ESM APPENDIX S1: OBTAINING AND MODIFYING PHYLOGENETIC AND GEOGRAPHIC DATA

---

1) Resolving taxonomic incongruences among datasets and assessing monophyly of ranks

Extended Methods:

To obtain a time-calibrated phylogeny of Percomorpha for all analyses, we extracted the clade Percomorpha as defined by Near et al. ([1]; i.e. the most recent common ancestor of Ophidiiformes and Perciformes) from a large phylogeny of all Actinopterygii [2], the most complete phylogeny published at the time of analysis.

To assess total regional richness and phylogenetic sampling of regions in downstream analyses, we obtained a list of all described percomorph species from FishBase.org in August 2016 [3], totaling 17,458 species (dataset S1). To do this, we compiled species lists from the summary pages of each family in the orders known to belong to Percomorpha (Atheriniformes, Batrachoidiformes, Beloniformes, Cetomimiformes, Cyprinodontiformes, Gasterosteiformes, Gobiesociformes, Lophiiformes, Mugiliformes, Ophidiiformes, Perciformes, Pleuronectiformes, Scorpaeniformes, Synbranchiformes, Syngnathiformes, and Tetraodontiformes). Note that the order Cetomimiformes was outside of Percomorpha in Near et al. [1], but was nested within Percomorpha by Rabosky et al. [2] so we included it in our analyses.

We resolved conflicts between taxonomies used in the different data sources (FishBase, OBIS, GBIF, IUCN, and names of terminal taxa in the published phylogeny) by validating names against FishBase taxonomy [3,5]. We removed some terminal taxa from the phylogeny in

order to facilitate downstream analyses and to correspond with the updated species list from FishBase, using three criteria. First, we removed 12 terminal taxa that were considered synonyms with other species also sampled in the phylogeny (following taxonomy in FishBase). Second, we removed 19 tips that were subspecies of another species already sampled in the tree (leaving one tip per named species). In these cases, we kept the first subspecies in alphabetical order (any choice of subspecies to keep should produce identical results). Third, we removed 10 species that caused non-monophyly of their families, most likely due to systematic errors in phylogenetic reconstruction (see below for individual justification). After removing 41 tips, the resulting phylogeny contained 4,571 species (~26% of the described species in Percomorpha). See table S1 for a list of all tips removed with justification.

Monophyly of families

Our analyses of weighted mean net diversification rates (appendix S3) relied on delimiting monophyletic groups. We also checked the monophyly of families in order to detect terminal taxa potentially placed incorrectly in the phylogeny. We assessed monophyly of sampled families using the R package *MonoPhy* [4]. We used FishBase as a standard taxonomy for all ranks, due to the ease of validating names from varied data sources [3,5]. The use of other taxonomies (such as that of [6]) need not modify our results (see below).

A total of 25 families were identified as non-monophyletic. Of these, 18 could be easily resolved by aggregating families to form monophyletic groups (dataset S2). Thus, many families were non-monophyletic because one family was paraphyletic with respect to another family (i.e. one family was nested inside another). In these cases, we simply considered both families to form a clade. In many cases, this generated congruence between FishBase taxonomy and phylogenetically-based taxonomies [6]. For example, the family Caesionidae is recognized by FishBase, but is sometimes considered part of Lutjanidae rather than a distinct family [6]. We used a clade containing Caesionidae and Lutjanidae (as defined by FishBase) to resolve the paraphyly of Lutjanidae.

The remaining seven families were polyphyletic. Six of these families had a single species or genus that was distantly related to other members of that family that were represented in the phylogeny. These were: (i) Cetomimidae (whalefishes; due to *Parataeniophorus brevis*); (ii) Gobiidae (gobies; due to the genus *Lythrypnus*); (iii) Labridae (wrasses; due to *Decodon melasma*); (iv) Siganidae (rabbitfishes; due to *Siganus rivulatus*); (v) Lutjanidae (snappers; due to *Pristipomoides aquilonaris*); and (vi) Scorpaenidae (scorpionfishes; due to *Pterois lunulata*). The seventh polyphyletic family, (vii) Serranidae (seabasses) contained six clades that were not closely related to each other.

We referred to the primary literature to assess whether polyphyly in these seven families was explained by one of two causes. First, was polyphyly caused by errors in phylogenetic reconstruction (such as incorrectly identified species in GenBank, limited gene sampling for the seemingly misplaced taxon, or poor overlap of representative genes within a family [2])?

Second, was polyphyly instead associated with the correct phylogenetic placement of that species but incorrect assignment of that species to a family (e.g. indicating families in need of taxonomic revision)? We looked for precedence of the non-monophyly of the family in the primary literature as the main criterion for distinguishing between these scenarios. If there was no precedent in the previous literature for the placement of the species causing polyphyly in the tree of Rabosky et al. [2], we considered this to potentially be caused by an error in phylogeny estimation, and we removed the outlier species from the phylogeny. We then considered that species as part of its named family for downstream analyses (e.g. for counting species richness in calculations of net diversification rates).

Below, we provide justifications for our decisions for all seven cases of polyphyly:

(i) In the phylogeny of Rabosky et al. [2], *Parataeniophorus brevis* was nested within Syngnathiformes instead of the other members of Cetomimidae. Within Cetomimidae, *P. brevis* was once considered to belong to the family Mirapinnidae, but the membership of this family within Cetomimidae was supported using a molecular phylogeny [7]. We therefore considered the polyphyly of Cetomimidae to be an error in the tree of Rabosky et al. [2]. We removed *Parataeniophorus brevis* from the phylogeny to avoid complications in downstream analyses. Cetomimidae was otherwise monophyletic.

(ii) The genus *Lythrypnus* (Gobiidae), with *L. dalli* and *L. zebra* sampled in the phylogeny, was previously found to be nested within Gobiidae [8–10]. However, this genus was placed in Uranoscopidae in the phylogeny. Since the placement of this genus outside of Gobiidae has no precedent, we removed these two species from the phylogeny. Gobiidae was otherwise paraphyletic, so we used a clade containing nine families to resolve its monophyly (Gobiidae, Eleotridae, Odontobutidae, Rhyacichthyidae, Microdesmidae, Kraemeriidae, Kurtidae, Apogonidae, Platycephalidae).

(iii) *Decodon melasma* (Labridae) was placed in the (otherwise monophyletic) family Moronidae in the phylogeny. It is the only sampled member of *Decodon*. Although *Decodon* has not (to our knowledge) previously been included in a molecular phylogeny, it was included in the tribe Hypsigenyini within Labridae in a morphological examination of the group ([11]; although this was not a phylogenetic analysis). Since the membership of *Decodon* in Labridae has not been previously questioned, we removed *Decodon melasma* from the phylogeny. Labridae was otherwise paraphyletic, so we used a clade containing Labridae, Scaridae, and Odacidae.

