

ESM APPENDIX S3: ANALYSES OF REGIONAL DIVERSIFICATION RATES

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3) References

Extended comparisons of weighted mean net diversification rates

Methods summary

We performed regressions of log₁₀-transformed regional richness (table S2) with the region's weighted mean net diversification rate. The weighted mean rate (e.g. [1]) represents the average diversification rate of clades occurring in each region, weighted by the clade's richness in the region. Thus, groups that dominate regional richness will have more weight in determining the average diversification rate of each region.

To calculate the weighted mean rates, we first delimited monophyletic higher taxa, analyzing families in one set of analyses and genera in another (see appendix S1). Non-monophyletic families were aggregated with related families until they formed a clade. The exception was the polyphyletic Serranidae, which we divided into four clades (see appendix S1 for details and justification). Non-monophyletic genera were simply excluded. Next, we calculated the net diversification rate [2] of each clade. Generally, this rate represents the number of species accumulated over the clades' history (i.e. speciation minus extinction), with a correction for the failure to sample extinct taxa ($\epsilon = \lambda/\mu$, or speciation rate/extinction rate). Note that ϵ corrects for entire clades that were not included due to extinction, and is not an estimate of extinction rates in individual clades. Thus, an analysis is typically performed using a single ϵ for all clades across the tree, but using a series of analyses to examine the robustness of the results to different ϵ values. The number of species for each clade was taken from FishBase [3], and incorporates all described species in each named taxon, including those not sampled in the phylogeny (table S2). We calculated rates using either the stem or crown age. Following standard practice, we performed analyses assuming $\epsilon = 0, 0.5, \text{ or } 0.9$. Clades with only 1 species (or 1 species sampled in the phylogeny) only have a stem age, and so were excluded from analyses using crown ages. Therefore, each clade had either 3 or 6 different rate estimates. Overall, we performed analyses including diversification rates for 200 family-level clades (181 monophyletic families, 4 serranid subclades, 15 aggregate families) and 1,131 monophyletic genera. All clades, their richness, and rates can be found in ESM dataset S2.

Finally, we calculated each region's weighted mean rate by multiplying the rate of each clade by its richness in the region (database S1), summed across all clades present in the region, and divided by the total regional richness of these clades in the region. Alternatively, we also calculated weighted mean rates by using endemic richness (species only found in that region) rather than total regional richness of clades. Endemic richness may be considered a proxy for the relative diversity of species originating in each region (e.g. [4]). We only did this alternative scheme at the family level, because the small number of endemic species in each genus complicated this comparison. We performed different regressions using weighted means calculated with each rank type (families or genera), with each rate estimate (stem or crown, assumed ϵ value), and each weight type (total or endemic regional richness) for a total of 18 separate regression analyses.

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Table S8. Results of regression between regional richness and weighted mean net diversification rates.

Rank	Age of clades	ϵ	Weighted by total regional richness		Weighted by endemic regional richness	
			P	r^2	P	r^2
Families	Stem	0	0.156	0.265	0.140	0.284
Families	Stem	0.5	0.185	0.236	0.149	0.2725
Families	Stem	0.9	0.306	0.149	0.246	0.187
Families	Crown	0	0.184	0.237	0.173	0.247
Families	Crown	0.5	0.204	0.219	0.181	0.239
Families	Crown	0.9	0.383	0.110	0.246	0.187
Genera	Stem	0	0.265	0.173	-	-
Genera	Stem	0.5	0.239	0.192	-	-
Genera	Stem	0.9	0.217	0.210	-	-
Genera	Crown	0	0.816	0.008	-	-
Genera	Crown	0.5	0.790	0.011	-	-
Genera	Crown	0.9	0.623	0.036	-	-

DIVERSIFICATION RATES AMONG REGIONS

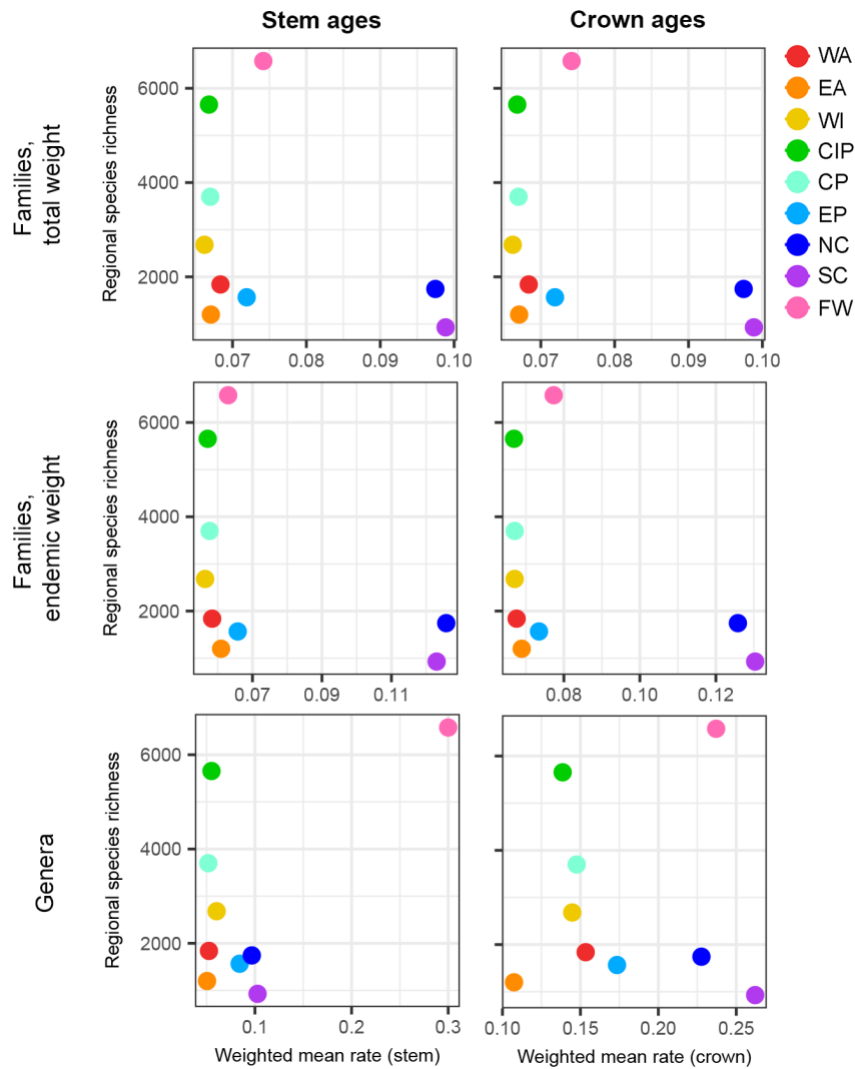


Figure S8: Relationships between regional richness and each region’s weighted mean net diversification rate. Weighted mean rates were calculated using either stem or crown ages, families or genera, and a weighting scheme based on a clade’s total richness or endemic richness in a region. All diversification rates shown were calculated assuming $\epsilon=0.5$. No relationships are significant with $P<0.05$ (table S8).

