The evolution of latitudinal range limits in tropical reef fishes: heritability, limits, and inverse Rapoport's rule

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ABSTRACT

Aim

In this study we explore patterns and evolutionary processes of tropical reef fish latitudinal ranges, namely the degree of similarity in range size between ancestor and descendant lineages (i.e. phylogenetic signal); the evolution of range limits; and the latitudinal distribution of range sizes, particularly with respect to Rapoport's rule.

Location

Global.

Taxon

Tropical reef fishes.

Methods

We integrate data on the latitudinal distribution and evolutionary history of 5,071 tropical reef fish species with phylogenetic comparative methods to assess the level of phylogenetic signal in latitudinal range size, low- and high-latitude limits, and range medians, and to estimate rates of evolution of those traits. Finally, we test whether latitudinal ranges become smaller near the equator, as predicted by Rapoport's rule, using phylogenetic generalized least squares.

Results

There were varying levels of phylogenetic signal in latitudinal range size, low- and high-latitude limits, and range medians. Despite these differences, latitudinal medians were consistently shown to have the highest phylogenetic signal among all measured geographic features. Interestingly, the position of high-latitude limits in general evolved at substantially faster rates than their low-latitude counterparts. Finally, we confirm for the first time the existence of an inverse Rapoport's rule in marine fishes using phylogenetic comparative methods.

Main conclusions

We uncovered several congruent patterns in latitudinal ranges of tropical reef fish, despite vastly disparate biogeographical distributions and ecological differences between the studied fish lineages. Such broad congruence suggests that the evolution of latitudinal ranges of reef fishes may be governed by common principles.

Key words: geographical distribution, macroecology, macroevolution, Rapoport's rule, coral reefs, latitudinal diversity gradient.

INTRODUCTION

Some of the most pervasive patterns in the distribution of life on earth, such as the latitudinal gradient in species diversity (Willig, Kaufman & Steven, 2003; Hillebrand, 2004; Mittelbach et al., 2007) and the differences in faunal composition between regions (Ficetola, Mazel & Thuiller, 2017; Cowman et al., 2017), are fundamentally determined by the evolution of the position and limits of geographical ranges of different organisms. For instance, phylogenetic niche conservatism posits that the ancestral niche can determine the regions and habitats that a clade can colonize, and those in which it will persist in the face of environmental change (Wiens & Donoghue, 2004). Therefore, understanding the evolution of geographical ranges has far implications for many areas in ecology, conservation and evolution, from biogeography to the response of species to climate change. In this study we focus on three fundamental properties of geographical distributions: the degree of similarity in latitudinal range size between ancestor and descendant lineages, the evolution of range limits, and the geographical distribution of range sizes using tropical reef fishes as a model system. Tropical reef fishes are an ideal group for studying patterns and processes in range size in the marine realm. They are conspicuous members of shallow coral reef ecosystems, facilitating the surveys that provide presence-absence data needed to quantify range sizes. Furthermore, reef fishes are among the most diverse groups of vertebrates in the world, exhibiting extraordinary taxonomic breadth and endemism, with many closely related species that vary greatly in both their range size and in many of the potential biological traits that may influence range size (Ruttenberg & Lester, 2015).

The seminal paper of Jablonski (1987) demonstrated that sister species of Cretaceous mollusks exhibited correlation in their range sizes, thus suggesting that there may be heritability in this emergent trait. However, the generality of species-level "heritability" of emergent traits in general, and of geographical range size in particular, is still unclear. For example, although studies on terrestrial taxa have shown mixed support for range size heritability (e.g. Ricklefs & Latham, 1992; Blackburn & Gaston, 1996; Waldron, 2007), some inferences might have been biased by the low statistical power of the early methods used to test for species level heritability (more recently referred to as phylogenetic signal, see Revell, Harmon & Collaret, 2008), such as variance partitioning. On the other hand, even though model-based methods were more successful in detecting phylogenetic signal in range size (Cardillo, 2015; Pie & Meyer, 2017), they also found substantial differences among lineages depending on their biological characteristics (e.g. Freckleton, Harvey & Pagel, 2002, see also Ricklefs & Latham, 1992). Interestingly, although the original study of Jablonski (1987) involved marine mollusks, no study to date tested for range size heritability in extant marine taxa.

One cannot understand the evolution of geographical range size without first recognizing what determines its limits (Gaston, 2009; Sexton et al., 2009). This issue was well presented by Merriam (1894): "What naturalists wish to know is not how species are dispersed, but how they are checked in their efforts to overrun the earth". The study of range limits is particularly intriguing in the ocean, given that there are few hard biogeographical barriers that inhibit species dispersal when compared with terrestrial habitats (Palumbi, 1994, but see Gaines et al., 2009). Within marine habitats, the proximate mechanisms driving the distribution of species might involve some combination of environmental tolerances (Rezende & Bozinovic, 2019; Deutsch, Penn & Seibel, 2020; Marshall et al., 2020), species-level traits that have the potential to impact species' distributions by influencing colonization ability and/or post-colonization survival or persistence (Luiz et al., 2013), and the

impact of ocean currents on larval dispersal (e.g. Gaylord & Gaines, 2000; Mora & Sale, 2002; Álvarez-Noriega et al., 2020). While these proximate mechanisms have been scrutinized in the macroecological literature, the ultimate (evolutionary) mechanisms driving range limit evolution in marine species are still poorly known. In terrestrial organisms, tolerance to heat is largely conserved across lineages, whereas tolerance to cold varies between and within species, a pattern that was interpreted as evidence for hard physiological boundaries constraining the evolution of tolerances to high temperatures (Araújo et al., 2013, see also Qu & Wiens, 2020). Indirect evidence of environmental tolerances can be obtained by recording the minimum and maximum latitudes of occurrence of a given species, given the widespread association between geographical distributions and physiological processes, particularly in marine fish (Stuart-Smith et al., 2015; Stuart-Smith, Edgar & Bates, 2017; Waldock et al., 2019; Dahlke et al., 2020). Given that many climatic variables vary consistently with latitude, such limits can serve as a proxy for the corresponding environmental limits. Indeed, Pie & Meyer (2017) found that, for terrestrial vertebrates, rates of evolution of high-latitude limits were 1.6–4 times faster than low-latitude limits, suggesting that different mechanisms drive the evolution of "warm" and "cold" range boundaries. The extent to which this pattern is shared with marine organisms is currently unknown.

Rapoport's rule states that species that are characteristic of high-latitude locations have greater latitudinal range than species which inhabit low-latitude locations (Rapoport, 1982), and it therefore could provide a mechanism to explain the latitudinal gradient in species richness (Stevens, 1989). Although evidence for Rapoport's rule has been obtained for several terrestrial taxa, its generality has been called into question (Gaston, Blackburn & Spicer, 1998). Moreover, it has rarely been assessed in marine organisms. For instance, the few studies to date testing Rapoport's rule for marine fishes found that, not only the rule did not apply, but also that ranges actually became larger towards the equator (Rohde, Heap & Heap, 1993; Macpherson & Duarte, 1994; Macpherson, Hastings & Robertson, 2009, but see Fortes & Absalão, 2010). However, it is important to note that, given the often significant phylogenetic signal in geographical ranges (e.g. Cardillo, 2015; Pie & Meyer, 2017), it is possible that the obtained results might have been affected by phylogenetic nonindependence between species, potentially biasing both the direction and the significance of the estimated relationships. To the best of our knowledge, no study to date tested for the existence of Rapoport's rule in marine fishes using phylogenetic comparative methods.

In this study we provide a comprehensive assessment of the evolution of geographical ranges in marine reef fishes. In particular, we focus on three main questions: (1) is there significant phylogenetic signal in their latitudinal range sizes? (2) do low- and high-latitude range limits evolve at different rates during their evolution? and (3) do patterns of reef fish latitudinal range size variability support Rapoport's rule?

MATERIALS AND METHODS

Data collection

Latitudinal limits were obtained from the presence-absence dataset of Rabosky et al. (2018). This dataset consists of global occurrences of marine species in geographic grid cells of 150 km^2, and it was built through the AquaMaps algorithm (Ready et al., 2010). From this dataset, we first filtered species that are considered reef-associated (see Siqueira et al., 2020), to then calculate the highest,

lowest and median latitudinal points of the geographic distribution of each species. Our final dataset contained distribution data for 5,071 species of tropical reef fishes. We also used the phylogenetic trees produced by Siqueira et al. (2020) to perform our comparative analyses. This set of 100 phylogenies was produced by the taxonomic imputation of missing species into the backbone tree of Rabosky et al. (2018) using the TACT algorithm (Chang, Rabosky & Alfaro, 2020).

Analyses

We estimated the phylogenetic signal of the latitudinal median, as well as the high- and low-latitude limits of tropical reef fishes using Pagel's λ (Pagel, 1999) and Blomberg et al.'s *K* (2003) using the *phylosig* function in PHYTOOLS 0.7-47 (Revell, 2012). More specifically, we tested whether a model with an estimated λ provides a better fit than a simpler alternative where λ=0, whereas *K* estimates were based on 1,000 resamplings of the original data. Latitudinal range size data were ln-transformed prior to the analyses. We used phylogenetic generalized least squares (PGLS, Freckleton et al., 2002) to test the relationship between the latitudinal range (difference between high and low latitude limits as the response variable) and latitudinal position (predictor variable) using the *pgls* function in CAPER 1.0.1 (Orme et al., 2008). We estimated the rate of evolution of each geographic feature based on the σ^2 parameter under a Brownian Motion (BM) model using the *fitContinuous* function in GEIGER 2.0.7 (Harmon et al., 2008). Differences in rates of evolution of low- and high-latitude limits were tested using the *mvBM* function in mvMORPH 1.1.3 (Clavel, Escarguel & Merceron, 2015). This test contrasts the fit of a model in which low- and high-latitude limits share the same rates against an alternative where each limit has a separate rate using likelihood ratio tests. To account for phylogenetic uncertainty, we repeated all analyses on each of the 100 alternative topologies and report the median of the estimates of each parameter and model likelihood. However, given that the phylogenetic imputation used to provide those topologies might have introduced noise in the inferred parameters, we repeated all analyses using a smaller phylogeny (2,585 tips) that included only those species for which genetic data were available. We refer to these datasets as *expanded* and *reduced*, respectively. The random imputation of species based on taxonomy can also bias the inferred evolutionary signal of distribution features. Therefore the tests of phylogenetic signal were performed using the reduced dataset only. In each of the above mentioned analyses, we pruned the trees to estimate separately the evolutionary rates and phylogenetic signal for different families and orders, as long as the resulting subtrees had at least 20 tips. All analyses were carried out in R 4.0.2 (R Core Team, 2020).

