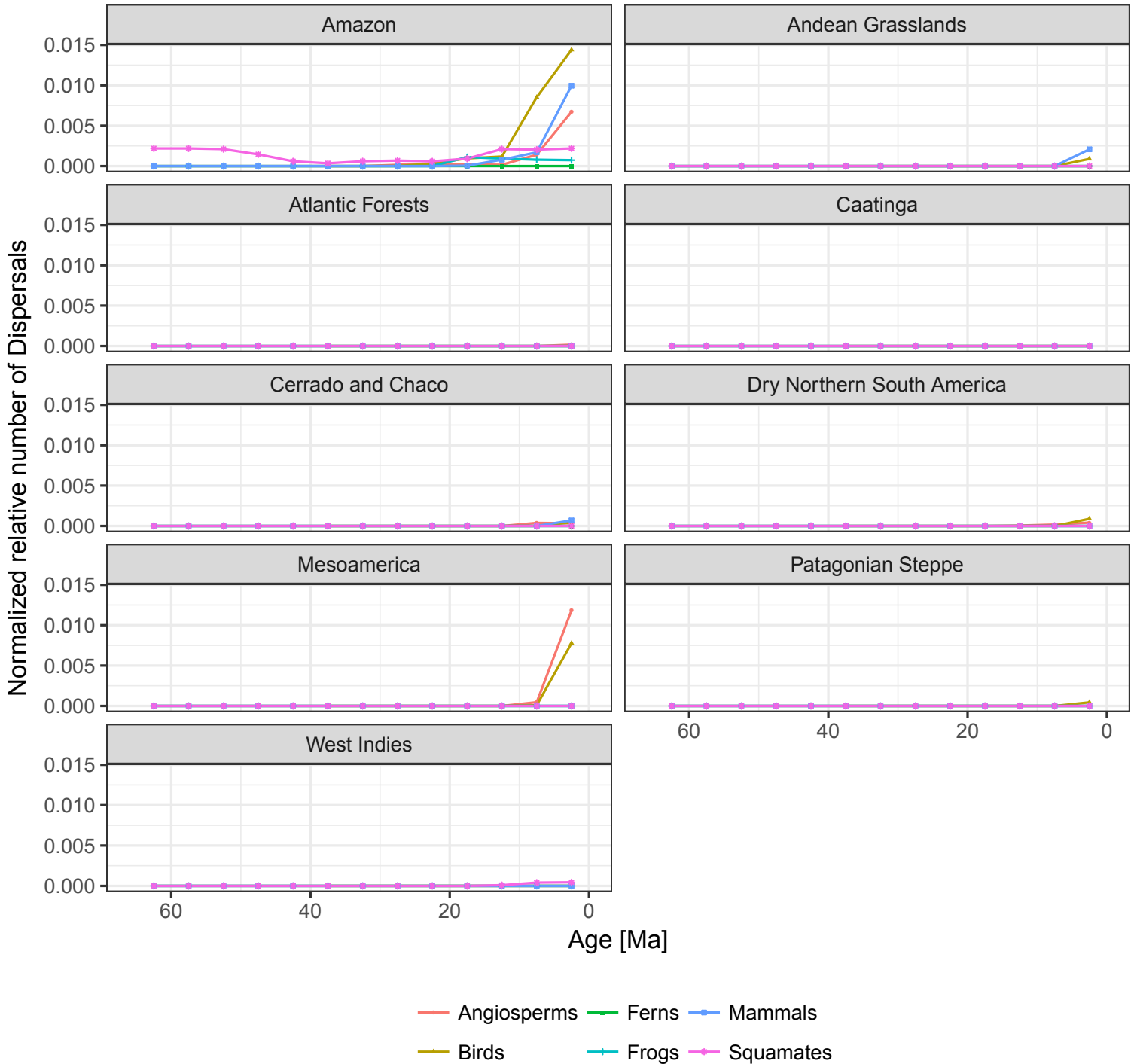
Dry Northern South America

Fig. S11: Dispersals through time (Time-stratified model)



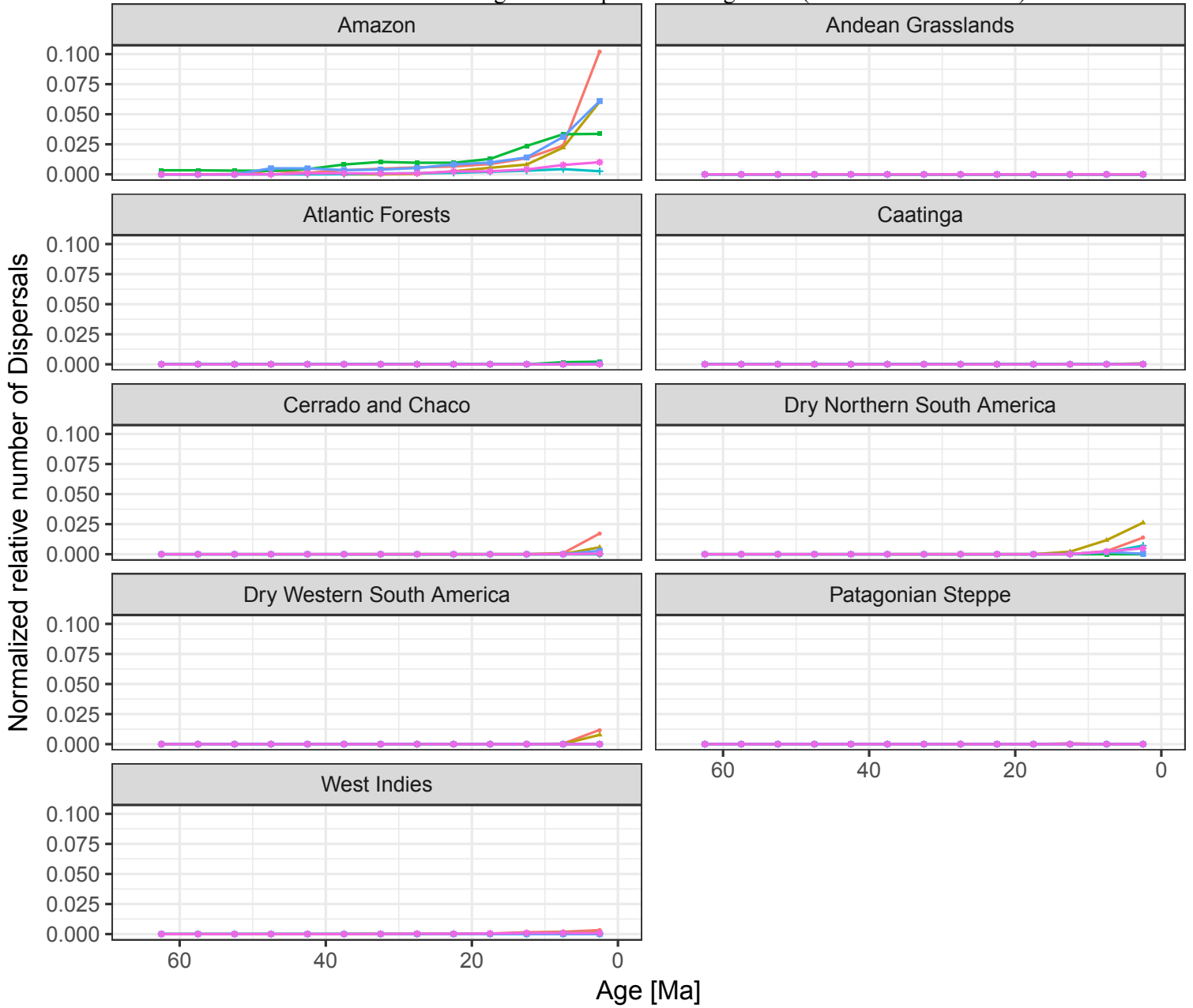
Dry Western South America

Fig. S11: Dispersals through time (Time-stratified model)



Mesoamerica

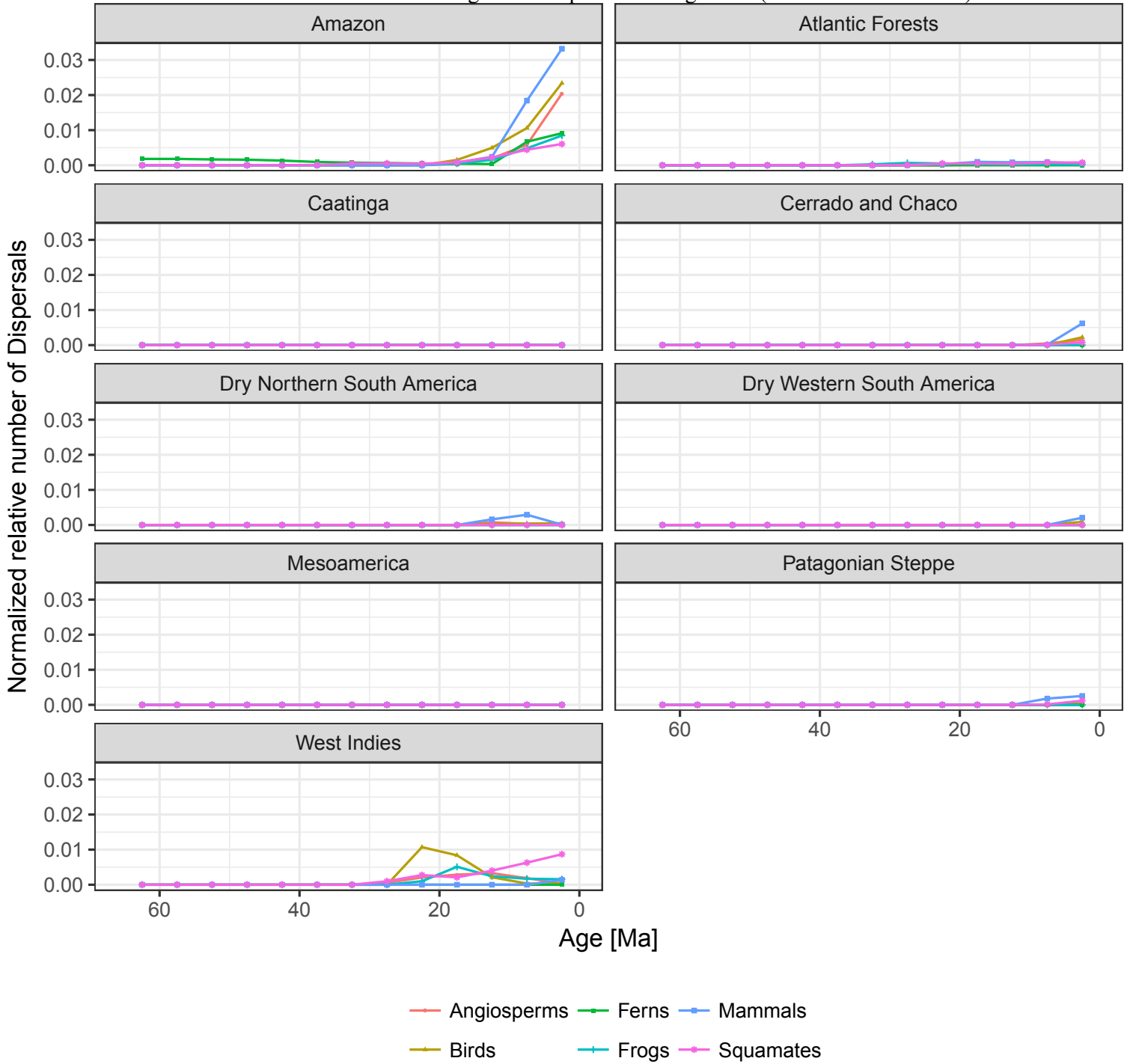
Fig. S11: Dispersals through time (Time-stratified model)



—●— Angiosperms —■— Ferns —▲— Mammals
 —◆— Birds —×— Frogs —●— Squamates

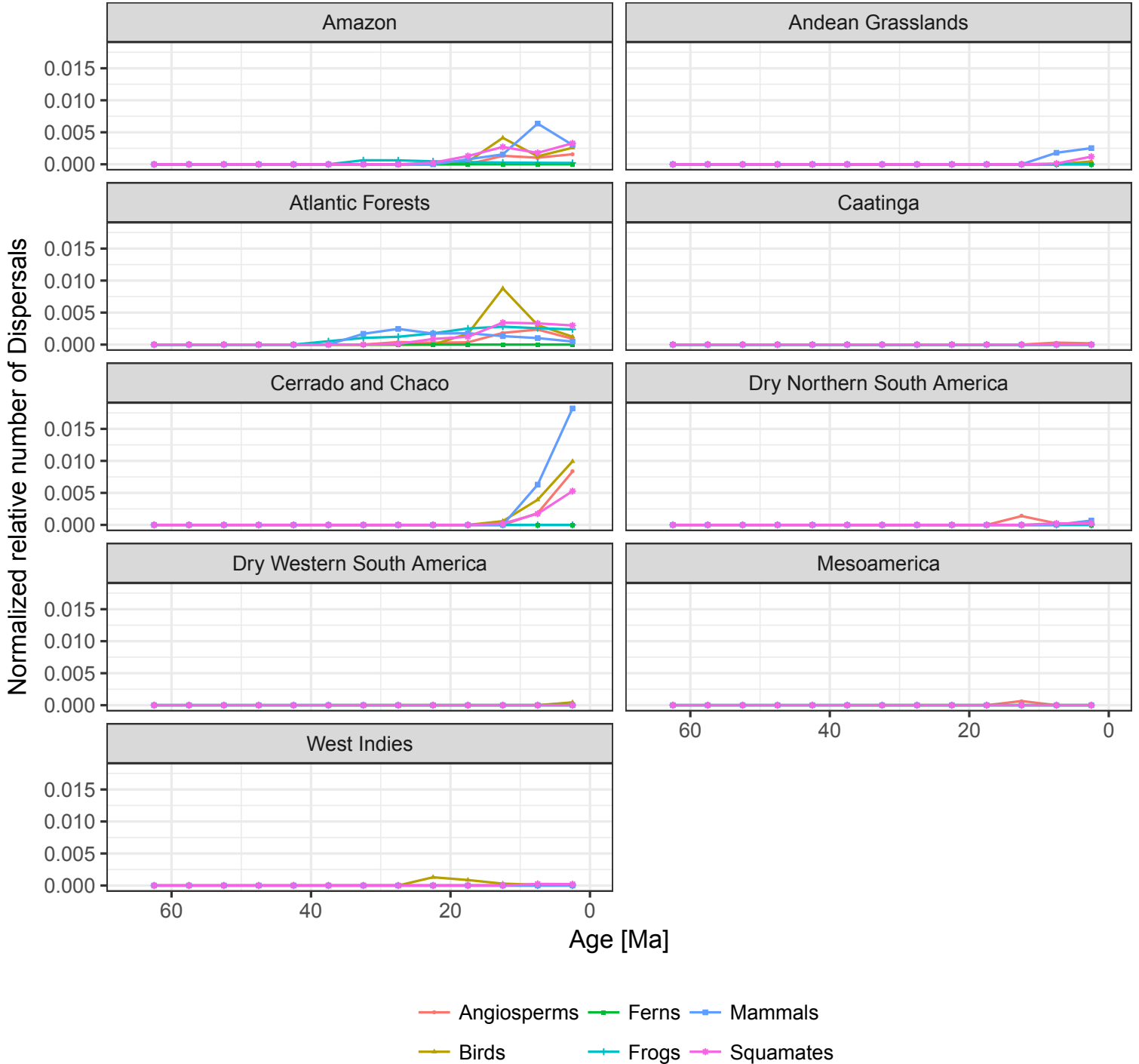
Andean Grasslands

Fig. S11: Dispersals through time (Time-stratified model)



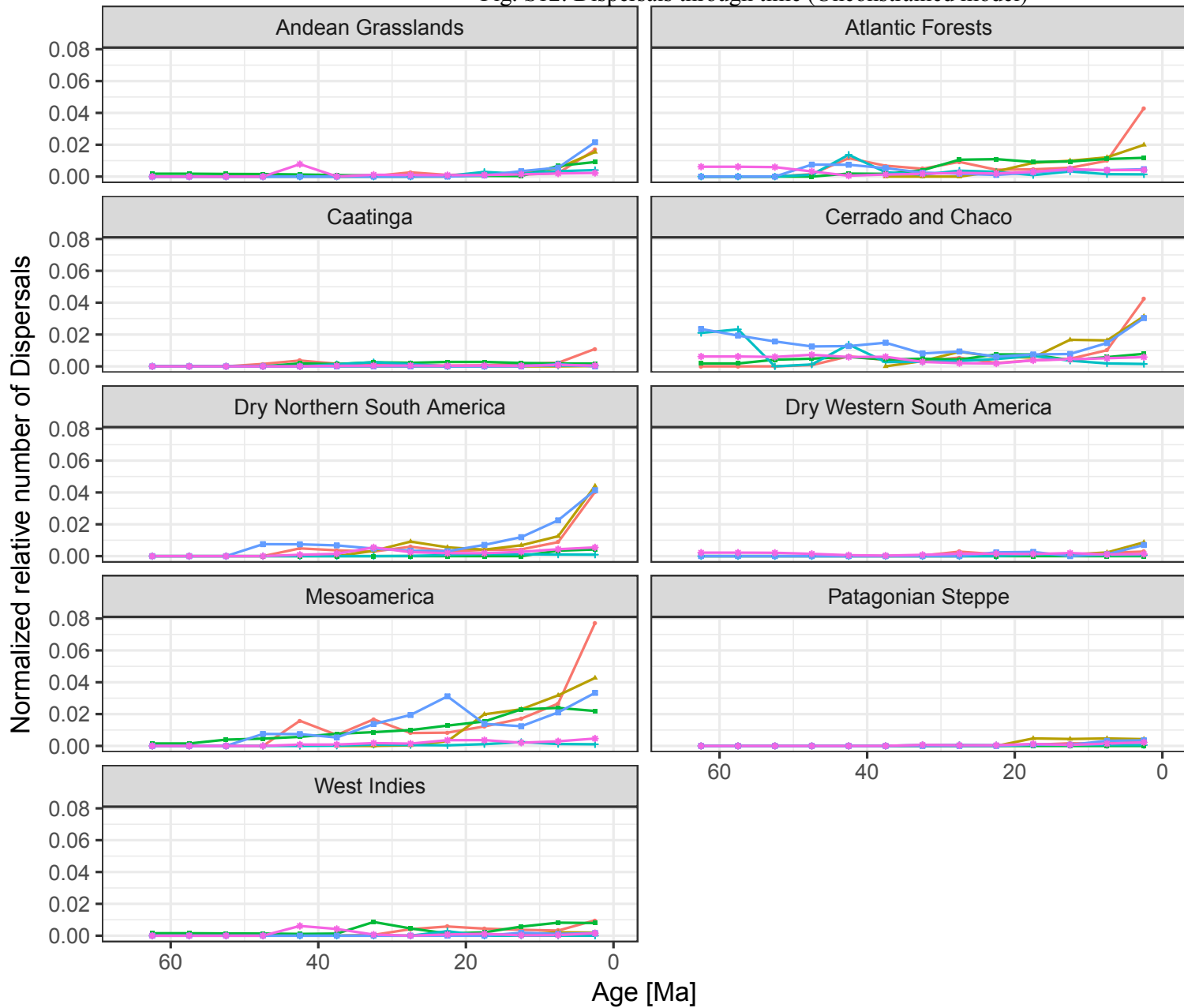
Patagonian Steppe

Fig. S11: Dispersals through time (Time-stratified model)