DIVERSIFICATION RATES AMONG REGIONS

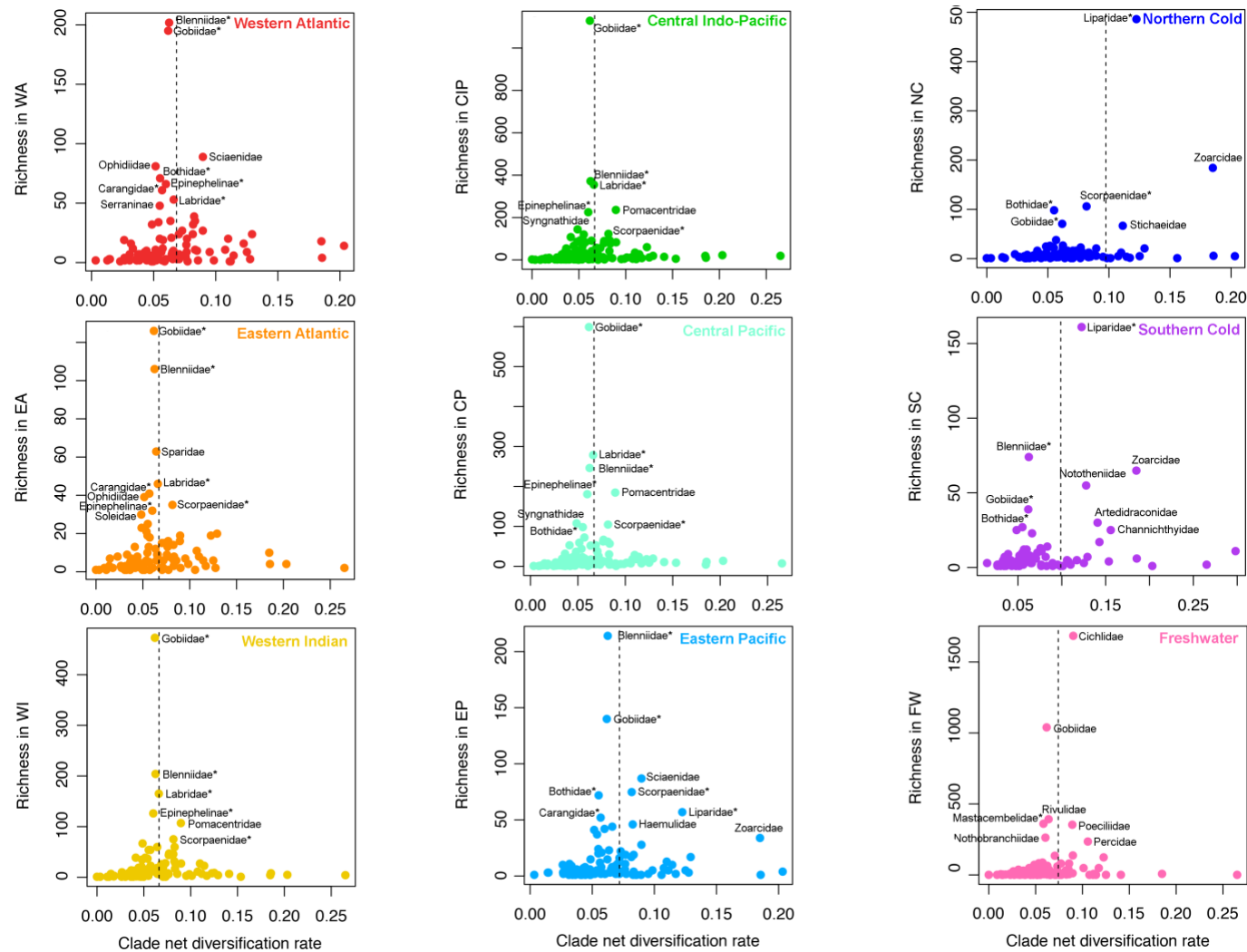


Figure S9. Clades with the greatest contribution to regional richness and thus weighted mean net diversification rates for each region. Here, diversification rates of family-level clades were calculated using the crown age and assuming $\epsilon=0.5$. Dashed lines show the weighted mean rate (weighted by total regional richness of the clade). Clades with a * are aggregates of non-monophyletic families to resolve their monophyly; the most species-rich family in the aggregate is shown for context (appendix S1; datasets S1, S2).

2) Hidden State Speciation and Extinction models (HiSSE and GeoHiSSE)

Extended Methods

i. Description of hidden-state speciation and extinction models

To further test if high diversification rates could explain the high richness of some regions, we used SSE models (state-dependent speciation and extinction), which do not depend on *a priori* clade delimitation. We used models allowing for unknown hidden states, which may co-vary with regions of interest and also affect diversification [5]. The inclusion of hidden states allows for more meaningful hypothesis testing, since SSE models normally assume a null model with no diversification-rate variation across the phylogeny. Since Percomorpha is an ecologically diverse clade, it is likely that many traits other than geography influence their diversification. We fit models where geography influenced diversification, with or without hidden states that also influence diversification. Conceptually, a HiSSE model compares diversification between two binary states, but also partitions diversification-rate heterogeneity within each state among two additional, unknown hidden states. The *hisse* R package (version 1.8.5 [5]) optimizes turnover ($\tau = \lambda + \mu$, where λ =speciation rate and μ =extinction rate) and the extinction fraction ($\epsilon = \mu/\lambda$) separately for region-hidden state combinations 1A, 1B, 0A, and 0B, where 1 and 0 represent the observed states, and A and B represent the alternative hidden states. The results are reported with τ and ϵ estimates converted to speciation (λ) and extinction (μ) rates for clarity (as automatically implemented in *hisse*).

ii. Binary comparisons of regions

We performed analyses using HiSSE [5] and the newly available GeoHiSSE [6]. Both HiSSE and GeoHiSSE are limited to comparing two states (or regions) of interest. Thus, we restricted our analyses to three binary comparisons: (i) the Indo-West Pacific (combined WI, CIP, and CP) versus other warm oceans (EP, WA, and EA); (ii) warm (WI, CIP, CP, EP, WA, and EA) versus cold oceans (NC and SC); and (iii) freshwater (FW) versus marine (all other areas). Note that although our primary goal is to explain the richness of the CIP compared to other warm oceans, we used the combined Indo-West Pacific instead of CIP separately in these analyses, because of evidence suggesting that faunas of the WI and CP are predominately the result of colonization from the CIP (figure S5 in appendix S2). Regional comparisons are described in table S9. For each analysis, we pruned the phylogeny of Percomorpha to only include species occurring in at least one of the regions of comparison. We made two pruned phylogenies, one containing only fishes occurring in warm marine regions (2,661 species), and one containing only marine fishes (2,979 species). No pruning was needed for the third analysis, since it included all sampled percomorph fishes (4,571 species).

