# Comparative phylogeography of the western Indian Ocean reef fauna

Borsa Philippe [1, 2, 8, 9, *], Durand Jean-Dominique [3], Chen Wei-Jen [4], Hubert Nicolas [5], Muths Delphine [6, 7], Mou-Tham Gerard [1, 2], Kulbicki Michel [1, 2]

[1] IRD, UMR EMTROPI, Noumea, New Caledonia.
[2] LabEx Corail, Noumea, New Caledonia.
[3] IRD, UMR MARBEC, Montpellier, France.
[4] Natl Taiwan Univ, Inst Oceanog, Taipei 10764, Taiwan.
[5] IRD, UMR ISEM, Montpellier, France.
[6] IFREMER, Delegat Ocean Indien, Le Port, Reunion.
[7] Univ Europeenne Bretagne, Rennes, France.
[8] IRD UMR 250 EMTROPI, Jl Raya Sesetan Gang Markisa 6, Denpasar 80322, Indonesia.
[9] Univ Udayana, LabEx Corail, Jl Raya Sesetan Gang Markisa 6, Denpasar 80322, Indonesia.

* Corresponding author : Philippe Borsa, email address : philippe.borsa@ird.fr; jean-dominique.durand@ird.fr;;wjchen.actinops@gmail.com; nicolas.hubert@ird.fr;;muthsdelphine@yahoo.fr; gerard.mou-tham@ird.fr; michel.kulbicki@ird.fr

**Abstract :**

Assessing patterns of connectivity at the community and population levels is relevant to marine resource management and conservation. The present study reviews this issue with a focus on the western Indian Ocean (WIO) biogeographic province. This part of the Indian Ocean holds more species than expected from current models of global reef fish species richness. In this study, checklists of reef fish species were examined to determine levels of endemism in each of 10 biogeographic provinces of the Indian Ocean. Results showed that the number of endemic species was higher in the WIO than in any other region of the Indian Ocean. Endemic species from the WIO on the average had a larger body size than elsewhere in the tropical Indian Ocean. This suggests an effect of peripheral speciation, as previously documented in the Hawaiian reef fish fauna, relative to other sites in the tropical western Pacific. To explore evolutionary dynamics of species across biogeographic provinces and infer mechanisms of speciation, we present and compare the results of phylogeographic surveys based on compilations of published and unpublished mitochondrial DNA sequences for 19 Indo-Pacific reef-associated fishes (rainbow grouper *Cephalopholis argus*, scrawled butterflyfish *Chaetodon meyeri*, bluespot mullet *Crenimugil* sp. A, humbug damselfish *Dascyllus abudafur*/*Dascyllus aruanus*, areolate grouper *Epinephelus areolatus*, blacktip grouper *Epinephelus fasciatus*, honeycomb grouper *Epinephelus merra*, bluespotted cornetfish *Fistularia commersonii*, cleaner wrasse *Labroides* sp. 1, longface emperor *Lethrinus* sp. A, bluestripe snapper *Lutjanus kasmira*, unicornfishes *Naso brevirosris*, *Naso unicornis* and *Naso vlamingii*, blue-spotted maskray *Neotrygon kuhlii*, largescale mullet *Planiliza macrolepis*, common parrotfish *Scarus psicattus*, crescent grunter *Terapon jarbua*, whitetip reef shark

*Triaenodon obesus*) and three coastal Indo-West Pacific invertebrates (blue seastar *Linckia laevigata*, spiny lobster *Panulirus homarus*, small giant clam *Tridacna maxima*). Heterogeneous and often unbalanced sampling design, paucity of data in a number of cases, and among-species discrepancy in phylogeographic structure precluded any generalization regarding phylogeographic patterns. Nevertheless, the WIO might have been a source of haplotypes in some cases and it also harboured an endemic clade in at least one case. The present survey also highlighted likely cryptic species. This may eventually affect the accuracy of the current checklists of species, which form the basis of some of the recent advances in Indo-West Pacific marine ecology and biogeography.

**Highlights**

► Checklists of reef fish species were used to assess provincial endemism in the Indian Ocean. ► The number of endemic species was highest in the western Indian Ocean. ► Phylogeographic patterns for 22 Indo-Pacific reef-associated species were reviewed and compared. ► Among-species discrepancies in phylogeographic patterns precluded generalization on the evolutionary processes at play. ► A proportion of likely cryptic species was highlighted.

## 1. Introduction

*1.1. Background*

Marine biologists define biogeographic provinces as regions of the ocean characterized by the presence of distinct communities that are thought to have some cohesion at the evolutionary timescale and found to be distinct from adjacent provinces (Spalding et al., 2007; Briggs and Bowen, 2012, and references therein). Thus-called marine biogeographic provinces generally harbour a proportion of endemic species. The extent of biogeographic provinces generally coincides with geologic and/or oceanographic boundaries (Spalding et al., 2007, and references therein; Briggs and Bowen, 2012; Obura, 2012; Veron et al., 2015). Quantitative delineation of biogeographic provinces based on 169 reef fish checklists from across all tropical oceans (Kulbicki et al., 2013a) showed less clear-cut province boundaries, than those described in the above surveys. The delimitation of biogeographic provinces is viewed as important to help establish patterns of connectivity at the community and the population levels, which in turn has relevance in resource management and conservation (Spalding et al., 2007; Obura, 2012; Kulbicki et al., 2013a; Veron et al., 2015).

Ocean currents transport larvae of sedentary marine species, allowing the connection of geographically-distant habitats suitable for adults. Larval transportation also enables sedentary marine species to colonize new habitats (e.g., recent volcanic islands), and to recolonize habitats where the species have been extirpated. Although the direction and intensity of currents may determine levels of contemporary gene flow, a species' geographic structure over evolutionary time is more likely to be influenced by geographic distance between suitable habitats (Crandall et al., 2014). Albeit not a primary determinant of distribution range size, variability in pelagic larval duration may partly contribute to differences in the distribution of reef fish species in the Indo-Pacific, as species with longer larval duration have a greater chance to disperse over habitats unsuitable to adults than those with shorter pelagic larval duration (Scheltema, 1968; Woodland, 1990; Lester et al., 2007; Treml et al., 2012; Luiz et al., 2013). Adult body size is another factor affecting a species' distribution range (Luiz et al., 2013). Larger adults have higher reproductive output and higher-quality offspring (Beldade et al., 2012; Hixon et al., 2014), which enhances the probability of achieving long-distance dispersal. At the intraspecific level, higher larval survival rate potentially translates into higher dispersal ability which in turn translates into potential for higher gene flow between populations. Population genetic differentiation decreases with pelagic larval duration in the tropical Indo-West Pacific fish family Siganidae (Lemer et al. 2007), where geographic range size also increases with pelagic larval duration (Woodland, 1990). Tropical Pacific fishes from families Chaetodontidae, Labridae and Pomacentridae show a similar correlation (Lester and Ruttenberg, 2005; Lester et al., 2007). Selkoe and Toonen (2011) found that pelagic larval duration and genetic differentiation estimates, i.e. S. Wright's *Fst* and the slope of the isolation-by-distance correlation (Rousset, 1997), typically reflect scales of dispersal if the sampling design is adequate. Gene flow counteracts genetic differentiation by natural selection and genetic drift (Slatkin, 1985), thus hampering adaptation to local conditions.

*1.2. The western Indian Ocean (WIO) province*

The present study focuses on the western Indian Ocean (WIO) province, the westernmost of the tropical Indo-West Pacific domain. The WIO province is defined here as the oceanic region bounded by the eastern coast of Africa from Somalia to Mozambique and extending to the East so as to include the Seychelles and Mascarene archipelagoes. This approximately coincides with Obura's (2012) and Spalding et al.'s (2007) definitions of the Western Indian Ocean province. Briggs and Bowen (2012) did not mention the WIO as a particular biogeographic province in terms of endemism or as a diversity hotspot.