RESULTS

The distribution of latitudinal ranges in the studied tropical reef fish species follows the typical pattern found in terrestrial organisms, with an approximately lognormal distribution with a left skew (Figure 1). The truncation on the right-hand side of the distribution is probably the result of a geometric constraint in terms of the size of ocean basins, given that the largest possible range (i.e. the natural logarithm of the difference between the maximum and minimum latitudes across all studied species) would be ≈ 4.7. Despite this hard boundary condition, the latitudinal ranges of studied lineages on average tended to be relatively broad, with many species approaching the largest latitudinal range classes. There were varying levels of phylogenetic signal in latitudinal range size, low- and high-latitude limits and range medians, both at the order (Figure 2) and the family levels

(Figure S1). Despite these differences, range medians consistently showed the highest levels of phylogenetic signal, both for Pagel's λ and Blomberg et al.'s *K* (Tables S1, S2).

Results of statistical tests for variation in rates of evolution between high- and low-latitude limits for different fish orders are shown in Table 1. Significant rate differences were detected in 17 and 13 out of the 19 and 16 tested orders for the expanded and reduced datasets, respectively. These significant differences predominantly involved faster rates in high-latitude limits (16 out of 17 and 10 out of 12 for the expanded and reduced datasets, respectively). At the family level, significant rate differences were detected in 36 and 17 families out of the 41 and 27 tested for the expanded and reduced datasets, respectively (Table S3). Again, significant differences predominantly involved faster rates in high-latitude limits (33 versus 3 and 13 versus 4 for the expanded and reduced datasets, respectively). Therefore, although not universal, a faster rate of evolution of high-latitude range limits is widespread among marine fish lineages. Finally, contrary to the expectation based on Rapoport's rule, in general there was a negative relationship between latitude and latitudinal range (Figure 3), which was significant in 11 out of 15 orders (Table 2) and 19 out of 23 families for the reduced dataset (Table S4). There was no case of the positive relationship between latitude and latitudinal range predicted by Rapoport's rule for any of the tested orders and families.

It is important to note that, given that the Atlantic and Indo-Pacific ocean basins were influenced by different histories and environmental gradients, we repeated our analyses separately for evolutionary rate tests, and considered whether species were present in either (or both) ocean basins as a covariate in PGLS analyses. Rate tests provided qualitatively similar results (Table S5 for orders, Table S6 for families). Likewise, the PGLS for different families (Table S7) and orders (Table S8) did not show a significant effect of ocean basin on the relationship between latitude and latitudinal range except for the order Perciformes and the family Scorpaenidae. However, when the corresponding data were visualized (Figure S2), it becomes clear that the significant effect of ocean basin on Perciformes is mostly due to species with very large range sizes that occur in both basins whose range size is not related to latitude (Figure S2). Although there was also a significant effect of ocean basin on the scorpaenid range data, it was mostly reflected in different slopes of relationships that were still negative, thus corroborating that none of the studied fish taxa showed evidence for a positive relationship between range size and latitude that is expected based on Rapoport's rule.

DISCUSSION

In this study we provide the most comprehensive assessment of the evolution of latitudinal ranges of marine fishes to date. In particular, we uncover several general principles governing geographical range evolution in reef-associated fishes, namely (1) there was stronger phylogenetic signal in latitudinal midpoint than in latitudinal limits; (2) high-latitude range limits evolve substantially faster than low-latitude range limits; and (3) latitudinal range sizes tend to become larger in species whose medians are closer to the equator.

The detection of phylogenetic signal in traits related to geographical ranges might provide insight into important mechanisms driving their evolution. For instance, if closely related species show range overlap, they could experience similar conditions that would lead to expansions and contractions in their geographical ranges in parallel when faced with climate change, as seems to be the case in birds (Mouillot & Gaston, 2009). However, our results indicate that not all properties of reef fish latitudinal ranges share similar levels of phylogenetic signal. Rather, range medians tended

to show higher phylogenetic signal than either latitudinal range or limits. These differences suggest that the evolution of latitudinal ranges takes place at a relatively constant rate, whereas range size and limits might experience stronger heterotachy, thus obscuring patterns of phylogenetic autocorrelation. These results are particularly intriguing when compared to the estimates of evolutionary rates (Table 1, Table S3). The combination of relatively lower phylogenetic signal in high-latitude range limits and their higher evolutionary rates is not obvious, given that higher rates do not necessarily entail lower phylogenetic signal (Revell et al., 2008). Rather, these results provide a scenario in which tropical reef fish gradually change the median position and site of their latitudinal ranges, whereas range limits (particularly those at higher latitudes) show a faster and more heterogeneous rate of evolution. One potential mechanism to explain this pattern is the observation that higher latitudes have experienced more variation in temperatures through time (Siqueira et al., 2016; Gaboriau et al., 2019). More detailed studies, particularly using more precise geographical distribution data, as well as more detailed phylogenetic comparative methods of range evolution, might provide important insight into the extent to which this scenario is representative of reef fish range evolution in general.

We confirmed previous studies suggesting an inverse Rapoport rule for marine fishes (Rohde et al., 1993; Macpherson & Duarte, 1994). It is important to note that Macpherson (2003) and Fortes & Absalão (2010) actually found patterns consistent with Rapoport's rule in smaller and larger datasets than ours, respectively, of marine fishes. However, they used the method proposed by Stevens (1989), which compares the mean latitudinal range of all species within each 5° latitudinal band within the latitudinal gradient. As indicated by Rohde et al. (1993), in this method the same species are counted multiple times as they are distributed across different latitudinal bands, leading to statistical issues of nonindependence (see also Rohde & Heap, 1996; Ribas & Schoereder, 2006). Interestingly, an inverse Rapoport's rule was also found for marine prosobranch gastropods living on the shelves of the western Atlantic and eastern Pacific Oceans (Roy et al., 1998) and for marine bivalves in the western and eastern Pacific and western Atlantic coasts (Tomašových et al., 2015). The reverse Rapoport's rule appears to be common among marine organisms because of the nonlinearity of the latitudinal gradient of temperature in the sea, with much weaker spatial variation in annual minimum, mean and maximum daily temperature at low than at mid latitudes. These effects may be a general factor shaping latitudinal gradients in range size, because at the global scale, as shallow thermal gradients within the tropics and steep thermal gradients at higher latitudes also characterize some terrestrial environments (Tomašových et al., 2015).

To what extent do latitudinal ranges in marine and terrestrial organisms evolve according to the same rules? Other than the fact that latitudinal ranges of marine organisms are commonly considered much larger than those of terrestrial organisms (Gaston, 2003), there have been few attempts to assess the extent to which geographical range evolution might differ between these two environments. We argue that, despite the obvious differences between marine and terrestrial life, their geographical ranges actually share several important characteristics, namely (1) approximately lognormal distributions with a left skew (Gaston, 2003; Macpherson, 2003; Mora & Robertson, 2005; Figure 1); (2) phylogenetic signal in geographical range properties (Cardillo, 2015; Pie & Meyer, 2017; Figure 2, Figure S1, Tables S1, S2); (3) asymmetry in evolutionary rates between high- and low-latitude limits (Pie & Meyer, 2017; Table 1, Table S3). Although these characteristics seem to represent general principles regarding geographical range evolution that transcend differences

between land and ocean habitats, there are several taxa that seem to depart from this expectation. Therefore, one of the main contributions of our study is that we can now actually recognize those taxa as exceptional, and we can now seek to understand why they are not constrained by the same mechanisms as other taxa.

There are some important caveats with respect to our analyses. For instance, we have not explicitly considered differences among species with respect to depth, which might be an important confounding factor for marine fish (e.g. Macpherson & Duarte, 1994). However, in the case of reef fishes, depth does not seem to play an important role in explaining interspecific variation in range size (Luiz et al., 2012, 2013). It is also important to note that our estimates of rates of evolution depend fundamentally on (1) the accuracy of the phylogenetic relationships between the studied species and (2) the extent to which distribution ranges evolve according to a Brownian motion model. Formally assessing phylogenetic accuracy is a challenging task, particularly for large-scale phylogenies with thousands of species, in which the level of topological error might vary across lineages based on the level of phylogenetic and taxonomic sampling. Such inaccuracies have been shown to affect downstream analyses (e.g. Title & Rabosky, 2019). We concede that some level of error is present in the phylogenetic relationships used in the present study, particularly when using phylogenetic imputation (Chang et al., 2020). However, we believe that such inaccuracies are unlikely to alter our conclusions for three main reasons. First, any error in the analyzed phylogenies would lead to undirected random noise as opposed to differentially overestimating high-latitude limits in relation to low-latitude limits, which would in fact cause the estimated rate differences to be conservative. Second, the consistency in the results across fish taxa of widely different ecologies and biogeographical distributions (and with terrestrial organisms as well) would be unlikely due to chance alone. Finally, the sensitivity analyses carried out in our study, varying the phylogenies in both the expanded and reduced datasets, indicates that our conclusions are largely unaffected by the topological variation in the underlying trees. With respect to the adequacy of Brownian motion (BM) as a model of range evolution, we can most certainly say that it is not. For instance, BM assumes that species are identical in their trait values at the time of speciation, which would be unrealistic for all but some specific cases of sympatric speciation. Also, BM is unbounded, whereas ranges are bounded both by continents and by the poles. However, our goal was not to provide a realistic model of range size but rather a first approximation to estimate rates of range size evolution. At the present, there are adaptations of BM-like processes to model specifically the evolution of geographical ranges. We hope that our results, particularly the asymmetry in the evolutionary rates between low- and high-latitude limits, would become an important component of such models in the future.