Unlike HiSSE, GeoHiSSE allows widespread species (species found in both regions) to take on separate rate parameters, and explicitly models geographic range evolution as a third observed state. However, HiSSE allows each possible hidden state transition to vary, while GeoHiSSE and similar models [7] use a universal transition rate among hidden state categories. GeoHiSSE is currently in development, and this feature may be available in the future. However, we suspect this constraint led to problematic parameter estimates using GeoHiSSE (see below).

Therefore, we used both HiSSE and GeoHiSSE in this study, even though HiSSE is not designed for geographic data.

iii. HiSSE comparisons, assignment of widespread species, and model fitting

Since HiSSE does not allow species to occupy both states at the same time (unlike GeoHiSSE), we performed alternative analyses that changed the coding of species occurring in both regions of comparison. These are termed “inclusive” and “endemic only” hereafter.

In the inclusive analysis, we coded all species occurring in the Indo-West Pacific (IWP) as belonging to binary state 1 even if they also occurred in the East Pacific or Atlantic (comparison 1). In the alternative “endemic only” analysis, we only coded species entirely restricted to the Indo-West Pacific as state 1, and all other species were coded as state 0 (comparison 2). For example, a species with the range CIP+CP+EP was coded as 1 in the inclusive analysis and 0 in the endemic-only analyses; a species with the range CIP+CP was coded as state 1 in both analyses. Similarly, the “inclusive” analysis coded all species entering cold marine waters as state 1 (comparison 3), versus only species restricted to cold waters as state 1 (comparison 4). The “inclusive” analysis coded all species entering freshwater+brackish habitats as state 1 even if they also occurred in marine habitats (comparison 5), versus only species restricted to freshwater+brackish habitats as state 1 (comparison 6).

The alternative coding of widespread species described here will cause a respective change in the modelling of range evolution as follows, using the warm oceans comparison as an example. In inclusive analyses, in order to transition from the IWP to the other warm oceans, a lineage occurring in the IWP can either expand its range to the other warm oceans (either the Atlantic or East Pacific) and then become locally extinct in the IWP, or directly disperse from the IWP to the other warm oceans (note that since this is not a geographic model, it cannot distinguish between the different processes modelled in DEC versus DEC+J [8]). However, in order to transition from the other warm oceans to the IWP, a lineage only needs to expand its range to the IWP, or directly disperse there without range expansion (it does not need to become locally extinct in the other warm oceans). This is because all species present in the IWP are coded as IWP regardless of the extent of their range. In *endemic only* analyses, the reverse is true. A lineage transitioning from the IWP to the other warm oceans needs only to expand its range or directly disperse there, and does not need to become locally extinct in the IWP. In order to transition from the other warm oceans to the IWP, a lineage must both expand its range and then become locally extinct, or directly disperse there.

To summarize, in inclusive analyses it is easier to transition from other warm oceans to the IWP than the reverse, because fewer range changes are required. In endemic only analyses, it is easier to transition from the IWP to the other warm oceans than the reverse for the same reason. This difference may be expected to reverse the magnitude of inferred transition rates between regions between inclusive and endemic only comparisons. However, we found that the magnitude of transitions is generally similar between comparisons. For example, the transition rate from other warm oceans to the IWP is higher than the reverse in both inclusive and endemic only analyses. Therefore, we do not expect that this assignment of widespread ranges has strongly biased our results due to differences in assumptions about range evolution.

HiSSE model characteristics and relative fits are given in table S10. For all comparisons, we calculated the fraction of species sampled in each range category using our georeferenced

dataset of 17,453 species (dataset S1; table S9). We fit a total of six alternative models to each of the six datasets. We first fit a full BiSSE model without hidden states [9]. Fitting a set of models without equally-complex null models can increase the rate of type-1 error. This presumably happens when a model with greater complexity (i.e. a full HiSSE model) is preferred due to rate heterogeneity across the phylogeny, even if there is no effect of the trait of interest on diversification [5,6]. Therefore, we fit two null models: one with the same number of diversification parameters as a BiSSE model (“Null-2”, or “CID-2” of [5]), and one designed with the same number of diversification-rate parameters as a full HiSSE model (“Null-4”, or “CID-4” of [5]). The increased complexity of the Null-4 model is achieved by adding four hidden state categories to the model, instead of two. In the null models, diversification varies with hidden states but not the observed states (geography). We then fit a full HiSSE model, a HiSSE model with turnover constrained between regions, and the extinction fraction constrained between regions. All models allowed transitions to freely vary among hidden state and region categories. Dual transitions were not allowed (e.g. instantaneous transition from 0A to 1B). At the time our analyses were performed, only restricted dispersal parameters could be implemented with the Null-4 model using the *hisse* R package; we used a three-rate model to characterize transitions.