The reef fish fauna of the WIO has attracted increased interest from the scientific community. Smith and Heemstra (1986) described a large proportion of the species occurring in South Africa and adjacent waters (Mozambique, Madagascar). Subsequently, a number of country-based checklists have been proposed in this region (e.g. Iles Eparses, the Comores archipelago, Seychelles, Mascarene Islands). These species checklists were used to delineate biogeographic regions (Kulbicki et al., 2013a), and to relate species richness to a number of large-scale environmental factors, including sea-surface temperature, island size and its degree of isolation, distance from the Coral Triangle, and reef area (Parravicini et al., 2013). These studies, along with previous work on reef fish macro-ecology (Santini and Winterbottom, 2002; Bellwood et al., 2012; Kulbicki et al., 2013b; Mouillot et al., 2013), suggest that the WIO has some specific characteristics. In particular, this part of the Indian Ocean holds more species than expected from modeling based on geomorphologic, biogeographic and environmental explanatory variables (Parravicini et al., 2013; Pellissier et al., 2014). This leads us to hypothesize that the WIO represents either a species sink, a center of origin, or a zone of overlap. Possible routes of migration for reef fishes include along the eastern African coast, from the Maldives-Chagos archipelagoes towards the Seychelles, or from temperate southern Africa towards the North-East. Obura (2012) (p. 1) posits that diversity patterns in WIO corals are consistent with the oceanography of the western Indian Ocean, "*reflecting inflow of the South Equatorial Current, maintenance of high diversity in the northern Mozambique Channel, and export from this central region to the north and south, and to the Seychelles and Mascarene islands.*" This amounts to suggesting that the WIO may harbour specific communities that both receive and export species.

*1.3. Comparative phylogeography as an approach to test biogeographic hypotheses*

Community assembly, the sum of the processes leading to the aggregation of species in ecological communities (Emerson and Gillespie 2008), results from intricate interactions at the regional and local scales (Ricklefs, 1987; Leibold et al., 2004; Leibold et al., 2010). Community assembly is affected by the dynamics of diversification, which drives the biodiversity build-up in a regional pool, and by the ecological dynamics within communities, which limits the number of species that coexist (Hubert et al., 2015). Historical biogeography has traditionally focused on the contribution of geological and paleoecological landscape histories on species diversification at the regional scale (Nelson and Platnick, 1981; Myers and Giller, 1988; Ricklefs and Schluter, 1993). For this, the distributions of species have been analyzed to detect coinciding geographical boundaries, which in turn have been linked to known past events (Cracraft and Prum, 1988; Morrone 1994; Morrone and Escalante, 2002). The introduction of genetic markers into historical biogeography

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has led to the development of comparative phylogeography, which aims at uncovering shared patterns in the distribution of intraspecific genetic diversity (Avise, 2000). Phylogeography offers the tools and concepts to study the historical processes that may be responsible for the contemporary geographic distributions of gene genealogies. Thus, phylogeography addresses some of the conservation issues that are at the core of modern marine biogeography. This approach has proven to be informative in exploring evolutionary dynamics of species across biogeographical boundaries and in revealing the temporal dynamics underpinning the coincidence of species distributions (Bermingham and Moritz, 1998; Hubert et al., 2007; Lee and Johnson, 2009). Phylogeographic subdivisions generally corroborate biogeographic provinces based on species lists, with a notable exception at the Indian-Pacific boundary (Briggs and Bowen, 2012). Studying phylogeographic structure (i.e., generally at the intraspecific level) allows one to test hypotheses on geographic connectivity inferred from species endemicity and species richness data (e.g., Obura, 2012; Kulbicki et al., 2013a).

*1.4. Objectives*

The first objective of this study is to determine whether the reef fish assemblages found in the WIO hold specific properties by (1) comparing species richness in the WIO to other provinces in the Indian Ocean, and (2) examining if the general structure of the WIO's reef fish assemblages is different from adjacent regions. Subsequently, one may hypothesize that the WIO is a species sink, or source, or zone of overlap, which may have important consequences in conservation.

Then, we review the phylogeography of coral reef species with wide Indo-West Pacific distribution to: (i) detect possible multiple-species patterns of differentiation for WIO populations; (ii) test the biogeographic hypotheses derived from data on reef fish assemblages. Our emphasis is on coral reef fishes, but comparative information on coral reef invertebrates is also included.

## 2. Materials and Methods

*2.1. Partitioning the Indian Ocean into biogeographic provinces*

Spalding et al. (2007) defined biogeographic regions or provinces based on expert advice and estimated that the resulting classification should apply to a large set of marine flora and fauna. Basing their work on coral species lists, Veron et al. (2015) did a cluster analysis which resulted in the eastern African coast, Madagascar, the Mascarene Islands, the Maldives, and Chagos being grouped together. However, the basic biogeographical units they used were derived from Spalding et al.'s (2007) provinces. Kulbicki et al. (2013a) distinguished biogeographical regions for reef fishes using a dissimilarity matrix to build clusters. These authors found that beyond large biogeographical units, the classification of reef fish into small biogeographic units was unstable. Nevertheless, their study showed that the eastern African reef fish fauna was distinct from that of Madagascar and the Mascarene Islands.

In the present work, provinces in the Indian Ocean were primarily defined according to Kulbicki et al. (2013a). For Australia, we chose the partition proposed by the Atlas of Living Australia (http://regions.ala.org.au/#rt=imcras). The Andaman-Nicobar archipelago, the Cocos

(Keeling) islands and Christmas Island were set apart as this group of islands has a depauperate fauna when compared to the nearby coastal areas of Sumatra and peninsular Malaysia. They are also thought to lie at the boundary between Indian and Pacific ocean faunas as they boast a number of Indian-Pacific geminate species pairs (Hobbs et al., 2009; Hobbs et al., 2014), a peculiarity that has not yet been documented for the coastal areas of Sumatra and peninsular Malaysia. We applied Ward's algorithm of aggregation (Legendre and Legendre, 2012) on reef fish checklists to help confirm biogeographical units defined from the literature (see above). Depending on the distance metric (Supplementary material, Fig, S1), Madagascar grouped either with eastern Africa (from tropical South Africa to Somalia), or with the Seychelles and the Mascarene Islands. Similarly, the Maldives and Chagos clustered together but depending on the distance metric would do so either with India, Sri Lanka and Lakshadweep, or with the Seychelles, Mascarene Islands, and other localities from eastern Africa (Supplementary material, Fig, S1). Therefore, we deemed it difficult to assign checklists to a given biogeographical region or province. The final classification proposed here (Fig. 1) combined the views of Spalding et al. (2007), Kulbicki et al. (2013a), Veron et al. (2015), and the results presented in Supplementary material, Fig. S1. This is intended as a consensus, reached with a certain part of subjectivity. The separation of the eastern African coast from the Madagascar-Seychelles-Mascarene group was a posteriori justified by the results of species-richness analysis.

## 2.2. Analysis of reef fish checklists

Checklists of reef fishes were obtained as detailed previously (Kulbicki et al., 2013a; Parravicini et al., 2013; Pellissier et al., 2014; Supplementary material, Table S1). Checklists of fishes from Australia were obtained from the Atlas of Living Australia website. Only fish species associated with either coral reefs or rocky reefs were retained for our analyses. For each species, size was obtained from FishBase (Froese and Pauly, 2013) and from other sources (see all references under label "General" in Supplementary material, Table S1). A geographic-range index was obtained for each species by counting the number of checklists on which it was found. A total of 289 species lists worldwide were used to build this index. Species lists were grouped into 10 Indian-Ocean provinces (Fig.1). The geographic locations of checklist sites are given in Supplementary material, Table S1.

Species-richness analyses were restricted to reef fish checklists from the Indian-Ocean region. These checklists suggest that the WIO could be split into two sub-provinces, namely the eastern African (EAF) sub-province, and the Madagascar-Seychelles-Mascarene Islands (WII, for Western Indian Ocean Islands) sub-province. As confirmed by the present work, these sub-provinces show distinct patterns of reef fish endemism. Therefore, to explain some of the patterns we considered EAF and WII as separate biogeographic entities. Species were classed into four main categories of endemism according to their geographical range: (i) "local endemics", i.e. species known from only one checklist; (ii) "province endemics", i.e. species known from only two checklists within a province ; (iii) "regional endemics", i.e. species known from three to five checklists; (iv) "non endemics", i.e. species found in six or more checklists. Species found on checklists from non-adjacent biogeographical provinces were not considered endemics.