(iv) *Pristipomoides aquilonaris* (Lutjanidae) was placed as the sister clade to Sciaenidae in the phylogeny, instead of being placed with other sampled members of Lutjanidae. It is the only sampled member of *Pristipomoides* in the phylogeny. This species (and the genus *Pristipomoides*) were nested within Lutjanidae in previous molecular phylogenies [12–14]. Since there is no precedent for placing this species near Sciaenidae, we removed *Pristipomoides aquilonaris* from the phylogeny. Lutjanidae was otherwise paraphyletic, so we used a clade containing Caesionidae and Lutjanidae.

(v) *Siganus rivulatus* was the only member of *Siganus* to be found outside of Siganidae in the phylogeny. It was nested within a clade containing Labridae and Scaridae. The other 28 sampled species of Siganidae formed a monophyletic group. This species was found to be nested within Siganidae in a previous molecular phylogeny [15]. We therefore removed *Siganus rivulatus* from the phylogeny. Signanidae was otherwise monophyletic.

(vi) *Pterois lunulata* (Scorpaenidae) was placed within Platycephalidae in the phylogeny, while the other five sampled members of *Pterois* were nested within Scorpaenidae. This species was found to be nested in a clade with other *Pterois* in a previous molecular phylogeny of Pteroinae (Scorpaenidae; [16]). We therefore removed *Pterois lunulata* from the phylogeny. Scorpaenidae was otherwise paraphyletic, so we used a clade containing Scorpaenidae and Sebastidae.

(vii) Unlike the previous six families, Serranidae was hypothesized to be polyphyletic in previous molecular phylogenetic analyses [17]. The six distinct serranid clades in the phylogeny of Rabosky et al. [2] are: (a) *Cephalopholis argus;* (b) *Niphon spinosis;* (c) *Acanthistius ocellatus;* (d) subfamily Serraninae; (e) subfamilies Epinephelinae, Diploprioninae, Grammistinae, Liopropomatinae, and some members of Anthiinae; and (f) the anthiines *Caesioperca lepidoptera* and *Plectranthias japonicus.* Ultimately, we split Serranidae into four clades for downstream analyses (see below for justification for each case). We retained clades b-e as distinct since they were congruent with the primary literature (see below). We treated clades a and f as erroneous, and counted their richness as part of clade e.

(a) In the phylogeny [2], *Cephalopholis argus* (subfamily Epinephelinae) is the sister to a clade including members of Labridae and Odacidae. Other sampled members of *Cephalopholis* are nested within clade e, which includes Epinephelinae and others (see below). *Cephalopholis argus* is nested within *Cephalopholis* in Epinephelinae in previous molecular phylogenies [18–20]. Therefore, we removed *Cephalopholis argus* from the phylogeny, and counted it in species richness counts of Epinephelinae (clade e) for downstream analyses.

(b and c) *Niphon spinosis* (monotypic subfamily Niphoninae) and *Acanthistius ocellatus* (subfamily Anthiinae) were found to be phylogenetically distinct from the rest of Serranidae in this phylogeny [2] and in a previous phylogeny [17]. Whereas *Acanthistius ocellatus* was the only member of its genus sampled in these two studies, Smith and Craig [17] posited that the entire genus *Acanthistius* was outside of Serranidae (implying monophyly for the genus). We considered the subfamily Niphoninae and the genus *Acanthistius* to each represent distinct clades for the purposes of our net diversification analyses (dataset S2).

(d) The subfamily Serraninae was found to be distinct from other serranids in the present phylogeny [2] and in earlier studies [17,21]. We considered Serraninae to be a separate clade in downstream analyses.

(e) The phylogeny included a clade encompassing the subfamilies Epinephelinae, Diploprioninae, Grammistinae, Liopropomatinae, and most members of Anthiinae. The subfamily Anthiinae is included except for the genus *Acanthistius,* which forms a distinct clade

(see clade c above), and the species *Caesioperca lepidoptera* and *Plectranthias japonicas* (see clade f below). The monophyly of clade e is supported by many previous molecular phylogenies [17,19,20,21]. We thus treated clade e as distinct in downstream analyses.

Note that the species *Plectranthias kelloggi* (as per [2]; now *Zalanthias kelloggi*) is traditionally placed in Anthiinae, but was suggested to belong to Serraninae given its placement in the phylogeny of Smith and Craig [17]. Following FishBase taxonomy [3], it is considered to be in Serraninae. However, in the phylogeny of Rabosky et al. [2], it is nested within Anthiinae as its traditional taxonomic placement would suggest. This would cause polyphyly of Serraninae in the present phylogeny [2]. However, unlike FishBase, the Catalogue of Fishes [22] instead denotes this species as belonging to Anthiinae. We considered this species to belong to Anthiinae and our clade e, in spite of its FishBase taxonomic placement, in order to facilitate analyses and because its placement still appears to be unresolved.

(f) *Caesioperca lepidoptera* and *Plectranthias japonicas* (both Anthiinae) together form a distinct clade in phylogeny, as sister to a clade containing Nototheniidae, Channichthyidae, and others. This relationship is contradicted by previous studies. The membership of *Caesioperca* in Anthiinae is supported by morphology [23] and DNA barcoding data [24]. *Plectranthias japonicas* was nested in Anthiinae in the molecular phylogenetic tree of Smith and Craig [17]. Therefore, we removed both these species from the phylogeny, and included the richness of the genera *Caesioperca* and *Plectranthias* in our tallies for clade e (above).

Note that the species *Caesioscorphis theagenes* and *Hemilutjanus macrophthalmos* (included in the FishBase list of 17,458 percomorph species but not in the phylogeny) are members of Serranidae, but were not assigned to a subfamily ("Incertae sedis" in FishBase). We excluded these two species from the weighted mean net diversification rate, because we split the family Serranidae into four clades based on subfamilies for downstream analyses, and we lacked phylogenetic information to assign these species to one of these four clades.

Using the modified phylogeny (after removing tips, table S1), we calculated diversification rates of 200 family-level clades (181 monophyletic families, 15 aggregate clades, and 4 serranid subclades). All clades are given in dataset S2.

Monophyly of genera

We also assessed the monophyly of sampled genera to calculate their net diversification rates (appendix S3; dataset S2). Of 1,454 total genera sampled in the tree of Rabosky et al. [2], 323 were non-monophyletic (22.2%). We excluded these non-monophyletic genera from analyses because the remaining 1,131 genera were sufficient to assess regional differences in net diversification rates. Among the monophyletic genera, the majority (751 genera; 66.4%) had only one species sampled in the phylogeny (or were monotypic). For these genera, only the stem age could be obtained from the phylogeny. We obtained a crown and stem age for the remaining 380 genera with at least 2 species sampled for use in net diversification rate analyses (dataset S2).

Table S1: A total of 41 taxa removed from the phylogeny of Rabosky et al. [2]. Taxonomy follows FishBase [3] as of August 2016. Subspecies that were retained in the phylogeny were treated as representing the entire species for biogeographic coding. For details and justification, see Extended Methods in section 1 of this document (Resolving taxonomic incongruences among datasets and assessing monophyly of families).