Amazon

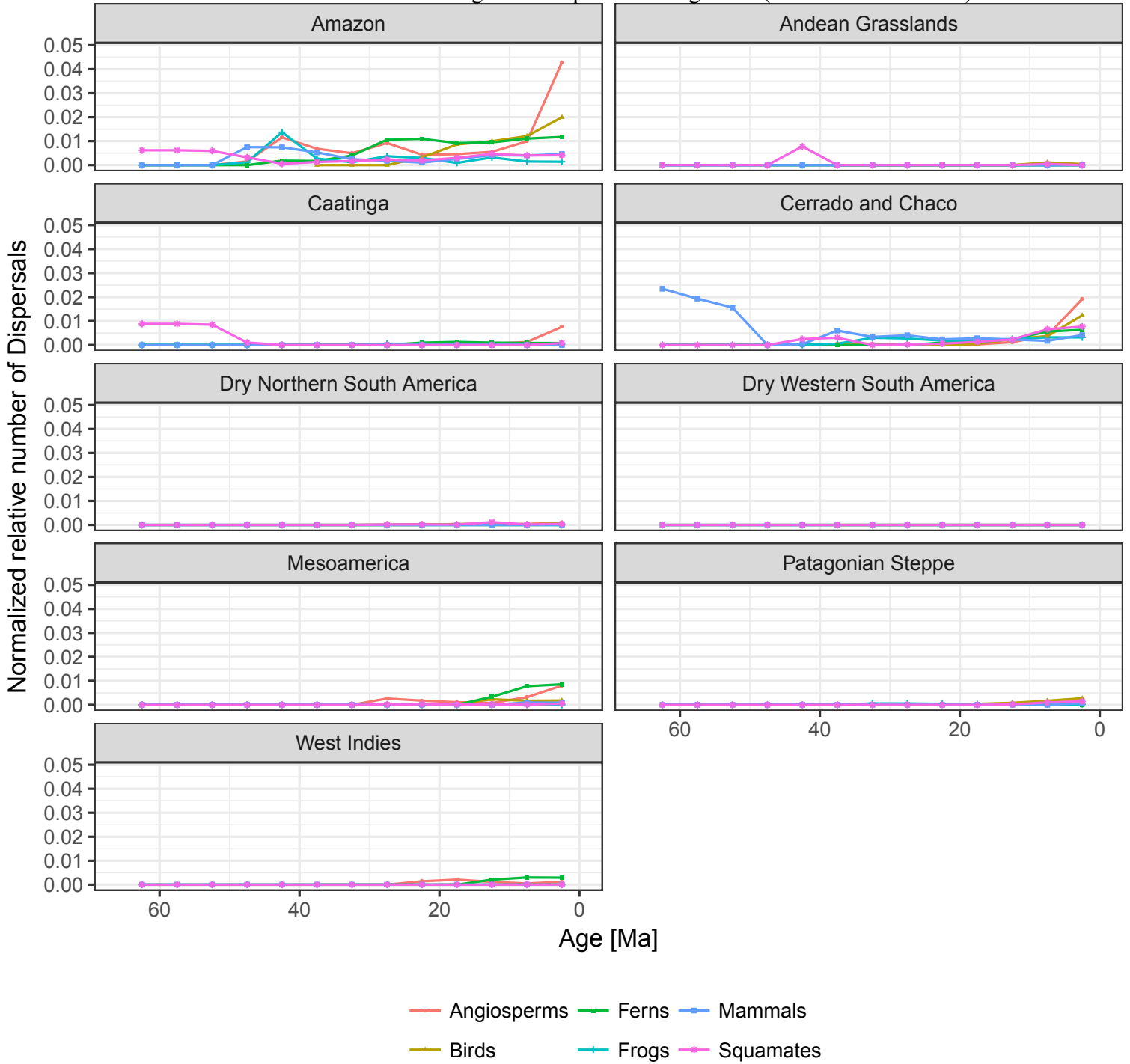
Fig. S12: Dispersals through time (Unconstrained model)



- Angiosperms
- Ferns
- ▲— Mammals
- ◆— Birds
- ×— Frogs
- *— Squamates

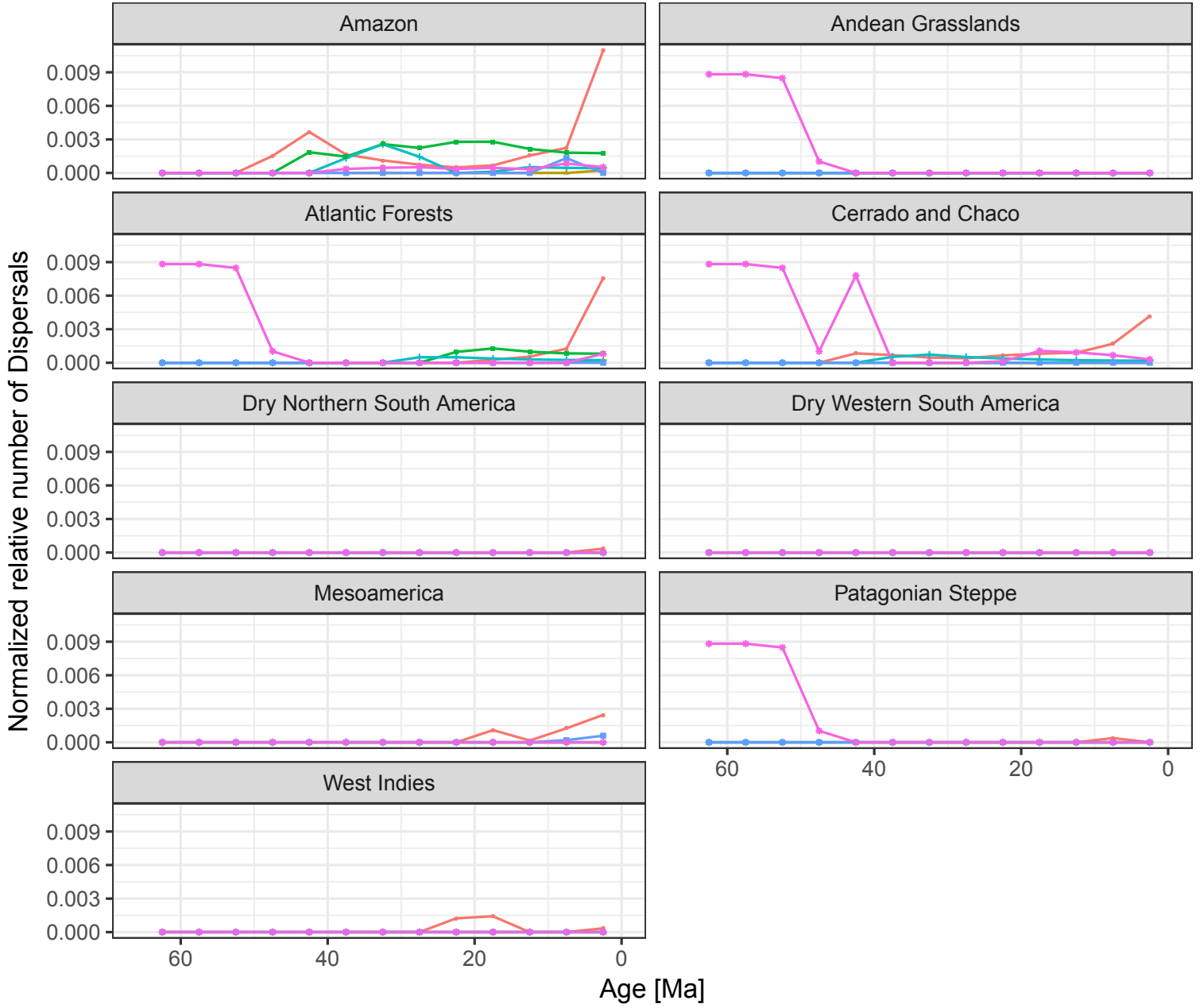
Atlantic Forests

Fig. S12: Dispersals through time (Unconstrained model)



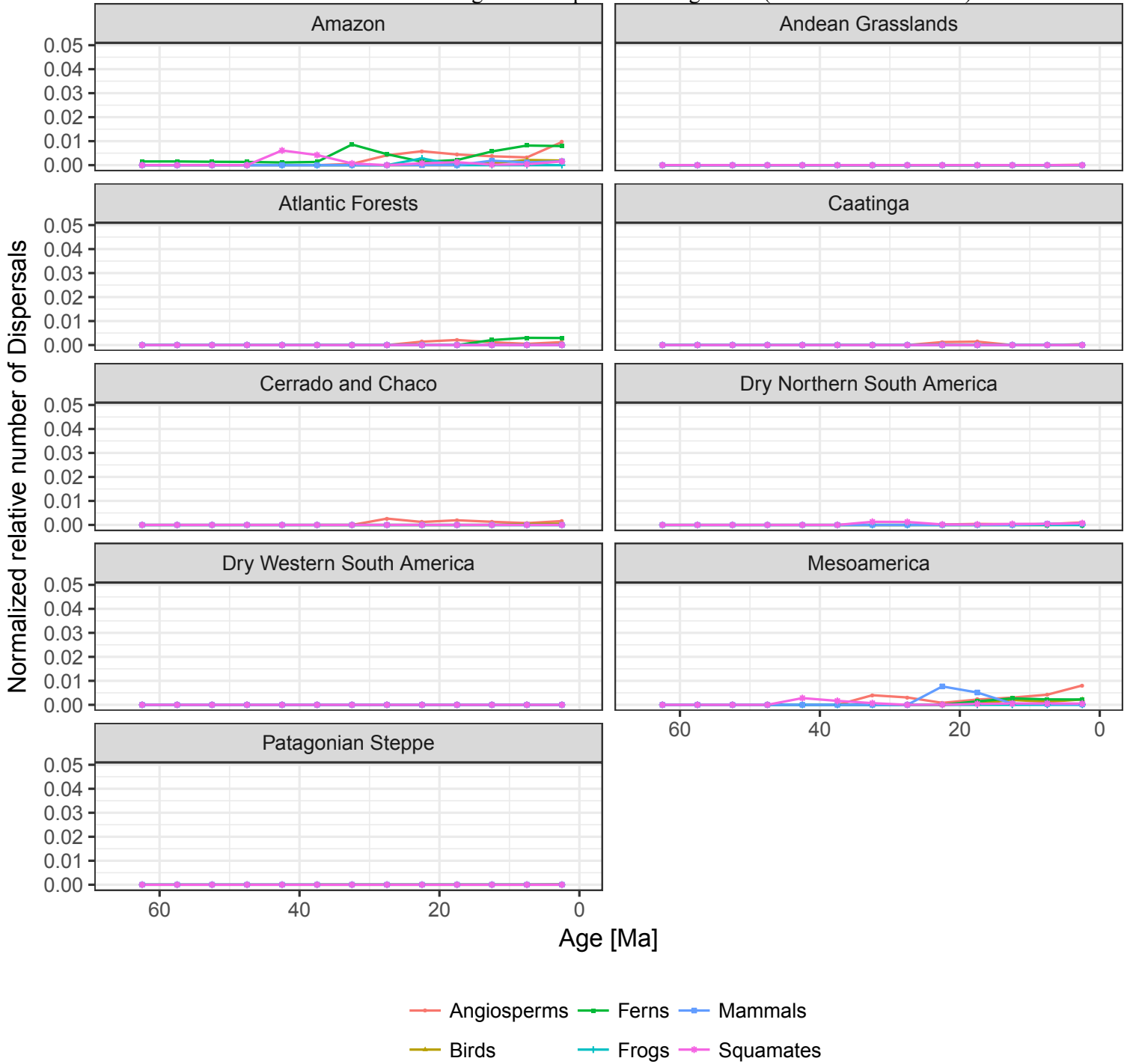
Caatinga

Fig. S12: Dispersals through time (Unconstrained model)



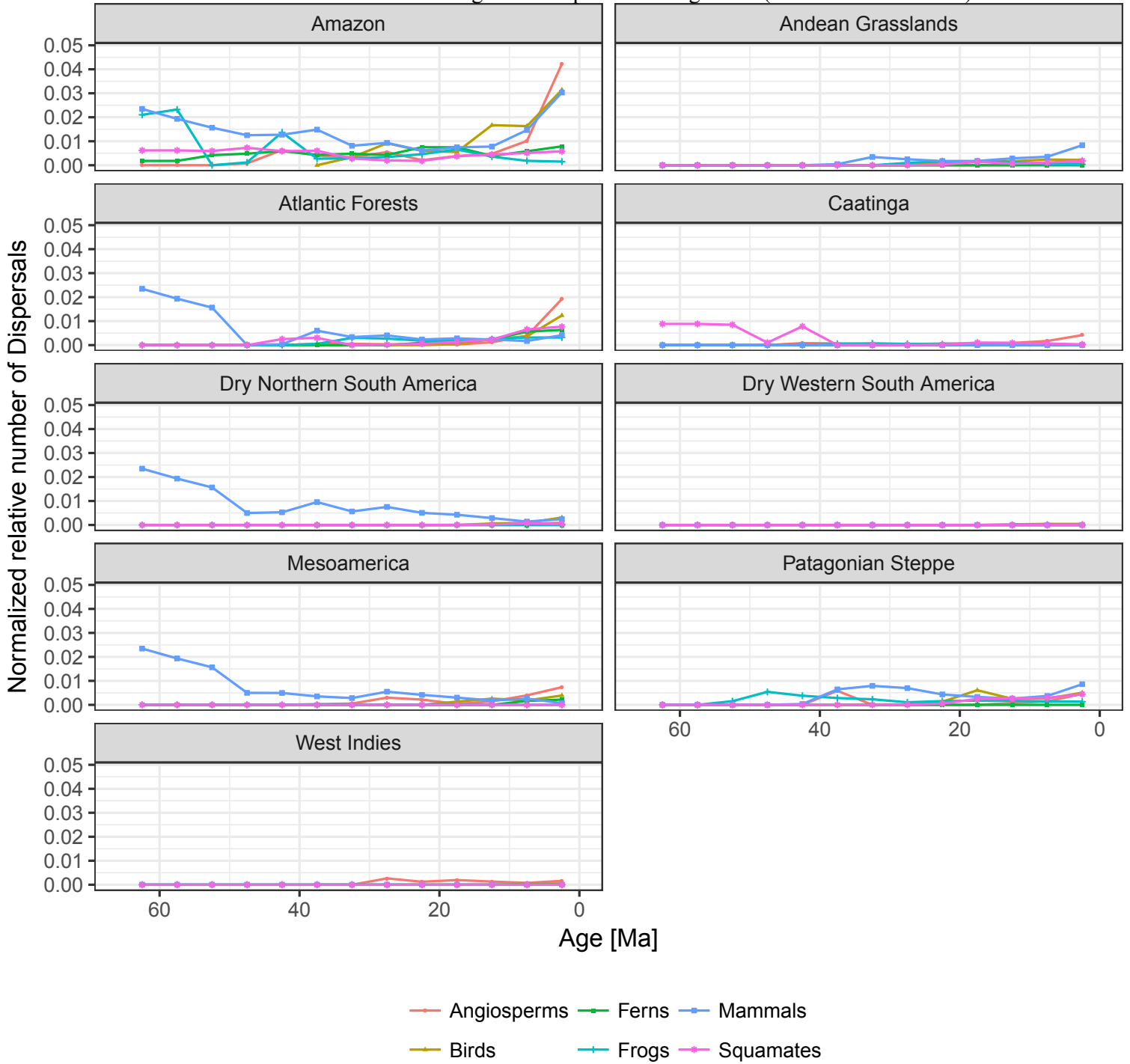
West Indies

Fig. S12: Dispersals through time (Unconstrained model)