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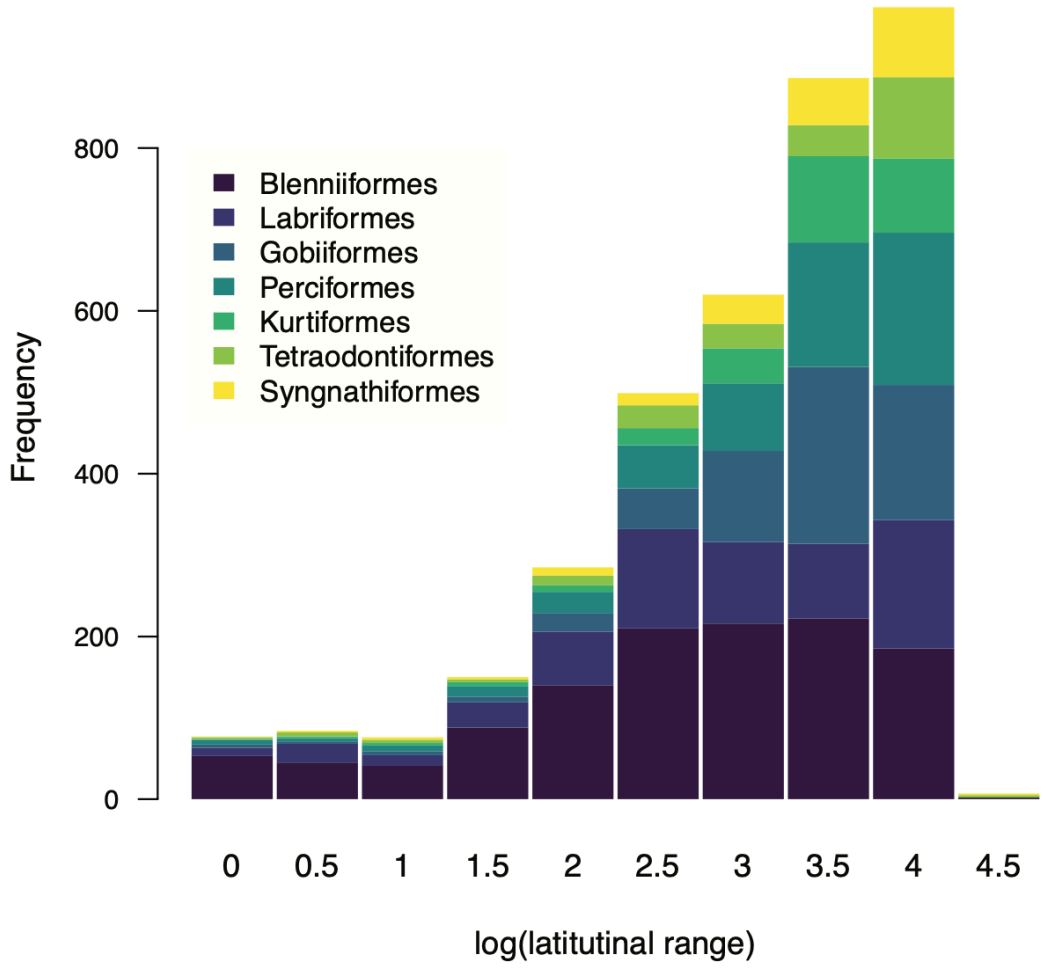
Figure captions

Figure 1. Distribution of log-transformed latitudinal ranges of the seven most species-rich marine fish orders in our dataset. The largest possible range (i.e. the natural logarithm of the difference between the maximum and minimum latitudes across all studied species) would be ≈ 4.7.

Figure 2. Phylogenetic signal, according to Pagel's λ (Pagel 1999), of properties of geographical ranges of tropical reef fish orders. Details on estimates, corresponding likelihoods and p-values are indicated in Table S1.

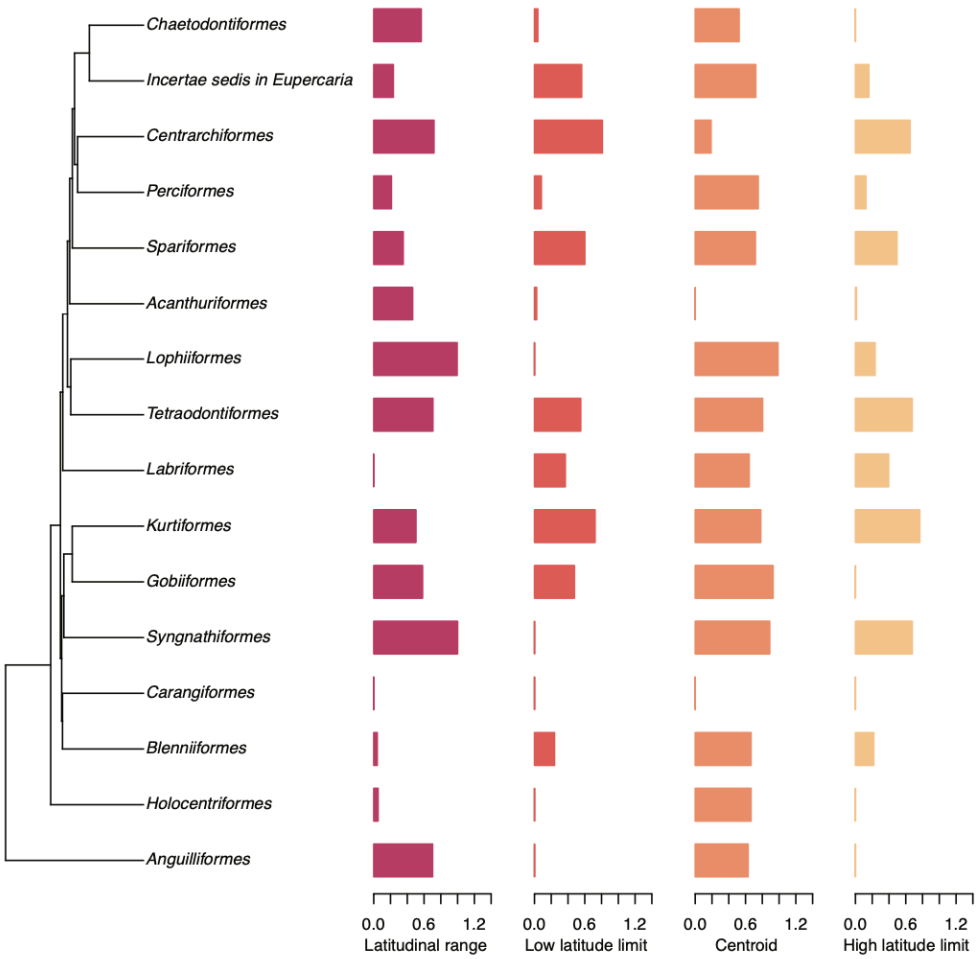
Figure 3. Latitudinal variation in the northern limit (A), median (B), and southern limit (C) of marine fishes, as well as the latitudinal distribution of their corresponding latitudinal range sizes.

Figure 1


Blenniiformes
Labriformes
Gobiiformes
Perciformes
Kurtiformes
Tetraodontiformes
Syngnathiformes
Frequency
0
200
400
600
800
0
0.5
1
1.5
2
2.5
3
3.5
4
4.5
log(latitutinal range)

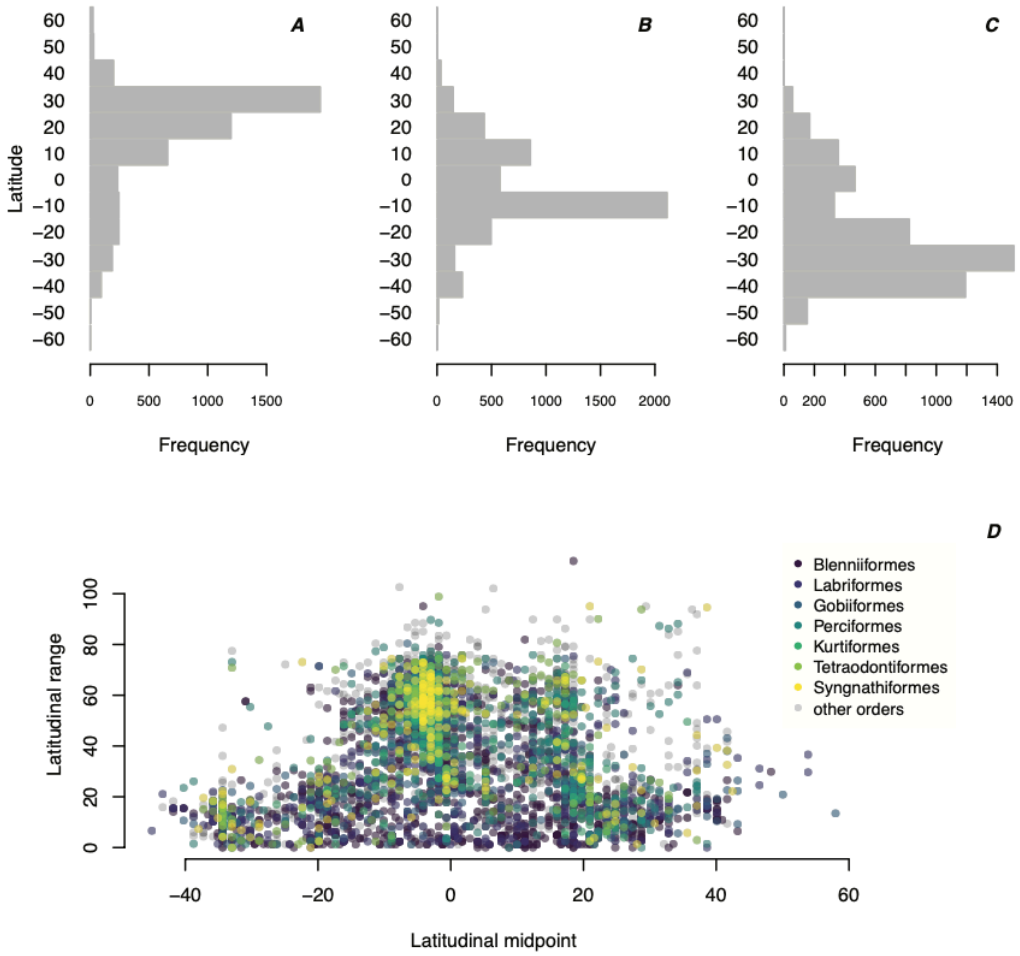
1

Figure 2



2
3
4

Figure 3


A
B
C
D
Latitude
Frequency
Latitudinal range
Latitudinal midpoint
Blenniiformes
Labriformes
Gobiiformes
Perciformes
Kurtiformes
Tetraodontiformes
Syngnathiformes
other orders

1

Table 1. Relative fit of models in which high- and low-latitude range limits of marine fish orders evolve at the same or different rates: lik1: log likelihood of multiple-rate model; lik2: likelihood of single-rate model; σ^2 high and σ^2 low indicate estimated rates of evolution for high- and low-latitude range limits, respectively; N: number of analyzed species. Values for the expanded dataset indicate medians across 100 alternative topologies. Bold-face rates are significantly different.