Species	Reason for removing from phylogeny
1. *Cheilopogon antoncichi*	Synonymous with *Cheilopogon furcatus,* already sampled in phylogeny.
2. *Evynnis japonica*	Synonymous with *Evynnis tumifrons,* already sampled in phylogeny (now called *Dentex tumifrons*)
3. *Mugil gyrans*	Synonymous with *Mugil trichodon,* already sampled in phylogeny.
4. *Pampus cinereus*	Synonymous with *Pampus argenteus,* already sampled in phylogeny.
5. *Sebastes marinus*	Synonymous with *Sebastes norvegicus,* already sampled in phylogeny.
6. *Takifugu fasciatus*	Synonymous with *Takifugu obscurus*, already sampled in phylogeny.
7. *Telmatochromis burgeoni*	Synonymous with *Telmatochromis temporalis*, already sampled in phylogeny.
8. *Cyprichromis zebra*	Synonymous with *Cyprichromis zonatus*, already sampled in phylogeny.
9. *Cyprichromis jumbo*	Synonymous with *Cyprichromis zonatus*, already sampled in phylogeny.
10. *Mugil platanus*	Synonymous with *Mugil liza*, already sampled in phylogeny.
11. *Mastacembelus stappersii*	Synonymous with *Mastacembelus frenatus*, already sampled in phylogeny.
12. *Elacatinus inornatus*	Synonymous with *Tigrigobius digueti*, already sampled in phylogeny (as *Elacatinus digueti*).
13. *Oreochromis niloticus baringoensis*	Subspecies of *Oreochromis niloticus*, already sampled in phylogeny.
14. *Aphanius dispar richardsoni*	Subspecies of *Aphanius dispar; A. d. dispar* kept in tree to represent species
15. *Cheilopogon pinnatibarbatus pinnatibarbatus*	Subspecies of *Cheilopogon pinnatibarbatus; C. p. californicus* kept in tree to represent species

16. *Craterocephalus stercusmuscarum stercusmuscarum*	Subspecies of *Craterocephalus stercusmuscarum; C. s. fulvus* kept in tree to represent species
17. *Diplodus sargus lineatus*	Subspecies of *Diplodus sargus; D. s. cadenati* kept in tree to represent species
18. *Diplodus sargus sargus*	Subspecies of *Diplodus sargus; D. s. cadenati* kept in tree to represent species
19. *Ditrema temminckii temminckii*	Subspecies of *Ditrema temminckii; D. t. pacificum* kept in tree to represent species
20. *Melanotaenia splendida rubrostriata*	Subspecies of *Melanotaenia splendida; M. s. inornata* kept in tree to represent species
21. *Melanotaenia splendida splendida*	Subspecies of *Melanotaenia splendida; M. s. inornata* kept in tree to represent species
22. *Melanotaenia splendida tatei*	Subspecies of *Melanotaenia splendida; M. s. inornata* kept in tree to represent species
23. *Mullus barbatus ponticus*	Subspecies of *Mullus barbatus; M. b. barbatus* kept in tree to represent species
24. *Oxyporhamphus micropterus similis*	Subspecies of *Oxyporhamphus micropterus; O. m. micropterus* kept in tree to represent species
25. *Sarotherodon galilaeus multifasciatus*	Subspecies of *Sarotherodon galilaeus*; *S. g. galilaeus* kept in tree to represent species
26. *Sarotherodon galilaeus sanagaensis*	Subspecies of *Sarotherodon galilaeus*; *S. g. galilaeus* kept in tree to represent species
27. *Sebastes pachycephalus pachycephalus*	Subspecies of *Sebastes pachycephalus*; *S. p. chalcogrammus* kept in tree to represent species
28. *Strongylura notata notata*	Subspecies of *Strongylura notata*; *S. n. forsythia* kept in tree to represent species
29. *Tylosurus acus. imperialis*	Subspecies of *Tylosurus acus*; *T. a. acus* kept in tree to represent species
30. *Tylosurus acus melanotus*	Subspecies of *Tylosurus acus*; *T. a. acus* kept in tree to represent species
31. *Tylosurus acus rafale*	Subspecies of *Tylosurus acus*; *T. a. acus* kept in tree to represent species
32. *Parataeniophorus brevis*	Caused polyphyly of Cetomimidae; placement likely to be an error in phylogenetic reconstruction

33. *Lythrypnus dalli*	Caused polyphyly of Gobiidae; placement likely to be an error in phylogenetic reconstruction
34. *Lythrypnus zebra*	Caused polyphyly of Gobiidae; placement likely to be an error in phylogenetic reconstruction
35. *Decodon melasma*	Caused polyphyly of Labridae; placement likely to be an error in phylogenetic reconstruction
36. *Pristipomoides aquilonaris*	Caused polyphyly of Lutjanidae; placement likely to be an error in phylogenetic reconstruction
37. *Siganus rivulatus*	Caused polyphyly of Siganidae; placement likely to be an error in phylogenetic reconstruction
38. *Pterois lunulata*	Caused polyphyly of Scorpaenidae; placement likely to be an error in phylogenetic reconstruction
39. *Cephalopholis argus*	Caused polyphyly of Serranidae; placement likely to be an error in phylogenetic reconstruction
40. *Caesioperca lepidoptera*	Caused polyphyly of Serranidae; placement likely to be an error in phylogenetic reconstruction
41. *Plectranthias japonicus*	Caused polyphyly of Serranidae; placement likely to be an error in phylogenetic reconstruction

2. Biogeographic coding and data quality

Extended Methods:

Biogeographic regions

Analyses of historical biogeography require assigning species to one or more discrete regions. We defined nine regions (figure 1 in main text), which correspond closely to the areas delimited by Briggs [25], Briggs and Bowen [26], and Kulbicki et al. [27] (based on patterns of endemism of coastal fishes). Note that "warm-temperate" and "warm" marine provinces identified by previous authors are combined herein following recommendations of Briggs and Bowen [26], because warm-temperate faunas tend to be phylogenetically more closely related to tropical faunas than cold-temperate or polar faunas. Although our primary goal was examining richness differences among warm marine regions, we incidentally included cold marine and freshwater habitats in our biogeographic analyses since a large portion of percomorph diversity occurs exclusively in these habitats.

Shapefiles, created in QGIS version 2.16.1 'Nødebo' (http://www.qgis.org/en/site/index.html), containing exact regional boundaries are available from the Dryad package associated with this paper. Approximate boundaries are briefly described here.

We used six discrete regions corresponding to warm and warm-temperate marine biogeographic regions:

1. Western Indian Ocean ("WI"): western boundary at the Cape of Good Hope (exclusive), eastward to the Maldives (inclusive); encompassing Eastern Africa, the Red Sea, and Madagascar.

2. Central Indo-Pacific ("CIP"): western boundary at the western coast of Pakistan (inclusive), east to the Solomon Islands (inclusive) and Cape Otway, Victoria, Australia (exclusive), northern boundaries at Shanghai, China and Port Hamada in Japan (exclusive); encompassing the Indo-Australian Archipelago region and the northern Great Barrier Reef.

3. Central Pacific ("CP"): northern boundary at Port Douglas, Australia (exclusive), southern boundary at Hamilton on the northern tip of North Island, New Zealand (inclusive), eastern boundary at Isla Salas and Gomez (inclusive); encompassing the Coral Sea, Palau, Hawaii, and other Pacific islands. We also included Juan Fernandez Island off the coast of Chile because its fauna are more closely aligned with the Central Pacific [25]. The island was subsumed in the Eastern Pacific region and not contiguous with the rest of the Central Pacific.