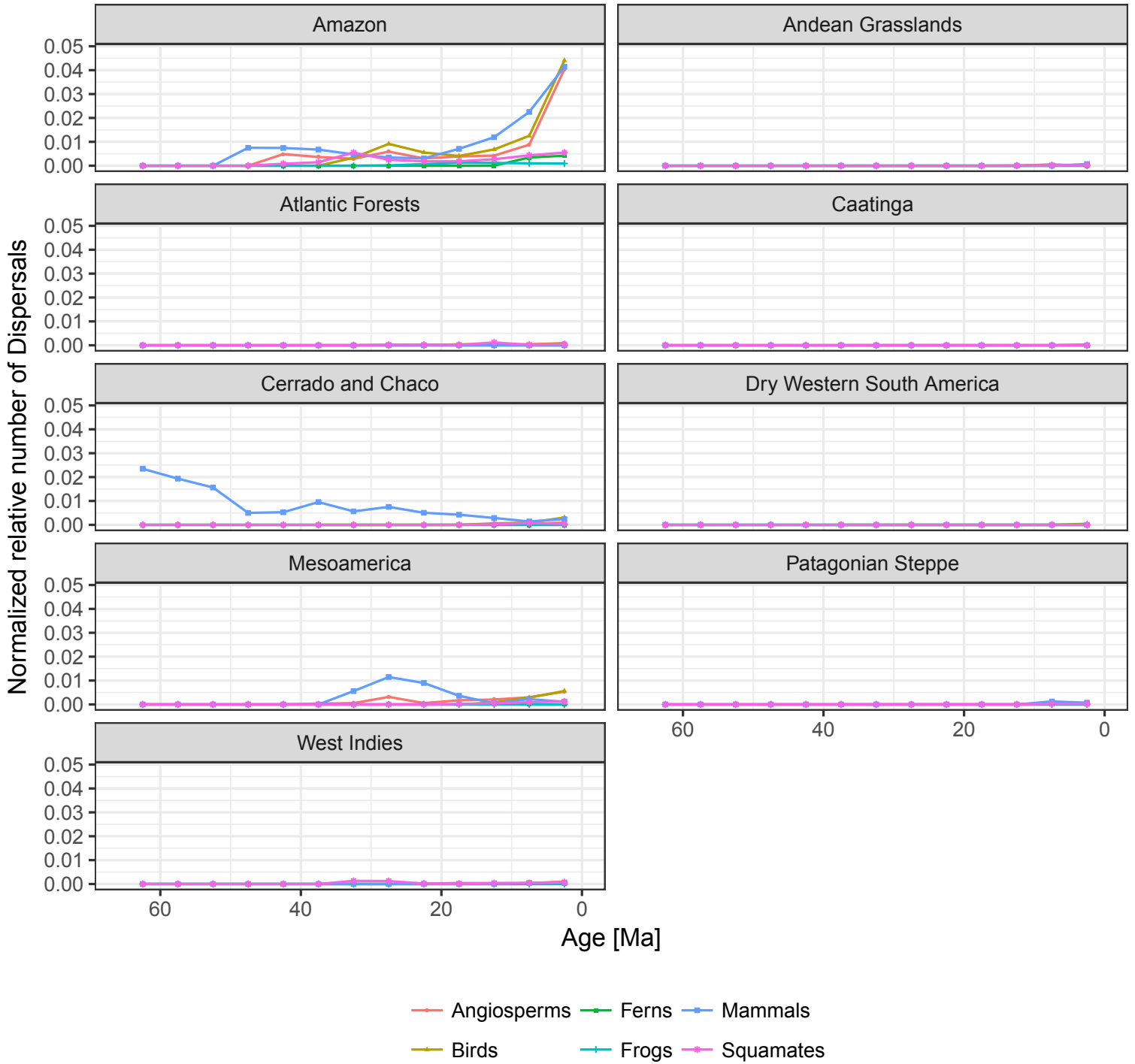
Cerrado and Chaco

Fig. S12: Dispersals through time (Unconstrained model)



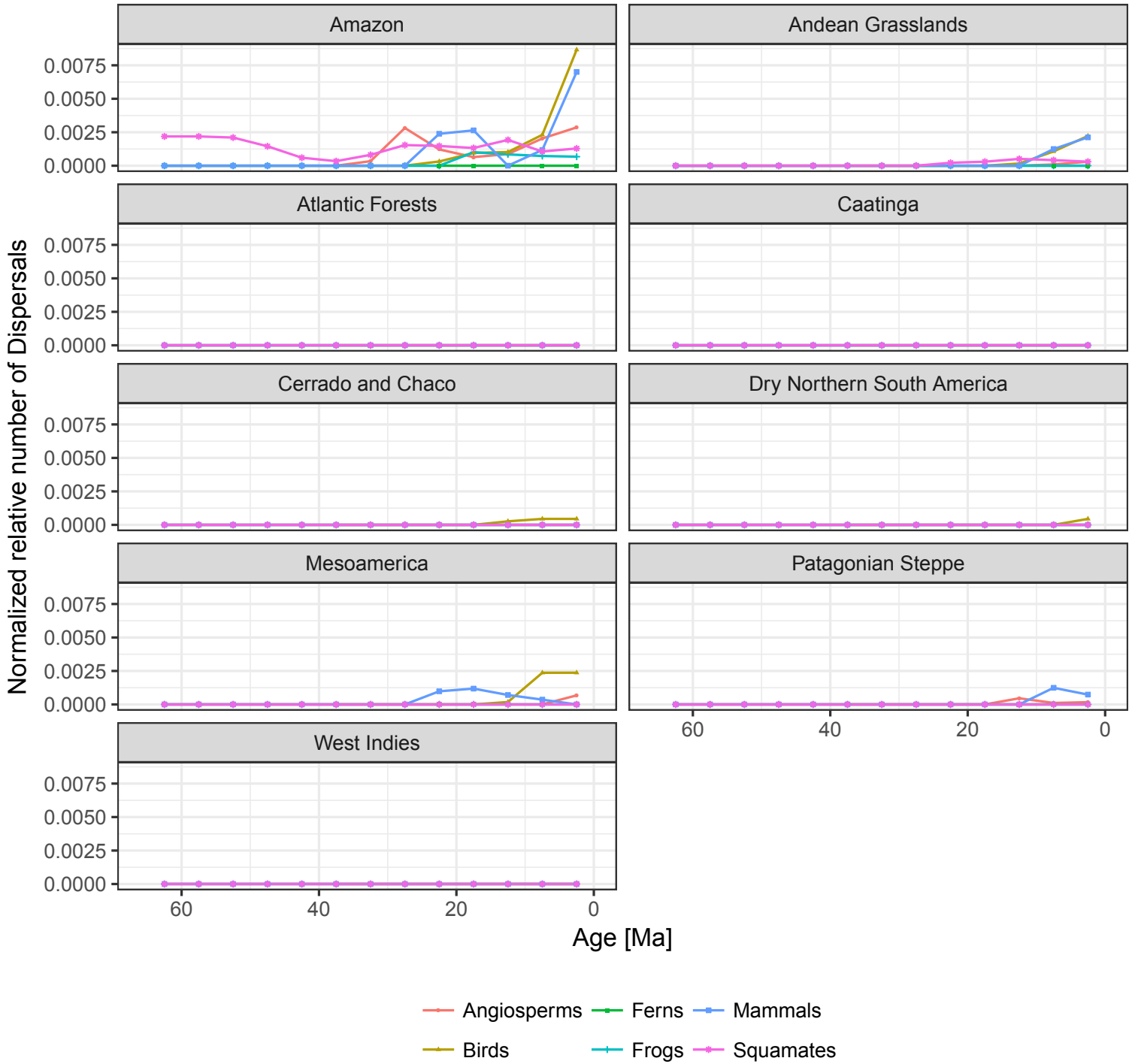
Dry Northern South America

Fig. S12: Dispersals through time (Unconstrained model)



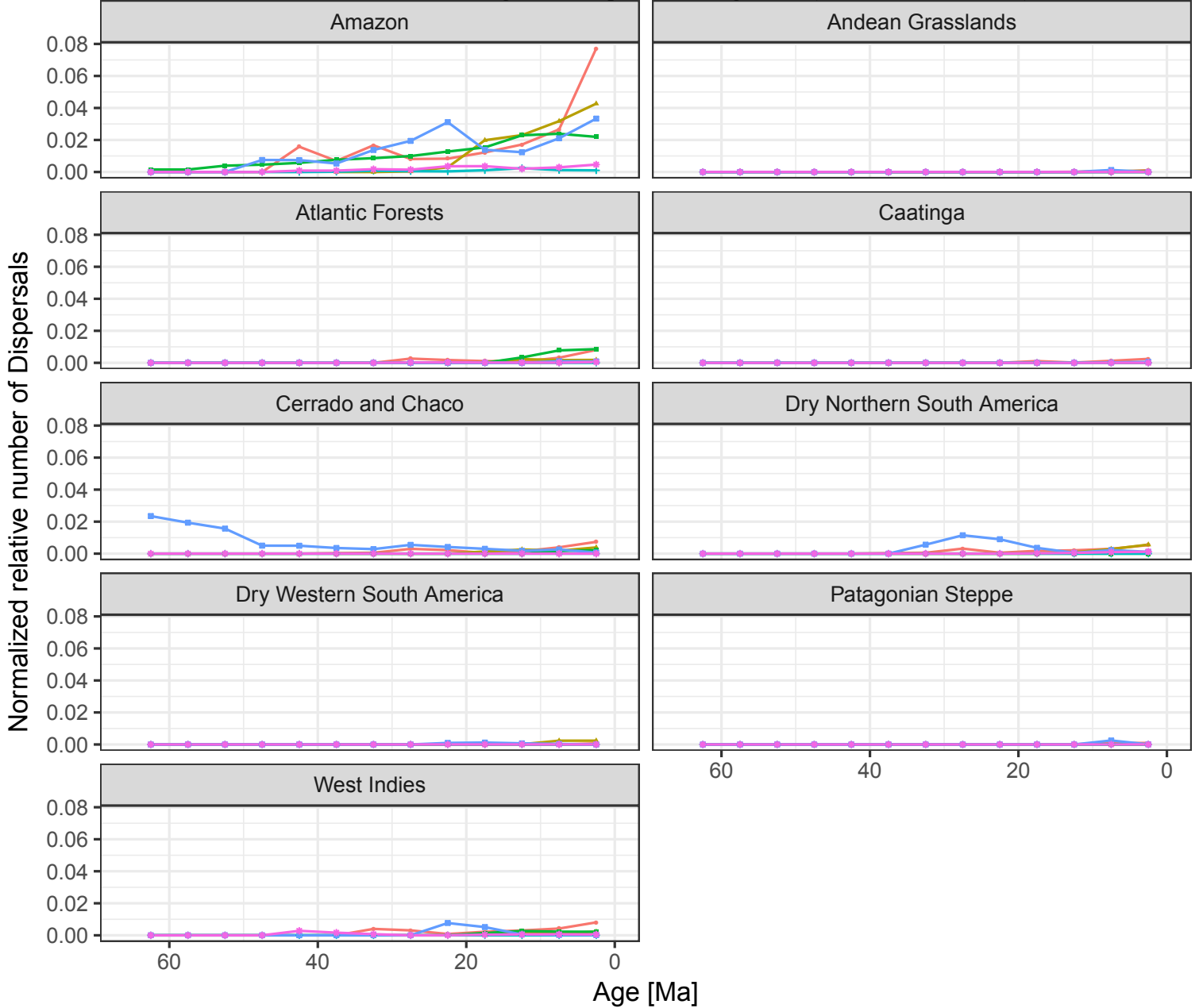
Dry Western South America

Fig. S12: Dispersals through time (Unconstrained model)



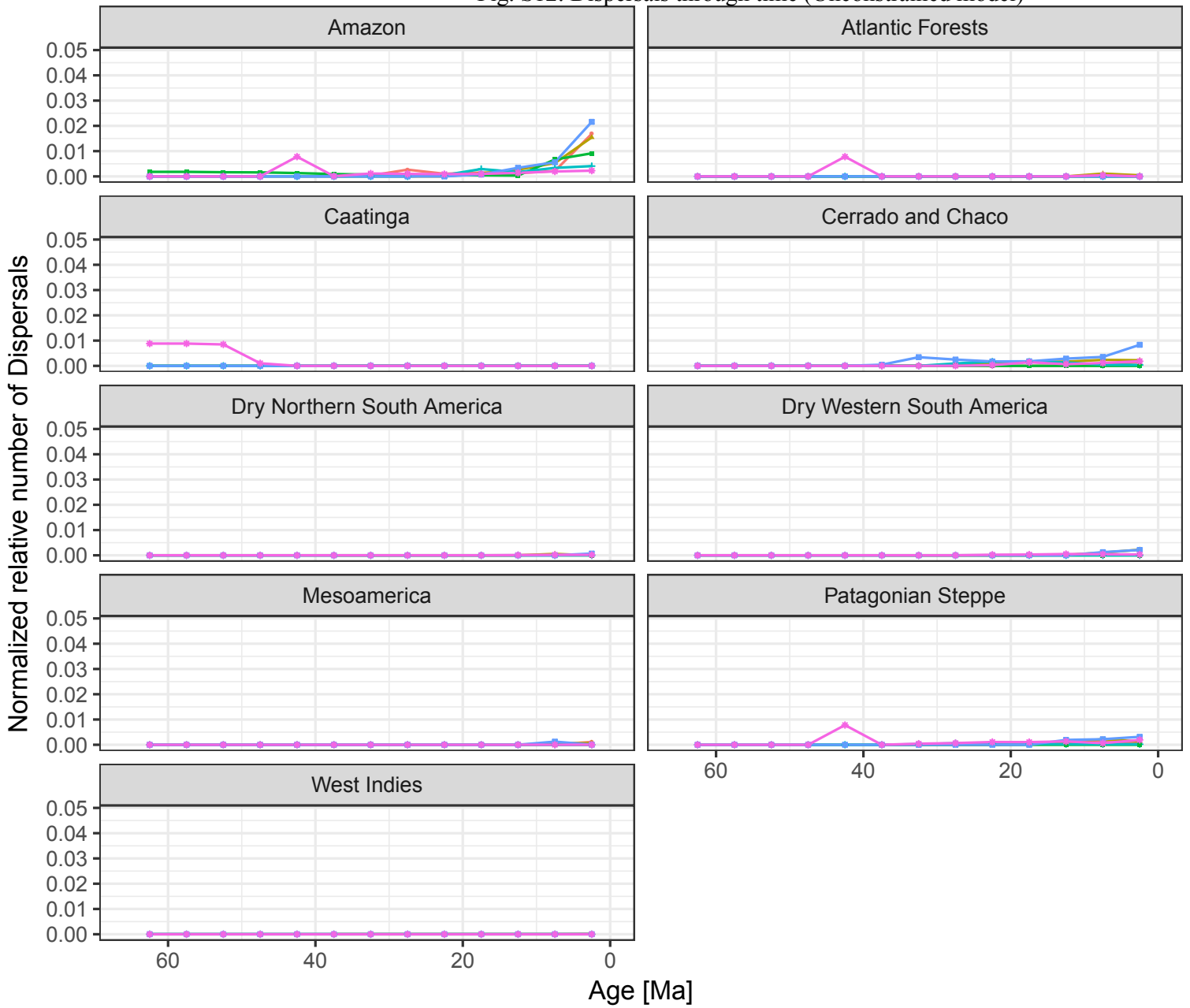
Mesoamerica

Fig. S12: Dispersals through time (Unconstrained model)



Andean Grasslands

Fig. S12: Dispersals through time (Unconstrained model)



- Angiosperms
- Ferns
- Mammals
- Birds
- Frogs
- Squamates

Patagonian Steppe

Fig. S12: Dispersals through time (Unconstrained model)