Order	Reduced dataset						Expanded dataset					
	lik1	lik2	p	σ^2 high	σ^2 low	N	lik1	lik2	p	σ^2 high	σ^2 low	N
Acanthuriformes	-1145.94	-1150.06	0.0041	213.978	**331.472**	108	-1427.40	-1427.88	0.1081	260.114	307.808	135
Anguilliformes	-560.49	-560.65	0.5686	34.277	31.687	61	-1372.24	-1376.89	0.0027	**99.221**	72.834	140
Aulopiformes	-	-	-	-	-	-	-360.50	-362.70	0.0968	116.731	75.955	35
Blenniiformes	-4728.02	-4735.69	8.97E-05	**194.439**	135.536	443	-13366.55	-13405.09	1.49E-29	**504.293**	283.336	1216
Carangiformes	-1436.49	-1477.34	1.57E-19	**2985.984**	1265.937	118	-1582.83	-1627.14	2.51E-21	**2686.822**	1150.022	132
Centrarchiformes	-490.79	-493.67	0.0164	**77.843**	41.272	51	-759.12	-764.46	0.0019	**158.289**	87.511	75
Chaetodontiformes	-988.34	-997.42	2.05E-05	**432.543**	251.434	96	-1334.66	-1344.95	3.10E-05	**465.602**	255.737	127
Gobiiformes	-1877.79	-1878.94	0.1279	60.823	286.250	196	-6338.19	-6376.85	4.38E-06	176.709	**195.677**	587
Holocentriformes	-374.41	-375.24	0.1977	80.619	69.369	43	-657.22	-661.15	0.0218	**249.886**	226.536	67
Incertae sedis in Eupercaria	-2182.43	-2196.15	1.63E-07	**107.478**	49.228	195	-2915.40	-2946.68	2.05E-12	**182.877**	95.700	287
Kurtiformes	-580.86	-581.02	0.5795	15.736	14.598	69	-2868.24	-2890.32	3.23E-12	**275.721**	145.130	281
Labriformes	-3577.24	-3606.32	2.41E-14	**2508.761**	1396.061	337	-7203.53	-7292.78	8.34E-39	**1609.595**	847.875	617
Lophiiformes	-236.62	-241.82	0.0013	**91.312**	42.242	25	-345.93	-351.15	0.0007	**111.138**	64.588	37
Ophidiiformes	-	-	-	-	-	-	-766.24	-774.12	0.0008	**231.625**	167.159	77
Perciformes	-2885.74	-2917.10	2.39E-15	118.891	**292.006**	267	-5893.84	-5893.89	0.0003	**290.563**	284.386	535
Spariformes	-1365.29	-1378.52	2.68E-07	**94.444**	30.936	136	-1930.65	-1953.29	1.09E-10	**157.028**	56.131	189
Syngnathiformes	-1089.65	-1097.96	4.58E-05	**54.871**	45.639	94	-2375.75	-2414.93	2.29E-09	**222.812**	135.129	218
Tetraodontiformes	-1588.55	-1596.32	8.01E-05	**142.239**	83.969	153	-2404.48	-2417.01	4.06E-08	**422.725**	226.461	225
Uranoscopiformes	-	-	-	-	-	-	-369.34	-373.47	0.0133	**385.331**	227.516	35

Table 2. Phylogenetic generalized least squared analyses of the relationship between absolute latitude and latitudinal range of different fish orders.

Order	Slope	SE	t	P	R^2	N
Acanthuriformes	-0.032	0.002	-17.676	0	0.747	108
Anguilliformes	-0.016	0.004	-4.217	0	0.232	61
Blenniiformes	0.006	0.02	0.281	0.779	0	443
Carangiformes	-0.045	0.003	-16.805	0	0.709	118
Centrarchiformes	0	0.002	-0.228	0.821	0.001	51
Chaetodontiformes	-0.061	0.005	-12.73	0	0.633	96
Gobiiformes	-0.081	0.004	-19.611	0	0.665	196
Holocentriformes	-0.042	0.009	-4.909	0	0.37	43
Incertae sedis in Eupercaria	0.063	0.012	5.257	0	0.125	195
Kurtiformes	-0.009	0.006	-1.607	0.113	0.037	69
Labriformes	-0.067	0.017	-3.885	0	0.043	337
Perciformes	-0.055	0.004	-12.673	0	0.377	267
Spariformes	-0.013	0.007	-1.873	0.063	0.026	136
Syngnathiformes	-0.039	0.019	-2.101	0.038	0.046	94
Tetraodontiformes	-0.041	0.004	-10.016	0	0.399	153

Supplementary material

Figure S1. Phylogenetic signal, according to Pagel's λ (Pagel 1999), of properties of geographical ranges of tropical reef fish families. Details on estimates, corresponding likelihoods and p-values are indicated in Table S2.

Figure S2. Relationship between latitudinal range size (ln-transformed) and latitudinal position for the clades for which Ocean basin had a significant effect, based on PGLS analyses. We only tested taxa that had at least 10 tips in each of the groups.

Table S1. Tests of phylogenetic signal of latitudinal range size, lower latitude, median and higher latitude limits for different reef fish families.

Table S2. Tests of phylogenetic signal of latitudinal range size, lower latitude, median and higher latitude limits for different reef fish orders.

Table S3. Relative fit of models in which high- and low-latitude range limits of marine fish families evolve at the same or different rates: lik1: log likelihood of multiple-rate model; lik2: likelihood of single-rate model; σ^2 high and σ^2 low indicate estimated rates of evolution for high- and low-latitude range limits, respectively; N: number of analyzed species. Values for the expanded dataset indicate medians across 100 alternative topologies. Bold-face rates are significantly different.

Table S4. Phylogenetic generalized least squares analyses of the relationship between absolute latitude of the range median and latitudinal range of different fish orders

Table S5. Relative fit of models in which high- and low-latitude range limits of marine fish orders evolve at the same or different rates, analyzing separately each ocean basin: lik1: log likelihood of multiple-rate model; lik2: likelihood of single-rate model; σ^2 high and σ^2 low indicate estimated rates of evolution for high- and low-latitude range limits, respectively; N: number of analyzed species. Values for the expanded dataset indicate medians across 100 alternative topologies. Bold-face rates are significantly different.

Table S6. Relative fit of models in which high- and low-latitude range limits of marine fish families evolve at the same or different rates, analyzing separately each ocean basin: lik1: log likelihood of multiple-rate model; lik2: likelihood of single-rate model; σ^2 high and σ^2 low indicate estimated rates of evolution for high- and low-latitude range limits, respectively; N: number of analyzed species. Values for the expanded dataset indicate medians across 100 alternative topologies. Bold-face rates are significantly different.

Table S7. Phylogenetic generalized least squares analyses of the relationship between absolute latitude of the range median and latitudinal range of different fish orders using ocean basin as a covariate.

Table S8. Phylogenetic generalized least squares analyses of the relationship between absolute latitude of the range median and latitudinal range of different fish families using ocean basin as a covariate.

Figure S1

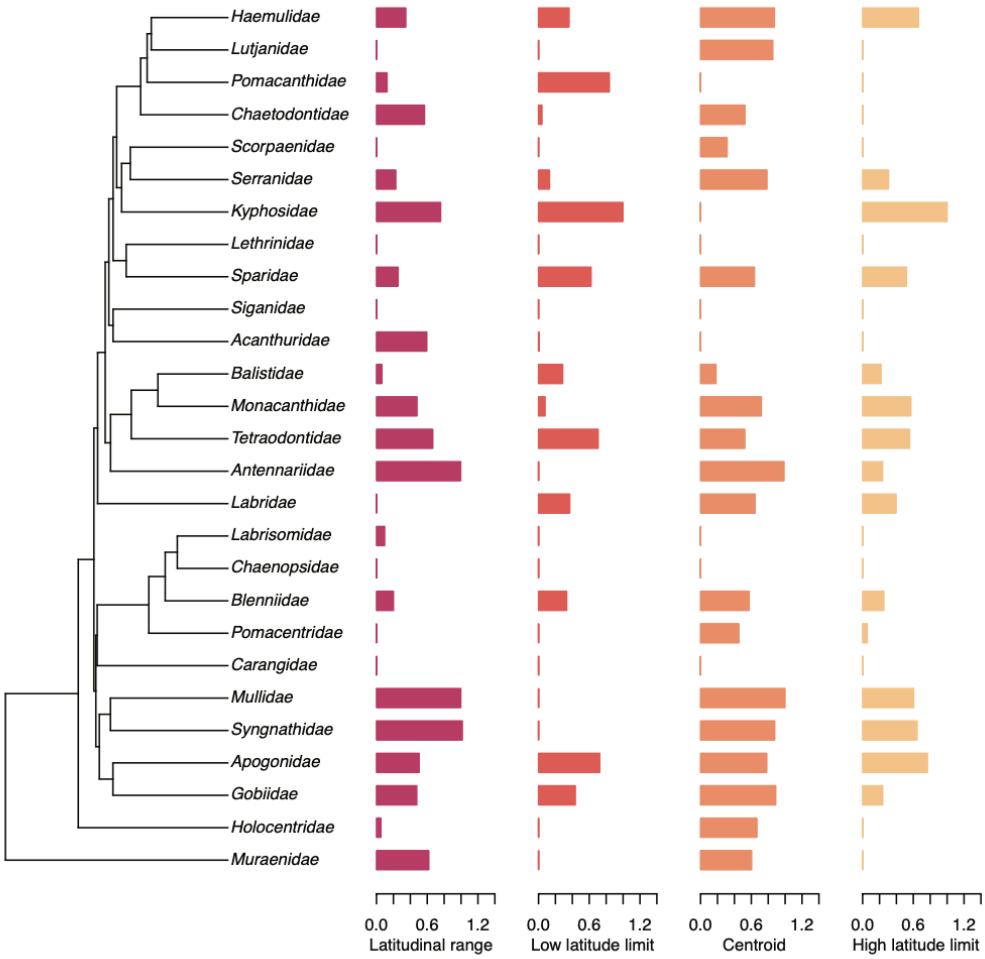

Haemulidae
Lutjanidae
Pomacanthidae
Chaetodontidae
Scorpaenidae
Serranidae
Kyphosidae
Lethrinidae
Sparidae
Siganidae
Acanthuridae
Balistidae
Monacanthidae
Tetraodontidae
Antennariidae
Labridae
Labrisomidae
Chaenopsidae
Blenniidae
Pomacentridae
Carangidae
Mullidae
Syngnathidae
Apogonidae
Gobiidae
Holocentridae
Muraenidae
0.0 0.6 1.2
Latitudinal range
0.0 0.6 1.2
Low latitude limit
0.0 0.6 1.2
Centroid
0.0 0.6 1.2
High latitude limit