4. Eastern Pacific ("EP"): extending from east of Hawaii (exclusive) to the Pacific coasts of North, Middle, and South America, south from Point Conception, California (inclusive), and north of Parque Nacional Laguna San Rafael in Chile (exclusive).

5. Western Atlantic ("WA"): northern boundary at the Virginia-North Carolina border (inclusive), south to the Valdes Peninsula, Argentina (exclusive), eastern boundary at the mid-Atlantic ridge, and encompassing the Caribbean.

6. Eastern Atlantic ("EA"): east of the mid-Atlantic ridge, northern boundary at the English Channel (inclusive), southern boundary at the Cape of Good Hope (inclusive); encompassing the Mediterranean, European inland seas, and Western Africa. We also included the St. Paul and Amsterdam islands in the southern Indian Ocean following Briggs and Bowen [26]. Although these islands are not contiguous with the EA region described here, their faunas are predominately of EA origin due to the West Wind Drift [25].

Cold marine regions were divided into two regions:

7. Northern Cold ("NC"): extending north of the boundaries described above, and from (and exclusive of) Point Conception, North Carolina, the English Channel, and Shanghai, China, and including the Yellow Sea, north of Port Hamada, Japan (inclusive), and the Arctic Sea.

8. Southern Cold ("SC"): extending south of the boundaries described above, and south from southern Chile (Parque Nacional Laguna San Rafael) and Argentina (Valdes Peninsula), Victoria, Australia (inclusive), and including Tasmania, part of North Island south of Hamilton and the South Island of New Zealand, and Antarctica.

9. Finally, we considered freshwater and brackish habitats as a ninth area irrespective of geography ("FW"). We assigned this "region" based on habitat designations in FishBase profiles. FishBase considers "freshwater", "brackish", and "saltwater" as separate habitats. A single species could potentially occur in all three habitats. We coded species in "freshwater" and "brackish" habitats as freshwater, and refer to "saltwater" habitats as "marine" in the text. If a species occurred in freshwater (and/or brackish) but not marine habitats according to our definition, that species was coded as absent in all eight marine regions (even if it had georeferenced occurrences in the ocean). One alternative coding scheme that would result in a change of a species' assigned range is if we instead coded "brackish" as marine. If so, the only species that would be affected are those occurring in "brackish" but not "saltwater" habitats. Only 510 species were brackish and not marine (3% of all species) so assignment of these species to one or more marine regions is unlikely to change our overall results.

Assigning presence/absence in regions using georeferenced data

A total of 17,453 percomorph species (all but 5), were assigned to one or more of these nine regions as follows. First, we assigned species to the freshwater "region" if they had the designations "freshwater" and/or "brackish" in their FishBase profiles. These profiles were viewed by downloading "Environment" designations (fields "Fresh", "Brack", and "Saltwater" for each species) using the *rfishbase* package version 2.1.1 [5]. We checked the Fishbase website manually for 187 species for which we could not retrieve information on habitat using *rfishbase.*

A total of 5,019 species were freshwater or brackish only (not saltwater) and so we recorded them as absent from all eight marine areas.

Next, to assign the remaining 12,439 marine species to one or more of eight marine regions, we mapped georeferenced occurrence points for each species from the Ocean Biogeographic Information System [28] onto shapefile polygons to assign their presence or absence among the eight regions, using the R package *robis* version 0.1.2 [29]. Prior to mapping, we cleaned georeferenced points using the following quality control options implemented in *robis* (numbers refer to quality control codes described by table 1 of Vandepitte et al. [30]): (code #1) all required OBIS fields were completed, (#2) taxon name matched an existing name in the WoRMS database [31]; (#3) taxon name was lower than the family level, (#4) latitude and longitude were nonzero, (#5) latitude and longitude values were within the range of possible values (i.e. longitude not greater than 180º), (#6) coordinates were on the coastline or ocean, (#9) coordinates were in the expected geographic region given metadata, (#10) the record was documented with a valid code, (#9) the minimum depth value for the record was smaller or equal to the maximum depth value (#18), and the sampled depth was a possible value (#19).

Preliminary analyses suggested that even this degree of cleaning overestimated species' range sizes due to erroneous points, so when possible we excluded occurrences deemed to be spatial outliers. The goal of outlier analysis is to remove occurrences that are possibly erroneous, presumably due to misidentifications or other errors that may not otherwise be detected. Occurrences were excluded if they occurred >3 times farther away in space than the interquartile distance of the center of the species' range (implemented in *robis* as quality control code #28 of Vandepitte et al. [30]). A total of 9,647 species had georeferenced data in OBIS (77.6% of marine species). Of these, 9,557 (99.1%) had sufficient data to perform outlier analysis, with the remaining 90 species assigned based on cleaned data only.

If OBIS did not contain any georeferenced data for the species, we instead used GBIF [32] and the *rgbif* package version 0.9.4 [33]. We removed occurrence points that failed quality control checks for the following reasons (implemented in the R package *speciesgeocodeR* v. 1.0–4 [34]): latitude/longitude were NA, latitude/longitude were non-numeric, latitude/longitude were not within possible values, latitude/longitude were equal to zero, latitude equaled longitude, the coordinates did not fall within a threshold rectangle surrounding the country assigned to the occurrence, and the coordinates fell at GBIF headquarters in Copenhagen. This allowed us to assign regions for 2,096 species without georeferenced data in OBIS (16.9% of marine species).

We assigned the remaining 691 species (5.6% of marine species) using FishBase profiles (see detailed procedure in following section) for the following reasons. For 599 species, there were no georeferenced occurrence data in either OBIS or GBIF repositories. For 90 of these species, the FishBase profile contained unclear or incomplete information to assign ranges, so we supplemented FishBase with primary literature sources (see References in this document). We also used FishBase in some cases to resolve taxonomic incongruences among data sources. We assigned regions to 55 species that were valid species according to FishBase but not in OBIS, and so the same OBIS data would have otherwise applied to multiple named species under the

FishBase taxonomy. We then assigned ranges for 42 species in which OBIS data were only available for one subspecies, thereby making sure the assigned range reflected the entire species.

After this procedure, only 5 remaining species of the original 17,458 species could not be assigned to one or more regions because their range was unknown. These were removed from the species list for downstream analyses, leaving a total of 17,453 species.

Finally, we checked to ensure that the assigned ranges reflected the species' native range and not human introductions. We used the World Register of Introduced Marine Species [35] to identify and eliminate any georeferenced localities that might reflect human introductions. We edited the ranges of 24 species for this reason: 19 species were Lessepsian migrants from the Western Indian Ocean into the Eastern Atlantic via the Suez Canal, 2 were introduced to Australia and California from other regions, and 3 were introduced to the Western Atlantic from other regions.