After fitting models, we used Akaike weights to assess their relative fit, as advocated by [5,6]. A full HiSSE model will give separate rates for each region-hidden state combination (tables S12–S15). However, since our goal is to understand average rate differences between regions, the hidden states may complicate interpretation. This is because species possessing hidden states with slow or fast diversification rates may be present in unequal proportion between regions, even if a null model has the best fit. To summarize rate differences across hidden states and to improve interpretation of the results, we used the function `GetModelAveRates` to obtain an average rate for each region. These model-averaged rates (figures S10–S13) will reflect the proportion of species in a region with each hidden state category. In all but one case, one model had an Akaike weight greater than or equal to 0.99 (table S10), so we did not include poorly fitting models in model-averaged results. In one case (comparison 3 in table S10), two of the six models had high Akaike weights, so we model-averaged results from these two models.

iv. GeoHiSSE comparisons and model fitting

We used the newly-available GeoHiSSE ([6], implemented in *hisse* version 1.8.6), in addition to HiSSE, because GeoHiSSE explicitly models range evolution and allows species to occupy both ranges. However, as noted above, we generally found problematic parameter estimates using GeoHiSSE. Specifically, transition rates in some hidden state categories were problematically high (e.g. a per-lineage rate of >30 events per myr), and some transitions were zero. We suggest this occurred because the currently-available implementation of GeoHiSSE uses a universal transition rate among hidden states (unlike HiSSE). We fit models that constrained range expansion and extirpation in attempt to ameliorate this problem. This improved parameter estimates when comparing among warm oceans, but not when comparing warm and cold oceans or marine and freshwater habitats. Thus, we only report the comparison of the IWP and other warm oceans here.

GeoHiSSE model characteristics and relative fits are described in table S11. Note that unlike HiSSE, which optimizes turnover (τ), the extinction fraction (ϵ), and transitions between binary states (q), GeoHiSSE optimizes in-situ speciation (s), range contraction or extirpation (x), dispersal from a narrow to widespread range (d), and vicariant speciation or the splitting of widespread ranges among daughter lineages ($s01$). There is a shared transition rate among hidden state categories (q). Transitions among hidden state categories are only permitted within the same observed range (i.e. dual transitions are not allowed to occur simultaneously). We fit a total of 10 GeoHiSSE models that differed in whether diversification was geography-dependent or independent, whether the widespread range was allowed to have a hidden area, whether transitions to the widespread area were allowed to differ among hidden state categories, and whether extirpation rates were constrained to be the same among regions. Four models were excluded from the model set (which happened to be the three models with the greatest number of free diversification rate parameters) because they had problematic parameter estimates as described above. All models allowed diversification in the IWP and other warm oceans to be split into two hidden state categories A and B. We input the proportion of sampled species in each range of 0.3866, 0.1828, and 0.3273 for widespread, IWP, and other warm species respectively, calculated using our OBIS/GBIF data (dataset S1). As for HiSSE, we used Akaike weights to determine the best-fitting models relative to others in the set, and summarized rates among hidden-state categories using the function `GetModelAveRates`.

v. GeoSSE simulations and type-1 error

Note that we did not use GeoSSE (Geographic State Speciation and Extinction; [10]), which, unlike HiSSE, unites the DEC and the SSE frameworks by modeling inheritance of two geographic areas along with diversification rates. Unlike GeoHiSSE, GeoSSE does not include hidden states. We did not use this approach because we found that GeoSSE had an unacceptable rate of type-1 error given our data. We followed the recommendations of Rabosky and Goldberg [11] for assessing type-1 error rates under the GeoSSE model. First, we randomly permuted our geographic data for the analysis of warm-water fishes (2,661 species) among species across the tree, randomly assigning species to the Indo-West Pacific region (inclusive of widespread species) and to “other warm oceans”, while keeping richness in each region constant. We analyzed this dataset because it is the smallest of the three trees analyzed with HiSSE, since type-1 error is expected to be exacerbated with larger trees due to greater rate heterogeneity. Therefore, if there are problems with this smaller dataset, it seems likely that they will also apply to the larger datasets. After permutating the data, we compared the fit of a model with speciation rates constrained to be equal to that of a full model with speciation rates freely variable between geographic states. We performed 100 trials using this procedure. The model with speciation constrained to be equal was preferred in only 32 trials, even though this should be the correct model in most replicates (since there should be no association between diversification rates and randomized character data). However, in 65 of 100 trials, the model with differences in speciation rates between the two states was strongly preferred with $\Delta AIC \geq 4$. In 3 trials, the difference was not significant. These analyses were performed in the R package *diversitree* version 0.9–7 [12].

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Table S9. Summary of group comparisons and sampling proportions used to account for incomplete sampling in HiSSE analyses. Proportions of species sampled were calculated from georeferenced data of 17,453 species (table S2; database S1). In each comparison, we trimmed the phylogeny to only include species occurring in at least one of the regions of interest.

Comparison	Taxa included	Trait 1	Trait 0	Sampled proportion, trait 1	Sampled proportion, trait 0
1	Warm marine species	Indo-West Pacific (WI, CIP, CP), Inclusive	Other warm oceans (WA, EA, EP)	0.2008	0.3273
2	Warm marine species	Indo-West Pacific (WI, CIP, CP), Endemic only	Other warm oceans (WA, EA, EP)	0.1828	0.3378
3	Marine species	Cold oceans (NC, SC), Inclusive	Warm oceans (WA, EA, EP, WI, CIP, CP)	0.3851	0.2006
4	Marine species	Cold oceans (NC, SC), Endemic only	Warm oceans (WA, EA, EP, WI, CIP, CP)	0.2575	0.2376
5	All species	Freshwater (FW), Inclusive	Marine (all marine regions)	0.3389	0.2153
6	All species	Freshwater (FW), Endemic only	Marine (all marine regions)	0.3172	0.2396

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Table S10. HiSSE model properties and relative model fit based on Akaike weights. When two models had high support (e.g. comparison 3), we model averaged the results. - = Akaike weight <0.01. Here, 0 and 1 represent the observed traits (region) and A–D represent the unknown hidden states. Regional comparisons are listed in table S9.

Model characteristics	Description	Model					
		1	2	3	4	5	6
		Full BiSSE	Null-2	Null-4	Full HiSSE	HiSSE, $\epsilon_0=\epsilon_1$	HiSSE, $\tau_0=\tau_1$
	Number of hidden states	0	2	4	2	2	2
	Diversification associated with geography?	yes	no	no	yes	yes	yes
	Diversification rate parameters	$\epsilon_0, \epsilon_1, \tau_0, \tau_1$	$\epsilon_A, \epsilon_B, \tau_A, \tau_B$	$\epsilon_A, \epsilon_B, \epsilon_C, \epsilon_D, \tau_A, \tau_B, \tau_C, \tau_D$	$\epsilon_{0A}, \epsilon_{0B}, \epsilon_{1A}, \epsilon_{1B}, \tau_{0A}, \tau_{0B}, \tau_{1A}, \tau_{1B}$	$\epsilon_A, \epsilon_B, \tau_{0A}, \tau_{0B}, \tau_{1A}, \tau_{1B}$	$\epsilon_{0A}, \epsilon_{0B}, \epsilon_{1A}, \epsilon_{1B}, \tau_A, \tau_B$
	Total number of free parameters	6	12	11	16	14	14
Model fit	Akaike weight, comparison 1	-	1	-	-	-	-
	Akaike weight, comparison 2	-	-	-	-	1	-
	Akaike weight, comparison 3	-	-	-	0.27	0.73	-
	Akaike weight, comparison 4	-	-	-	-	-	1
	Akaike weight, comparison 5	-	-	1	-	-	-
	Akaike weight, comparison 6	-	-	-	-	0.99	0.01