Figure S2

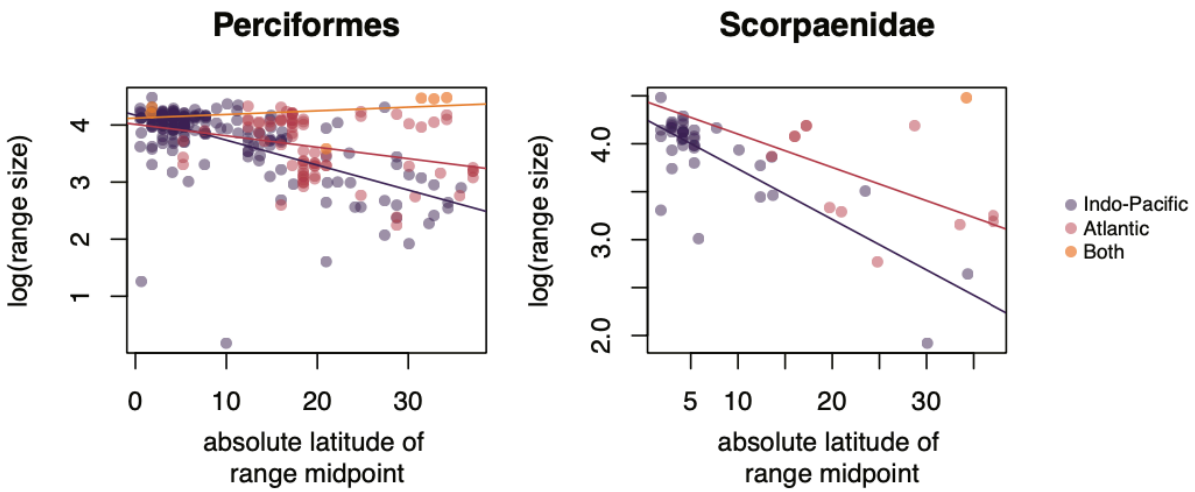

Perciformes
Scorpaenidae
log(range size)
absolute latitude of
range midpoint
Indo-Pacific
Atlantic
Both

Table S1. Tests of phylogenetic signal of latitudinal range size, lower latitude, median and higher latitude limits for different reef fish orders.

		Range size						Lower latitude						Midpoint latitude						Higher latitude					
Order	N	λ	logL	logL0	P	K	P	λ	logL	logL0	P	K	P	λ	logL	logL0	P	K	P	λ	logL	logL0	P	K	P
Acanthuriformes	108	0.464	-65.69	-70.788	0.001	0.02	0.6	0.026	-503.849	-504.014	0.565	0.024	0.39	0	-398.605	-398.604	1	0.011	0.614	0.012	-523.759	-523.796	0.786	0.054	0.112
Anguilliformes	61	0.702	-15.39	-18.566	0.012	0.383	0.103	0	-278.311	-278.31	1	0.243	0.939	0.631	-240.244	-241.073	0.198	0.388	0.077	0	-286.924	-286.924	1	0.271	0.701
Blenniiformes	443	0.042	-1062.26	-1064.68	0.028	0.025	0.876	0.239	-1940.18	-1970.2	0	0.05	0.098	0.666	-1768.39	-1856.88	0	0.088	0.028	0.218	-2071.46	-2078.92	0	0.058	0.232
Carangiformes	118	0	-90.272	-90.271	1	0.019	0.594	0	-550.437	-550.435	1	0.01	0.68	0	-488.245	-488.242	1	0.026	0.4	0	-583.486	-583.484	1	0.007	0.841
Centrarchiformes	51	0.719	-57.57	-64.829	0	0.278	0.001	0.81	-230.282	-233.246	0.015	0.215	0.003	0.189	-229.751	-231.137	0.096	0.012	0.367	0.652	-248.052	-255.006	0	0.234	0.002
Chaetodontiformes	96	0.567	-88.414	-93.133	0.002	0.198	0.002	0.04	-438.873	-439.073	0.527	0.068	0.968	0.524	-379.647	-385.358	0.001	0.143	0.053	0	-469.41	-469.409	1	0.071	0.966
Gobiiformes	196	0.583	-133.372	-156.499	0	0.052	0.477	0.477	-866.305	-872.988	0	0.023	0.544	0.929	-748.956	-793.93	0	0.266	0.025	0	-883.246	-883.244	1	0.117	0.499
Holocentriformes	43	0.052	-20.997	-21.135	0.6	0.23	0.221	0	-191.918	-191.918	1	0.164	0.37	0.666	-159.248	-158.923	1	0.297	0.022	0	-194.359	-194.358	1	0.157	0.541
Incertae sedis in Eupercaria	195	0.234	-148.255	-151.935	0.007	0.015	0.884	0.563	-854.744	-861.942	0	0.137	0.01	0.722	-719.789	-749.633	0	0.126	0.015	0.16	-897.599	-898.793	0.122	0.092	0.27
Kurtiformes	69	0.504	-24.795	-29.024	0.004	0.577	0.057	0.723	-306.029	-306.661	0.261	0.536	0.047	0.782	-245.508	-266.887	0	0.783	0.002	0.767	-308.385	-312.756	0.003	0.729	0.018
Labriformes	337	0	-851.823	-851.822	1	0.023	0.858	0.368	-1533.91	-1549.92	0	0.006	0.819	0.644	-1381.52	-1461.45	0	0.041	0.151	0.396	-1642.07	-1665.1	0	0.006	0.826
Lophiiformes	25	0.995	-22.368	-29.026	0	1.053	0.001	0	-117.001	-117.001	1	0.402	0.089	0.987	-95.452	-103.404	0	1.08	0.001	0.235	-122.891	-123.214	0.422	0.33	0.21
Perciformes	267	0.211	-228.836	-238.082	0	0.029	0.371	0.082	-1206.22	-1207.14	0.176	0.022	0.334	0.752	-1058.34	-1092.22	0	0.09	0.004	0.125	-1256.22	-1256.22	0.917	0.079	0.036
Spariformes	136	0.352	-153.525	-164.396	0	0.145	0.357	0.601	-594.371	-607.054	0	0.187	0.057	0.718	-586.586	-608.458	0	0.223	0.003	0.496	-661.565	-669.179	0	0.156	0.199
Syngnathiformes	94	1	-228.541	-263.008	0	0.614	0.038	0	-433.929	-433.928	1	0.145	0.085	0.889	-402.909	-413.482	0	0.325	0.001	0.678	-460.881	-464.505	0.007	0.232	0.006
Tetraodontiformes	153	0.706	-141.621	-152.565	0	0.102	0.01	0.552	-697.975	-703.747	0.001	0.099	0.004	0.804	-626.259	-650.638	0	0.129	0.001	0.677	-740.412	-754.521	0	0.11	0.002

Table S2. Tests of phylogenetic signal of latitudinal range size, lower latitude, median and higher latitude limits for different reef fish families.