Constructing alternative datasets from FishBase and IUCN

We cleaned the georeferenced locality data extensively to account for common errors, but there was still some variation among data sources in the assignment of particular species to the eight marine regions. This variation may be caused by real uncertainties about a species' geographic range, or errors caused by poor data quality (i.e. [36]). To assess the extent of uncertainty regarding assignment of species to regions, we manually constructed two alternative datasets using regional assignments from either FishBase [3] or IUCN profiles [37]. We did this for just a subset of species, focusing on the 4,571 species included in the phylogeny (and thus included in the ancestral-area reconstructions).

To construct the FishBase dataset for marine species, we read the "Distribution" information displayed on each species' profile, and assigned each species to marine regions based on the verbal description of the species' range. For many species, this was sufficient to determine the range. We did not include areas listed in the verbal description as only entered based on larvae or "stray individuals", or if records were noted to be uncertain. Of 4,571 species considered, 1,580 were freshwater or brackish only (not assigned to marine regions). Of the remaining 2,991 marine species, 1,889 were assigned based on the verbal range description alone (63.1%). If the verbal description of the range was not sufficient to assign the species to one or more of the eight marine regions (because it was too general or unclear), we then inspected the computer-generated native distribution maps on the species' profile provided by AquaMaps (www.aquamaps.org) to clarify ambiguities. For these species, we only considered the parts of the range projected with 80–100% probability of occurrence. We observed that AquaMap projections tended to overextend species' ranges when compared to the verbal descriptions. Since the projected range is based on environmental parameters, and may not reflect the realized range, we cautiously used these maps only to clarify areas already mentioned in the description, and did not add additional areas portrayed in the map. For example, if the description of the species' distribution was "Japan," which could potentially include CIP and/or NC, we inspected

only the range surrounding Japan in the computer-generated map. We used AquaMaps to assign ranges to 967 species (32.3% of marine species), 170 of which had maps edited by professionals. The remaining 135 marine species (only 3.0%) could not have their ranges confidently assigned using this procedure because their range description was not detailed enough and they lacked AquaMap projections; these species were not considered in these comparisons. Freshwater assignments were identical to those in the OBIS/GBIF dataset (based on "Environment" in FishBase).

Similarly, we constructed an alternative dataset using IUCN profiles to assign species to marine regions. We considered the comparison between FishBase and IUCN area assignments as a "baseline" for assessing uncertainty in species ranges. Since both of these alternative datasets were constructed manually, differences in area assignments between them are more likely to be due to differences in expert opinion regarding the species' range rather than erroneous occurrence records as for OBIS/GBIF (although some errors may still be present in AquaMap projections). IUCN maps are constructed using a combination of georeferenced data and environmental parameters and then vetted by experts (in contrast, only 17.6% of the AquaMap projections we viewed were vetted by professionals). We first visually inspected maps of each species to assign each species to one or more of eight marine geographic regions. Some species did not have constructed maps. In these cases, we used the verbal "Range Description" of the species' range, which tended to be less specific than the maps. We assigned the freshwater state using the "Systems" designation under "Habitat and Ecology" in species profiles. Of 4,571 species considered, 1,764 did not have IUCN profiles. 865 were freshwater only according to the "System" designation and were not assigned to marine areas. Of the remaining 1,942 marine species, 1,810 were assigned based on the range map (93.2%). 40 species lacked a map, and were assigned based on the range description in the species profile, 9 of which had additional supplemental information available to assign the range. Only 92 species (2.0%) could not be assigned to one or more of the nine regions because they lacked a range map, clear range description, and/or system designation.

Pairwise comparisons of FishBase, IUCN, and OBIS datasets

We performed pairwise comparisons of species assignments to the nine regions between: (a) FishBase and IUCN ("baseline"), (b) FishBase and OBIS/GBIF, and (c) IUCN and OBIS/GBIF. In each comparison, we only included species shared by both datasets (eliminating those that were not sampled in the phylogeny, or where the range was not confidently assigned in one or both datasets). For comparisons using the OBIS/GBIF dataset, we only compared marine species assigned using georeferenced data from either repository and not species that were assigned using FishBase, primary literature, or that were freshwater only (because these are identical to FishBase assignments). For all comparisons, we identified species that matched completely in all regional assignments between the two datasets. Next, we performed linear regression of regional richness between the two datasets

1. Fishbase vs. IUCN: 2,664 species were shared between the two datasets. Of these, 83.6% matched in assignment among all eight marine regions. Of the 437 species that did not match, the majority (75.5%) had mismatches in only one area. The average % of marine regions matching was 83% (for reference, if a species differed by only one region between sources, its % of match was 7/8 = 87.5%). Richness in the nine regions was very strongly related between FishBase and IUCN ($P<0.001$; $r^2=0.957$). IUCN slightly overestimated richness in NC (meaning individual species tended to be assigned to NC in IUCN maps and not assigned there in FishBase profiles). Thus, 34% of mismatches were associated with the NC region, compared to 10–18% for the other seven marine regions. Otherwise, assignment to the eight marine regions was very similar (figure S1a). FishBase "Environment" designations were more likely to assign presence to freshwater than IUCN "System" designations. Freshwater assignments matched for 87.8% of the 2,664 shared species. Mismatches were likely because IUCN lacks a "brackish" category, and only considers "freshwater" and "marine" as habitats. We ultimately used FishBase habitat assignments in our analyses because dataset covers more species than IUCN.

2. FishBase vs. OBIS/GBIF: 2,781 marine species were shared between the two datasets. Of these, 1,731 matched in assignment among all eight marine regions (62.2%). Despite the lower proportion of complete matches compared to the FishBase vs. IUCN comparison, the proportion of matches within the eight marine regions was high (91–96% of species within each region matched in presence/absence in that region between the two datasets). Of 1,050 species that did not completely match, the average % of match between the eight regions was 83.0% (the same as the comparison between FishBase and IUCN), indicating that the majority of mismatches involved only one region. Despite mismatches, richness patterns among the eight regions were strongly related in these two datasets ($P<0.001$; $r^2=0.977$). After outlier analysis, richness in WI, CIP, CP, and NC tended to be underestimated by OBIS (i.e. a species was not assigned to WI in OBIS but assigned there in FishBase). WA was the only region that tended to be overestimated by OBIS in comparison (figure S1b). However, the rank order of regions by richness was the same. Most mismatches involved presence/absence in WI (25% of mismatches) followed by NC (23%) and EP (20%); the remaining five marine regions were involved in 10–17% of mismatches.

3. IUCN vs. OBIS/GBIF: 1,772 marine species were shared between the two datasets. A total of 1,062 species matched in their distribution among all eight regions (59.9%). Again, despite mismatches, matches within the eight regions was high (87–95% of species matched in their presence/absence distribution, with the lowest percentage of matches within NC and the highest in CIP). Again, among 710 species that did not match entirely, the average % of match was 82%, indicating that most mismatches involved only one area. Richness in the eight regions between the two datasets was strongly related ($P<0.001$, $r^2=0.903$). Richness in WA and EP tended to be overestimated by OBIS/GBIF (i.e. assigned to WA by OBIS but not by IUCN), whereas WI, NC, and SC tended to be overestimated by IUCN (i.e. assigned to WI by IUCN but not by OBIS; figure S1c). However, the rank order of regions by richness was the same. Among mismatches, 33% involved the NC region and 25% involved the WI region, with 12–17% involving the other six marine regions. However, 34% of mismatches between FishBase vs.