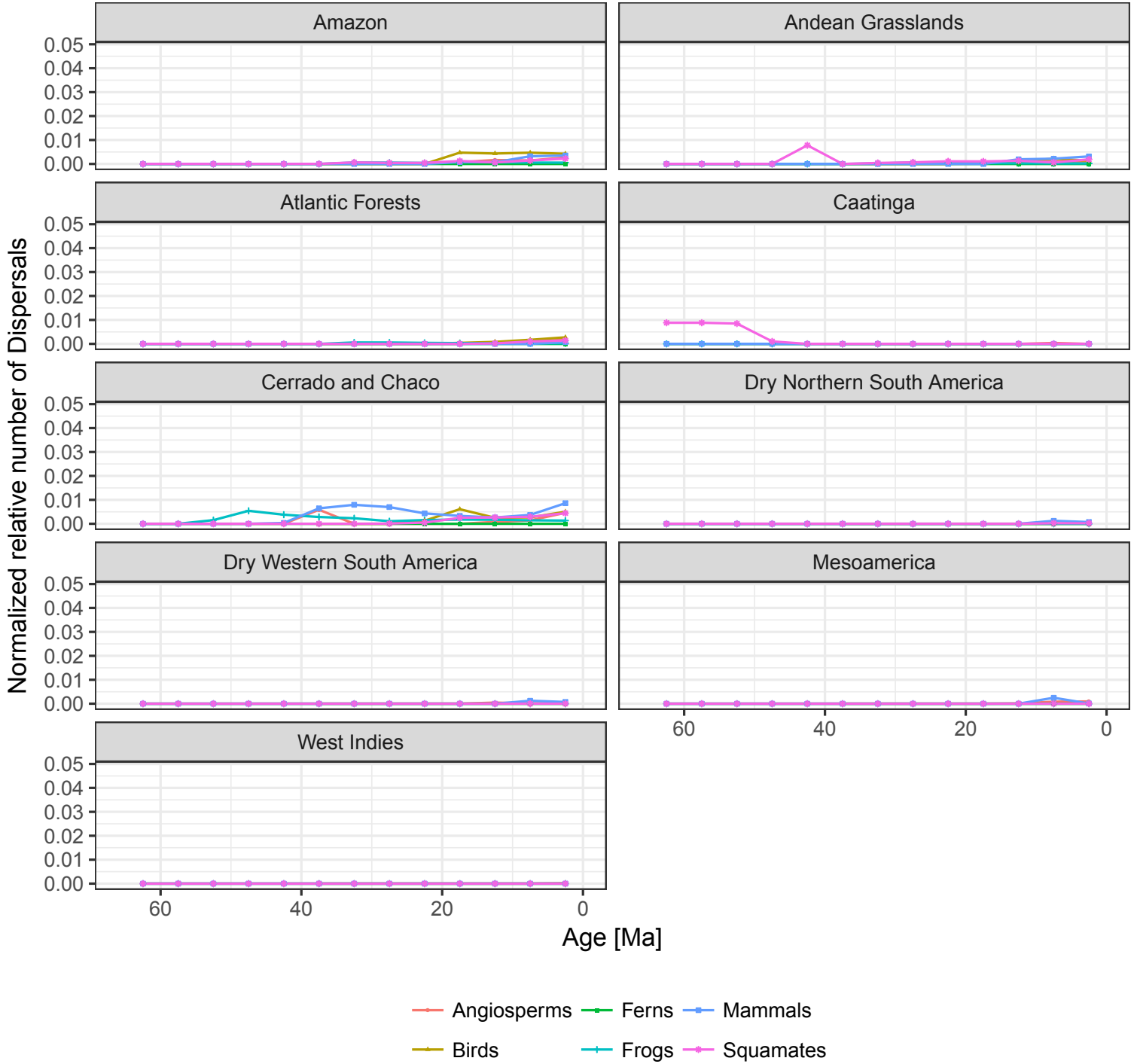
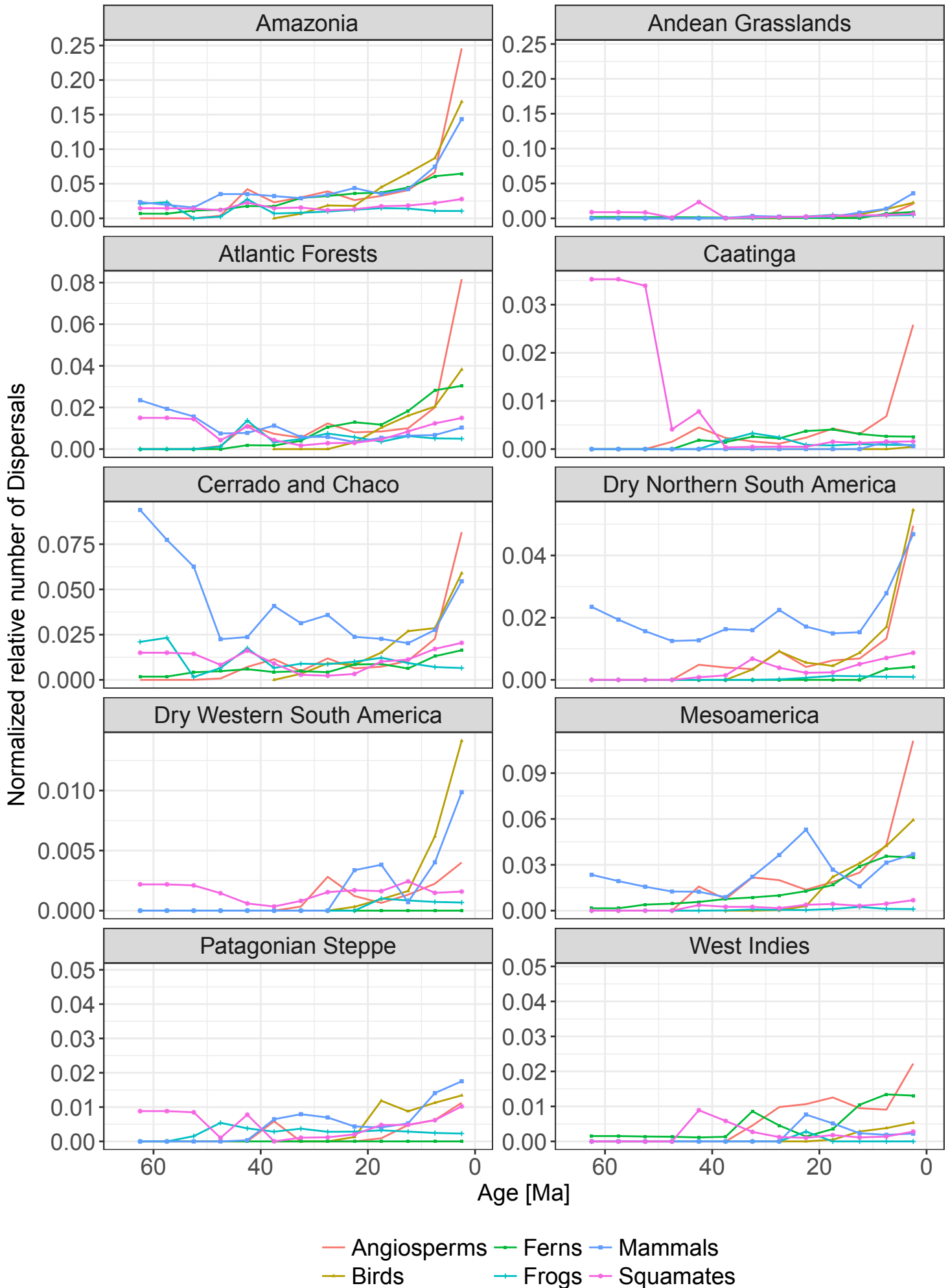


Fig. S13: Dispersal events (immigration + emigration) for each clade and region.



Emigrations from all study areas split by taxon

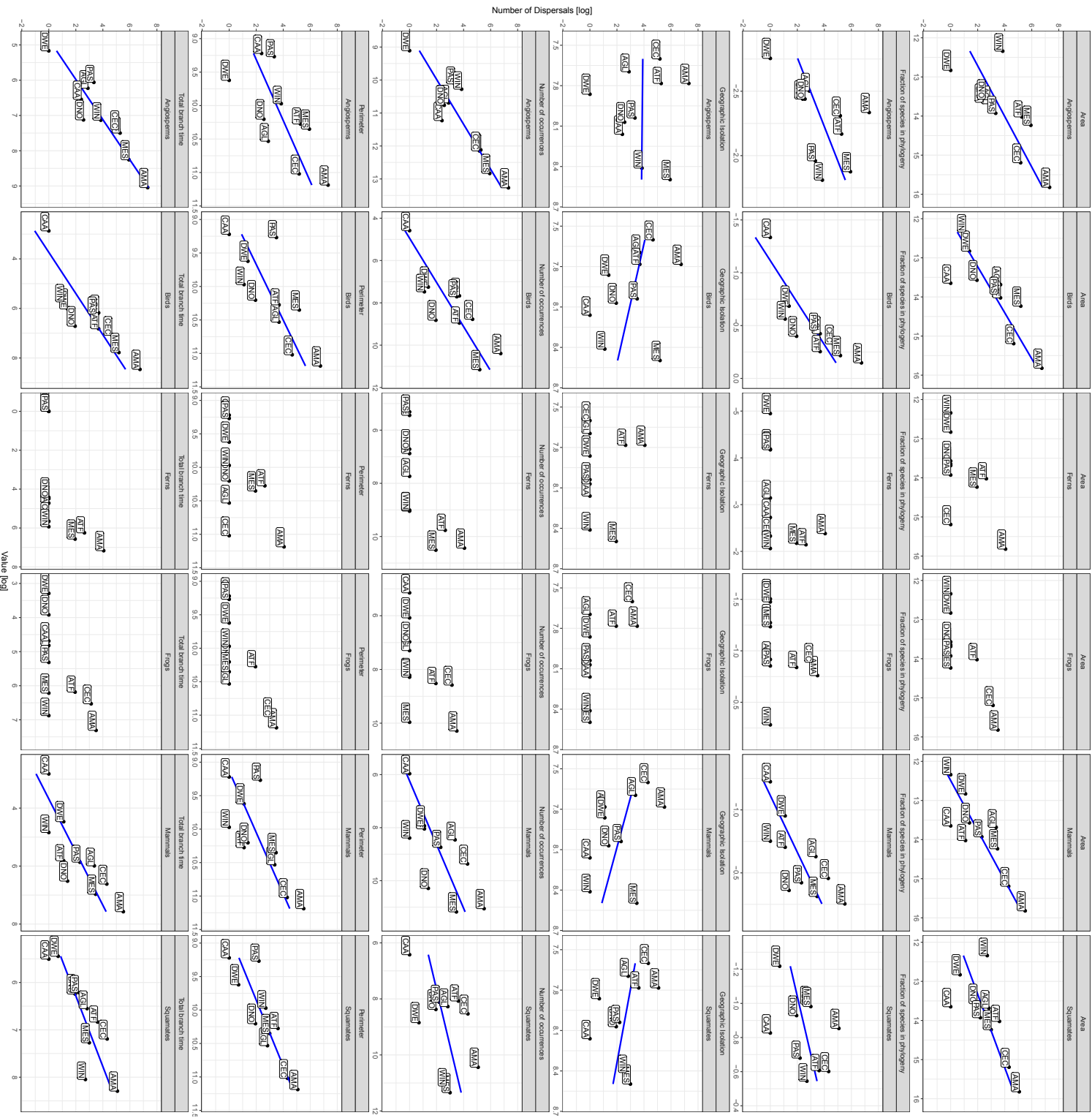


Fig. S15: Relation between phylogenetic sampling and branch time per region and clade. Colored lines show simple linear regression smoothers per clade. The black line shows a simple linear regression for the overall model.

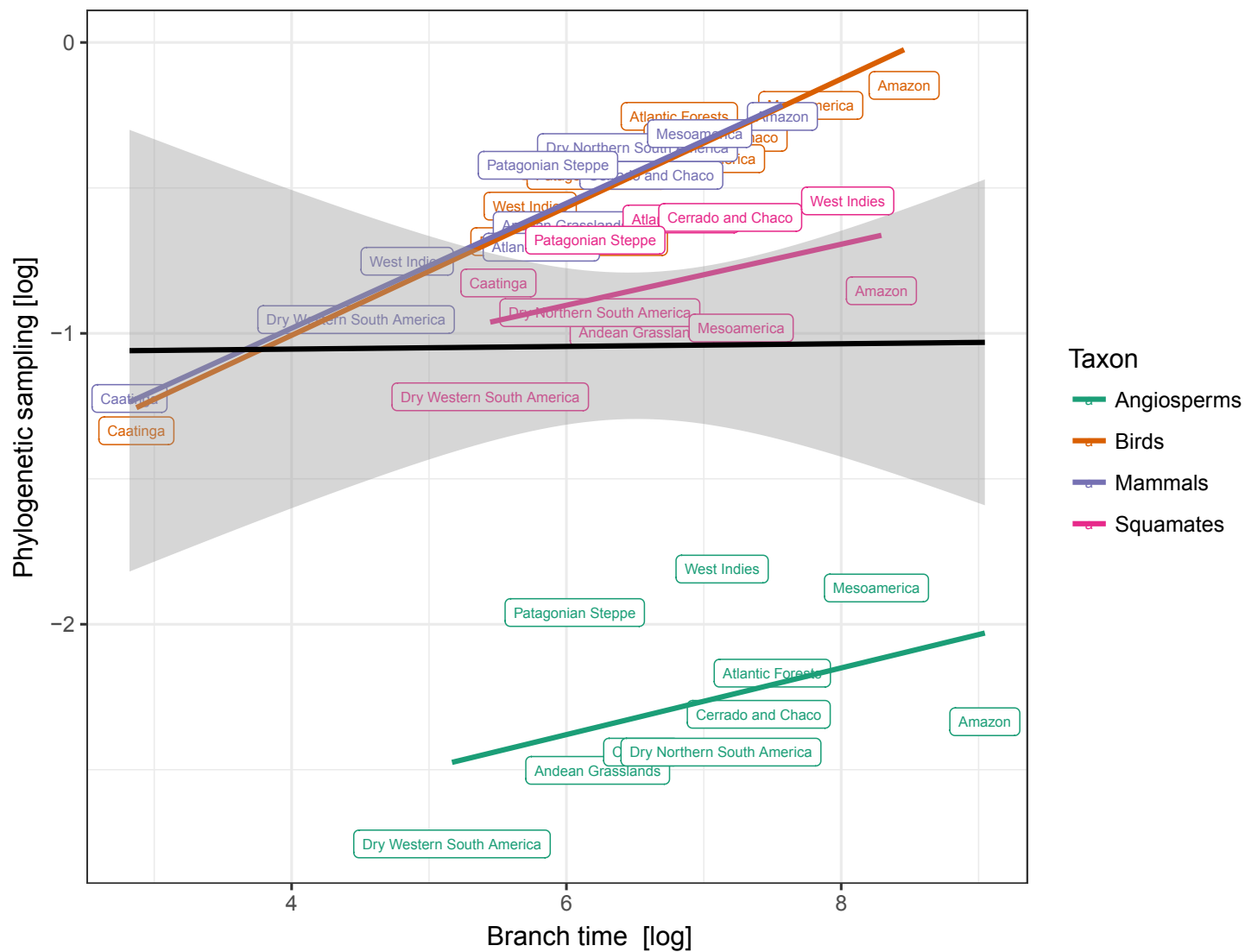


Fig. S16: Relation between phylogenetic sampling and number of occurrence records per area and clade. Colored lines show individual simple linear regression smoothers for each clade, the black line shows a simple overall linear regression. Note that the overall model suggests a negative relation due to the low phylogenetic sampling fraction in angiosperms.

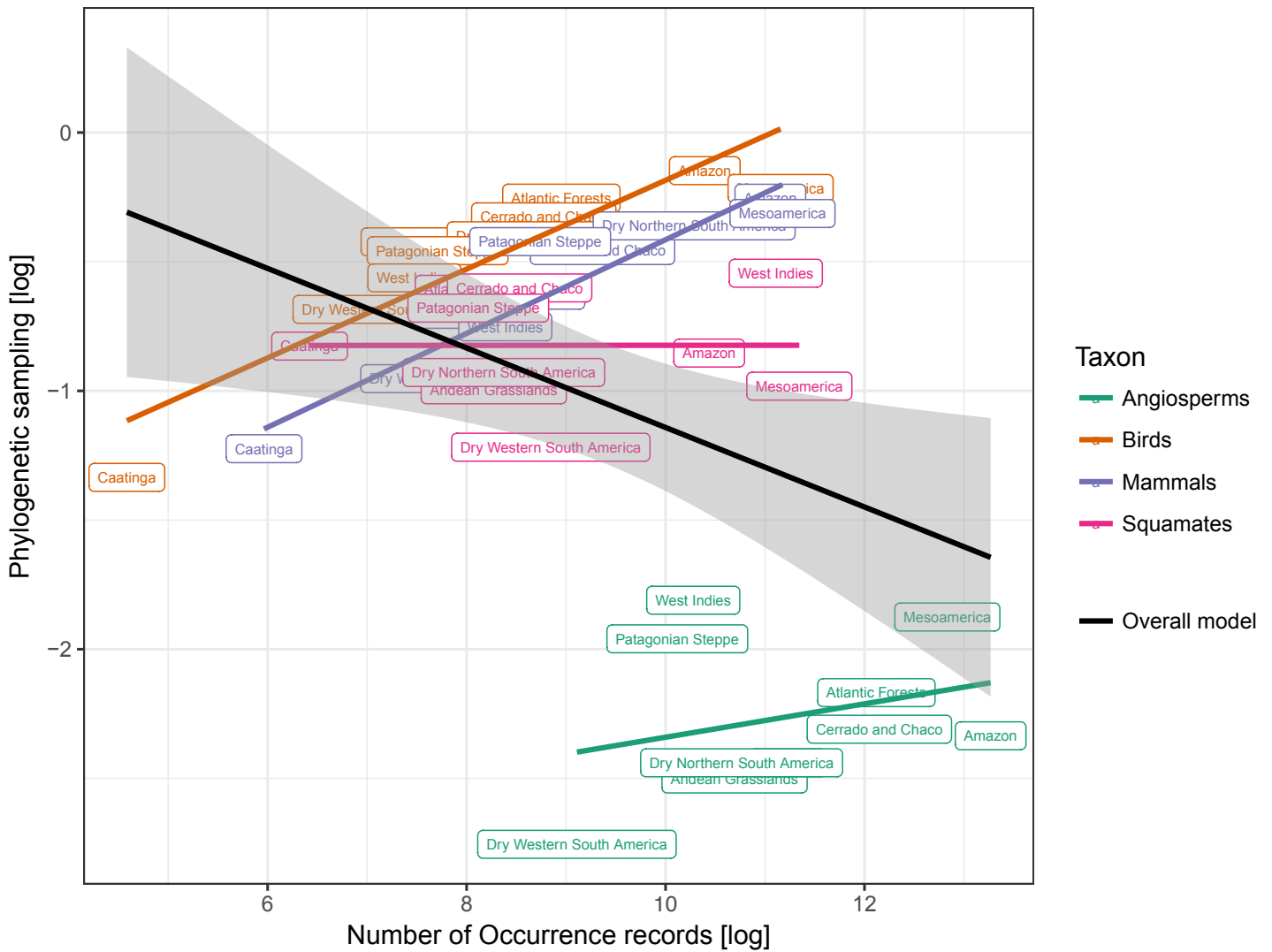


Fig. S17: Relation between emigration events and phylogenetic sampling for each study clade with sufficient data. The colored lines are individual simple linear regression smoothers.