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Table S11. Parameters of GeoHiSSE models and their relative fits based on Akaike weights. We only used GeoHiSSE to compare the Indo-West Pacific (here state 0, combined WI, CIP, and CP) with other warm oceans (here state 1, combined WA, EA, and EP). Species were allowed to occupy both range categories. All models allowed diversification to be associated with two hidden state categories A and B. Note that unlike HiSSE, which optimizes turnover (τ), the extinction fraction (ϵ), and transitions between binary states (q), GeoHiSSE optimizes in-situ speciation (s), range contraction or extirpation (x), dispersal from a narrow to widespread range (d), and vicariant speciation or splitting of widespread ranges among daughter lineages (s_{01}). The transition rate q characterizes changes between hidden state categories. *= Model was excluded due to biologically unrealistic parameter estimates. - = Akaike weight <0.01 .

Model	Description	Diversification associated with geography?	Diversification rate parameters	Transition parameters	Total number of free parameters	Akaike weight
1	Full (unconstrained) GeoHiSSE	yes	$S_{1A}, S_{0A}, S_{01A}, X_{1A}, X_{0A}, S_{1B}, S_{0B}, S_{01B}, X_{1B}, X_{0B}$	$d_{0A}, d_{1A}, d_{1B}, d_{0B}, q_{\text{hidden}}$	15	*
2	GeoHiSSE with no hidden state associated with s_{01}	yes	$S_{1A}, S_{0A}, S_{01}, X_{1A}, X_{0A}, S_{1B}, S_{0B}, X_{1B}, X_{0B}$	$d_{0A}, d_{1A}, d_{1B}, d_{0B}, q_{\text{hidden}}$	14	*
3	GeoHiSSE with no hidden state associated with s_{01} or transitions to 01	yes	$S_{1A}, S_{0A}, S_{01}, X_{1A}, X_{0A}, S_{1B}, S_{0B}, X_{1B}, X_{0B}$	$d_0, d_1, q_{\text{hidden}}$	12	*
4	Area-independent with 2 hidden states	no	S_A, S_B, X_A, X_B	$d_{0A}, d_{1A}, d_{1B}, d_{0B}, q_{\text{hidden}}$	9	*
5	Area-independent with s_{01} free	no	$S_A, S_B, X_A, X_B, S_{01}$	$d_{0A}, d_{1A}, d_{1B}, d_{0B}, q_{\text{hidden}}$	10	1
6	Area-independent with constrained dispersal rates	no	S_A, S_B, X_A, X_B	$d_0, d_1, q_{\text{hidden}}$	7	-
7	Area-independent with s_{01} free and constrained dispersal rates	no	$S_A, S_B, X_A, X_B, S_{01}$	$d_0, d_1, q_{\text{hidden}}$	8	-

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8	GeoHiSSE with area-independent x	yes	$S_{1A}, S_{0A}, S_{01A}, S_{1B}, S_{0B}, S_{01B}, X_A, X_B$	$d_{0A}, d_{1A}, d_{1B}, d_{0B}, Q_{\text{hidden}}$	13	-
9	GeoHiSSE with area-independent x, no hidden state associated with s01	yes	$S_{1A}, S_{0A}, S_{1B}, S_{0B}, S_{01}, X_A, X_B$	$d_{0A}, d_{1A}, d_{1B}, d_{0B}, Q_{\text{hidden}}$	12	-
10	GeoHiSSE with area-independent x, no hidden state associated with s ₀₁ or transitions to 01	yes	$S_{1A}, S_{0A}, S_{1B}, S_{0B}, S_{01}, X_A, X_B$	$d_0, d_1, Q_{\text{hidden}}$	10	-

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Table S12. Maximum likelihood estimates for diversification and transition parameters for comparison between warm marine regions using HiSSE. λ = speciation rate. μ = extinction rate. r = net diversification rate.

Comparison 1: Indo-West Pacific (inclusive) vs. other warm oceans

Best model: Null-2 Akaike weight = 1.00

Rates				Transition Matrix				
State	λ	μ	r		Other-A	IWP-A	Other-B	IWP-B
Other-A	0.0360	0.0006	0.0355	Other-A	NA	0.0054	0.0074	0
Other-B	0.3111	0.2169	0.0943	IWP-A	0.0030	NA	0	0.0077
IWP-A	0.0360	0.0006	0.0355	Other-B	0.0891	0	NA	0.0172
IWP-B	0.3111	0.2169	0.0943	IWP-B	0	0.0383	0.0078	NA

Comparison 2: Indo-West Pacific (endemic only) vs. other warm oceans

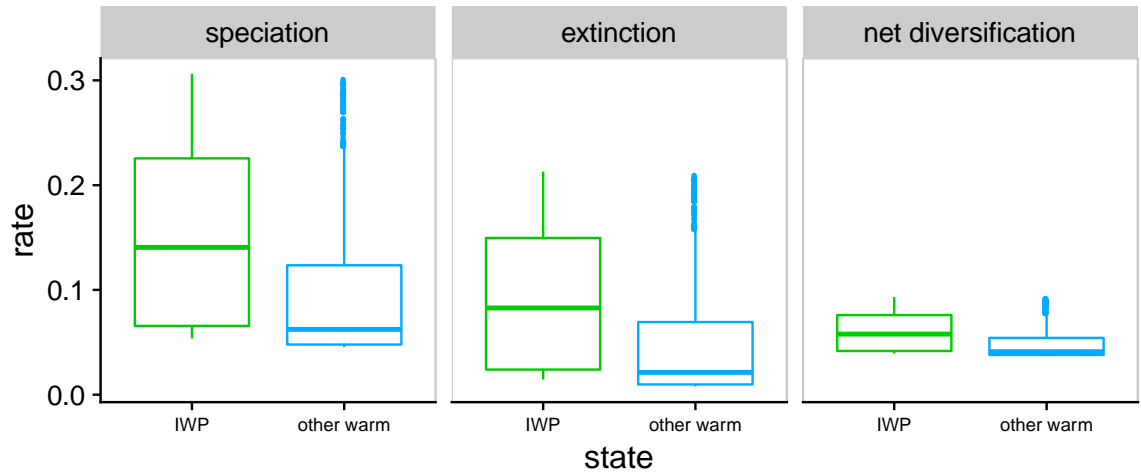
Best model: $\epsilon_0 = \epsilon_1$ Akaike weight = 1.00