*2.3. Nucleotide-sequence data*

We compiled mitochondrial nucleotide-sequence datasets for eight species or species complexes that matched the following criteria: (1) having a wide Indo-Pacific distribution; (2) being sampled in both the Indian and the Pacific Oceans; (3) having sampling localities in the Indian Ocean including, but not limited to, the WIO. The following species were selected: the humbug damselfish *Dascyllus abudafur* (Perciformes: Pomacentridae) and its Pacific-Ocean sibling *D. aruanus*, the areolate grouper *Epinephelus areolatus* (Perciformes: Serranidae), the blacktip grouper *E. fasciatus*, the honeycomb grouper *E. merra*, the bluespotted cornetfish *Fistularia commersonii*, the bluestripe snapper *Lutjanus kasmira* (Perciformes: Lutjanidae), the spiny lobster *Panulirus homarus* (Decapoda: Palinuridae), and the crescent grunter, *Terapon jarbua* (Perciformes: Teraponidae). The sequence datasets used for these species were gathered from previous projects of ours (Muths et al., 2012; Borsa et al., 2014; Liu et al., 2014; Muths et al., 2015), together with homologous sequences from the literature (Ward et al., 2005; Kawahara et al., 2008; Gaither et al., 2010; Asgharian et al., 2011; Lakra et al., 2011; Zhang, 2011; Hubert et al., 2012; Jeena, 2013; Zhuang et al., 2013; Alcantara and Yambot, 2014; Lavergne et al., 2014; Lavery et al., 2014; Schoelinck et al., 2014; Senevirathna and Munasinghe, 2014; Jackson et al., 2015), from the CRYOBANK barcode database (http://cryobank.sinica.edu.tw/) and from the GENBANK nucleotide-sequence database (http://www.ncbi.nlm.nih.gov/). New cytochrome *b* gene sequences of 6 *D. aruanus* individuals from Madang, Bismarck Sea were produced according to the methods and protocols detailed in Liu et al. (2014). New *CO1* gene sequences were produced for *E. fasciatus* from Glorieuses Islands, Iles Eparses ($N$ = 1), as well as *T. jarbua* from Iles Eparses ($N$ = 7), Vietnam ($N$ = 3), and Taiwan ($N$ = 10). For this, genomic DNA was extracted using the PureLink® Genomic DNA Mini Kit (Life Technologies, Carlsbad CA) and a set of three primers (*FishF1*, *FishF2* and *FishR1*; Ward et al., 2005) was used to PCR-amplify a 650-bp fragment of the *CO1* gene. Purification of PCR products and sequencing were done by Macrogen (Amsterdam). CRYOBANK and GENBANK accession numbers are provided in Appendix A. Sequences were edited using the 4PEAKS DNA sequence file viewer software (Mekentosj.com, Amsterdam; Griekspoor and Groothuis, 2005).
For each species, sequences were aligned and trimmed to a common length under BIOEDIT ver. 7.1.11 (Hall, 1999).

*2.4. Nucleotide-sequence data analysis*

Median-joining parsimony networks were constructed using NETWORK ver. 4.6.1.3 (Bandelt et al., 1999), based on the matrices of individual nucleotide sequences; the default settings of the program were selected. Nucleotide distances between haplogroups were estimated using MEGA6 (Tamura et al., 2013), based on the most likely nucleotide substitution model according to the Bayesian information criterion. The model chosen for the 1058-bp cytochrome *b* gene fragment in *D. abudafur* / *D. aruanus* was TN93+G (Tamura and Nei, 1993). Although the best model determined by MEGA6 for the 803-bp cytochrome *b* gene fragment in *E. merra* was HKY+G (Hasegawa et al., 1985), the model chosen was the second-best, TN93+G, which contrary to HKY+G, is available for estimating nucleotide distances in MEGA6. The model chosen for the 547-bp *CO1* gene fragment in *P. homarus* was T92+G (Tamura, 1992). The model chosen for the 475-bp

cytochrome *b* gene fragment in *L. kasmira* and for the 551-bp *CO1* gene fragment in *T. jarbua* was K2P (Kimura, 1980).

In all networks, we distinguished haplotypes sampled in the Pacific Ocean from those sampled in the Indian Ocean. Within the latter, we distinguished those sampled in the WIO or from tropical South Africa [even though the latter formally belonged to the nearby southwestern Indian Ocean province (SWI) as defined in Section 2.1] from the rest of the Indian Ocean.

Levels of genetic divergence between populations were estimated with the $\phi_{ST}$ fixation index (Excoffier et al., 1992) computed using ARLEQUIN 3.5 (Excoffier and Lischer, 2010). For estimating $\phi_{ST}$, nucleotide differences were based on the nucleotide substitution model determined as the most likely according to the Bayesian information criterion. Because the HKY model is not implemented in ARLEQUIN, the more inclusive TN93 model was used instead. Significance of $\phi_{ST}$ for all possible pairwise population comparisons was assessed using 1,000 random permutations.

*2.5. Survey of the phylogeographic literature*

The core collection of the Web of Science ver. 2014 (Thomson Reuters, London; http://apps.webofknowledge.com/) was searched for additional articles on the marine phylogeography of the Indo-West Pacific. Combinations of the keywords "Indian", "Pacific" and "phylogeography", or their derivatives, were entered into the "topic" field of the Basic Search tool of the Web of Science. Among the articles thus retrieved, we retained those for which samples from both the Indian and the Pacific oceans were characterized genetically at the mitochondrial locus, including at least one sample from the WIO or tropical South Africa and one sample from the rest of the Indian Ocean. The eligible phylogeographic surveys in reef fishes and invertebrates included the peacock grouper *Cephalopholis argus* (Gaither et al., 2011), the scrawled butterflyfish *Chaetodon meyeri* (DiBattista et al., 2012), the cleaner wrasse *Labroides dimidiatus* (Drew et al., 2008; Sims et al., 2014), the longface emperor *Lethrinus* sp. A (one of the two biological species formerly under *L. olivaceus*; Borsa et al., 2013b), the blue sea star, *Linckia laevigata* (Crandall et al., 2014), the spotted and bluespine unicornfishes, *Naso brevirostris* and *N. unicornis* (Horne et al., 2008), the bignose unicornfish *N. vlamingii* (Klanten et al., 2007), the blue-spotted maskray *Neotrygon kuhlii* (Arlyza et al., 2013), the common parrotfish *Scarus psittacus* (Winters et al., 2010), the whitetip reef shark *Triaenodon obesus* (Whitney et al., 2012), and the small giant clam *Tridacna maxima* (Hui, 2012). An additional taxonomic survey of species in the family Mugilidae (Durand and Borsa, 2015) provided preliminary insights into the phylogeographies of the bluespot mullet, *Crenimugil* sp. A (one of the cryptic species under *Moolgarda seheli*; see Durand et al., 2012), and the largescale mullet, *Planiliza macrolepis* (formerly *Chelon macrolepis*; Durand et al., 2012). While grey mullets are generally not understood as coral reef-associated fishes, the habitats of *Crenimugil* sp. A and *P. macrolepis* include reef-associated mangroves and reef flats and lagoons.

The topology of the phylogenetic trees of *Labroides dimidiatus* mitochondria (Drew et al., 2008; Sims et al., 2014), together with correlated differences in morphology, imply that *L. dimidiatus* consists of two distinctly evolved entities which either have retained morphological and behavioural similarity, or have converged morphologically and behaviourly. It is thus sensible to treat the two forms of *L. dimidiatus* separately. One form, which corresponds to mitochondrial clade 1 of Sims et al. (2014), is distributed from the western Indian Ocean to the western Pacific Ocean;

the other form (clade 2) has so far been sampled exclusively in the southwestern Pacific (Drew et al., 2008; Sims et al., 2014). We examined the phylogeographic structure of the clade 1 form, coined *Labroides* sp. 1 hereafter.

## 3. Results

### 3.1. Species richness patterns inferred from reef fish assemblages

The total number of reef fish species per province (Fig.1A; Supplementary material, Table S2) varied from 612 in the subtropical southeastern Indian Ocean province (SCI), to 1931 in the adjacent Western Australian province (WAU). The WIO province ($N$ = 1826) had nearly as many species as WAU but it was the largest in size of all Indian Ocean provinces. When we split the WIO into two provinces, namely WII and EAF, the WII had 1572 species and the EAF had 1532. The WIO had a number of reef fish species higher than, or equal to that in the East India–Thailand-Malaysia province (EI) ($N$ = 1728), even though the latter is much closer to the Coral Triangle, the epicenter of Indo-West Pacific species richness for reef fishes (Briggs, 2003; Bellwood et al., 2005; Allen and Erdmann, 2012). Species richness in the WII sub-province was also higher than in the northwestern Indian Ocean (NWI) province. No gradient in species richness was observed among provinces.