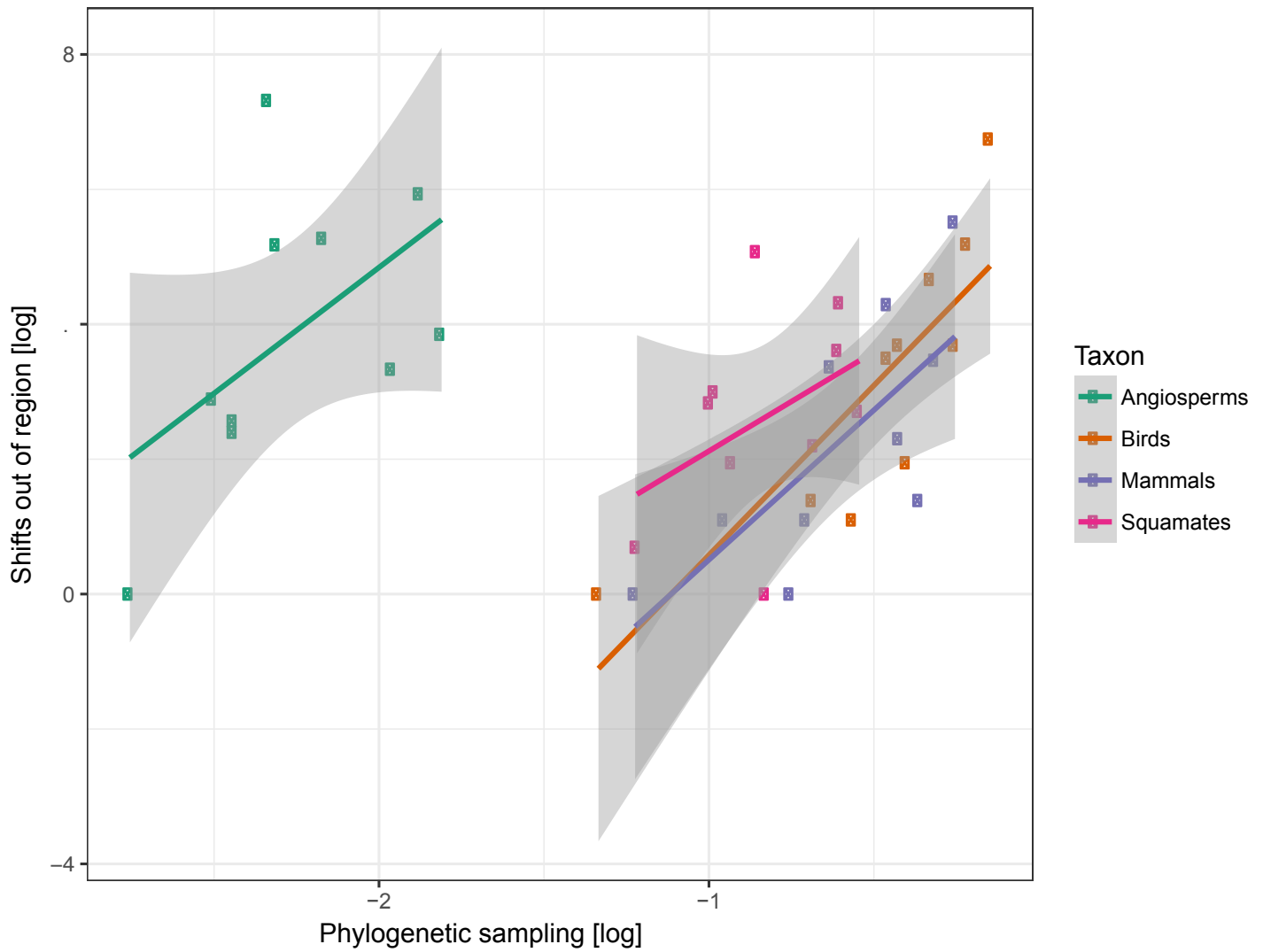


Fig. S18: Relation between emigration events and phylogenetic sampling, as identified by a simple overall linear regression across all study clades with sufficient data.

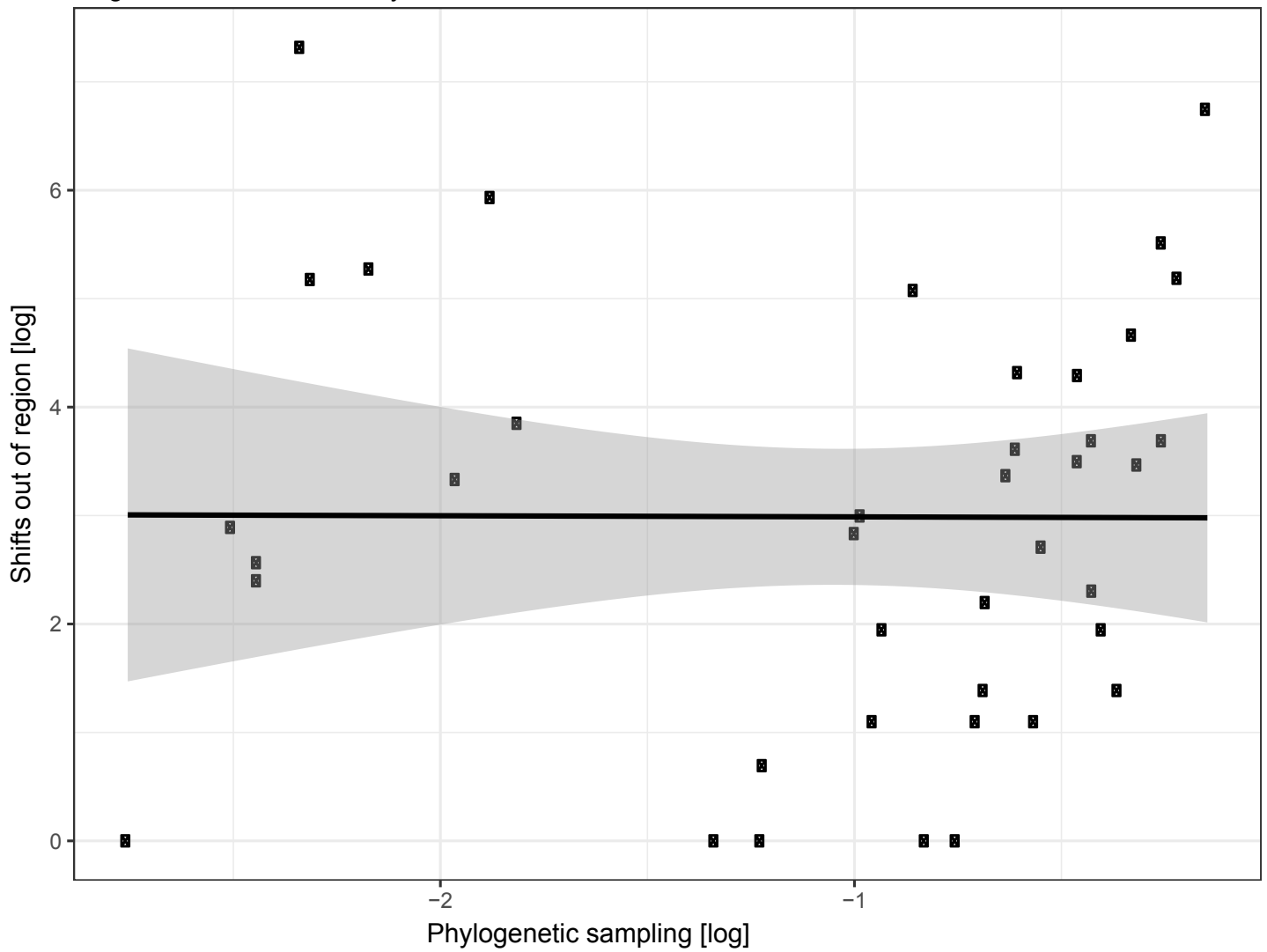


Fig. S19: Relation between emigration events and phylogenetic sampling as represented in the linear mixed effects model described in the main text. The colored lines show the partial response of emigration events to phylogenetic sampling for the four study clades with sufficient data, assuming all other predictors at their mean values. The points show raw data for illustration.

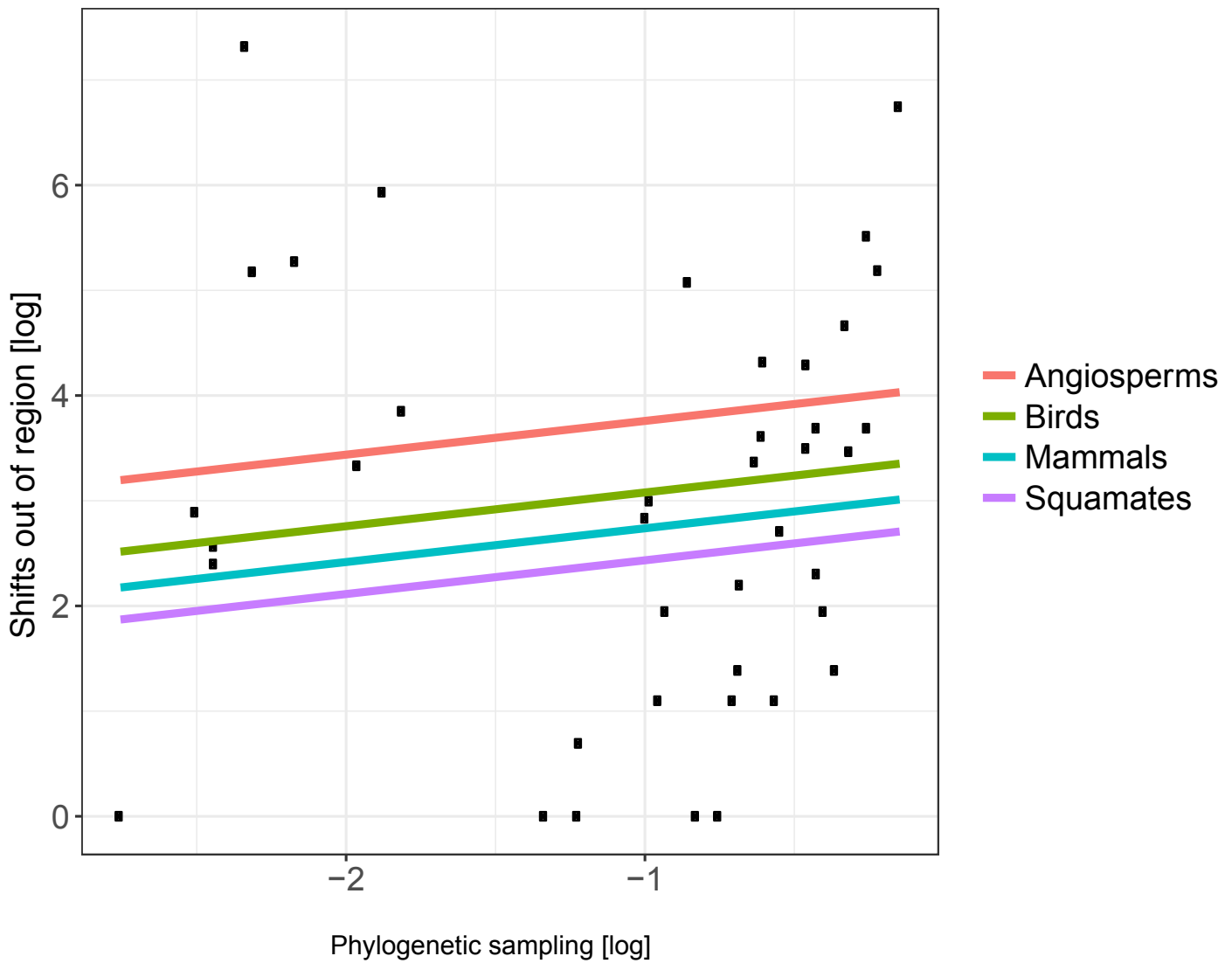


Fig. S20: Assessment of the altitudinal range comprised within the “Andean grasslands” region used in our analysis. The assessment was made by super-imposing the limits of this region on a topographic map obtained from WorldClim (www.worldclim.org). Altitudes are provided as meters above sea level.

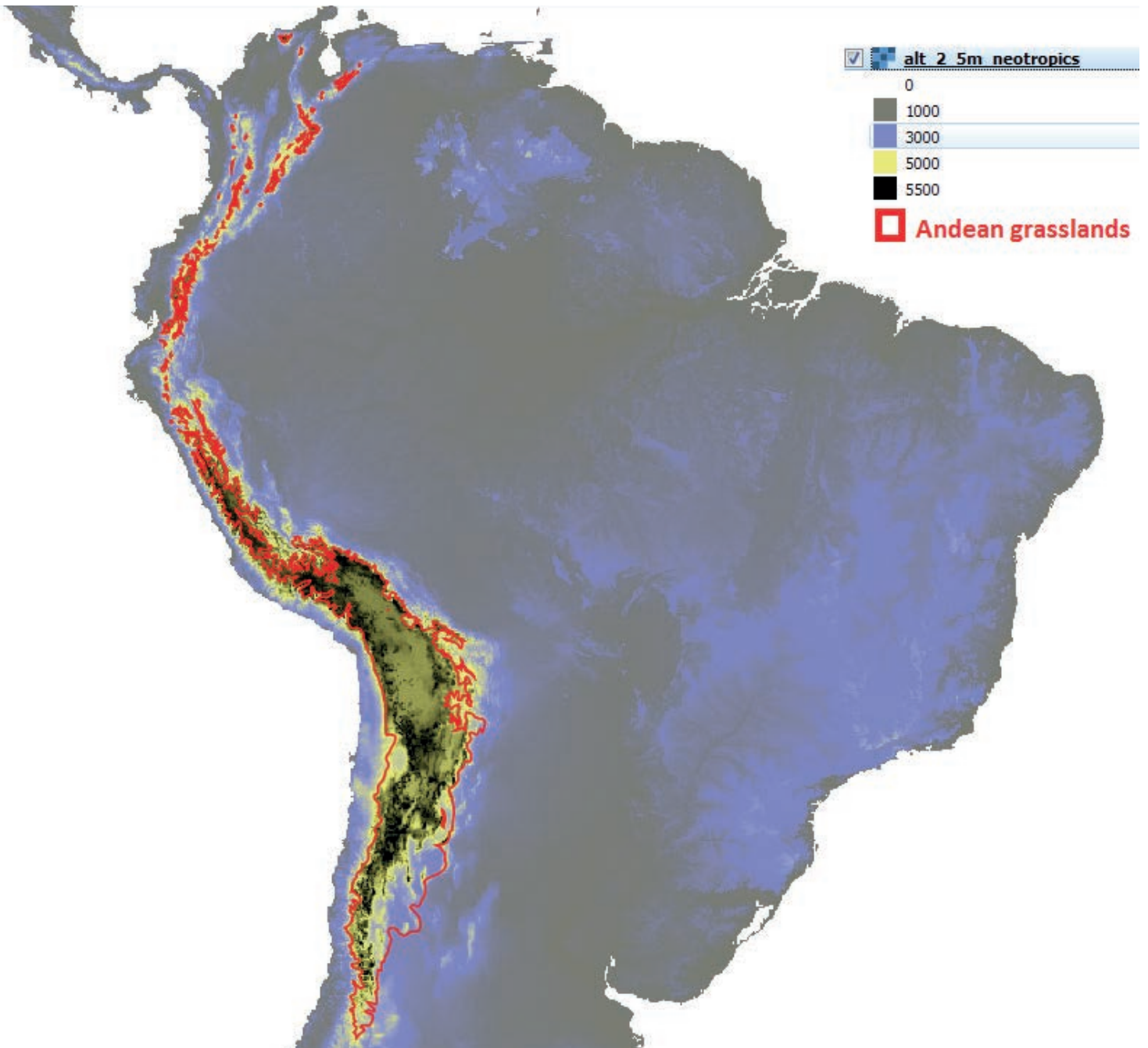
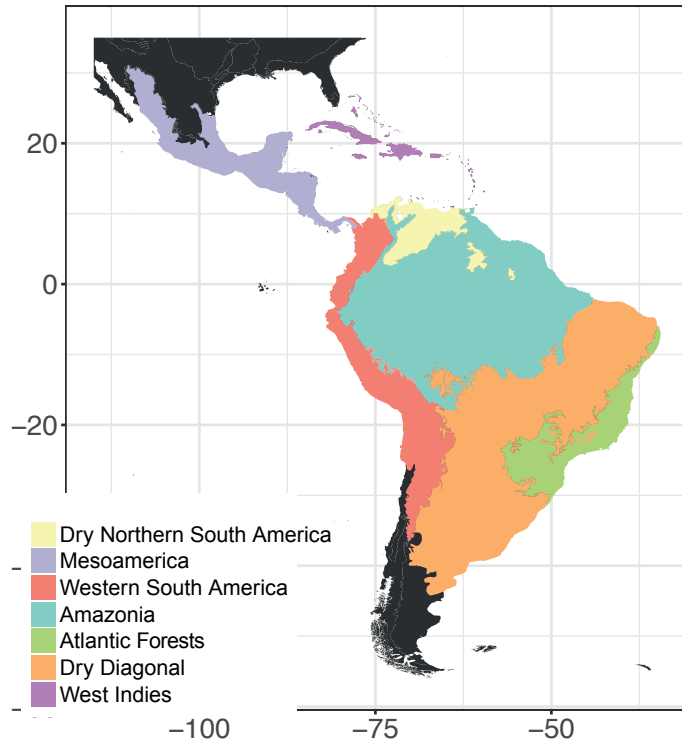


Fig. S21: Expert-defined area classification with simplified regions combining both biome borders and geological history, and the resulting cross-regional dispersal patterns inferred from the biogeographic analysis of all taxa surveyed.