		Range size						Lower latitude						Midpoint latitude						Higher latitude					
Family	N	λ	logL	logL0	P	K	P	λ	logL	logL0	P	K	P	λ	logL	logL0	P	K	P	λ	logL	logL0	P	K	P
Acanthuridae	67	0.594	-38.915	-47.681	0	0.036	0.498	0.005	-312.711	-312.714	0.937	0.037	0.373	0	-253.909	-253.908	1	0.016	0.572	0	-326.736	-326.735	1	0.102	0.123
Antennariidae	25	0.995	-22.368	-29.026	0	1.053	0.001	0	-117.001	-117.001	1	0.402	0.111	0.987	-95.452	-103.404	0	1.08	0.001	0.235	-122.891	-123.214	0.422	0.33	0.206
Apogonidae	69	0.504	-24.795	-29.024	0.004	0.577	0.036	0.723	-306.029	-306.661	0.261	0.536	0.046	0.782	-245.508	-266.887	0	0.783	0.003	0.767	-308.385	-312.756	0.003	0.729	0.017
Balistidae	32	0.063	-12.398	-12.48	0.684	0.15	0.863	0.285	-145.041	-146.249	0.12	0.266	0.341	0.182	-120.716	-120.988	0.461	0.228	0.527	0.218	-150.894	-151.43	0.3	0.344	0.178
Blenniidae	105	0.2	-127.323	-130.537	0.011	0.014	0.479	0.333	-478.926	-482.893	0.005	0.135	0.024	0.574	-444.613	-463.605	0	0.064	0.128	0.251	-506.339	-509.252	0.016	0.05	0.319
Carangidae	114	0	-87.386	-87.385	1	0.019	0.587	0	-531.931	-531.929	1	0.009	0.7	0	-473.102	-473.099	1	0.027	0.38	0	-564.094	-564.092	1	0.007	0.88
Chaenopsidae	44	0	-137.88	-137.879	1	0.355	0.744	0	-157.381	-157.38	1	0.372	0.534	0	-147.785	-147.784	1	0.398	0.429	0	-169.73	-169.729	1	0.391	0.522
Chaetodontidae	96	0.567	-88.414	-93.133	0.002	0.198	0.003	0.04	-438.873	-439.073	0.527	0.068	0.957	0.524	-379.647	-385.358	0.001	0.143	0.059	0	-469.41	-469.409	1	0.071	0.959
Gobiidae	182	0.476	-125.996	-147.777	0	0.056	0.524	0.435	-803.021	-810.508	0	0.024	0.563	0.888	-697.082	-739.883	0	0.293	0.054	0.236	-822.491	-823.219	0.228	0.149	0.412
Haemulidae	68	0.346	-41.046	-45.384	0.003	0.328	0.242	0.361	-303.642	-303.829	0.541	0.384	0.037	0.873	-232.245	-257.55	0	0.959	0.001	0.661	-311.738	-314.979	0.011	0.467	0.015
Holocentridae	43	0.052	-20.997	-21.135	0.6	0.23	0.225	0	-191.918	-191.918	1	0.164	0.391	0.666	-159.248	-158.923	1	0.297	0.019	0	-194.359	-194.358	1	0.157	0.495
Kyphosidae	21	0.758	-20.829	-24.267	0.009	0.385	0.001	0.998	-90.954	-96.423	0.001	0.325	0.005	0	-97.952	-97.952	1	0.015	0.351	0.999	-102.973	-106.027	0.013	0.291	0.01
Labridae	337	0	-851.823	-851.822	1	0.023	0.859	0.368	-1533.912	-1549.919	0	0.006	0.824	0.644	-1381.52	-1461.45	0	0.041	0.136	0.396	-1642.067	-1665.097	0	0.006	0.823
Labrisomidae	32	0.096	-29.509	-29.683	0.555	0.319	0.817	0	-119.237	-119.237	1	0.358	0.618	0	-105.72	-105.72	1	0.348	0.696	0	-109.742	-109.742	1	0.334	0.696
Lethrinidae	30	0	-15.931	-15.93	1	0.251	0.706	0	-125.687	-125.687	1	0.123	0.837	0	-97.291	-97.29	1	0.357	0.297	0	-135.543	-135.543	1	0.115	0.774
Lutjanidae	60	0	-36.639	-36.639	1	0.199	0.078	0	-249.58	-249.58	1	0.19	0.047	0.854	-208.605	-222.372	0	0.308	0.001	0	-257.771	-257.771	1	0.19	0.163
Monacanthidae	48	0.479	-45.054	-51.073	0.001	0.283	0.016	0.077	-214.884	-214.986	0.652	0.215	0.092	0.718	-198.54	-210.28	0	0.507	0.001	0.571	-230.741	-239.087	0	0.44	0.001
Mullidae	31	0.996	-16.13	-19.838	0.006	0.523	0.05	0	-144.901	-144.901	1	0.34	0.112	0.998	-122.201	-132.802	0	0.913	0.001	0.604	-151.39	-153.085	0.066	0.502	0.03
Muraenidae	59	0.618	-14.631	-18.659	0.005	0.55	0.032	0	-269.621	-269.62	1	0.296	0.988	0.603	-231.237	-233.3	0.042	0.57	0.021	0	-278.167	-278.167	1	0.373	0.595
Pomacanthidae	54	0.124	-55.981	-56.179	0.529	0.012	0.943	0.837	-233.937	-240.937	0	0.263	0.017	0	-215.839	-215.839	1	0.102	0.315	0	-256.714	-256.714	1	0.105	0.347
Pomacentridae	219	0	-525.813	-525.813	1	0.021	0.952	0	-957.216	-957.215	1	0.04	0.576	0.453	-846.955	-853.287	0	0.173	0.003	0.053	-1028.391	-1029.011	0.266	0.104	0.238
Scorpaenidae	54	0	-38.245	-38.245	1	0.155	0.066	0	-248.792	-248.791	1	0.045	0.372	0.313	-220.739	-221.425	0.241	0.063	0.27	0	-256.879	-256.878	1	0.089	0.235
Serranidae	207	0.228	-181.841	-190.701	0	0.027	0.58	0.129	-929.19	-930.614	0.092	0.021	0.555	0.785	-809.132	-840.479	0	0.116	0.006	0.306	-966.934	-968.653	0.064	0.092	0.089
Siganidae	22	0	-16.039	-16.039	1	0.152	0.671	0	-100.478	-100.478	1	0.252	0.259	0	-58.236	-58.236	1	0.211	0.446	0	-103.144	-103.144	1	0.266	0.229
Sparidae	73	0.255	-98.923	-101.296	0.029	0.219	0.381	0.621	-325.318	-332.612	0	0.388	0.007	0.636	-330.532	-345.108	0	0.417	0.004	0.519	-364.837	-372.282	0	0.337	0.026
Syngnathidae	54	1.015	-143.408	-165.385	0	0.808	0.1	0	-244.083	-244.082	1	0.153	0.625	0.876	-234.695	-242.544	0	0.443	0.001	0.645	-262.741	-266.529	0.006	0.288	0.02
Tetraodontidae	46	0.665	-51.783	-52.765	0.161	0.138	0.177	0.705	-209.571	-215.532	0.001	0.195	0.01	0.523	-190.962	-194.203	0.011	0.113	0.216	0.556	-221.946	-227.818	0.001	0.123	0.11

Table S3. Relative fit of models in which high- and low-latitude range limits of marine fish families evolve at the same or different rates: lik1: log likelihood of multiple-rate model; lik2: likelihood of single-rate model; σ^2 high and σ^2 low indicate estimated rates of evolution for high- and low-latitude range limits, respectively; N: number of analyzed species. Values for the expanded dataset indicate medians across 100 alternative topologies. Bold-face rates are significantly different.

Family	Reduced dataset						Expanded dataset					
	lik1	lik2	p	σ^2 high	σ^2 low	N	lik1	lik2	p	σ^2 high	σ^2 low	N
Acanthuridae	-715.894	-720.5781	0.002208	226.2312	**435.3725**	67	-847.1445	-849.4384	0.025684	263.4660	**398.1629**	80
Antennariidae	-236.6154	-241.8212	0.001252	**91.3118**	42.2423	25	-345.9285	-351.1459	0.000685	**111.1379**	64.5881	37
Apogonidae	-580.8648	-581.0183	0.579536	15.7358	14.5983	69	-2868.245	-2890.315	3.23E-12	**275.7211**	145.1296	281
Balistidae	-307.404	-309.8569	0.026768	**102.3164**	97.1714	32	-330.1385	-330.6827	0.21595	98.3615	99.2456	35
Blenniidae	-1143.789	-1175.172	2.33E-15	**468.7975**	106.1315	105	-4478.406	-4486.341	1.47E-03	**679.9777**	311.9288	397
Bythitidae	-	-	-	-	-	-	-766.2368	-774.1206	0.000795	**231.6250**	167.1588	77
Caesionidae	-	-	-	-	-	-	-203.6906	-205.183	0.134949	344.8768	277.6458	22
Carangidae	-1400.158	-1419.303	6.10E-10	**3096.9080**	1271.6520	111	-1533.504	-1577.193	5.65E-21	**2770.4831**	1182.8515	128
Chaenopsidae	-349.2045	-351.063	0.053859	9.8629	5.8710	44	-714.4874	-724.7961	1.18E-05	**39.5422**	16.4533	86
Chaetodontidae	-988.3425	-997.4151	2.05E-05	**432.5426**	251.4344	96	-1334.664	-1344.945	3.10E-05	**465.6020**	255.7371	127
Cirrhitidae	-	-	-	-	-	-	-179.3231	-181.7152	0.037152	**18.3677**	11.5892	21
Gobiidae	-1732.974	-1735.161	0.03649	55.6645	**298.7900**	182	-5867.375	-5974.661	5.89E-14	164.1384	**198.7332**	538
Haemulidae	-600.2037	-600.4436	0.488514	30.2821	26.9926	68	-731.1711	-735.0596	0.013278	**46.3973**	30.9952	81
Holocentridae	-374.4097	-375.2394	0.197688	80.6194	69.3687	43	-657.2199	-661.1467	0.021788	**249.8858**	226.5361	67
Kyphosidae	-257.9288	-304.6504	4.18E-22	**158.9750**	68.0348	21	-314.3982	-318.9424	3.34E-03	**328.9833**	170.1817	32
Labridae	-3577.24	-3606.322	2.41E-14	**2508.7607**	1396.0607	337	-7203.531	-7292.776	8.34E-39	**1609.5954**	847.8747	617
Labrisomidae	-244.7889	-245.9008	0.135904	4.4873	7.4853	32	-775.2444	-799.9723	1.2E-10	**61.1856**	25.2484	89
Lethrinidae	-266.434	-281.5991	3.64E-08	**95.8053**	47.7441	30	-354.418	-359.1593	8.67E-04	**112.0650**	67.9711	37
Lutjanidae	-521.1885	-522.1982	0.155303	38.9112	29.2656	60	-894.1694	-896.8238	0.025584	**76.1103**	61.1429	98
Malacanthidae	-	-	-	-	-	-	-238.5797	-245.2924	0.000533	**128.8070**	55.4729	25
Microdesmidae	-	-	-	-	-	-	-368.1481	-372.0998	0.002075	**233.6594**	139.7501	38
Monacanthidae	-488.6201	-489.332	0.232806	98.7080	63.5934	48	-722.7282	-724.2802	0.063192	163.6213	107.4630	73
Mullidae	-370.7273	-391.6774	9.60E-11	**57.4360**	48.7029	31	-685.7773	-689.2305	2.22E-02	**156.4179**	104.5292	67
Muraenidae	-541.2364	-541.3894	0.580146	35.3737	32.7344	59	-1324.426	-1330.097	0.005191	**102.8522**	75.4421	135
Nemipteridae	-	-	-	-	-	-	-262.0745	-268.5817	0.000216	**43.7251**	15.8457	30
Opistognathidae	-	-	-	-	-	-	-207.5297	-211.6421	1.10E-02	**147.8849**	69.6053	21
Ostraciidae	-	-	-	-	-	-	-232.3962	-237.6737	0.008862	**286.5435**	127.3213	23
Pinguipedidae	-	-	-	-	-	-	-369.3351	-373.4651	0.013265	**385.3315**	227.5163	35
Platycephalidae	-	-	-	-	-	-	-216.6895	-218.1961	4.34E-02	**374.6075**	224.0807	21
Plesiopidae	-	-	-	-	-	-	-287.5903	-295.589	0.000744	**406.2531**	122.0868	28
Pomacanthidae	-554.6885	-579.4551	1.95E-12	**211.1563**	46.9552	54	-892.9476	-906.866	2.41E-07	**337.8422**	101.4341	86
Pomacentridae	-2244.803	-2250.26	0.000954	158.9223	**218.8449**	219	-3717.498	-3732.717	2.12E-06	**271.2223**	206.3474	357
Pseudochromidae	-	-	-	-	-	-	-949.5722	-967.0143	6.15E-07	**251.4024**	178.3282	93
Scorpaenidae	-570.7577	-571.4274	0.247122	190.9743	277.4313	54	-1707.534	-1754.077	2.87E-11	**297.2604**	253.9547	155
Serranidae	-2219.834	-2254.953	5.26E-17	101.7128	**304.1805**	207	-3924.376	-3925.284	6.00E-05	247.3192	**271.6305**	359
Siganidae	-197.0595	-197.6959	0.25924	181.2096	150.6831	22	-228.1092	-229.1887	0.142626	241.4189	148.2401	25
Sparidae	-725.5706	-740.1027	7.00E-08	**116.1207**	31.6637	73	-993.3856	-1011.655	1.44E-09	**191.1765**	52.3892	97
Syngnathidae	-531.9438	-535.9734	0.004527	**57.8061**	47.5836	54	-1408.09	-1415.888	0.000136	**226.3597**	118.2476	133
Synodontidae	-	-	-	-	-	-	-360.4968	-362.7041	0.09683	116.7308	75.9550	35
Tetraodontidae	-482.3235	-490.0647	8.33E-05	**242.0808**	105.2646	46	-863.1374	-872.7336	2.26E-05	**684.9577**	268.3767	80
Tripterygiidae	-	-	-	-	-	-	-1398.034	-1419.005	3.39E-08	**402.4512**	189.9152	134