The number of endemic species was much higher in the WIO than in any other region of the Indian Ocean (Fig. 1B; Supplementary material, Table S2). The WIO also had a highpercentage of endemics (11.2%), close to those of the Red Sea/NWI province (13.4%) or the SWI province (13.3%). The majority of these endemics were regional endemics. No correlation was found between the number of endemics, or their proportion or their level of endemism, and sea-surface temperature, reef area, island size, degree of isolation, or distance to the Coral Triangle (as the assumed epicenter of Indo-West Pacific marine species richness). Within the WIO, endemic species were more abundant and more frequent in the WII than in the EAF. In the latter, the numbers and proportions of local and provincial endemics were among the lowest in the Indian Ocean.

Endemic reef fish species showed among-region variation in size distributions (Supplementary material, Fig. S2). The WIO displayed a heterogeneous composition, with the size distribution of endemic species in the EAF being rather similar to that in SWI. Both EAF and SWI had larger endemic species than the other regions of the Indian Ocean. All the other provinces were dominated by small endemic species (with a peak in size at 5-10 cm). However, the WII also showed a mode at 15-30 cm, like the continental African provinces, suggesting that similar processes may be at play in EAF, WII and South Africa.

### 3.2. Multiple-species phylogeographic survey

In the pair *Dascyllus abudafur* / *D. aruanus*, mitochondrial haplotypes were split into two main haplogroups (Fig. 2) separated by 0.6% net nucleotide distance. One haplogroup comprised all haplotypes sampled in the Indian Ocean, the other one comprised all haplotypes sampled in the Pacific Ocean. Most haplotypes from the Red Sea, all private, formed a sub-lineage nested within the WIO haplogroup. This suggests that Red Sea haplotypes derive from either the WIO, or from a geographically larger population that encompasses the WIO. Population-pairwise $\phi_{ST}$ estimates

(Supplementary material, Table S3) showed no heterogeneity within the WIO ($\phi_{ST}$ not significantly different from 0), while all comparisons between WIO populations and the other Indian-Ocean population, i.e. the Red Sea (RS) ($\phi_{ST}$ = 0.353-0.386) were highly significant, indicating strong restriction in gene flow.

Strong phylogeographic structure was also evident in *Epinephelus areolatus* (Fig. 3). The only haplotype sampled in the WIO clustered with the other Indian-Ocean haplotypes (except those sampled in Western Australia) whereas all Pacific-Ocean haplotypes clustered together with Western Australian haplotypes as a separate haplogroup. Three distinct haplogroups were observed in *E. fasciatus* (Fig. 4A). The longest branch of the network separated haplotypes found exclusively in the WIO and the Red Sea, from the rest, i.e. from the central and eastern Indian Ocean and from the Pacific Ocean. No clear geographic segregation was observed within the latter ensemble, although haplotypes from different geographic origins were apparently not distributed randomly. Most haplotypes from the Coral Triangle clustered around the dominant haplotype, while the second-dominant haplotype mostly comprised haplotypes from the central and eastern Indian Ocean. The mitochondrial haplotype network produced for *E. merra* (Fig. 5A) can be easily superimposed on the map of samples (Fig. 5B), indicating phylogeographic structure. An Indian vs. Pacific phylogeographic partition was evident, where haplogroups from the two oceans were separated by 4.6% nucleotide distance, pointing to a geographic barrier between the two mitochondrial forms. The geographic barrier is located east of the Maldives and west of New Caledonia. Indian-Ocean haplotypes clustered into two distinct haplogroups, each centered around a dominant haplotype in a star-like fashion. One of the two haplogroups exclusively comprised haplotypes sampled from the WIO. The other haplogroup, which appeared to be an offshoot of the first haplogroup, comprised all haplotypes sampled in the Maldives together with a proportion of WIO haplotypes. In other words, the Maldives haplogroup was nested within the WIO haplogroup, suggesting past asymmetrical gene flow from the WIO, or from a geographically larger population encompassing the WIO, towards the central Indian Ocean. Population-pairwise $\phi_{ST}$ estimates (Supplementary material, Table S4) indicated substantial heterogeneity within the WIO (with $\phi_{ST}$ up to 0.344) and highly significant differences with the only other sample from the Indian Ocean, i.e. the Maldives (MAL) (average $\phi_{ST}$ = 0.269±0.125).

No obvious phylogeographic structure was observed in *Fistularia commersonii*, although all haplotypes from Baja California clustered as a single branch of the network and the two haplotypes from Reunion Island (WIO) were distant from the rest of the network (Fig. 6).

*Lutjanus kasmira* haplotypes were organized as a star-like network with a dominant central haplotype that was shared between the WIO, the central and eastern Indian Ocean, and the Pacific Ocean. Little heterogeneity in haplotype frequencies was visible overall, except for the occurrence of a derived, predominantly Pacific-Ocean haplogroup (Fig. 7). Population-pairwise $\phi_{ST}$ estimates (Supplementary material, Table S5) singled out the Marquesas population ($\phi_{ST}$ = 0.499-0.627) but otherwise showed only weak differentiation, with population-pairwise $\phi_{ST}$ values ranging from 0 to 0.077. The $\phi_{ST}$ estimates between the WIO and the other Indian-Ocean populations ranged from 0 to 0.050 and were hardly significantly different from 0 considering adjustment for multiple tests (Rice, 1989).

Two major haplogroups were observed in *Panulirus homarus*, separated by 5.8% net nucleotide distance at the *CO1* locus (Fig. 8A). While the dominant haplogroup included haplotypes

from the whole distribution of *Panulirus homarus*, the second haplogroup (delineated by a dashed ellipse on Fig.8A) comprised haplotypes from the WIO exclusively. The WIO haplogroup, which corresponds to morphological subspecies *P. h. rubellus* (Lavery et al., 2014), was discarded for $\phi_{ST}$ analysis. At the Indian-Ocean scale, the dominant haplogroup showed no obvious structure, while the $\phi_{ST}$ analysis distinguished the northwestern Indian-Ocean samples from all the rest ($\phi_{ST}$ = 0.108 ± 0.106) (Supplementary material, Table S6).

Three main haplogroups were observed in *Terapon jarbua* (Fig. 9). A haplogroup that included all haplotypes sampled in Juan de Nova, WIO, together with a haplotype from the Red Sea, was separated from the rest of the nucleotide sequence dataset by 7.6% net nucleotide distance at the *CO1* locus. Within the latter, a predominantly Indian haplogroup was separated from a predominantly Pacific haplogroup by 2.6% net nucleotide distance. High levels of genetic differentiation were estimated between populations, but no clear geographic pattern was apparent. The reason for this was the geographically widespread occurrence of the three haplogroups, in variable proportions. The Iles Eparses sample was strongly differentiated from the other populations ($\phi_{ST}$ = 0.472-0.628; Supplementary material, Table S7) because all of its individuals harboured the Juan de Nova haplotype which was not sampled elsewhere except in the Red Sea.

### 3.3. Additional cases drawn from the phylogeographic literature

Fourteen additional cases were investigated (Supplementary material, Figs. S3-S14; Durand and Borsa, 2015), eleven of which concerned reef-associated bony fishes. In *Cephalopholis argus*, two major haplogroups were observed, with an Indian vs. Pacific phylogeographic partition. However, the 'Indian' haplogroup also harboured haplotypes sampled in the Pacific Ocean and vice versa, suggesting either incomplete lineage sorting, or secondary contact between the two oceans (Gaither et al., 2011). Haplotypes sampled in the WIO were nested within the 'Indian' haplogroup exclusively, suggesting that 'Pacific' haplotypes under Gaither et al.'s (2011) overlap hypothesis have not reached the WIO (Supplementary material, Fig. S3). In *Chaetodon meyeri* (Supplementary material, Fig. S4), only moderate Indian vs. Pacific phylogeographic partition was observed, suggesting weak differentiation between populations from the two oceans. In *Labroides* sp. 1, a loose Indian vs. Pacific genetic-differentiation was visible (Supplementary material, Fig. S5), compatible with isolation by distance (Wright, 1942). This is the hypothesis favoured by Sims et al. (2014) on the basis of observed correlation-between $\phi_{ST}$ and geographic distance. From the limited dataset available in *Lethrinus* sp. A (Supplementary material, Fig. S6), we observed a clear Indian vs. Pacific phylogeographic partition. In *Linckia laevigata* (Supplementary material, Fig. S7), two major clusters of haplotypes were observed, one of which included a few WIO haplotypes. This cluster included a substantially higher proportion of Indian-Ocean haplotypes than the other cluster, which was predominantly Pacific. The dominant WIO haplotypes occupied a central position in the network, implying that one, the other, or possibly both, of the two major haplogroups may derive from an ancestral WIO stock. No phylogeographic structure was observed in *Naso brevirostris, N. unicornis and N. vlamingii* (Supplementary material, Figs. S8-S10). No phylogeographic structure was visible from the haplotype network in *Scarus psittacus* (Supplementary material, Fig. S12) although peripheral genetic differentiation has been reported. Genetic differences in *Triaenodon obesus* indicated geographic isolation between populations either side of the Indo-Pacific barrier