Rates				Transition Matrix				
State	λ	μ	r		Other-A	IWP-A	Other-B	IWP-B
Other-A	0.0380	0.0080	0.0300	Other-A	NA	0.0047	0.0091	0
Other-B	0.3681	0.2537	0.1144	IWP-A	0.0021	NA	0	0.0052
IWP-A	0.0410	0.0086	0.0324	Other-B	0.1002	0	NA	0.0267
IWP-B	0.2875	0.1982	0.0893	IWP-B	0	0.0357	0.0114	NA

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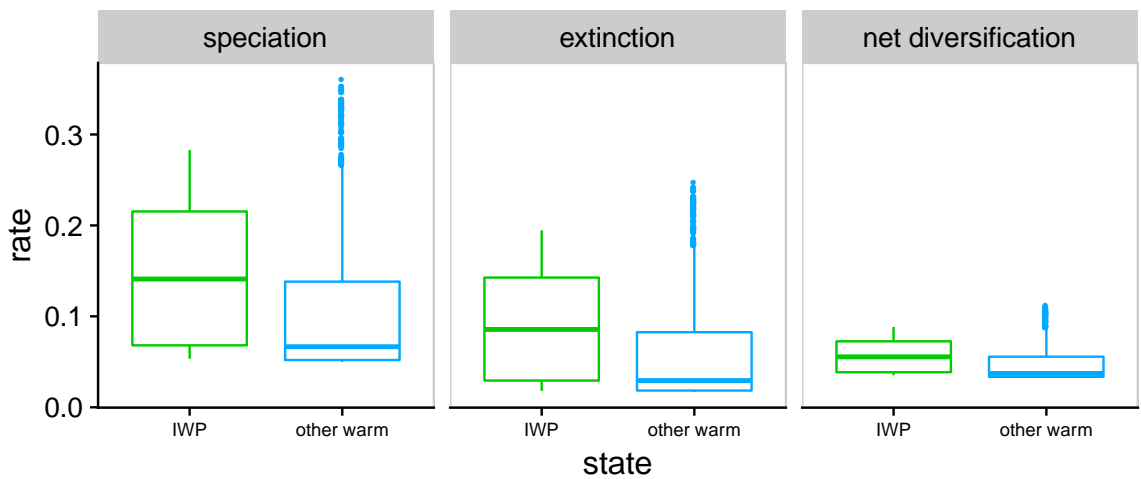
Figure S10. Speciation, extinction, and net diversification rates from HiSSE for warm marine regions based on averaging across hidden-state categories according to their frequency at the tips. Rate averaging takes uncertainty in state reconstructions into consideration [6].

Comparison 1: Indo-West Pacific (inclusive) vs. other warm oceans



Frequency of hidden states	
Region-hidden state combination	Number of species
IWP-A	962
IWP-B	633
other-A	889
other-B	177

Comparison 2: Indo-West Pacific (endemic only) vs. other warm oceans



Frequency of hidden states	
Region-hidden state combination	Number of species
IWP-A	748
IWP-B	576
other-A	1,125
other-B	212

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Table S13. Maximum likelihood estimates from for diversification and transition parameters for comparison between warm marine regions, using GeoHiSSE. s = speciation rate. x = extirpation rate. r = net diversification rate. Note that the speciation rate for the widespread range represents vicariant speciation (split into two narrow-ranged daughter lineages). The widespread area does not have an extirpation rate.

Best model: Area-independent diversification with s_{01} (vicariant speciation) as a free parameter (model 5 in table S11)

Diversification rates:

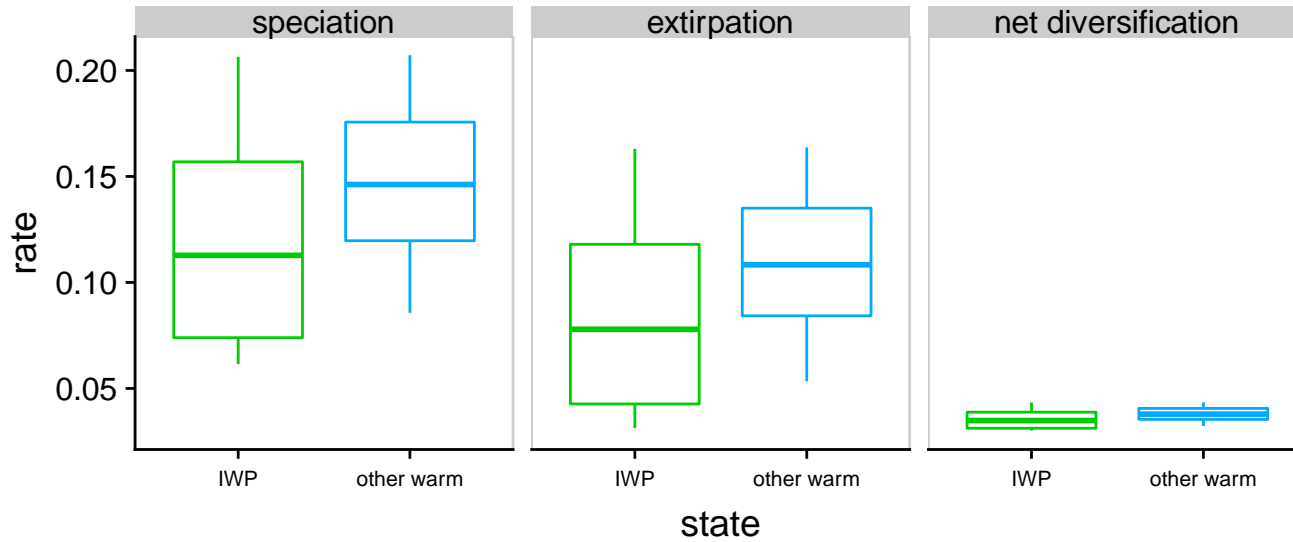
Region	s	x	r
Other-A	0.0269	<0.0001	0.0269
Other-B	0.2095	0.1657	0.0437
IWP-A	0.0269	<0.0001	0.0269
IWP-B	0.2095	0.1657	0.0437
Widespread	<0.0001	-	-