Table S4. Phylogenetic generalized least squared analyses of the relationship between absolute latitude and latitudinal range of different fish orders.

Family	Slope	SE	t	P	R^2	N
Acanthuridae	-0.032	0.001	-24.485	0	0.902	67
Apogonidae	-0.009	0.006	-1.607	0.113	0.037	69
Balistidae	-0.049	0.007	-7.479	0	0.651	32
Blenniidae	0.094	0.008	11.905	0	0.579	105
Carangidae	-0.045	0.003	-16.456	0	0.707	114
Chaenopsidae	0.139	0.125	1.113	0.272	0.029	44
Chaetodontidae	-0.061	0.005	-12.73	0	0.633	96
Gobiidae	-0.081	0.004	-18.968	0	0.667	182
Haemulidae	-0.024	0.01	-2.321	0.023	0.075	68
Holocentridae	-0.042	0.009	-4.909	0	0.37	43
Labridae	-0.067	0.017	-3.885	0	0.043	337
Labrisomidae	0.014	0.018	0.775	0.444	0.02	32
Lethrinidae	-0.058	0.016	-3.605	0.001	0.317	30
Lutjanidae	-0.021	0.009	-2.362	0.022	0.088	60
Monacanthidae	-0.027	0.012	-2.3	0.026	0.103	48
Mullidae	-0.005	0.008	-0.582	0.565	0.012	31
Muraenidae	-0.017	0.004	-4.342	0	0.249	59
Pomacanthidae	0.088	0.025	3.572	0.001	0.197	54
Pomacentridae	-0.374	0.057	-6.584	0	0.167	219
Scorpaenidae	-0.019	0.004	-5.151	0	0.338	54
Serranidae	-0.071	0.005	-13.05	0	0.454	207
Sparidae	-0.01	0.01	-1.024	0.309	0.015	73
Syngnathidae	-0.055	0.029	-1.86	0.069	0.062	54
Tetraodontidae	-0.048	0.006	-8.15	0	0.602	46

Table S5. Relative fit of models in which high- and low-latitude range limits of marine fish orders evolve at the same or different rates, analyzing separately each ocean basin: lik1: log likelihood of multiple-rate model; lik2: likelihood of single-rate model; σ^2 high and σ^2 low indicate estimated rates of evolution for high- and low-latitude range limits, respectively; N: number of analyzed species. Values for the expanded dataset indicate medians across 100 alternative topologies. Bold-face rates are significantly different.

Ocean basin	Order	Atlantic species - Reduced dataset						Atlantic species - Expanded dataset					
		lik1	lik2	p	σ^2 high	σ^2 low	N	lik1	lik2	p	σ^2 high	σ^2 low	N
Atlantic	Anguilliform	-	-	-	-	-	-	-239.4415	-241.2547	0.0701	7.6876	10.0884	28
	Blenniiform	-1181.1514	-1242.1150	2.39E-28	**395.3121**	58.1123	111	-2728.8265	-2952.8627	6.68E-62	**289.3318**	91.2962	237
	Carangiform	-570.9478	-573.5860	0.021616	294.9806	202.2604	53	-573.7065	-581.9524	0.0007	**281.5779**	192.7803	56
	Gobiiformes	-545.7935	-588.0517	3.81E-20	97.9125	**968.0432**	52	-986.9269	-1056.4500	1.11E-30	82.9629	**588.5996**	90
	Incertae sec	-501.4051	-505.3175	0.005153	**43.8581**	21.3180	54	-642.9340	-644.6400	0.1388	48.0963	22.4075	66
	Kurtiformes	-128.7619	-141.5289	4.35E-07	0.8350	**12.0692**	18	-188.4443	-203.5088	1.02E-07	1.6097	**18.1141**	25
	Labriformes	-723.2023	-725.6925	0.025636	**315.0155**	33.5789	71	-950.3881	-966.8081	2.23E-07	**263.1413**	30.4702	92
	Perciformes	-758.4841	-805.0762	4.76E-22	5.9511	**40.7417**	83	-1332.8449	-1333.6581	0.1549	53.9095	47.6556	137
	Spariformes	-454.5379	-464.6421	6.94E-06	**104.5980**	26.0320	45	-563.6316	-579.2944	4.72E-08	**126.6616**	29.8389	56
	Syngnathifo	-263.3301	-268.2449	0.001717	7.5552	24.7948	29	-413.5300	-413.8101	0.2339	45.2026	36.0967	42
	Tetraodonti	-392.9620	-412.0387	6.54E-10	**163.6776**	22.2329	39	-496.8844	-509.4881	6.51E-07	**201.1066**	57.4332	48
Indo-pacific	Acanthurifo	-	-	-	-	-	-	-1338.0476	-1338.5295	0.06955	270.2204	324.4574	126
	Anguilliform	-367.2436	-369.6244	0.029101	42.7126	36.8513	43	-1107.1079	-1114.5038	0.00103	**104.9235**	76.3355	113
	Blenniiform	-3699.4227	-3871.9973	4.82E-77	125.7009	**158.8776***	337	-10759.3669	-10815.2746	1.44E-21	**458.3540**	269.6945	985
	Carangiform	-1040.4561	-1105.5936	3.57E-30	3920.7860	1646.2719	88	-1209.7415	-1249.3904	8.02E-19	**3497.9963**	1476.2727	99
	Chaetodonti	-	-	-	-	-	-	-1190.7205	-1200.1647	3.32E-05	**491.2029**	278.8051	113
	Gobiiformes	-1303.3148	-1309.6897	0.00036	**47.0256**	38.5519	145	-5178.5073	-5205.0298	7.84E-11	**169.8634**	110.8642	503
	Holocentrifo	-	-	-	-	-	-	-549.6664	-553.0318	0.04528	213.3577	189.1824	56
	Incertae sec	-1517.5773	-1536.9996	4.59E-10	**98.3537**	52.2836	143	-2624.8257	-2643.4335	8.15E-08	**180.0870**	99.7587	225
	Kurtiformes	-431.8717	-439.7590	7.14E-05	**20.8160**	15.4419	51	-2614.4856	-2638.7091	1.67E-09	**254.8747**	143.6512	257
	Labriformes	-3242.7675	-3330.7814	3.57E-40	**3092.7302**	1759.1249	266	-6230.3769	-6312.7740	3.95E-36	**1790.9933**	975.6635	527
	Lophiiforme	-	-	-	-	-	-	-282.6165	-289.3837	0.00086	**110.9116**	67.5180	30
	Ophidiiform	-	-	-	-	-	-	-586.6882	-597.4441	1.76E-05	**227.9829**	106.7890	59
	Perciformes	-2004.1696	-2005.8140	0.069752	159.9265	131.2123	190	-4400.4380	-4446.3651	1.62E-11	**303.4668**	210.0539	406
	Spariformes	-952.5719	-955.3492	0.018432	58.4632	32.6861	97	-1405.4976	-1423.3490	6.49E-08	**112.6119**	50.5275	140
	Syngnathifo	-676.7544	-677.8425	0.140163	66.9882	51.3369	68	-1865.8678	-1882.2227	3.57E-07	**207.7451**	122.1819	181
	Tetraodonti	-1247.2410	-1249.0763	0.055385	119.3173	91.9784	127	-2069.4174	-2086.2325	1.05E-08	**331.9662**	219.6183	192

Table S6. Relative fit of models in which high- and low-latitude range limits of marine fish families evolve at the same or different rates, analyzing separately each ocean basin: lik1: log likelihood of multiple-rate model; lik2: likelihood of single-rate model; σ^2 high and σ^2 low indicate estimated rates of evolution for high- and low-latitude range limits, respectively; N: number of analyzed species. Values for the expanded dataset indicate medians across 100 alternative topologies. Bold-face rates are significantly different.