(Supplementary material, Fig. S13). Strong phylogeographic structure was observed in *Tridacna maxima* across the Indo-Pacific barrier and within the Indian Ocean (Supplementary material, Fig. S14). Within the Indian Ocean, three distinct *T. maxima* clades were evident from maximum-likelihood analysis. One clade corresponded to Hui's (2012) clade 5, exclusively found in the WIO; a second clade corresponded to Hui's (2012) clade 2, exclusive to the eastern Indian Ocean and the Sunda Shelf; a third clade corresponded to Hui's (2012) clades 4 and 6 from the WIO and the Red Sea (Supplementary material, Fig. S14). Similarly strong, parapatric geographic structure was observed in *Neotrygon kuhlii*, where 7 clades had been sampled by Arlyza et al. (2013), all from the sole Coral Triangle region (Supplementary material, Fig. S11). The two *Neotrygon kuhlii* haplotypes sampled from the WIO formed a lineage distinct from all other sites sampled in the Indian Ocean and on the Indian-Ocean side of the Coral Trangle.

In addition, little genetic differentiation was evident in *Crenimugil* sp. A, where the same mitochondrial haplotype was sampled from the WIO to the southwestern Pacific. However, a distinct sub-clade from the northwestern Indian Ocean was observed (Durand and Borsa, 2015). In *Planiliza macrolepis*, haplotypes sampled in the Maldives and further east belonged to a clade distinct from haplotypes sampled in the western and northwestern Indian Ocean (see figures 1A and 4E of Durand and Borsa, 2015).

## 4. Discussion

### 4.1. Species diversity and endemism patterns

The WIO showed higher reef-fish species richness than provinces geographically closer to the Coral Triangle, the epicenter of species richness in the Indo-West Pacific, for reef fishes (Briggs, 2003; Bellwood et al. 2005; Allen and Erdmann, 2012) and more generally for the coastal marine fauna and flora (Sanciangco et al., 2013). This was unexpected for several reasons. First, the number of species usually decreases as distance from the biodiversity center increases (Briggs, 2003; Parravicini et al., 2013). Pellissier et al. (2014) proposed that this is in part due to evolutionary history, with regions close to the assumed diversity center also being close to coral refuges during cold climate episodes. In addition, the WII has many small islands which typically harbour low species richness, because species richness decreases with island size (Parravicini et al., 2013). One would therefore expect fewer species in the WII than on the continental shelf of Africa (EAF and SWI). We observed the opposite.

The number of endemic species in the WIO was higher than in the northwestern part of the Indian Ocean (NWI province), as already shown by Kulbicki et al. (2013a), despite the fact that NWI has the highest rate of local endemism in the Indo-Pacific after Easter Island and Hawaii (Allen, 2008). We do not know if these endemic species are of local origin or if they are relicts from wider, past distributions. Dedicated phylogeographic surveys of these endemic species, that would also examine phylogenetically related species would help uncover their origin(s). The analysis of body-length distributions nevertheless provided some interesting information. Along the western shores of the Indian Ocean (NWI, EAF, SWI), endemic species were larger than elsewhere in the Indian Ocean. This is to be related to a similar situation in Hawaii where local endemics are larger than endemics in other parts of the Pacific Ocean (DeMartini and Friedlander, 2004). Hawaii, just as the

eastern African coast, lies at the edge of its realm. Species size is a primary determinant of species distribution and large species tend to be better dispersers and better colonizers than small species (Luiz et al., 2013). As a consequence, larger species are more frequent in assemblages on small or remote islands, just as in the present case off the eastern African coast. In the other part of the WIO, WII endemics are, in majority, small species, although with a second mode of larger species. This suggests a complex origin for endemics. Small-size endemics dominate in the northwestern part of the Indian Ocean, which suggests that the continental or island coastal type was not a major determinant of the distribution of sizes. Both the Red Sea and Madagascar held coral reef refuges during the last 3 million years (Pellissier et al., 2014). These refuges could have sheltered small species which subsequently may have not re-colonized a wide range and therefore became endemic.

*4.2. Variability in phylogeographic structure*

As shown by the case studies used for the present review, geographic sampling design in phylogeographic surveys of Indo-West Pacific reef species was mostly uneven and unbalanced. Even the aggregative survey of *Linckia laevigata* by Crandall et al. (2014), presented (p. 399) as "*one of the most geographically comprehensive genetic studies of any Indo-Pacific species to date*", had gaps in its sampling design, with the western and central Indian-Ocean regions being noticeably under-sampled. This, together with the low number of comprehensive case studies available, are weaknesses of the present multiple-species phylogeographic survey.

Remarkable variability in phylogeographic patterns and in intensity of genetic differentiation was observed. In several cases (*Dascyllus abudafur/D. aruanus*, *Epinephelus areolatus, E. merra*, *Lethrinus* sp. A, *Tridacna maxima*), a marked Indian vs. Pacific partition was observed, suggesting geminate species formed by allopatry on either side of the Indo-Pacific barrier. Weaker Indian vs. Pacific phylogeographic partition was apparent in *Cephalopholis argus*, *Labroides* sp. 1 and *Linckia laevigata*, which could result either from secondary contact and incomplete re-homogenization across the Indo-Pacific barrier (*C. argus*; Gaither et al., 2011), incomplete lineage sorting, or isolation by distance. In all three cases, as in a number of other cases from the phylogeographic literature reviewed by Carpenter et al. (2011) and Gaither and Rocha (2013), the phylogeographic structure was consistent with incipient genetic divergence of Indian vs. Pacific populations. Among reef-associated animals, this also includes the neritid snail *Nerita albicilla* (Crandall et al. 2008) and the bigscale soldierfish *Myripristis berndti* (Muths et al., 2011). Another phylogeographic break located in the mid-Indian Ocean was observed in both *E. fasciatus* and *Planiliza macrolepis*. In these and several of the above cases, the western Indian Ocean populations showed phylogeographic originality compared to the eastern Indian Ocean populations, presumably because of the geographic-isolation effect of the mid-Indian Ocean oceanic barrier west of the Lakshadweep-Maldives-Chagos archipelagoes.

Little phylogeographic structure was evident in *Fistularia commersonii*, where the dominant haplotypes were present in all regions sampled. No phylogeographic structure was detected in seven other species, namely *Chaetodon meyeri*, *Crenimugil* sp. A, *Lutjanus kasmira*, *Naso brevirostris*, *N. unicornis*, *N. vlamingii*, and *Panulirus homarus* (*P. h. rubellus* and the Marquesas sub-lineage excluded). Among reef fishes, *Chaetodon ornatissimus* (the sister-species of *C. meyeri*; DiBattista et

al., 2012), *F. commersonii*, *L. kasmira* and *N. lituratus* (congeneric with *N. brevirostris* and *N. vlamingii*, and sister species to *N. unicornis*; Klanten et al., 2004) have pelagic larval durations >30 d, i.e. longer than the other reef fishes considered in this review (see Supplementary material, Table S8). The *Dascyllus abudafur*/*D. aruanus* species pair, which had the highest levels of population differentiation, is also among those with the shortest pelagic larval duration (18.6-24.3 d). However, this handful of case studies is not sufficient to draw conclusions on a possible effect of pelagic larval duration on phylogeographic structure in Indian-Ocean reef fishes. Complex phylogeographic structure was uncovered in *Terapon jarbua*, where the WIO, the northwestern Indian Ocean, and the Coral Triangle might be centers of diversification. One may suspect that *T. jarbua* actually consists of two, perhaps three biological species whose geographic distributions partly overlap. This possibility cautions against interpreting $\phi_{ST}$ estimates without prior sorting of samples by species.