IUCN also involved NC, so these mismatches are perhaps more likely to be related to differences in expert opinion on the range of these species than mismatches for other regions.

In summary, we do not expect our results in the main text to be artefactual due to uncertainty in a species' range or errors in georeferenced data. First, whereas variation in data quality within and between data repositories is common [36], the rank order of richness in the eight marine regions is the same in all comparisons, and the proportion of matches within the eight regions are high (i.e. 87–96% of species are correctly assigned within a single region). Second, mismatches between georeferenced data and FishBase/IUCN profiles tended to be caused by a retraction of the range when using georeferenced data due to outlier analysis (figure S1). This indicated that the georeferenced data after outlier analysis tended to be conservative, and mismatches were unlikely to result in type-1 error (i.e. detection of a time-for-speciation effect due to oversampling of some areas). Finally, we performed time-for-speciation analyses with combined regions (Indo-West Pacific and Atlantic regions), which should further minimize variation in regional assignments, and found similar results (appendix S2).

All range assignments across the three datasets are available in dataset S1.

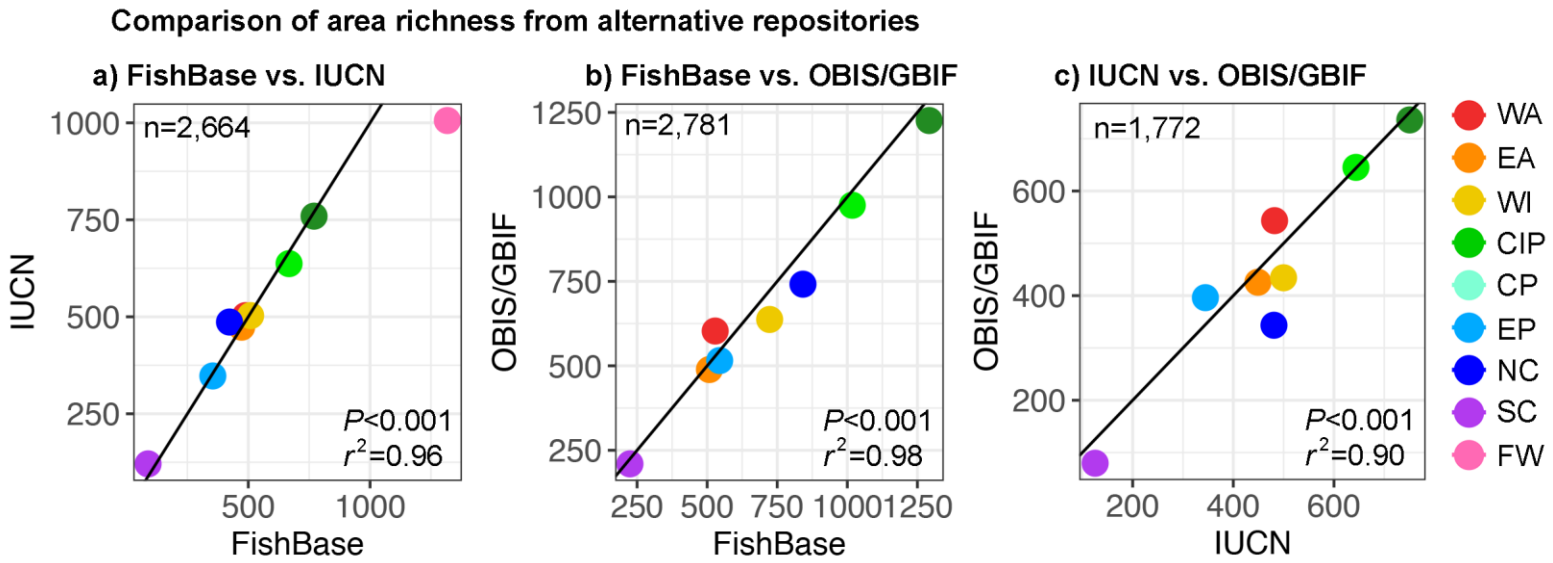

Figure S1: Results of pairwise regressions of regional richness between alternative biogeographic data repositories: FishBase vs. IUCN (left), georeferenced data from OBIS/GBIF vs. FishBase (middle), and OBIS/GBIF vs. IUCN (right). Straight line represents a 1-1 relationship in richness; n= the number of species shared between the two datasets. Range assignments based on OBIS/GBIF were used for all analyses, because this dataset included >99% of all Percomorph species.

Table S2. Percentage of percomorph species occurring in each region that were sampled in the phylogeny relative to the total number of described species in each region, estimated across nine regions. Values are derived from marine georeferenced occurrences (OBIS/GBIF) and FishBase habitat data, totaling 17,453 species. Linear regression shows that sampled richness is strongly related to total richness (P=0.0001, r^2=0.89).

Region	Total richness	Percent sampled (species sampled)
Western Atlantic (“WA”)	1,845	34.2% (631)
Eastern Atlantic (“EA”)	1,210	43.1% (522)
Western Indian (“WI”)	2,677	25.3% (677)
Central Indo-Pacific (“CIP”)	5,659	23.8% (1,346)
Central Pacific (“CP”)	3,697	28.0% (1,037)
Eastern Pacific (“EP”)	1,570	35.0% (549)
Northern Cold (“NC”)	1,749	46.3% (810)
Southern Cold (“SC”)	929	24.9% (231)
Freshwater (“FW”)	6,584	33.9% (2,231)