All taxa – only edges with weight > 10 shown

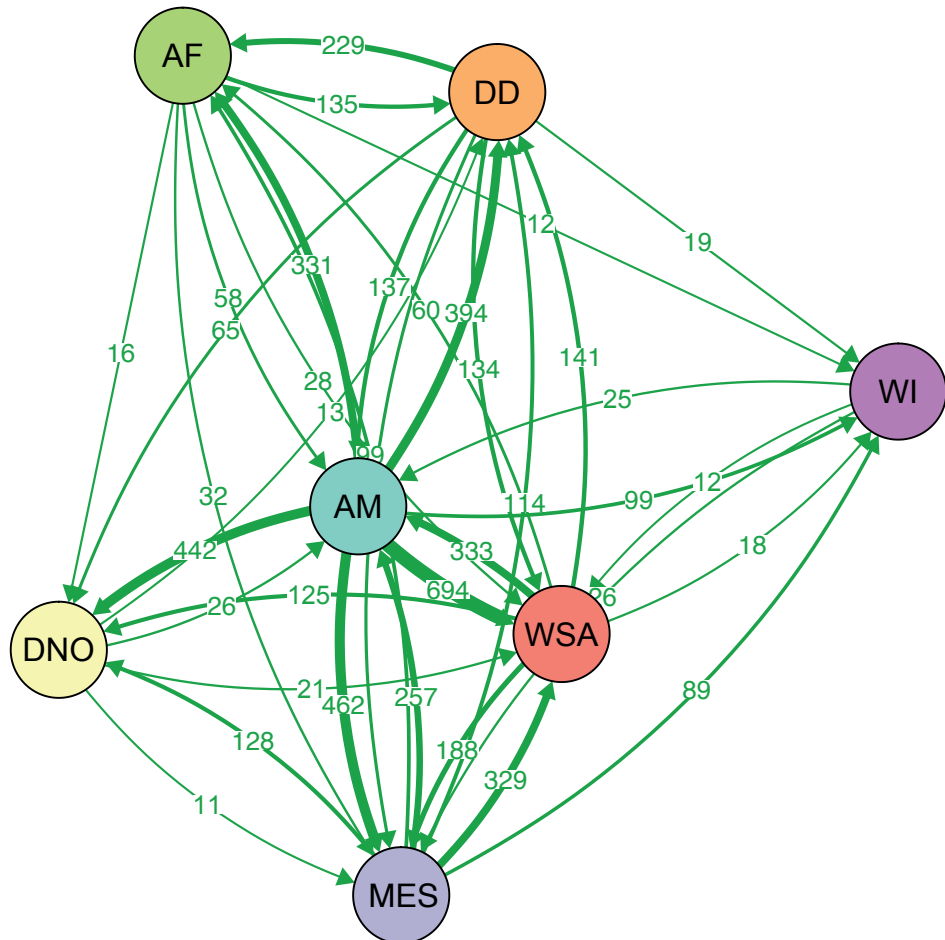
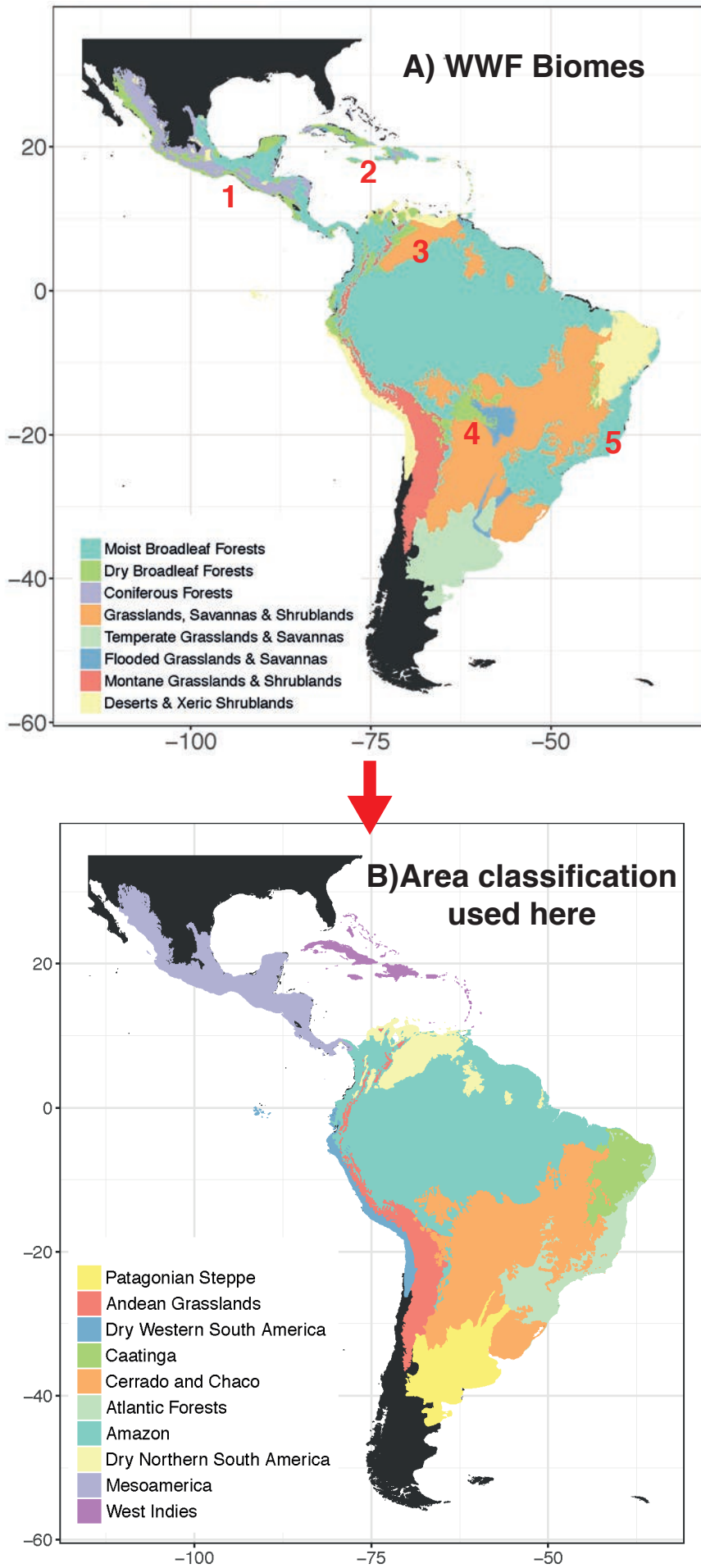


Fig. S22: Modifications of the biome classification to generate the operational units in this study.



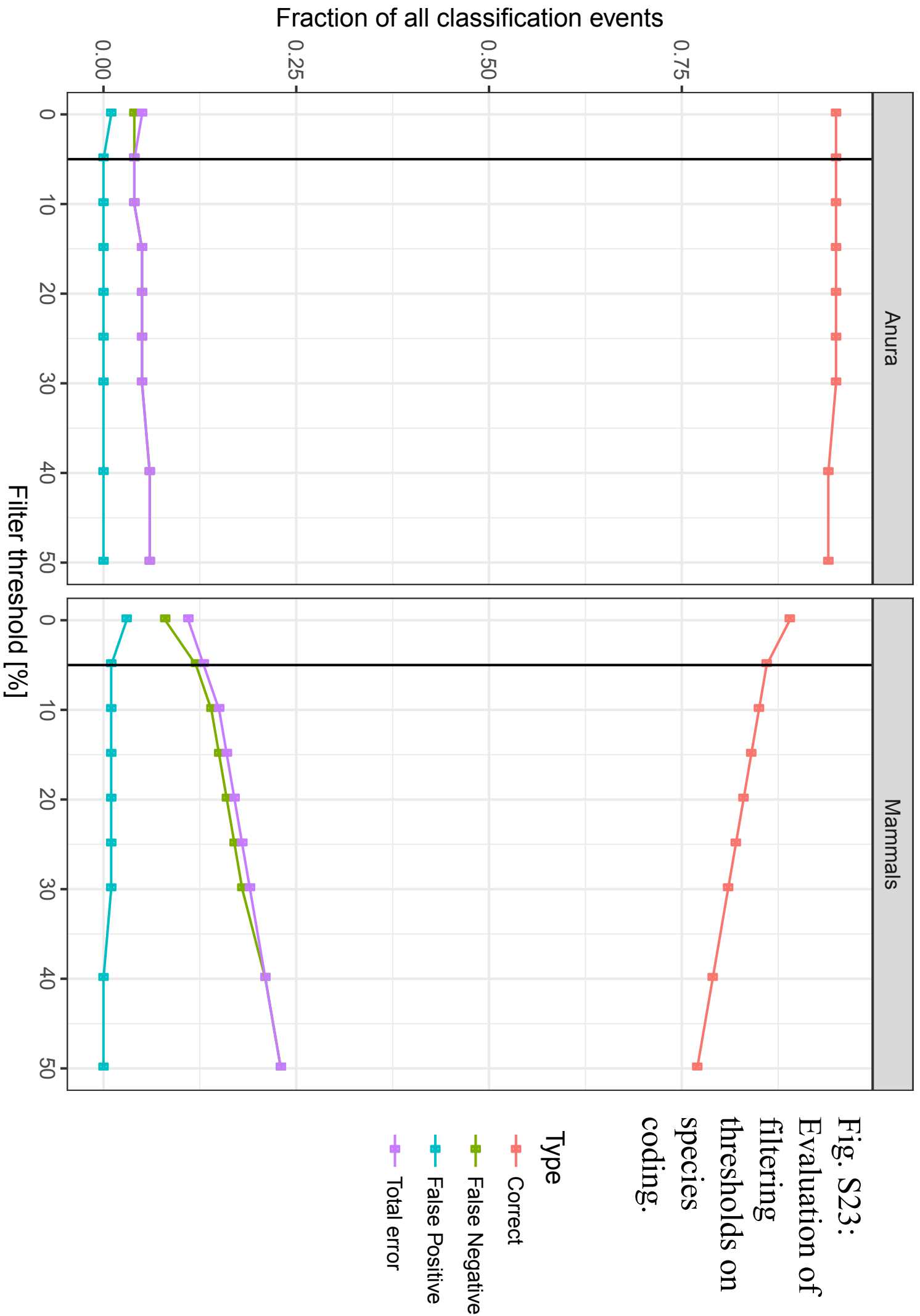


Table S1. Number of occurrence records per region, after the automated data cleaning.

Region	Angiosperms	Birds	Ferns	Frogs	Mammals	Squamates
Amazon	578216	32670	34056	29412	63131	34144
Andean Grasslands	44069	2141	2285	1476	4714	3917
Atlantic Forests	183352	7728	17405	5014	3118	3210
Caatinga	75284	98	970	172	389	615
Cerrado and Chaco	188925	6474	8473	5325	11684	5079
Dry Northern South America	47310	6766	825	1068	29368	4330
Dry Western South America	9038	1412	231	437	2789	6949
Mesoamerica	374241	69994	36705	21246	71324	84522
Patagonian Steppe	24786	2228	203	3705	6245	3352
West Indies	29092	1765	8159	3968	4397	66718

36	Angiosperms	10	22.7	5	2	0	3	2	0	0	9	1	0	0	9	1	0	0	Adenaria, Cuphea	
37	Angiosperms	10	19.6	9	1	0	2	1	3	0	6	0	0	0	6	0	0	0	Bellucia, Henriettea, Henrietteia, Loreya	
38	Angiosperms	90	12	78	22	4	8	18	28	2	53	0	0	0	53	0	0	0	Adelobotrys, Gliemia, Conostegia, Eriocnema, Grafjenrieda, Leandra, Anathallis, Barbosella, Brachionidium, Dracula, Dryadella, Echinosepala, Fronderia, Lepanthes, Lepanthopsis, Masdevallia, Myoxanthus, Pabstella, Phileophila,	
39	Angiosperms	41	6.4	28	6	1	2	1	2	0	18	4	0	0	18	4	0	0	Solanum	
4	Angiosperms	25	1.3	22	11	1	2	11	2	0	10	1	3	0	10	1	3	0	Solanum	
40	Angiosperms	10	4.2	7	8	3	1	5	0	0	2	0	1	0	2	0	1	0	Colyptroanthus, Luma, Martleria, Myrcia,	
41	Angiosperms	8	42.7	6	3	1	0	3	0	1	2	1	0	0	2	1	0	0	Carica, Jacaratia, Vasconcellea	
42	Angiosperms	11	35.7	7	2	0	0	2	1	3	3	6	3	0	3	6	3	0	Tropaeolum	
43	Angiosperms	12	8.7	8	3	1	0	5	1	1	1	0	0	0	1	0	0	0	Eriotheca, Pachira	
44	Angiosperms	54	20.6	30	4	1	3	6	8	0	25	0	0	0	25	0	0	0	Bursera, Commiphora, Crepidospermum,	
45	Angiosperms	9	1	8	6	3	1	7	1	0	6	0	0	0	6	0	0	0	Carilospermum, Paullinia, Serjania, Urvillea	
46	Angiosperms	10	2.2	8	2	1	0	4	4	0	4	0	0	0	4	0	0	0	Cupania, Diiodendron, Matayba, Vouarava	
47	Angiosperms	9	1.6	9	7	2	0	3	2	0	2	0	0	0	2	0	0	0	Simba	
48	Angiosperms	18	26.6	16	4	2	1	3	8	0	5	0	0	0	5	0	0	0	Chrysobalanus, Caeplia, Hirella, Licania	
49	Angiosperms	15	6.5	8	3	2	6	5	4	0	6	1	1	0	6	1	1	0	Phyllanthus	
5	Angiosperms	21	5.9	11	7	6	5	7	3	0	8	0	0	0	8	0	0	0	Amphitecna, Crescentia, Cybistox,	
50	Angiosperms	12	2.9	4	4	1	1	0	1	0	12	0	0	0	12	0	0	0	Godmania, Handroanthus, Sportosperma, Prosthechea	
51	Angiosperms	30	41.4	22	5	3	4	2	8	0	16	1	0	0	16	1	0	0	Chrysobalanus, Clusia, Dystovomita,	
52	Angiosperms	16	18.7	11	8	3	1	7	0	0	8	2	1	0	8	2	1	0	Possiflora, Tetrastylis	
53	Angiosperms	13	31.4	10	2	1	1	3	2	0	4	2	2	0	4	2	2	0	Abatia, Banara, Neosprucea, Prockia	
54	Angiosperms	20	69.2	15	5	4	4	6	8	0	4	0	0	0	4	0	0	0	Acantharea, Blepharandra, Byssonima, Coleostachys, Diacida, Galpinia,	
55	Angiosperms	12	14.1	2	4	2	0	8	0	0	3	0	0	0	3	0	0	4	Aspicarpa, Cordobia, Gallardo,	
56	Angiosperms	17	37	13	3	2	1	6	8	0	8	1	1	0	8	1	1	0	Chiloscolus, Glycydendron, Hevea, Manihot,	
57	Angiosperms	14	10.6	4	2	0	4	4	0	0	6	1	3	0	6	1	3	0	Croton	
58	Angiosperms	11	2.8	6	4	4	3	3	2	0	5	0	0	0	5	0	0	0	Croton	
59	Angiosperms	10	1.8	7	4	1	1	3	0	0	4	1	1	0	4	1	1	0	Doyerea, Gurania, Helmontia, Psiguria,	
6	Angiosperms	11	3.2	9	1	0	0	0	1	0	8	0	0	0	8	0	0	0	Columnnea, Dymonia, Glossoloma,	
60	Angiosperms	24	25.5	23	2	0	0	2	1	0	10	0	0	0	10	0	0	0	Castilla, Helicostylis, Maguire, Naucleopsis,	
61	Angiosperms	13	4.4	5	2	0	0	1	2	0	8	0	0	0	8	0	0	0	Barleria, Caularthron, Epidendrum,	
62	Angiosperms	18	13.2	16	5	1	1	8	5	0	10	1	0	0	10	1	0	0	Ficus	
63	Angiosperms	11	2.8	11	0	0	0	0	6	0	0	0	0	0	0	0	0	0	Brownea, Elizabetha, Macrolobium	
64	Angiosperms	10	1.1	2	1	0	1	1	1	1	8	0	0	0	8	0	0	0	Leucaena, Lysiloma	
65	Angiosperms	28	4	19	11	7	2	15	6	0	9	1	4	0	9	1	4	0	Microlobus, Mimosa, Parapiptadenia,	
66	Angiosperms	56	1.1	55	11	4	1	12	15	2	26	1	0	0	26	1	0	0	Aburerna, Albizia, Cathartium, Cedrelinga,	
67	Angiosperms	15	15.7	10	7	4	3	7	2	1	4	1	0	0	4	1	0	0	Brya, Centriolobium, Cranocarpus,	
68	Angiosperms	13	25.3	10	2	1	1	2	1	0	2	0	0	0	2	0	0	0	Andira, Hymenolobium, Vataireopsis	
69	Angiosperms	52	28.1	48	8	4	0	11	8	1	8	0	0	0	8	0	0	0	Aldina, Amburana, Atetia, Bacoa,	
7	Angiosperms	18	4.7	14	0	0	0	3	2	2	10	1	0	0	10	1	0	0	Candolleodendron, Cyathostegia, Digteryx,	
70	Angiosperms	17	18.7	10	7	6	5	8	5	0	9	1	1	0	9	1	1	0	Amalophyllon, Diasterna, Gloxinia, Goyazia,	
71	Angiosperms	10	20.3	4	1	0	4	1	3	0	6	0	0	0	6	0	0	0	Heppelia, Kohleria, Monogyte, Moussonia,	
																			Camptosema, Canavalia, Cleobulia, Cratylia,	
																				Coccoloba, Neornilispauighia