The relative lack of consistency in the phylogeographic structures apparent from the 22 cases that we examined precludes any generalization about the evolutionary processes that have shaped the phylogeographic structure of species in the WIO. More research is certainly necessary to possibly draw generalities, and possibly alter this conclusion. Nevertheless, novel information arose from the present review. For instance, the observed phylogeographic structures in some species (*D. abudafur*, *E. merra*, *Linckia laevigata*) tended to designate the WIO as a possible source of haplotypes. The WIO also harboured endemic clades in *Panulirus homarus* (*P. h. rubellus*) and in *Tridacna maxima*, suggesting either long-term past geographic isolation or unique ecological characteristics suitable to the latter.

*4.3. Need for taxonomic updates*

Previous phylogeographic work has shown that several widespread Indo-West Pacific reef species actually consist of distinct evolutionary units that qualify as separate species (e.g. Wörheide et al., 2008; Fauvelot and Borsa, 2011; Vogler et al., 2012; Borsa et al. 2013a; Hoareau et al., 2013;Huelsken et al., 2013). This is also the case of *D. aruanus* which is now recognized to consist of the geminate Indo-Pacific species pair *D. abudafur*/*D. aruanus* (Borsa et al., 2014), and of *Labroides dimidiatus* (Sims et al., 2014; see section 2.4), whose pattern of cryptic speciation parallels that of *Lethrinus olivaceus* (Borsa et al., 2013b). *L. olivaceus* consists of two biological species provisionally designated as *Lethrinus* sp. A in the Indo-West Pacific, and *Lethrinus* sp. B, from the western and central Pacific (Borsa et al., 2013b). The subspecies of *P. homarus* endemic to the WIO, *P. h. rubellus*, should similarly be raised to the species status, because of concurring morphological and genetic distinctness (Lavery et al., 2014). Hypothesizing that the distinction of the *rubellus* form pertains to intraspecific variation does not hold given the long pelagic larval stage in *P. homarus* which lasts up to several months, as in other *Panulirus* species (Goldstein et al., 2008; Phillips and Matsuda, 2011). It has also been argued that the western and northwestern-Indian Ocean clade of *Planiliza macrolepis* represents a species distinct from the populations east of the mid-Indian Ocean barrier, for which the provisional species name *Planiliza* sp. H has been proposed (Durand and Borsa, 2015). The present study highlights additional cases where the current taxonomy of species may not reflect their evolutionary history, thus flagging potential cryptic species. For instance, *E. areolatus, E. merra* and *Lethrinus* sp. A may each consist of a pair of geminate Indian / Pacific

species. Phylogeographic patterns in *E. fasciatus* (present work) lead us to similarly hypothesize two cryptic species separated by the mid-Indian Ocean barrier. One of the potential biological species under *Terapon jarbua* appears to be endemic to the western and northwestern Indian Ocean. Taxonomic investigations of *Neotrygon kuhlii* and *Tridacna maxima* are also warranted.

Based on preliminary barcoding surveys, the occurrence of cryptic species might well occur in up to 30%-60% of Indo-West-Pacific reef fishes (Zemlak et al., 2009; Hubert et al., 2012). If this is confirmed by further taxonomic investigations, the species checklists at the basis of a number of recent advances in the biogeography and ecology of reef fishes (e.g. Bellwood et al., 2005; Bellwood et al., 2012; Kulbicki et al., 2013a; Mouillot et al., 2013; Parravicini et al., 2013; Pelissier et al., 2014) will likely become partly obsolete. Consequently, the delineation of biogeographic provinces evoked in the present paper might also have to be revised. However, if most of the additional cryptic species result from thus-far neglected Indian vs. Pacific differences, it is unlikely that the partition into biogeographic provinces within each ocean will change drastically from the current one.

**Authors' contributions**

Designed the study: PB, WJC, JDD, MK. Contributed samples / materials / analysis tools: PB, WJC, JDD, MK, GMT, DM. Analyzed and interpreted the data: PB, JDD, MK, DM. Wrote the paper: PB, NH, MK. All authors read and approved the final manuscript.

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**Appendix A. Database accession numbers for nucleotide sequences**

CRYOBANK accession number for *E. fasciatus* was ASIZP0800173. GENBANK accession numbers for *D. abudafur / D. aruanus* were KF754733-KF754795 and 6 additional cytochrome *b* gene sequences from Madang (GENBANK nos. KT258989-KT258994); those for *E. areolatus* were DQ107866-DQ107870, GU324187, FJ237756-FJ237763, HQ149838, HQ913572, HQ945841, JN208569-JN208572, JX674967-JX674969, KC593374, KC970469, KF009590-KF009591, KJ130964-KJ130965, KJ202151-KJ202152, KJ607969, KM077914, KP058460 and NC_020785; those for *E. fasciatus* were DQ107873-DQ107876, EU392207-EU392208, EU600145-EU600146, FJ459561-FJ459563, GU805082, JQ431717, JX093907, JX674994-JX674996, KC970470, KF009593, KF489582, KF714942, KF8029400, KJ130967-KJ130969, KJ202153-KJ202155 and KJ594972-KJ594972, and an additional *CO1* gene sequences from Glorieuses Islands (GENBANK no. KT258995); those for *E. merra* were AY78644, JN255254–JN255345 and JN545057–JN545096; those for *F. commersonii* were EF607383- EF607384, JF493489, JQ349978- JQ349979, JQ431740-JQ431741, KP053133-KP053237, KP260463 and NC_010274; those for *L. kasmira* were JF514414–JF514500 and FJ754049–FJ754133; those for *P. homarus* were JN418937, JN542716, JN591360, JQ229883-JQ229888, JQ229910-JQ229926, KC959890-KC959891, KF548571, KF715528-KF715550, KF715552, and KJ802748-KJ802782; those for *T. jarbua* included EU871691, EU871692, FJ237549, FJ265859, HQ149959-HQ149961, JF494663-JF494666, JN021254, JN021255, JQ342095-JQ342111, JX260979, KC241987, KC417308, KC774674, KC970423, KF009671, KF268188, KF268189, KJ466137 and KJ466138, and 20 additional *CO1* gene sequences from Iles Eparses (GENBANK nos. KT231909-KT231915), Vietnam (GENBANK nos KT231926-KT231928) and Taiwan (GenBank nos KT231916- KT231925). Sequences nos. EU541344, HM909801 and KJ130970 labeled "*Epinephelus fasciatus*" were discarded because they were found outside the *E. fasciatus CO1* haplotype cluster in a preliminary Neighbour-Joining tree of serranid barcodes, hence were thought to be possibly from misidentified specimens.

**Appendix B. Supplementary data**

Supplementary data related to this article can be found at http://dx.doi.org/10.1016/j.actao.2015.xxx

**References**

Alcantara, S.G., Yambot A.V., 2014. DNA barcoding of commercially important grouper species (Perciformes, Serranidae) in the Philippines. Mitochondrial DNA. doi: 10.3109/19401736.2014.958672

Allen, G.R., 2008. Conservation hotspots of biodiversity and endemism for Indo-Pacific coral reef fishes. *Aquat. Conserv. Mar. Freshw. Ecosyst.* 18, 541-556.

Allen, G.R., Erdmann, M.V., 2012. Reef fishes of the East Indies, vols. I-III. Tropical Reef Research,

Perth, 1292 p.

Arlyza, I.S., Shen, K.-N., Durand, J.-D., Borsa, P., 2013. Mitochondrial haplotypes indicate parapatric-like phylogeographic structure in blue-spotted maskray (*Neotrygon kuhlii*) from the Coral Triangle region. J. Hered. 104, 725-733. doi:10.1093/jhered/est044

Asgharian, H., Sahafi, H.H., Ardalan, A.A., Shekarriz, S., Elahi, E., 2011. Cytochrome c oxidase subunit 1 barcode data of fish of the Nayband National Park in the Persian Gulf and analysis using meta-data flag several cryptic species. Mol. Ecol. Resour. 11, 461-472.

Avise, J.C., 2000. Phylogeography: the history and formation of species. Harvard University Press, Cambridge MA, 447 p.

Bandelt, H.J., Forster, P., Röhl, A., 1999. Median-joining networks for inferring intraspecific phylogenies. Mol. Biol. Evol. 16, 37–48.

Beldade, R., Holbrook, S.J., Schmitt, R.J., Planes, S., Malone, D., Bernardi, G., 2012. Larger female fish contribute disproportionately more to self-replenishment. Proc. Roy. Soc. B Biol. Sci. 279: 2116–2121.