References

1. Near TJ *et al*. 2013 Phylogeny and tempo of diversification in the superradiation of spiny-rayed fishes. *Proc. Natl. Acad. Sci. USA* **110**, 12738–12743.
2. Rabosky DL, Santini F, Eastman J, Smith SA, Sidlauskas B, Chang J, Alfaro ME. 2013 Rates of speciation and morphological evolution are correlated across the largest vertebrate radiation. *Nat. Commun.* **4**, 1958.
3. Froese R, Pauly D. 2017 FishBase Version 2/2017. See http://www.fishbase.org/.
4. Schwery O, O'Meara BC. 2016 MonoPhy: a simple R package to find and visualize monophyly issues. *PeerJ. Comp. Sci.* **2**, e56.
5. Boettiger C, Lang DT, Wainwright PC. 2012 rfishbase: exploring, manipulating, and visualizing FishBase data from R. *J. Fish. Biol.* **81**, 2030–2039.
6. Betancur-R R, Wiley EO, Arratia G, Acero A, Bailly N, Miya M, Lecointre G, Orti G. 2017 Phylogenetic classification of bony fishes. *BMC Evol. Biol.* **17**, 162.
7. Johnson DG, Paxton JR, Sutton TT, Satoh TP, Sado T, Nishida M, Miya M. 2009 Deep-sea mystery solved: astonishing larval transformations and extreme sexual dimorphism unite three fish families. *Biol. Lett.* **5**, 235–239.
8. Thacker CE, Roje DM. 2011 Phylogeny of Gobiidae and identification of gobiid lineages. *Syst. Biodivers.* **9**, 329–347.
9. Maxfield JM, van Tassell JL, St. Mary CM, Joyeux JC, Crow KD. 2012 Extreme gender flexibility: using a phylogenetic framework to infer the evolution of variation in sex allocation, phylogeography, and speciation in a genus of bidirectional sex changing fishes (*Lythrypnus*, Gobiidae). *Mol. Phylogenet. Evol.* **64**, 416–427.
10. Tornabene L, Chen Y, Pezold F. 2013 Gobies are deeply divided: phylogenetic evidence from nuclear DNA (Teleostei: Gobioidei: Gobiidae). *Syst. Biodivers.* **11**, 345–361.
11. Gomon MF. 1997 Relationships of fishes of the Labrid tribe Hypsigenyini. *B. Mar. Sci.* **60**, 789–871.
12. Sarver SK, Freshwater DW, Walsh PJ. 1996 Phylogenetic relationships of Western Atlantic snappers (family Lutjanidae) based on mitochondrial DNA sequences. *Copeia* **1996**, 715–721.
13. Zhang J, Liu X. 2006 The phylogenetic relationship of the family Lutjanidae based on analyses of AFLP and mitochondrial 12S rRNA sequences. *Chinese Sci. Bull.* **51**, 143–148.
14. Guo Y, Bai Q, Yan T, Wang Z, Liu C. 2014 Mitogenomes of genus *Pristipomoides, Lutjanus*, and *Pterocaesio* confirm Caesionidae nests in Lutjanidae. *Mitochondr. DNA* **27**, 2198–2199.
15. Borsa P, Lemer S, Aurelle D. 2007 Patterns of lineage diversification in rabbitfishes. *Mol. Phylogenet. Evol.* **44**, 427–435.
16. Wilcox CL. 2014 Molecular investigations of the Pteroinae: Insights into the invasive lionfishes from the native range. PhD Dissertation, The University of Hawaii at Manoa.
17. Smith WL, Craig MT. 2007 Casting the Percomorph net widely: the importance of broad taxonomic sampling in the search for the placement of serranid and percid fishes. *Copeia* **2007**, 35–55.
18. Craig MT, Hastings PA. 2006 A molecular phylogeny of the groupers of the subfamily Epinephelinae (Serranidae) with a revised classification of the Epinephelini. *Ichthyol. Res.* **54**, 1–17.
19. Erisman BE, Craig MT, Hastings PA. 2009 A phylogenetic test of the size-advantage model: evolutionary changes in mating behavior influence the loss of sex change in a fish lineage. *Am. Nat.* **174**, E83–E99.

20. Schoelinck C, Hinsinger DD, Dettai A, Cruad C, Justine JL. 2014 A phylogenetic re-analysis of groupers with applications for ciguatera fish poisoning. *PLoS ONE* **9**, e98198.
21. Lautredou AC, Motomura H, Gallut C, Ozouf-Costaz C, Cruaud C, Lecointre G, Dettai A. 2013 New nuclear markers and exploration of the relationships among Serraniformes (Acanthomorpha, Teleostei): The importance of working at multiple scales. *Mol. Phylogenet. Evol.* **67**, 140–155.
22. Eschmeyer WN, Fricke R, van der Laan R. 2017 Catalogue of Fishes: Genera, Species, References. See http://researcharchive.calacademy.org/research/ichthyology/catalog/fishcatmain.asp/.
23. Baldwin CC, Johnson GD. 1993 Phylogeny of the Epinephelinae (Teleostei: Serranidae). *B. Mar. Sci.* **52**, 240–283.
24. Smith PJ, Steinke D, McMillan PJ, McVeagh SM, Struthers CD. 2008 DNA database for commercial marine fish. *NZAEBR* **22**, 1–63.
25. Briggs JC. 1995 *Global Biogeography*. Amsterdam, Netherlands: Elsevier.
26. Briggs JC, Bowen BW. 2012 A realignment of marine biogeographic provinces with particular reference to fish distributions. *J. Biogeogr*. **39**, 12–30.
27. Kulbicki M *et al*. 2013 Global biogeography of reef fishes: a hierarchical quantitative delineation of regions. *PLoS ONE* **8**, e81847.
28. OBIS. 2017 Data from the Ocean Biogeographic Information System. Intergovernmental Oceanographic Commission of UNESCO. See http://www.iobis.org/.
29. R package *robis* version 0.1.2. See https://github.com/iobis/robis.
30. Vandepitte L, Bosch S, Tyberghein L, Waumans F, Vanhoorne B, Hernandez F, De Clerck O, Mees J. 2015 Fishing for data and sorting the catch: assessing the data quality, completeness and fitness for use of data in marine biogeographic databases. *Database* **2015,** 1–14.
31. Boxshall GA *et al*. 2017 World Register of Marine Species. See http://www.marinespecies.org/.
32. Global Biodiversity Information Facility. 2017. See http://www.gbif.org/.
33. Chamberlain S, Boettiger C, Ram K, Barve V, Mcglinn D. 2017 rgbif: Interface to the Global 'Biodiversity' Information Facility 'API'. R package version 0.9.5. See http://CRAN.R-project.org/package=rgbif/.
34. Zizka A. 2015 speciesgeocodeR: Prepare species distributions for the use in phylogenetic analyses. See https://CRAN.R-project.org/package=speciesgeocodeR/.
35. Pagad S, Hayes K, Katsanevakis S, Costello MJ. 2016 World Register of Introduced Marine Species (WRIMS). See http://www.marinespecies.org/introduced on 2016-08/.
36. Robertson DR. 2008 Global biogeographical data bases on marine fishes: caveat emptor. *Diversity Distrib*. **14**, 891–892.
37. International Union for the Conservation of Nature. 2017 IUCN Red List of Threatened Species Version 2017.1. See http://www.iucnredlist.org/.

The following additional references were used to assign presence/absence to ranges for 90 species without georeferenced occurrence data or sufficient information in FishBase profiles (see dataset S1).