40	Birds	34	18	30	4	0	0	7	10	0	8	2	0	<i>Andigena, Aulacorhynchus, Pteroglossus,</i>
41	Birds	18	9.6	14	3	0	0	5	3	1	1	0	0	<i>Picumnus</i>
42	Birds	9	5.5	2	1	0	0	2	1	0	6	0	0	<i>Melanerpes</i>
43	Birds	12	3.5	9	3	0	0	4	4	1	0	1	1	<i>Veniliornis</i>
44	Birds	9	5.1	6	2	0	0	4	1	1	4	0	1	<i>Campephilus</i>
45	Birds	17	14.8	16	1	0	0	2	2	0	1	3	0	<i>Boissonneaua, Cytolaema, Ensifera, Heliodoxa, Ocreatus, Pterophanes,</i>
46	Birds	10	5.1	4	2	0	1	2	1	0	4	1	2	<i>Colaptes</i>
47	Birds	9	12.9	5	2	0	0	3	2	0	3	1	0	<i>Buteogallus, Harpyhaliaetus, Leucopternis</i>
48	Birds	9	23.9	5	4	0	0	5	1	0	3	1	3	<i>Aramides, Paratrialus</i>
49	Birds	14	16.2	8	2	1	3	4	3	1	7	0	2	<i>Patagoniornis</i>
5	Birds	63	16.3	35	15	0	6	18	22	8	26	0	3	<i>Attila, Casinornis, Deltarhynchus, Empidonomus, Legatus, Mochetornis, Megarynchus, Myiarchus, Myiodynastes,</i>
50	Birds	16	20.9	11	4	0	0	5	4	4	6	4	1	<i>Clarus, Columbiga, Metropelia, Uropelia</i>
51	Birds	15	14.2	14	0	0	0	4	2	2	0	7	0	<i>Aglaeactis, Coeligena, Lafresnaya</i>
52	Birds	27	20.8	16	2	0	5	8	7	0	9	1	0	<i>Androdon, Anthracoceros, Augastes, Coliitorax, Chrysolaemus, Colibri, Doryfera,</i>
53	Birds	31	22.7	28	3	0	0	3	6	1	9	1	0	<i>Eutoxeres, Glaucis, Phaeothornis,</i>
54	Birds	9	23	3	1	0	0	4	1	2	3	3	2	<i>Caracara, Daptrius, Ibycter, Milvago,</i>
6	Birds	80	17.2	28	12	0	2	19	8	3	28	15	14	<i>Agrionis, Aphanotriccus, Cnemarchus, Cnemotriccus, Cortopus, Empidonax, Hymenops, Knipolegus, Lathrotricus, Lessonia, Mitrephanes, Muscipipra, Iodopleura, Lanisoma, Laniocera,</i>
7	Birds	27	27.6	21	11	0	0	8	6	4	9	0	4	<i>Antiochia, Chiroxipha, Corapipo, Heterocercus, Illicura, Lepidochirus,</i>
8	Birds	45	14.6	39	4	0	0	7	12	0	7	1	0	<i>Botara, Cymbilaimus, Dichrozona, Frederickena, Hypoedeleus, Mackenziaena,</i>
9	Birds	16	16.6	12	4	0	0	2	1	0	2	0	1	<i>Aspleniium</i>
1	Ferns	9	39.5	7	7	0	4	3	0	0	6	0	0	<i>Campyloneurum, Microgramma, Niphidium</i>
2	Ferns	18	77.4	15	6	2	5	4	0	0	10	1	0	<i>Polypodium, Serpocaulon</i>
3	Ferns	16	69.3	13	4	2	1	5	2	0	9	4	0	<i>Trichomanes</i>
4	Ferns	10	99.5	8	2	0	4	1	0	0	6	0	0	<i>Chironectes, Didelphis, Lutreolina,</i>
1	Mammals	13	36.5	10	2	0	0	4	4	0	4	3	2	<i>Anoura, Brachyphylla, Choerorniscus, Choeronycteris, Epophylla, Glossophaga, Hylonycteris, Leptoncyteris, Lichonycteris,</i>
10	Mammals	33	22.7	15	1	2	7	0	9	2	15	0	0	<i>Ametrida, Artibeus, Carollia, Centurio, Chiroderma, Ectophylla, Enchisthenes, Mesophylla, Phyllopus, Platyrrhinus</i>
11	Mammals	67	22.8	57	3	0	4	8	30	3	31	1	1	<i>Eumops, Molossus, Promops</i>
12	Mammals	18	22.5	12	2	0	1	8	9	2	10	1	3	<i>Ctenomys</i>
13	Mammals	23	9.6	7	0	0	0	14	0	0	0	6	6	<i>Heteromys, Liomys</i>
2	Mammals	11	10.6	2	0	0	1	0	2	0	9	0	0	<i>Andalgalomys, Andinomys, Auliscomys, Bianomys, Calomys, Chirchillula, Delomys, Abrothrix, Akodon, Deltomys, Necromys, Chilomys, Elignodontia, Holochilus, Juscelinomys, Lundomys, Oligoryzomys,</i>
3	Mammals	51	15.7	29	4	0	0	21	8	6	1	18	5	
4	Mammals	38	15.2	24	5	0	0	15	0	2	0	16	6	
5	Mammals	24	9.6	13	3	0	0	14	2	2	2	8	5	

6	Mammals	26	71.3	15	7	0	0	15	11	0	8	5	8	<i>Bradyus, Cobassus, Collyptrophactus, Chaetophractus, Chlamyphorus, Choloepus, Cyclops, Desypus, Euphractus, Conepatus, Mephitis, Spilogale</i>
7	Mammals	8	14.7	1	0	0	0	1	1	1	6	1	2	<i>Balanitopteryx, Centronycteris, Cormura, Cytarops, Didelurus, Peronycteris, Chrototerus, Glyphonycteris, Lampronnycteris, Lophostoma, Macroty, Micronycteris, Mimon, Neonycteris, Coleodactylus, Pseudogonotodes, Anolis</i>
8	Mammals	18	34.9	13	0	0	0	0	11	0	9	0	0	<i>Malburya</i>
9	Mammals	29	28.4	26	1	0	1	2	14	0	19	0	0	<i>Bog, Corallus, Epicrates, Eunectes, Atropoides, Cerrophiidion, Porthidium, Bothriechis, Cerrophiidion, Lachesis, Micrurus</i>
1	Squamates	41	69.2	5	1	0	34	1	3	0	2	0	0	<i>Chironius, Dymarchon, Pseustes, Spilotes, Adelphicos, Atractus, Cryophis, Diapas, Geophis, Hydromorphus, Imantodes, Aisophis, Antillophis, Arrhyton, Darlingtonia, Erythrolamprus, Hysishynchus, Jaltrix, Sceloporus</i>
10	Squamates	11	36	0	0	0	11	0	0	0	0	0	0	<i>Philodryas, Pseudablabes, Xenoxybelis</i>
11	Squamates	24	33.1	0	0	0	24	0	1	0	1	0	0	<i>Boiruna, Clelia, Drepanoides, Hydrodynastes, Oxyrhopus, Phymophis, Ameiva, Chemidophorus, Dicrodon</i>
12	Squamates	17	25.2	11	7	1	1	6	2	0	3	1	2	<i>Bachia</i>
13	Squamates	11	44.8	6	1	0	4	4	3	0	4	0	0	<i>Amphisbaena, Anops, Aulura, Lepostemon</i>
14	Squamates	9	14.8	2	0	0	0	0	1	0	9	0	0	<i>Stenocercus</i>
15	Squamates	13	21.1	3	1	0	0	0	1	0	13	0	0	<i>Tropidurus</i>
16	Squamates	12	18.5	7	5	1	0	3	4	0	1	1	2	<i>Ctenosaura</i>
17	Squamates	13	26	9	6	0	0	3	4	0	5	0	0	<i>Enyalioides, Hoplacercus, Morunasaurus, Diplolaemus, Enyalius, Leiocaurus, Liolaemus</i>
18	Squamates	38	29.3	18	7	0	2	5	7	0	21	1	2	<i>Liolaemus</i>
19	Squamates	48	32.7	15	11	1	22	18	3	0	3	1	11	<i>Liolaeemus</i>
2	Squamates	38	19.8	0	0	0	0	0	0	0	38	0	0	<i>Anolis</i>
20	Squamates	10	25.1	6	4	2	0	7	0	0	0	2	4	<i>Anolis</i>
21	Squamates	26	31.3	18	10	1	1	12	5	0	2	1	4	<i>Anolis</i>
22	Squamates	8	65.3	5	3	1	0	5	2	1	0	1	2	
23	Squamates	17	32.2	2	0	0	14	2	0	1	0	1	2	
24	Squamates	11	45.9	10	1	0	1	1	2	0	0	0	0	
25	Squamates	17	45.4	5	5	2	7	6	0	0	0	0	2	
26	Squamates	32	43	27	1	0	0	3	0	9	0	8	1	
27	Squamates	11	24.4	4	4	3	0	7	1	0	0	1	0	
28	Squamates	9	20.3	0	0	0	0	0	0	0	9	0	0	
3	Squamates	12	81.2	12	4	1	0	2	3	2	2	0	0	
4	Squamates	9	42.2	2	2	0	0	4	0	0	0	4	5	
5	Squamates	23	26.1	2	0	0	0	1	0	1	0	20	3	
6	Squamates	11	11.8	1	0	0	0	1	0	1	0	10	0	
7	Squamates	7	13.8	0	0	0	0	1	0	0	0	2	7	
8	Squamates	37	39.9	29	0	0	7	0	5	1	4	2	0	
9	Squamates	17	39.6	0	0	0	17	0	0	0	0	0	0	

Table S3. Paleogeographic model used for the time-stratified biogeographic analyses implemented in the dispersal–extinction–cladogenesis (DEC) model. The model is built on connectivity matrices between areas, with connectivities evolving through time. For any combination of two areas, each matrix determines whether the areas are connected (1) or disconnected (0). When two areas are connected, dispersal events and range expansions are allowed in the biogeographic reconstruction, and an ancestor could have been distributed in a range composed of these two areas and more. This simple model is based on current knowledge of Neotropical paleogeography and biome evolution, but should be viewed as a hypothesis to be further refined and tested.

Time period: 0 to 9 Ma

	Amazonia	Atlantic Forests	Caatinga	West Indies	Cerrado and Chaco	Dry Northern South America	Dry Western South America	Andean Grasslands	Mesoamerica	Patagonian Steppe
Amazonia	1	0	1	1	1	1	1	1	1	0
Atlantic Forests	0	1	1	0	1	0	0	0	0	1
Caatinga	1	1	1	0	1	0	0	0	0	0
West Indies	1	0	0	1	0	1	0	0	1	0
Cerrado and Chaco	1	1	1	0	1	0	0	1	0	1
Dry Northern South America	1	0	0	1	0	1	0	1	0	0
Dry Western South America	1	0	0	0	0	0	1	1	0	0
Mesoamerica	1	0	0	1	0	0	0	0	1	0
Andean Grasslands	1	0	0	0	1	1	1	1	0	1
Patagonian Steppe	0	1	0	0	1	0	0	1	0	1

Some of the key events in the Neotropics underlying the model for this time period:

Emergence and expansion of several dry biomes in South America (45, 46) linked to global climatic cooling (47); highest increase in elevation in the Northern and Central Andes (48, 49); onset of the Amazon River (50).

Time period: 9 to 13 Ma

	Amazonia	Atlantic Forests	Caatinga	West Indies	Cerrado and Chaco	Dry Northern South America	Dry Western South America	Andean Grasslands	Mesoamerica	Patagonian Steppe
Amazonia	1	0	0	1	0	1	0	0	1	1
Atlantic Forests	0	1	0	0	0	0	0	0	0	1
Caatinga	0	0	0	0	0	0	0	0	0	0
West Indies	1	0	0	1	0	1	0	0	1	0
Cerrado and Chaco	0	0	0	0	0	0	0	0	0	0
Dry Northern South America	1	0	0	1	0	1	0	1	0	0
Dry Western South America	0	0	0	0	0	0	0	0	0	0
Mesoamerica	1	0	0	1	0	0	0	0	1	0
Andean Grasslands	0	0	0	0	0	1	0	1	0	1
Patagonian Steppe	1	1	0	0	0	0	0	1	0	1

Some of the key events in the Neotropics underlying the model for this time period:

Closure of the Central American Seaway connecting South America and Mesoamerica (51, 52); drainage of the Pebas system in Western Amazonia (48); global climatic cooling (47); development of the Patagonian Steppe (46); moderate uplift of the Andes (48).

Time period: 13 to 23 Ma

	Amazonia	Atlantic Forests	Caatinga	West Indies	Cerrado and Chaco	Dry Northern South America	Dry Western South America	Andean Grasslands	Mesoamerica	Patagonian Steppe
Amazonia	1	1	0	1	0	0	0	0	0	0
Atlantic Forests	1	1	0	0	0	0	0	0	0	0
Caatinga	0	0	0	0	0	0	0	0	0	0
West Indies	1	0	0	1	0	0	0	0	1	0
Cerrado and Chaco	0	0	0	0	0	0	0	0	0	0
Dry Northern South America	0	0	0	0	0	0	0	0	0	0
Dry Western South America	0	0	0	0	0	0	0	0	0	0
Mesoamerica	0	0	0	1	0	0	0	0	1	0
Andean Grasslands	0	0	0	0	0	0	0	0	0	0
Patagonian Steppe	0	0	0	0	0	0	0	0	0	0

Some of the key events in the Neotropics underlying the model for this time period:

Development of wetland conditions in western Amazonia (53, 54); low or absent Andes (48); Panama Arc not yet connected to South America (51).

Time period: 23 to 33 Ma

	Amazonia	Atlantic Forests	Caatinga	West Indies	Cerrado and Chaco	Dry Northern South America	Dry Western South America	Andean Grasslands	Mesoamerica	Patagonian Steppe
Amazonia	1	1	0	0	0	0	0	0	0	0
Atlantic Forests	1	1	0	0	0	0	0	0	0	0
Caatinga	0	0	0	0	0	0	0	0	0	0
West Indies	0	0	0	1	0	0	0	0	1	0
Cerrado and Chaco	0	0	0	0	0	0	0	0	0	0
Dry Northern South America	0	0	0	0	0	0	0	0	0	0
Dry Western South America	0	0	0	0	0	0	0	0	0	0
Mesoamerica	0	0	0	1	0	0	0	0	1	0
Andean Grasslands	0	0	0	0	0	0	0	0	0	0
Patagonian Steppe	0	0	0	0	0	0	0	0	0	0

Some of the key events in the Neotropics underlying the model for this time period:

South America is isolated from other landmasses; relative climatic stability following the Eocene/Oligocene climatic transition (47).

Time period: 33 to 35 Ma

	Amazonia	Atlantic Forests	Caatinga	West Indies	Cerrado and Chaco	Dry Northern South America	Dry Western South America	Andean Grasslands	Mesoamerica	Patagonian Steppe
Amazonia	1	1	0	1	0	0	0	0	0	0
Atlantic Forests	1	1	0	0	0	0	0	0	0	0
Caatinga	0	0	0	0	0	0	0	0	0	0
West Indies	1	0	0	1	0	0	0	0	1	0
Cerrado and Chaco	0	0	0	0	0	0	0	0	0	0
Dry Northern South America	0	0	0	0	0	0	0	0	0	0
Dry Western South America	0	0	0	0	0	0	0	0	0	0
Mesoamerica	0	0	0	1	0	0	0	0	1	0
Andean Grasslands	0	0	0	0	0	0	0	0	0	0
Patagonian Steppe	0	0	0	0	0	0	0	0	0	0

Some of the key events in the Neotropics underlying the model for this time period:

Proposed landbridge between the West Indies and South America (the GAARlandia) (55, 56).

Time period: 35 to 66 Ma

	Amazonia	Atlantic Forests	Caatinga	West Indies	Cerrado and Chaco	Dry Northern South America	Dry Western South America	Andean Grasslands	Mesoamerica	Patagonian Steppe
Amazonia	1	1	0	0	0	0	0	0	0	0
Atlantic Forests	1	1	0	0	0	0	0	0	0	0
Caatinga	0	0	0	0	0	0	0	0	0	0
West Indies	0	0	0	1	0	0	0	0	0	0
Cerrado and Chaco	0	0	0	0	0	0	0	0	0	0
Dry Northern South America	0	0	0	0	0	0	0	0	0	0
Dry Western South America	0	0	0	0	0	0	0	0	0	0
Mesoamerica	0	0	0	0	0	0	0	0	1	0
Andean Grasslands	0	0	0	0	0	0	0	0	0	0
Patagonian Steppe	0	0	0	0	0	0	0	0	0	0

Some of the key events in the Neotropics underlying the model for this time period:

Pan-Amazonia dominated large parts of northern South America (48). No evidence of several current biomes.

Table S4. Number of dispersal events per region and clade, sorted by decreasing order of total number of events.

Region	Direction	Angiosperms	Birds	Ferns	Frogs	Mammals	Squamates	Total
Amazonia	From	1506	850	58	33	248	160	2855
Mesoamerica	From	377	179	7	0	32	20	615
Cerrado and Chaco	From	177	106	1	23	73	75	455
Atlantic Forests	From	195	40	14	7	3	37	296
Andean Grasslands	From	18	40	0	1	29	17	105
Patagonian Steppe	From	28	33	0	1	10	9	81
West Indies	From	47	3	0	0	0	15	65
Dry Northern South America	From	13	7	0	0	4	7	31
Caatinga	From	11	0	0	0	1	0	12
Dry Western South America	From	1	4	0	0	3	2	10
Mesoamerica	To	471	192	26	4	72	23	788
Dry Northern South America	To	338	277	2	3	102	49	771
Cerrado and Chaco	To	399	235	13	9	55	55	766
Atlantic Forests	To	375	183	11	12	24	56	661
Amazonia	To	255	125	7	10	56	41	494
Andean Grasslands	To	122	89	5	11	38	33	298
Patagonian Steppe	To	64	57	0	9	31	49	210
West Indies	To	145	30	12	1	8	5	201
Caatinga	To	171	2	4	4	1	17	199
Dry Western South America	To	33	72	0	2	16	14	137

Table S5. Number of dispersal events per region and clade, sorted by **sink area** and in decreasing order of total number of events.