Bellwood, D.R., Hughes, T.P., Connolly, S.R., Tanner, J., 2005. Environmental and geometric constraints on Indo-Pacific coral reef biodiversity. Ecol. Lett. 8, 643–651. doi: 10.1111/j.1461-0248.2005.00763.x

Bellwood, D.R., Renema, W., Rosen, B.R., 2012. Biodiversity hotspots, evolution and coral reef biogeography: a review. In Gower, D.J., Johnson, K., Richardson, J., Rosen, B.R., Ruber, L., Williams, S.T. (eds.), Biotic evolution and environmental change in Southeast Asia. Cambridge University Press, Cambridge, pp. 216-245.

Bermingham, E., Moritz, C., 1998. Comparative phylogeography: concepts and applications. Mol. Ecol. 7, 367–369.

Borsa, P., Arlyza, I.S., Chen, W.-J., Durand, J.-D., Meekan, M.G., Shen, K.-N., 2013a. Resurrection of New Caledonian maskray *Neotrygon trigonoides* (Myliobatoidei: Dasyatidae) from synonymy with *N. kuhlii*, based on cytochrome-oxidase I gene sequences and spotting patterns. C. R. Biol. 336, 221-232. doi: 10.1016/j.crvi.2013.05.005

Borsa, P., Hsiao, D.-R., Carpenter, K.E., Chen, W.-J., 2013b. Cranial morphometrics and mitochondrial DNA sequences distinguish cryptic species of the longface emperor (*Lethrinus olivaceus*), an emblematic fish of the Indo-West Pacific coral reefs. C. R. Biol. 336, 505-514. doi: 10.1016/j.crvi.2013.09.004

Borsa, P., Sembiring, A., Fauvelot, C., Chen, W.-J., 2014. Resurrection of Indian-Ocean humbug damselfish, *Dascyllus abudafur* (Forsskål) from synonymy with its Pacific-Ocean sibling, *Dascyllus aruanus* (L.). C. R. Biol. 337, 709-716. doi: 10.1016/j.crvi.2014.09.001

Briggs, J.C., 2003. Marine centres of origin as evolutionary engines. J. Biogeogr. 30, 1-18.

Briggs, J.C., Bowen, B.W., 2012. A realignment of marine biogeographic provinces with particular reference to fish distributions. J. Biogeogr. 39, 12–30. doi:10.1111/j.1365-2699.2011.02613.x

Carpenter, K.E., Barber, P.H., Crandall, E.D., Ablan-Lagman, M.C.A., Ambariyanto, Mahardika, G.N., Manjaji-Matsumoto, B.M., Juinio-Meñez, M.A., Santos, M.D., Starger, C.J., Toha, A.H.A., 2011. Comparative phylogeography of the Coral Triangle and implications for marine management. J. Mar. Biol. 2011, 14.

Cracraft, J., Prum, R.O., 1988. Patterns and processes of diversification: speciation and historical congruence in some neotropical birds. Evolution 42, 603-620.

Crandall, E.D., Frey, M.A., Grosberg, R.K., Barber, P.H., 2008. Contrasting demographic history and phylogeographical patterns in two Indo-Pacific gastropods. Mol. Ecol. 17, 611–626.

Crandall, E.D., Treml, E.A., Liggins, L., Gleeson, L., Yasuda, N., Barber, P.H., Wörheide, G., Riginos, C., 2014. Return of the ghosts of dispersal past: historical spread and contemporary gene flow in the blue sea star *Linckia laevigata*. Bull. Mar. Sci. 90, 399–425. doi.org/10.5343/bms.2013.1052

DeMartini, E.E., Friedlander, A.M., 2004. Spatial patterns of endemism in shallow-water reef fish populations of the Northwestern Hawaiian Islands. Mar. Ecol. Prog. Ser. 271, 281-296.

DiBattista, J.D., Rocha, L.A., Craig, M.T., Feldheim, K.A., Bowen, B.W., 2012. Phylogeography of two closely related Indo-Pacific butterflyfishes reveals divergent evolutionary histories and discordant results from mtDNA and microsatellites. J. Hered. 103, 617–629. doi:10.1093/jhered/ess056

Drew, J., Allen, G.R., Kaufman, L., Barber, P.H., 2008. Endemism and regional color and genetic differences in five putatively cosmopolitan reef fishes. Conserv. Biol. 22, 965-975.

Durand, J.-D., Borsa, P., 2015. Mitochondrial phylogeny of grey mullets (Acanthopterygii: Mugilidae) suggests high proportion of cryptic species. C. R. Biol. 338, 266-277. doi: 10.1016/j.crvi.2015.01.007

Durand, J.-D., Chen, W.-J., Shen, K.-N., Fu, C., Borsa, P., 2012. Genus-level taxonomic changes implied by the mitochondrial phylogeny of grey mullets (Teleostei: Mugilidae). C. R. Biol. 335, 687–697.

Emerson, B.C., Gillespie, R.G., 2008. Phylogenetic analysis of community assembly and structure over space and time. Trends Ecol. Evol. 23, 519-530.

Excoffier, L., Lischer, H.E. L., 2010. Arlequin suite ver 3.5: A new series of programs to perform population genetics analyses under Linux and Windows. Mol. Ecol. Resour. 10, 564-567.

Excoffier, L., Smouse, P.E., Quattro, J.M., 1992. Analysis of molecular variance inferred from metric distances among DNA haplotypes - Application to human mitochondrial-DNA restriction data. Genetics 131, 479-491.

Fauvelot, C., Borsa, P., 2011. Patterns of genetic isolation in narrow-barred Spanish mackerel (*Scomberomorus commerson*) across the Indo-West Pacific. Biol. J. Linn. Soc. 104, 886-902.

Froese, R., Pauly, D., 2013. FishBase, World Wide Web electronic publication, www.fishbase.org, version (12/2013).

Gaither, M.R, Bowen, B.W., Bordenave, T.R., Rocha, L.A., Newman, S.J., Gomez, J.A., van Herwerden, L., Craig, M.T., 2011. Phylogeography of the reef fish *Cephalopholis argus* (Epinephelidae) indicates Pleistocene isolation across the Indo-Pacific Barrier with contemporary overlap in the Coral Triangle. BMC Evol. Biol. 11, 189.

Gaither, M.R. , Rocha, L.A., 2013. Origins of species richness in the Indo-Malay-Philippine biodiversity hotspot: evidence for the centre of overlap hypothesis. J. Biogeogr. 40, 1638-1648.

Gaither, M.R., Toonen, R.J., Robertson, D.R., Planes, S., Bowen, B.W., 2010. Genetic evaluation of marine biogeographical barriers: perspectives from two widespread Indo-Pacific snappers (*Lutjanus kasmira* and *Lutjanus fulvus*). J. Biogeogr. 37, 133–147.

Goldstein, J.S., Matsuda, H., Takenouchi, T., Butler, M.J.4, 2008. The complete development of larval Caribbean spiny lobster, *Panulirus argus*, in culture. J. Crustacean Biol. 28, 306–327.

Griekspoor, A., Groothuis, T., 2005. 4PEAKS: a program that helps molecular biologists to visualize and edit their DNA sequence files (http://mekentosj.com/4peaks/).

Hall, T.A., 1999. BioEdit: a user-friendly biological sequence alignment editor and analysis program

for Windows 95/98/NT. Nucl. Acids Symp. Ser. 41, 95-98.

Hasegawa, M., Kishino, H., Yano, T., 1985. Dating of the human-ape splitting by a molecular clock of mitochondrial DNA. J. Mol. Evol. 22, 160–74. doi:10.1007/BF02101694

He, B., Lai, T., Peng, Z., Wang, X., Pan,L., 2013. Complete mitogenome of the areolate grouper *Epinephelus areolatus* (Serranidae, Epinephelinae). Mitoch. DNA 24, 498-500.

Hixon, M.A., Johnson, D.W., Sogard, S.M., 2014. BOFFFFs: on the importance of conserving old-growth age structure in fishery populations. ICES J. Mar. Sci. 71, 2171–2185. doi:10.1093/icesjms/fst200

Hoareau, T.B., Boissin, E., Paulay, G., Bruggemann, J.H., 2013. The Southwestern Indian Ocean as a potential marine evolutionary hotspot: perspectives from comparative phylogeography of reef brittle-stars. J. Biogeogr. 40, 2167-2179. doi:10.1111/jbi.12155

Hobbs, J.-P.A., Frisch, A.J., Allen, G.R., Van Herwerden, L., 2009. Marine hybrid hotspot at Indo-Pacific biogeographic border. Biol. Lett. 5, 258-261.