38. Abbot JF. 1898 The marine fishes of Peru. *Proc. Acad. Nat. Sci. Philadelphia* **51**, 324–364.
39. Akihito P, Meguro K. 1988 Two new species of goby of the genus *Astrabe* from Japan. *Jpn. J. Ichthyol.* **34**, 409–420.
40. Anderson EM, Moller PR. 2007 Studies on the Zoarcidae (Teleostei: Perciformes) of the Southern Hemisphere. XIII. Two new species of *Lycenchelys* from the Southwestern Pacific. *Spec. Div.* **12**, 175–185.
41. Balushkin AV. 1993 *Patagonotothen thompsoni* sp. n., a new Patagonian notothen from the Strait of Magellan, South America (Pisces, Perciformes, Nototheniidae). *Arch Fischereiwiss* **41**, 223–229.
42. Bineesh KK, Akhilesh KV, Gopalakrishnan A, Jena JK. 2014 *Plectranthias alcocki*, a new anthiine fish species (Perciformes: Serranidae) from the Arabian Sea, off southwest India. *Zootaxa* **3785**, 490–496.
43. Randall JE, Lim KKP. 2000 A checklist of the fishes of the South China Sea. *Raffles Bull. Zool.*
44. Chernova NV. 2007 Systematics and phylogeny of fish of the genus *Liparis* (Liparidae, Scorpaeniformes). *J. Ichthyol.* **48**, 831–852.
45. Collette BB, Aadland CR. 1996 Revision of the frigate tunas (Scombridae, *Auxis*) with descriptions of two new subspecies from the eastern Pacific. *Fish. Bull.* **94**, 423–441.
46. Doiuchi R, Nakabo T. 2005 The *Sphryaena obtusata* group (Perciformes: Sphyraenidae) with a description of a new species from southern Japan. *Ichthyol. Res.* **52**, 132–151.
47. Fishes of Australia. See http://fishesofaustralia.net.au/.
48. Francis MP. 1996 Geographic distribution of marine reef fishes in the New Zealand region. *N. Z. J. Mar. Freshwater Res.* **30**, 35–55.
49. Fraser TH. 2016 A new species of cardinalfish (*Gymnapogon*, Gymnapogonini, Apogonidae, Percomorpha) from the Philippines. *Zootaxa* **4107**, 431–438.
50. Fukao R. 1987 Fishes of *Neoclinus bryope* species complex from Shirahama, Japan, with description of two new species. *Jpn. J. Ichthyol.* **34**, 291–308.
51. Galván DE, Venerus LA, Irigoyen AJ, Parma AM, Gosztonyi AE. 2005 Extension of the distributional range of the silver porgy, *Diplodus argenteus* (Valenciennes 1830), and the red porgy, *Pagrus pagrus* (Linnaeus 1758) (Sparidae) in northern Patagonia, south-western Atlantic. *J. Appl. Ichthyol.* **21**, 444–447.
52. Iwata A, Shibukawa K, Ohnishi N. 2007 Three new species of the shrimp-associated goby genus *Vanderhorstia* (Perciformes: Gobiidae: Gobiinae) from Japan, with re-descriptions of two related congeners. *Bull. Natl. Mus. Nat. Sci. Ser. A Suppl. 1* 185–205.
53. Kai Y, Nakabo T. 2004 A new species of *Sebastes* (Scorpaeniformes: Scorpaenidae) from the Pacific coast of southern Japan. *Ichthyol. Res.* **51**, 5–9.
54. Katafuchi H, Nakabo T. 2007 Revision of the East Asian genus *Ditrema* (Embiotocidae), with description of a new subspecies. *Ichthyol. Res.* **54**, 350–366.
55. Kimura S, Sato A. 2007 Descriptions of two new pricklebacks (Perciformes: Stichaeidae) from Japan. *Bull. Natl. Mus. Nat. Sci. Ser. A Suppl. 1* 67–79.
56. Love MS, Mecklenburg CW, Mecklenburg TA, Thorsteinson LK. 2005 Resource inventory of marine and estuarine fishes of the West Coast and Alaska: A checklist of North Pacific and Arctic Ocean species from Baja California to the Alaska-Yukon border. U.S.

Department of Interior, U.S. Geological Survey, Biological Resources Division, Seattle, WA, OCS Study MMS 2005-030 and USGS/NBII 2005-001.
57. Markle DF, Olney JE. 1990 Systematics of the pearlfishes (Pisces: Carapidae). *Bull. Mar. Sci.* **47**, 269–410.
58. Masuda H, Randall JE. 2001 *Rabaulichthys suzukii*, a new anthiine fish from Japan. *Ichthyol. Res.* **48**, 77–81.
59. Nielson JG, Schwarzhans W, Møller, PR. 2004 Reassignment of *Melodicthys paxtoni* to the genus *Fiordichthys* (Teleostei, Bythidae). *Cybium* **28,** 37–41.
60. Nielson JG. 2007 *Grammonus yunokawai* (Ophidiiformes: Bythitidae), a new marine cavefish from the Ryukyu Islands. *Ichthyol. Res.* **54**, 374–379.
61. Nogowa Y, Endo H. 2007 A new species of the genus *Priolepis* (Perciformes: Gobiidae) from Tosa Bay, Japan. *Bull. Natl. Mus. Nat. Sci. Ser. A Suppl. 1* 153–161.
62. Parenti P, Randall JE. 2000 An annotated checklist of the species of the labroid fish families Labridae and Scaridae. *Ichthyology Bulletin no. 8* (J. B. L. Smith Institute, Grahamstown, South Africa), pp 1–97.
63. Randall JE, Earle JL, Rocha LA. 2008 *Xyrichtys pastellus*, a new razorfish from the southwest Pacific, with discussion of the related *X. sciistius* and *X. woodi*. *AQUA* **14**, 149–158.
64. Sasaki D, Kimura S. 2013 Descriptions of two new silversides, *Hypoatherina golanii* and *Hypoatherina lunata*, from the Indo-West Pacific (Atheriniformes: Atherinidae). *Ichthyol. Res.* **60**, 103–111.
65. Senou H, Hirata T. 2000 A new labrid fish, *Cirrhilabrus katoi*, from southern Japan. *Ichthyol. Res.* **47**, 89–93.
66. Shibukawa K, Iwata A. 1998 *Siphonogobius nue*, a new genus and species of gobiid fish from Japan. *Ichthyol. Res.* **45**, 141–150.
67. Shibukawa K, Suzuki T, Aizawa M. 2013 *Gobiodon aoyagii*, a new coral goby (Actinopterygii, Gobiidae, Gobiinae) from the West Pacific, with redescription of a similarly-colored congener *Gobiodon erythrospilus* Bleeker, 1875. *Bull. Natl. Mus. Nat. Sci. Ser. A* **39**, 143–165.
68. Shinohara G, Narimatsu Y, Hattori T, Ito M, Takata Y, Matsuura K. 2009 Annotated checklist of deep-sea fishes from the Pacific coast off Tohoku District, Japan. *Natl. Mus. Nat. Sci. Mono.* **39**, 683–735.
69. Shiogaki M. 1988 A new gobiid fish of the genus *Clariger* from Mutsu Bay, Northern Japan. *Jpn. J. Ichthyol.* **35**, 127–132.
70. Song P, Lin L, Li Y, Zhong Z, Zhang R. 2014 Species composition and stability of nekton community structure in Sandu Bay, Fujian Province. *Biodivers. Sci.* **23**, 519–526.
71. Stevenson DE, Kenaley CP. 2013 Revision of the manefish genera *Caristius* and *Platyberyx* (Teleostei: Percomorpha: Caristiidae), with descriptions of five new species. *Copeia* **3**, 415–434.
72. Tsurouka O, Maruyama S, Yabe M. 2008 Revision of the cottid genus *Astrocuttus* Bolin (Perciformes: Cottoidei), with the description of a new species from Northern Japan. *Bull. Natl. Mus. Nat. Sci. Ser. A* 25–37.
73. Walsh F, Tanaka H. 2011 *Cirrhilabrus nahackyi*, a new wrasse (Perciformes: Labridae) from the South Pacific. *AQUA* **18**, 1–8.