Transition matrix:

	IWP-A	Other-A	Widespread-A	IWP-B	Other-B	Widespread-B
IWP-A	NA	0	<0.0001	0.0286	NA	NA
Other-A	0	NA	0.0102	NA	0.0286	NA
Widespread-A	0	0	NA	NA	NA	0.0286
IWP-B	0.0286	NA	NA	NA	0	0.0370
Other-B	NA	0.0286	NA	0	NA	0.0021
Widespread-B	NA	NA	0.0286	0	0	NA

DIVERSIFICATION RATES AMONG REGIONS

Figure S11. Speciation, extinction, and net diversification rates from GeoHiSSE for warm marine regions based on averaging across hidden-state categories according to their frequency at the tips. Rate averaging takes uncertainty in state reconstructions into consideration [6]. Note that the speciation rate for the widespread range represents vicariant speciation (a split into two narrower-ranged daughter lineages) and is not shown for clarity (see table S13). The widespread area does not have an extinction rate or a net diversification rate.



Frequency of hidden states

Region-hidden state combination	Number of species
IWP-A	707
IWP-B	617
widespread	271
other-A	251
other-B	815

DIVERSIFICATION RATES AMONG REGIONS

Table S14. Maximum likelihood estimates for diversification and transition parameters for comparison between cold and warm oceans, using HiSSE. For comparison 3, we model averaged results from the two models with high Akaike weights (figure S12). λ = speciation rate. μ = extinction rate. r = net diversification rate.

Comparison 3: Cold (inclusive) vs. warm oceans

Best model 1: $\epsilon_0=\epsilon_1$ Akaike weight = 0.73

Rates			
State	λ	μ	r
Warm-A	0.0525	0.0096	0.0429
Warm-B	0.2354	0.0945	0.1409
Cold-A	0.0304	0.0055	0.0248
Cold-B	0.2759	0.1108	0.1651

Transition Matrix				
	Warm-A	Cold-A	Warm-B	Cold-B
Warm-A	NA	0.0048	0.0036	0
Cold-A	0.0140	NA	0	0.0058
Warm-B	0.0676	0	NA	0.0065
Cold-B	0	0.1110	0.0206	NA

Best model 2: Full HiSSE Akaike weight = 0.27

Rates			
State	λ	μ	r
Warm-A	0.0432	<0.0001	0.0432
Warm-B	0.2613	0.1546	0.1067
Cold-A	0.0343	0.0232	0.0111
Cold-B	0.3367	0.1986	0.1381

Transition Matrix				
	Warm-A	Cold-A	Warm-B	Cold-B
Warm-A	NA	0.0057	0.0062	0
Cold-A	0.0087	NA	0	0.0074
Warm-B	0.0432	0	NA	0.0074
Cold-B	0	0.1076	0.0227	NA

Comparison 4: Cold (endemic only) vs. warm oceans

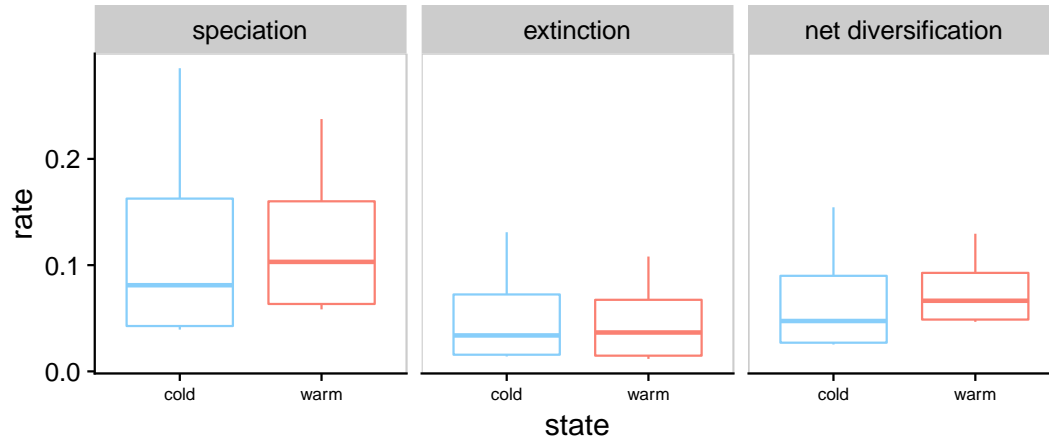
Best model: $\tau_0=\tau_1$ Akaike weight = 1.00

Rates			
State	λ	μ	r
Warm-A	0.0393	<0.0001	0.0393
Warm-B	0.2894	0.1898	0.0996
Cold-A	0.0393	<0.0001	0.0393
Cold-B	0.4120	0.0673	0.3447

Transition Matrix				
	Warm-A	Cold-A	Warm-B	Cold-B
Warm-A	NA	0.0004	0.0079	0
Cold-A	0.0101	NA	0	0.0197
Warm-B	0.0573	0	NA	0.0004
Cold-B	0	0.1785	0.0995	NA

Figure S12. Speciation, extinction, and diversification rates from HiSSE for warm and cold oceans, based on averaging across hidden state categories according to their frequency at the tips. Rate averaging takes uncertainty in state reconstructions into consideration [6]. For comparison 3, we model-averaged results from two best-fit models (table S14).

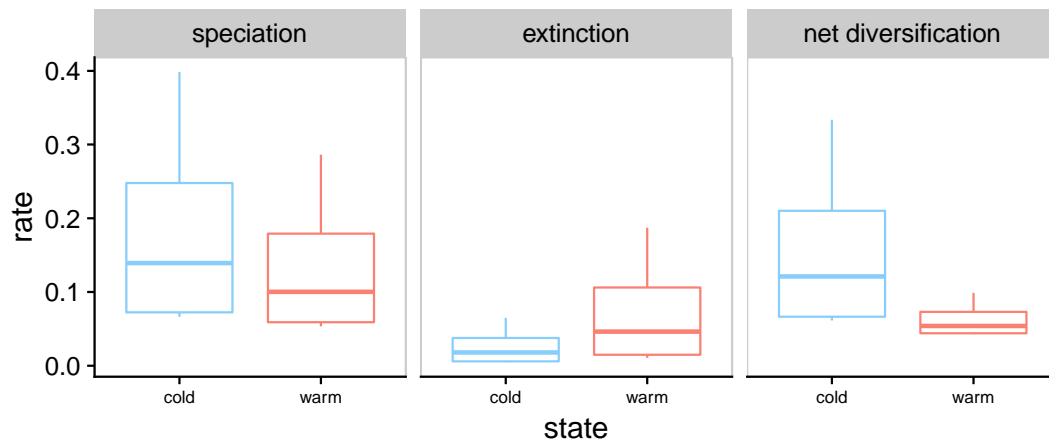
Comparison 3: Cold (inclusive) vs. warm oceans