To	From	Angiosperms	Birds	Ferns	Frogs	Mammals	Squamates	Total
Amazonia	Mesoamerica	157	89	3	0	14	13	276
Amazonia	Cerrado and Chaco	30	15	0	7	23	15	90
Amazonia	Atlantic Forests	36	3	4	2	1	4	50
Amazonia	Andean Grasslands	10	10	0	1	12	3	36
Amazonia	West Indies	13	1	0	0	0	6	20
Amazonia	Patagonian Steppe	5	5	0	0	1	0	11
Amazonia	Dry Northern South America	2	2	0	0	3	0	7
Amazonia	Caatinga	2	0	0	0	0	0	2
Amazonia	Dry Western South America	0	0	0	0	2	0	2
Amazonia	All above	255	125	7	10	56	41	494
Andean Grasslands	Amazonia	100	71	5	7	25	14	222
Andean Grasslands	Cerrado and Chaco	6	9	0	3	9	7	34
Andean Grasslands	Patagonian Steppe	7	5	0	1	3	5	21
Andean Grasslands	Mesoamerica	7	3	0	0	1	0	11
Andean Grasslands	Atlantic Forests	0	1	0	0	0	3	4
Andean Grasslands	Dry Northern South America	1	0	0	0	0	2	3
Andean Grasslands	Dry Western South America	0	0	0	0	0	2	2
Andean Grasslands	West Indies	1	0	0	0	0	0	1
Andean Grasslands	Caatinga	0	0	0	0	0	0	0
Andean Grasslands	All above	122	89	5	11	38	33	298
Atlantic Forests	Amazonia	265	118	9	6	12	31	441
Atlantic Forests	Cerrado and Chaco	54	42	1	6	10	22	135
Atlantic Forests	Mesoamerica	45	12	1	0	2	1	61
Atlantic Forests	Patagonian Steppe	4	8	0	0	0	0	12
Atlantic Forests	Dry Northern South America	2	0	0	0	0	2	4
Atlantic Forests	West Indies	3	0	0	0	0	0	3
Atlantic Forests	Andean Grasslands	0	3	0	0	0	0	3
Atlantic Forests	Caatinga	2	0	0	0	0	0	2
Atlantic Forests	Dry Western South America	0	0	0	0	0	0	0
Atlantic Forests	All above	375	183	11	12	24	56	661
Caatinga	Amazonia	73	1	3	2	1	5	85
Caatinga	Atlantic Forests	47	1	1	1	0	3	53
Caatinga	Cerrado and Chaco	29	0	0	1	0	7	37
Caatinga	Mesoamerica	18	0	0	0	0	0	18
Caatinga	West Indies	2	0	0	0	0	0	2
Caatinga	Dry Northern South America	2	0	0	0	0	0	2
Caatinga	Andean Grasslands	0	0	0	0	0	1	1
Caatinga	Patagonian Steppe	0	0	0	0	0	1	1
Caatinga	Dry Western South America	0	0	0	0	0	0	0
Caatinga	All above	171	2	4	4	1	17	199
Cerrado and Chaco	Amazonia	262	170	9	6	41	29	517
Cerrado and Chaco	Atlantic Forests	72	22	3	3	1	18	119
Cerrado and Chaco	Mesoamerica	41	18	1	0	3	0	63
Cerrado and Chaco	Patagonian Steppe	7	15	0	0	2	3	27
Cerrado and Chaco	Andean Grasslands	4	7	0	0	8	4	23
Cerrado and Chaco	West Indies	8	1	0	0	0	0	9
Cerrado and Chaco	Dry Northern South America	2	1	0	0	0	1	4
Cerrado and Chaco	Caatinga	3	0	0	0	0	0	3
Cerrado and Chaco	Dry Western South America	0	1	0	0	0	0	1
Cerrado and Chaco	All above	399	235	13	9	55	55	766
Dry Northern South America	Amazonia	275	225	2	3	82	35	622
Dry Northern South America	Mesoamerica	45	31	0	0	7	5	88
Dry Northern South America	Cerrado and Chaco	5	15	0	0	10	2	32
Dry Northern South America	Atlantic Forests	5	4	0	0	0	2	11
Dry Northern South America	West Indies	6	0	0	0	0	5	11
Dry Northern South America	Andean Grasslands	1	1	0	0	1	0	3
Dry Northern South America	Patagonian Steppe	1	0	0	0	2	0	3
Dry Northern South America	Dry Western South America	0	1	0	0	0	0	1
Dry Northern South America	Caatinga	0	0	0	0	0	0	0

Dry Northern South America	All above	338	277	2	3	102	49	771
Dry Western South America	Amazonia	26	44	0	2	10	13	95
Dry Western South America	Andean Grasslands	2	12	0	0	4	1	19
Dry Western South America	Mesoamerica	4	13	0	0	1	0	18
Dry Western South America	Cerrado and Chaco	0	2	0	0	0	0	2
Dry Western South America	Patagonian Steppe	1	0	0	0	1	0	2
Dry Western South America	Dry Northern South America	0	1	0	0	0	0	1
Dry Western South America	Atlantic Forests	0	0	0	0	0	0	0
Dry Western South America	Caatinga	0	0	0	0	0	0	0
Dry Western South America	West Indies	0	0	0	0	0	0	0
Dry Western South America	All above	33	72	0	2	16	14	137
Mesoamerica	Amazonia	420	182	22	4	66	17	711
Mesoamerica	Cerrado and Chaco	18	5	0	0	4	0	27
Mesoamerica	Atlantic Forests	15	1	4	0	0	1	21
Mesoamerica	West Indies	13	1	0	0	0	4	18
Mesoamerica	Patagonian Steppe	3	0	0	0	1	0	4
Mesoamerica	Caatinga	1	0	0	0	1	0	2
Mesoamerica	Dry Northern South America	1	0	0	0	0	1	2
Mesoamerica	Dry Western South America	0	2	0	0	0	0	2
Mesoamerica	Andean Grasslands	0	1	0	0	0	0	1
Mesoamerica	All above	471	192	26	4	72	23	788
Patagonian Steppe	Cerrado and Chaco	26	16	0	6	17	22	87
Patagonian Steppe	Amazonia	18	27	0	2	7	12	66
Patagonian Steppe	Atlantic Forests	10	8	0	1	1	6	26
Patagonian Steppe	Andean Grasslands	1	6	0	0	4	8	19
Patagonian Steppe	Mesoamerica	5	0	0	0	1	0	6
Patagonian Steppe	Dry Northern South America	1	0	0	0	0	1	2
Patagonian Steppe	Dry Western South America	1	0	0	0	1	0	2
Patagonian Steppe	Caatinga	1	0	0	0	0	0	1
Patagonian Steppe	West Indies	1	0	0	0	0	0	1
Patagonian Steppe	All above	64	57	0	9	31	49	210
West Indies	Amazonia	67	12	8	1	4	4	96
West Indies	Mesoamerica	55	13	2	0	3	1	74
West Indies	Atlantic Forests	10	0	2	0	0	0	12
West Indies	Cerrado and Chaco	9	2	0	0	0	0	11
West Indies	Dry Northern South America	2	3	0	0	1	0	6
West Indies	Caatinga	2	0	0	0	0	0	2
West Indies	Dry Western South America	0	0	0	0	0	0	0
West Indies	Andean Grasslands	0	0	0	0	0	0	0
West Indies	Patagonian Steppe	0	0	0	0	0	0	0
West Indies	All above	145	30	12	1	8	5	201

Table S6. Number of dispersal events per region and clade, sorted by **source area** and in decreasing order of total number of events. "Shift" refers to the probable sort of transition, as shown in Fig. 1: R (region-only), B (region and biome type), and A (ambiguous).

From	To	Shift	Angiosperms	Birds	Ferns	Frogs	Mammals	Squamates	Total
Amazonia	Mesoamerica	A	420	182	22	4	66	17	711
Amazonia	Dry Northern South America	B	275	225	2	3	82	35	622
Amazonia	Cerrado and Chaco	B	262	170	9	6	41	29	517
Amazonia	Atlantic Forests	A	265	118	9	6	12	31	441
Amazonia	Andean Grasslands	B	100	71	5	7	25	14	222
Amazonia	West Indies	A	67	12	8	1	4	4	96
Amazonia	Dry Western South America	B	26	44	0	2	10	13	95
Amazonia	Caatinga	B	73	1	3	2	1	5	85
Amazonia	Patagonian Steppe	B	18	27	0	2	7	12	66
Amazonia	All above		1506	850	58	33	248	160	2855
Andean Grasslands	Amazonia	B	10	10	0	1	12	3	36
Andean Grasslands	Cerrado and Chaco	R	4	7	0	0	8	4	23
Andean Grasslands	Dry Western South America	R	2	12	0	0	4	1	19
Andean Grasslands	Patagonian Steppe	R	1	6	0	0	4	8	19
Andean Grasslands	Atlantic Forests	B	0	3	0	0	0	0	3
Andean Grasslands	Dry Northern South America	R	1	1	0	0	1	0	3
Andean Grasslands	Caatinga	R	0	0	0	0	0	1	1
Andean Grasslands	Mesoamerica	A	0	1	0	0	0	0	1
Andean Grasslands	West Indies	A	0	0	0	0	0	0	0
Andean Grasslands	All above		18	40	0	1	29	17	105
Atlantic Forests	Cerrado and Chaco	B	72	22	3	3	1	18	119
Atlantic Forests	Caatinga	B	47	1	1	1	0	3	53
Atlantic Forests	Amazonia	A	36	3	4	2	1	4	50
Atlantic Forests	Patagonian Steppe	B	10	8	0	1	1	6	26
Atlantic Forests	Mesoamerica	A	15	1	4	0	0	1	21
Atlantic Forests	West Indies	A	10	0	2	0	0	0	12
Atlantic Forests	Dry Northern South America	B	5	4	0	0	0	2	11
Atlantic Forests	Andean Grasslands	B	0	1	0	0	0	3	4
Atlantic Forests	Dry Western South America	B	0	0	0	0	0	0	0
Atlantic Forests	All above		195	40	14	7	3	37	296
Caatinga	Cerrado and Chaco	R	3	0	0	0	0	0	3
Caatinga	Amazonia	B	2	0	0	0	0	0	2
Caatinga	Atlantic Forests	B	2	0	0	0	0	0	2
Caatinga	West Indies	A	2	0	0	0	0	0	2
Caatinga	Mesoamerica	A	1	0	0	0	1	0	2
Caatinga	Patagonian Steppe	R	1	0	0	0	0	0	1
Caatinga	Dry Northern South America	R	0	0	0	0	0	0	0
Caatinga	Dry Western South America	R	0	0	0	0	0	0	0
Caatinga	Andean Grasslands	R	0	0	0	0	0	0	0
Caatinga	All above		11	0	0	0	1	0	12
Cerrado and Chaco	Atlantic Forests	B	54	42	1	6	10	22	135
Cerrado and Chaco	Amazonia	B	30	15	0	7	23	15	90
Cerrado and Chaco	Patagonian Steppe	R	26	16	0	6	17	22	87
Cerrado and Chaco	Caatinga	R	29	0	0	1	0	7	37
Cerrado and Chaco	Andean Grasslands	R	6	9	0	3	9	7	34
Cerrado and Chaco	Dry Northern South America	R	5	15	0	0	10	2	32
Cerrado and Chaco	Mesoamerica	A	18	5	0	0	4	0	27
Cerrado and Chaco	West Indies	A	9	2	0	0	0	0	11
Cerrado and Chaco	Dry Western South America	R	0	2	0	0	0	0	2
Cerrado and Chaco	All above		177	106	1	23	73	75	455
Dry Northern South America	Amazonia	B	2	2	0	0	3	0	7
Dry Northern South America	West Indies	A	2	3	0	0	1	0	6
Dry Northern South America	Atlantic Forests	B	2	0	0	0	0	2	4
Dry Northern South America	Cerrado and Chaco	R	2	1	0	0	0	1	4
Dry Northern South America	Andean Grasslands	R	1	0	0	0	0	2	3
Dry Northern South America	Caatinga	R	2	0	0	0	0	0	2
Dry Northern South America	Mesoamerica	A	1	0	0	0	0	1	2
Dry Northern South America	Patagonian Steppe	R	1	0	0	0	0	1	2
Dry Northern South America	Dry Western South America	R	0	1	0	0	0	0	1
Dry Northern South America	All above		13	7	0	0	4	7	31
Dry Western South America	Amazonia	B	0	0	0	0	2	0	2
Dry Western South America	Mesoamerica	A	0	2	0	0	0	0	2
Dry Western South America	Andean Grasslands	R	0	0	0	0	0	2	2
Dry Western South America	Patagonian Steppe	R	1	0	0	0	1	0	2
Dry Western South America	Cerrado and Chaco	R	0	1	0	0	0	0	1
Dry Western South America	Dry Northern South America	R	0	1	0	0	0	0	1
Dry Western South America	Atlantic Forests	B	0	0	0	0	0	0	0

Dry Western South America	Caatinga	R	0	0	0	0	0	0	0
Dry Western South America	West Indies	A	0	0	0	0	0	0	0
Dry Western South America	All above		1	4	0	0	3	2	10
Mesoamerica	Amazonia	A	157	89	3	0	14	13	276
Mesoamerica	Dry Northern South America	A	45	31	0	0	7	5	88
Mesoamerica	West Indies	A	55	13	2	0	3	1	74
Mesoamerica	Cerrado and Chaco	A	41	18	1	0	3	0	63
Mesoamerica	Atlantic Forests	A	45	12	1	0	2	1	61
Mesoamerica	Caatinga	A	18	0	0	0	0	0	18
Mesoamerica	Dry Western South America	A	4	13	0	0	1	0	18
Mesoamerica	Andean Grasslands	A	7	3	0	0	1	0	11
Mesoamerica	Patagonian Steppe	A	5	0	0	0	1	0	6
Mesoamerica	All above		377	179	7	0	32	20	615
Patagonian Steppe	Cerrado and Chaco	R	7	15	0	0	2	3	27
Patagonian Steppe	Andean Grasslands	R	7	5	0	1	3	5	21
Patagonian Steppe	Atlantic Forests	B	4	8	0	0	0	0	12
Patagonian Steppe	Amazonia	B	5	5	0	0	1	0	11
Patagonian Steppe	Mesoamerica	A	3	0	0	0	1	0	4
Patagonian Steppe	Dry Northern South America	R	1	0	0	0	2	0	3
Patagonian Steppe	Dry Western South America	R	1	0	0	0	1	0	2
Patagonian Steppe	Caatinga	R	0	0	0	0	0	1	1
Patagonian Steppe	West Indies	A	0	0	0	0	0	0	0
Patagonian Steppe	All above		28	33	0	1	10	9	81
West Indies	Amazonia	A	13	1	0	0	0	6	20
West Indies	Mesoamerica	A	13	1	0	0	0	4	18
West Indies	Dry Northern South America	A	6	0	0	0	0	5	11
West Indies	Cerrado and Chaco	A	8	1	0	0	0	0	9
West Indies	Atlantic Forests	A	3	0	0	0	0	0	3
West Indies	Caatinga	A	2	0	0	0	0	0	2
West Indies	Andean Grasslands	A	1	0	0	0	0	0	1
West Indies	Patagonian Steppe	A	1	0	0	0	0	0	1
West Indies	Dry Western South America	A	0	0	0	0	0	0	0
West Indies	All above		47	3	0	0	0	15	65

Table S7. Residuals from the multiple predictor analysis on the effect of dispersal events, for each of the clades and regions included in the model.

Model	Direction	Taxon	Amazonia	Andean Grasslands	Atlantic Forests	Caatinga	Cerrado and Chaco	Dry Northern South America	Dry Western South America	Mesoamerica	Patagonian Steppe	West Indies
LME1	Emmigration	Angiosperms	0.25	-0.1	0.97	-0.5	-0.08	-0.98	-1.18	0.78	0.44	1.1
LME1	Emmigration	Birds	0.12	0.75	-0.01	0.37	-0.3	-1.24	-0.46	0.57	0.68	-0.25
LME1	Emmigration	Birds	-0.03	0.98	-1.31	0.72	0.09	-1.32	0.92	-0.13	0.1	-0.23
LME1	Emmigration	Squamates	-0.54	0.42	0.66	-1.25	0.01	-0.05	0.12	-0.33	0.1	0.15
LME2	Immigration	Angiosperms	-0.92	0.09	0.22	0.38	0.48	0.74	-0.45	0.65	-0.45	-0.06
LME2	Immigration	Birds	-0.95	0.06	0.31	-0.72	0.47	1.12	-0.08	0.48	-0.29	-0.09
LME2	Immigration	Mammals	-0.5	-0.05	-0.28	-0.86	-0.04	0.81	0.23	0.7	-0.09	-0.13
LME2	Immigration	Squamates	-0.67	0.02	0.3	0.34	0.1	0.98	-0.04	0.04	0.72	-2.59

Table S8. Descriptive statistics of the multiple predictor model on the effect of dispersal events.

Model	Direction	Taxa	Predictor	Coefficient mean	Coefficient 2.5%	Coefficient .97.5%	Importance
LME1	Emmigrations	Angiosperms + Birds + Mammals + Squamates	Area	0.738	0.38	1.093	*
LME1	Emmigrations	Angiosperms + Birds + Mammals + Squamates	Branch length	1.044	0.509	1.54	*
LME1	Emmigrations	Angiosperms + Birds + Mammals + Squamates	Fraction of species in Phylogeny	0.249	-0.415	1.142	
LME1	Emmigrations	Angiosperms + Birds + Mammals + Squamates	Geographic Isolation	-0.015	-0.328	0.298	
LME1	Emmigrations	Angiosperms + Birds + Mammals + Squamates	Perimeter	0.156	-0.292	0.601	
LME2	Immigrations	Angiosperms + Birds + Mammals + Squamates	Area	-0.103	-0.458	0.25	
LME2	Immigrations	Angiosperms + Birds + Mammals + Squamates	Branch length	1.012	0.461	1.527	*
LME2	Immigrations	Angiosperms + Birds + Mammals + Squamates	Fraction of species in Phylogeny	0.197	-0.536	1.139	
LME2	Immigrations	Angiosperms + Birds + Mammals + Squamates	Geographic Isolation	-0.335	-0.646	-0.026	*
LME2	Immigrations	Angiosperms + Birds + Mammals + Squamates	Perimeter	-0.155	-0.603	0.288	

Table S9. Statistics on the data gathered for all taxa analyzed and their sampling in the phylogenies.

Taxon	Number of occurrences in Neotropics	Number of species in Neotropics	Species in the phylogeny	Species in phylogeny with occurrence in the Neotropics	Number of monophyletic clades	Mean tip number per clade	Number of species sampled in all monophyletic clades
Angiosperms	992236	60031	30535	6202	104	20	2114(4%)
Frogs	42830	880	3126	431	11	14	155(18%)
Birds	55565	2622	9993	2443	54	23	1237(47%)
Ferns	45923	2595	1118	250	4	13	53(2%)
Mammals	131491	1025	5020	884	13	28	359(35%)
Squamates	63278	1176	4162	590	28	19	532(45%)
Total	1331323	68329	53954	10800	214	-	4450(7%)

Table_S10. Pearsons correlation of predictor variables for the multivariate regression model on number of shifts per region.

	Area	Geographic isolation	Perimeter	Phylogenetic sampling	No. occurrence records	Total branch length
Area	1	-0,47	0,68	0,11	0,37	0,53
Geographic isolation	-0,47	1	-0,44	0,03	0,09	-0,07
Perimeter	0,68	-0,44	1	0,14	0,5	0,68
Phylogenetic sampling	0,11	0,03	0,14	1	-0,38	0,01
No. occurrence records	0,37	0,09	0,5	-0,38	1	0,8
Total branch length	0,53	-0,07	0,68	0,01	0,8	1

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