Oceanic basin	Family	Reduced dataset						Expanded dataset					
		lik1	lik2	p	σ^2 high	σ^2 low	N	lik1	lik2	p	σ^2 high	σ^2 low	N
Atlantic	Apogonidae	-	-	-	-	-	-	-188.4443	-203.5088	1.02E-07	1.609686	**18.11406554**	25
	Blenniidae	-466.444	-491.105	2.17E-12	**984.373**	142.569	42	-871.0227	-877.0390	0.00039	**825.3754**	247.9183254	70
	Carangidae	-480.491	-483.728	0.01094	318.394	210.657	49	-539.3005	-544.1493	0.00259	**302.6071**	199.96553	52
	Chaenopsidae	-161.82	-175.265	2.15E-07	**11.5077**	2.10975	23	-396.3398	-406.0499	2.44E-05	*25.7436*	7.403890579	50
	Gobiidae	-543.074	-605.785	4.12E-29	103.879	**1027.28**	49	-928.7336	-999.2570	7.54E-29	83.22716	**623.1413124**	85
	Haemulidae	-243.382	-244.09	0.23399	3.02278	18.6024	29	-286.8138	-287.8529	0.13958	12.85642	19.37210459	33
	Labridae	-723.202	-725.693	0.02564	315.015	33.5789	71	-950.3881	-966.8081	2.23E-07	**263.1413**	30.4701678	92
	Labrisomidae	-	-	-	-	-	-	-436.3671	-476.8724	7.03E-19	**39.03681**	8.20107469	54
	Lutjanidae	-	-	-	-	-	-	-210.8576	-212.0543	0.40467	20.79599	21.41844825	24
	Muraenidae	-	-	-	-	-	-	-229.0300	-230.9449	0.03461	7.970814	10.44602587	27
	Pomacentridae	-191.488	-198.975	0.00011	**111.277**	17.7519	20	-326.3051	-335.1087	3.98E-05	**110.0313**	25.58961514	34
	Scorpaenidae	-	-	-	-	-	-	-398.2483	-399.2074	0.17381	46.17263	23.6662239	42
	Serranidae	-637.441	-671.928	9.98E-17	6.5569	**42.9331**	70	-977.1670	-978.0494	0.07867	52.06515	58.11280705	95
	Sparidae	-421.639	-431.073	1.40E-05	**111.953**	27.8557	42	-518.2855	-528.8057	6.69E-07	**133.7392**	31.50010332	53
	Syngnathidae	-	-	-	-	-	-	-255.8454	-256.9184	0.26151	21.77046	28.34427279	27
Indo-pacific	Antennariidae	-	-	-	-	-	-	-282.6165	-289.3837	0.00086	**110.9116**	67.5180	30
	Apogonidae	-431.872	-439.759	7.14E-05	**20.816**	15.4419	51	-2614.4856	-2638.7091	1.67E-09	**254.8747**	143.6512	257
	Blenniidae	-700.419	-711.736	1.96E-06	**122.619**	78.9225	66	-3533.6419	-3549.7840	4.80E-12	**554.3284**	276.4062	330
	Bythitidae	-	-	-	-	-	-	-586.6882	-597.4441	1.76E-05	**227.9829**	106.7890	59
	Carangidae	-1106.18	-1113.38	0.00015	**4058.9**	1704.24	85	-1177.4976	-1216.5988	2.78E-18	**3607.0637**	1522.2867	96
	Chaenopsidae	-163.251	-163.554	0.4359	7.4498	9.445	21	-291.4719	-293.1006	0.12039	15.0683	10.4788	36
	Chaetodontidae	-	-	-	-	-	-	-1190.7205	-1200.1647	3.32E-05	**491.2029**	278.8051	113
	Gobiidae	-1190.47	-1197.81	0.00013	**37.5776**	29.0081	134	-4677.9854	-4690.2839	6.33E-07	**158.7031**	104.4092	459
	Haemulidae	-355.627	-356.856	0.11704	33.5108	25.4916	41	-482.5195	-482.5760	0.48285	42.9448	30.5876	51
	Holocentridae	-	-	-	-	-	-	-549.6664	-553.0318	0.04528	213.3577	189.1824	56
	Labridae	-3242.77	-3330.78	3.57E-40	**3092.73**	1759.12	266	-6230.3769	-6312.7740	3.95E-36	**1790.9933**	975.6635	527
	Labrisomidae	-	-	-	-	-	-	-290.4084	-291.0646	0.27246	13.0499	13.8254	35
	Lutjanidae	-400.511	-403.032	0.02473	46.677	22.4252	43	-689.8165	-698.0432	0.01315	75.0617	47.1709	75
	Monacanthidae	-	-	-	-	-	-	-670.4496	-675.6282	0.02243	172.1422	107.0902	66
	Mullidae	-	-	-	-	-	-	-588.1888	-590.4983	0.05147	138.4902	99.9046	59
	Muraenidae	-357.092	-359.399	0.03174	43.662	37.6982	42	-1074.4323	-1079.3792	0.00273	**108.8236**	79.0646	109
	Pomacentridae	-2066	-2073.5	0.00011	162.147	**236.33**	201	-3382.2597	-3387.1817	0.00077	**247.0246**	213.1019	326
	Scorpaenidae	-463.028	-466.946	0.00512	240.209	**345.098**	42	-1314.1091	-1339.4677	2.19E-06	**304.6526**	303.2152	115
	Serranidae	-1404.54	-1426.71	2.75E-11	**140.296**	73.3754	142	-2851.7842	-2874.4602	4.32E-12	**251.9636**	140.3607	270
	Sparidae	-351.239	-351.253	0.86302	36.6853	34.6816	37	-510.4456	-516.3316	0.00154	90.1129	37.0899	51
	Syngnathidae	-377.838	-378.431	0.27613	75.5247	55.5575	37	-1132.0558	-1149.2665	5.98E-08	**224.0268**	96.7096	108
	Tetraodontidae	-391.915	-392.027	0.63505	132.609	117.173	39	-716.7563	-720.5728	0.0044	**425.0399**	269.2588	67
	Tripterygiidae	-	-	-	-	-	-	-1286.4126	-1300.3374	4.12E-06	**395.5660**	203.1879	123

Table S7. Phylogenetic generalized least squares analyses of the relationship between absolute latitude of the range median and latitudinal range of different fish orders using ocean basin as a covariate.

		Latitude of the distribution median					Ocean				
Family	N	Slope	SE	t	P		Slope	SE	t	P	R^2
Apogonidae	69	-0.011	0.007	-1.575	0.12		-0.067	0.173	-0.386	0.701	0.039
Blenniidae	105	0.097	0.008	12.326	0		0.599	1.006	0.595	0.553	0.603
Carangidae	114	-0.045	0.003	-16.351	0		0.292	0.251	1.161	0.248	0.712
Chaenopsidae	44	0.146	0.128	1.146	0.258		0.963	2.436	0.395	0.695	0.032
Chaetodontidae	96	-0.061	0.005	-12.667	0		0.045	0.207	0.217	0.828	0.633
Gobiidae	182	-0.083	0.004	-19.681	0		0.033	1.215	0.027	0.979	0.685
Haemulidae	68	-0.032	0.011	-2.86	0.006		0.148	0.372	0.398	0.692	0.135
Holocentridae	43	-0.057	0.009	-6.234	0		-0.673	0.424	-1.586	0.121	0.499
Labridae	337	-0.067	0.017	-3.882	0		-0.343	2.31	-0.149	0.882	0.043
Labrisomidae	32	0.013	0.018	0.735	0.468		-0.048	0.351	-0.138	0.892	0.02
Lutjanidae	60	-0.032	0.011	-2.998	0.004		-0.268	0.149	-1.793	0.078	0.136
Monacanthidae	48	-0.032	0.012	-2.66	0.011		-0.496	0.772	-0.642	0.524	0.158
Mullidae	31	-0.004	0.009	-0.485	0.632		0.051	0.309	0.163	0.871	0.013
Muraenidae	59	-0.02	0.006	-3.194	0.002		-0.068	0.123	-0.549	0.585	0.253
Pomacanthidae	54	0.094	0.025	3.765	0		1.042	0.865	1.205	0.234	0.219
Pomacentridae	219	-0.378	0.057	-6.596	0		-2.386	4.254	-0.561	0.575	0.168
Scorpaenidae	54	-0.035	0.003	-13.017	0		0.762	0.189	4.025	0	0.78
Serranidae	207	-0.007	0.009	-0.816	0.416		0.814	0.468	1.741	0.083	0.598
Sparidae	73	-0.015	0.01	-1.503	0.137		0.099	0.389	0.254	0.8	0.114
Syngnathidae	54	-0.057	0.03	-1.877	0.066		1.37	3.434	0.399	0.692	0.069

Table S8. Phylogenetic generalized least squares analyses of the relationship between absolute latitude of the range median and latitudinal range of different fish families using ocean basin as a covariate.

		Midpoint latitude				Ocean				
Order	N	Slope	SE	t	P	Slope	SE	t	P	R^2
Acanthuriformes	108	-0.032	0.002	-17.621	0	0.248	1.279	0.194	0.846	0.75
Anguilliformes	61	-0.02	0.006	-3.243	0.002	-0.09	0.121	-0.746	0.458	0.239
Blenniiformes	443	0.005	0.02	0.272	0.786	0.491	2.026	0.242	0.809	0
Carangiformes	118	-0.045	0.003	-16.657	0	0.286	0.23	1.243	0.216	0.714
Chaetodontiformes	96	-0.061	0.005	-12.667	0	0.045	0.207	0.217	0.828	0.633
Gobiiformes	196	-0.083	0.004	-20.329	0	0.047	1.175	0.04	0.968	0.683
Holocentriformes	43	-0.057	0.009	-6.234	0	-0.673	0.424	-1.586	0.121	0.499
Incertae sedis in Eupercaria	195	0.07	0.012	5.658	0	0.954	1.572	0.607	0.545	0.144
Kurtiformes	69	-0.011	0.007	-1.575	0.12	-0.067	0.173	-0.386	0.701	0.039
Labriformes	337	-0.067	0.017	-3.882	0	-0.343	2.31	-0.149	0.882	0.043
Perciformes	267	-0.019	0.005	-3.613	0	1.094	0.271	4.042	0	0.588
Spariformes	136	-0.018	0.007	-2.56	0.012	0.206	0.287	0.718	0.474	0.107
Syngnathiformes	94	-0.043	0.02	-2.192	0.031	0.699	2.115	0.331	0.742	0.053
Tetraodontiformes	153	-0.042	0.004	-10.495	0	-0.079	0.2	-0.395	0.694	0.442