Frequency of hidden states

Model 4		Model 5	
Region-hidden state combination	Number of species	Region-hidden state combination	Number of species
cold-A	756	cold-A	755
cold-B	255	cold-B	256
warm-A	1,233	warm-A	1,423
warm-B	735	warm-B	545

Comparison 4: Cold (endemic only) vs. warm oceans



Frequency of hidden states

Region-hidden state combination	Number of species
cold-A	223
cold-B	95
warm-A	1,878
warm-B	783

DIVERSIFICATION RATES AMONG REGIONS

Table S15. Maximum likelihood estimates for diversification and transition parameters for comparison between freshwater and marine habitats, using HiSSE. λ = speciation rate. μ = extinction rate. r = net diversification rate.

Comparison 5: Freshwater (inclusive) vs. marine

Best model: Null-4 Akaike weight = 1.00

Rates				Three-rate transition matrix	
State	λ	μ	r	rate	
hidden-A	0.0768	0.0001	0.0767	Between hidden states (A–D)	0.0166
hidden-B	0.0201	<0.0001	0.0201	Fresh to marine	0.0025
hidden-C	0.6953	0.6082	0.0871	Marine to fresh	0.0059
hidden-D	0.0122	<0.0001	0.0122		

Comparison 6: Freshwater (endemic only) vs. marine

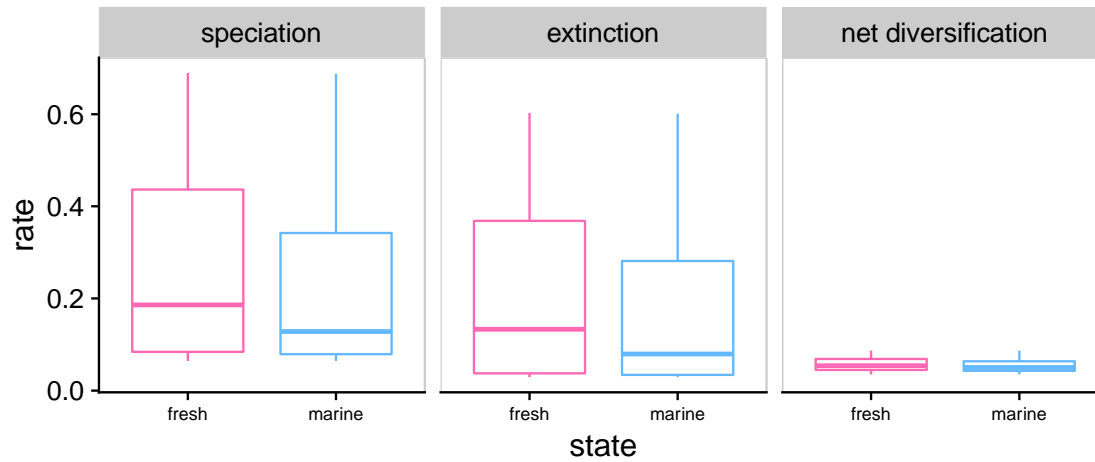
Best model: $\epsilon_0=\epsilon_1$ Akaike weight = 1.00

Rates				Transition Matrix				
State	λ	μ	r		Mar-A	Fresh-A	Mar-B	Fresh-B
Mar-A	0.0439	0.0041	0.0398	Mar-A	NA	0.0009	0.0065	0
Mar-B	0.3432	0.2117	0.1315	Fresh-A	0.0008	NA	0	0.0053
Fresh-A	0.0607	0.0057	0.0550	Mar-B	0.0754	0	NA	0.0009
Fresh-B	0.5042	0.3110	0.1932	Fresh-B	0	0.0935	0.0045	NA

DIVERSIFICATION RATES AMONG REGIONS

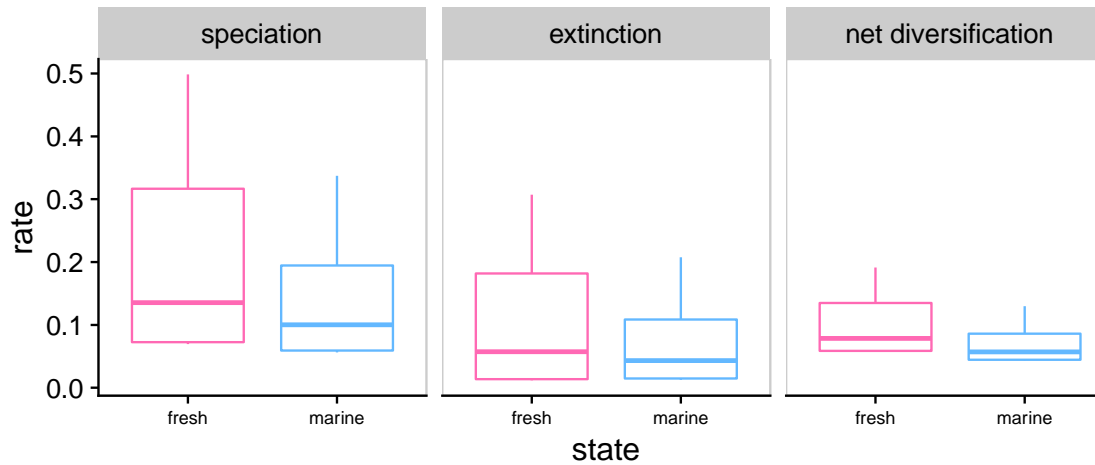
Figure S13. Speciation, extinction, and diversification from HiSSE for freshwater and marine habitats, based on averaging across hidden state categories according to their frequency at the tips. Rate averaging takes uncertainty in state reconstructions into consideration [6].

Comparison 5: Freshwater (inclusive) vs. marine



Frequency of hidden states	
Region-hidden state combination	Number of species
fresh-A	919
fresh-B	348
fresh-C	964
fresh-D	0
marine-A	1,118
marine-B	444
marine-C	778
marine-D	0

Comparison 6: Freshwater (endemic only) vs. marine



Frequency of hidden states	
Region-hidden state combination	Number of species
fresh-A	1,127
fresh-B	465
marine-A	2,229
marine-B	750

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