Hobbs, J.-P.A., Newman, S.J., Mitsopoulos, G.E.A., Travers, M.J., Skepper, C.L., Gilligan, J.J., Allen, G.R., Choat, H.J., Ayling, A.M., 2014. Checklist and new records of Christmas Island fishes: the influence of isolation, biogeography and habitat availability on species abundance and community composition. Raffles B. Zool. suppl. 30, 184-202.

Horne, J.B., van Herwerden, L., Choat, J.H., Robertson, D.R., 2008. High population connectivity across the Indo-Pacific: Congruent lack of phylogeographic structure in three reef fish congeners. Mol. Phyl. Evol. 49, 629-638.

Hubert, N., Calcagno, V., Etienne, R.S., Mouquet, N., 2015. Metacommunity speciation models and their implication in the understanding of diversification. Ecol. Lett. 18, 864-881. doi: 10.1111/ele.12458 .

Hubert, N., Duponchelle, F., Nuñez Rodiguez, J., Garcia Davila, C., Paugy, D., Renno, J. F., 2007. Phylogeography of the piranha genera *Serrasalmus* and *Pygocentrus*: implications for the diversification of the neotropical ichthyofauna. Mol. Ecol. 16, 2115-2136.

Hubert, N., Meyer, C.P., Bruggemann, H.J., Guérin, F., Komeno, R.J.L., Espiau, B., Causse, R., Williams, J.T., Planes, S., 2012. Cryptic diversity in Indo-Pacific coral-reef fishes revealed by DNA-barcoding provides new support to the Centre-of-Overlap hypothesis. PloS One 7, e28987.

Huelsken, T., Keyse, J., Liggins, L., Penny, S., Treml, E.A., Riginos, C., 2013. A novel widespread cryptic species and phylogeographic patterns within several giant clam species (Cardiidae: *Tridacna*) from the Indo-Pacific Ocean. PLoS One 8, e0080858.

Hui, M., 2012. Connectivity and evolution of giant clams (Tridacnidae): a molecular genetic approach. PhD dissertation, Universität Bremen, Bremen, xv+85 p.

Jackson, A.M., Tenggardjaja, K., Perez, G., Azzurro, E., Golani, D., Bernardi, G., 2015. Phylogeography of the bluespotted cornetfish, Fistularia commersonii: a predictor of bioinvasion success? Mar. Ecol., in press. doi: 10.1111/maec.12249

Jeena, N.S., 2013. Genetic divergence in lobsters (Crustacea: Palinuridae and Scyllaridae) from the Indian EEZ. PhD dissertation, Cochin University of Science and Technology, Kochi, xviii+238 p.

Kawahara R., Miya, M., Mabuchi, K., Lavoue, S., Inoue, J.G., Satoh, T.P., Kawaguchi A., Nishida, M., 2008. Interrelationships of the 11 gasterosteiform families (sticklebacks, pipefishes, and their relatives): A new perspective based on whole mitogenome sequences from 75 higher teleosts. Mol. Phyl. Evol. 46, 224–236.

Kimura, M., 1980. A simple method for estimating evolutionary rate of base substitutions through comparative studies of nucleotide sequences. J. Mol. Evol. 16, 111-120.

Klanten, S.O., Choat, J.H., van Herwerden, L., 2007. Extreme genetic diversity and temporal rather than spatial partitioning in a widely distributed coral reef fish. Mar. Biol. 150, 659–670. doi: 10.1007/s00227-006-0372-7

Klanten, S.O., van Herwerden, L., Choat, J.H., Blair, D., 2004. Patterns of lineage diversification in the genus *Naso* (Acanthuridae). Mol. Phyl. Evol. 32, 221–235.

Kulbicki, M., Parravicini, V., Bellwood, D.R., Arias-Gonzàlez, E., Chabanet, P., Floeter, S.R., Friedlander, A., McPherson, J., Myers, R.E., Vigliola, L., Mouillot, D., 2013a. Global biogeography of reef fishes: A hierarchical quantitative delineation of regions. PLoS One 8, e81847.

Kulbicki, M., Vigliola, L., Wantiez, L., Floeter, S., Hubert, N., Myers, R., 2013b. The biogeography of Chaetodontidae, a model for reef fishes ? In Berumen, M., Pratchett, M. (eds.), The biology and ecology of butterfly-fishes. Taylor & Francis, Boca Raton FL, pp. 70-106.

Lakra, W.S., Verma, M.S., Goswami, M., Lal, K.K., Mohindra, V., Punia, P., Gopalakrishnan, A., Singh, K.V., Ward, R.D., Hebert, P., 2011. DNA barcoding Indian marine fishes. Mol. Ecol. Resour. 11, 60-71.

Lavergne, E., Calvès, I., Meistertzheim, A.L., Charrier, G., Zajonz, U., Laroche, J., 2014. Complex genetic structure of a euryhaline marine fish in temporarily open/closed estuaries from the wider Gulf of Aden. Mar. Biol. 161, 1113–1126. doi: 10.1007/s00227-014-2404-z

Lavery, S.D., Farhadi, A., Farahmand, H., Chan, T.-Y., Azhdehakoshpour, A., Thakur, V., Jeffs, A.G., 2014. Evolutionary divergence of geographic subspecies within the scalloped spiny lobster *Panulirus homarus* (Linnaeus 1758). PLoS One 9, e97247. doi:10.1371/journal.pone.0097247

Lee, J.B., Johnson, J.B., 2009. Biogeography of the livebearing fish Poecilia gillii in Costa Rica: are phylogeographical breaks congruent with fish community boundaries? Mol. Ecol. 18, 4088-4101.

Legendre, P., Legendre, L., 2012. Numerical ecology, 3rd english edn. Elsevier, Amsterdam, 990 p.

Leibold, M.A., Economo, E.P., Peres-Neto, P., 2010. Metacommunity phylogenetics: separating the roles of environmental filters and historical biogeography. Ecol. Lett. 13, 1290-1299.

Leibold, M.A., Holyoak, M., Mouquet, N., Amarasekare, P., Chase, J.M., Hoopes, M.F., Holt, R.D., Shurin, J.B., Law, R., Tilman, D., Loreau, M., Gonzales A., 2004. The metacommunity concept: a framework for multi-scale community ecology. Ecol. Lett. **7**, 601-613.

Lemer, S., Aurelle, D., Vigliola, L., Durand, J.-D., Borsa, P., 2007. Cytochrome *b* barcoding, molecular systematics, and geographic differentiation in rabbitfishes (Siganidae). C. R. Biol. 330, 86-94.

Lester, S.E., Ruttenberg, B.I., 2005. The relationship between pelagic larval duration and range size in tropical reef fishes: a synthetic analysis. Proc. Roy. Soc. Lond. Ser. B 272, 585–591.

Lester, S.E., Ruttenberg, B.I., Gaines, S.D., Kinlan, B.P. 2007. The relationship between dispersal ability and geographic range size. Ecol. Lett. 10, 745–758. doi: 10.1111/j.1461-0248.2007.01070.x

Liu, S.-Y.V., Chang, F.-T., Borsa, P., Chen, W.-J., Dai, C.-F., 2014. Phylogeography of the humbug damselfish, *Dascyllus aruanus* (Linnaeus, 1758): evidence of Indo-Pacific vicariance and genetic differentiation of peripheral populations. Biol. J. Linn. Soc. 113, 931-942. doi:10.1111/bij.12378

Luiz, O.J., Allen, A.P., Robertson, D.R., Floeter, S.R., Kulbicki, M., Vigliola, L., Becheler, R., Madin, J.S., 2013. Adult and larval traits as determinants of geographic range size among tropical reef fishes. Proc. Natl. Acad. Sci. U.S.A. 110, 16498-16502.

Mouillot, D., De Bortoli, J., Leprieur, F., Parravicini, V., Kulbicki, M., Bellwood, D.R., 2013. The challenge of delineating biogeographical regions: nestedness matters for Indo-Pacific coral reef fishes. J. Biogeogr. 40, 2228-2237. doi:10.1111/jbi.12194

Morrone, J.J., 1994. On the identification of areas of endemism. Syst. Biol. 43, 438-441.

Morrone, J.J., Escalante, T., 2002. Parsimony analysis of endemicity (PAE) of Mexican terrestrial mammals at different area units: when size matters. J. Biogeogr. 29, 1095-1104.

Muths, D., Gouws, G., Mwale, M., Tessier, E., Bourjea, J., 2012. Genetic connectivity of the reef fish *Lutjanus kasmira* at the scale of the West Indian Ocean. Can. J. Fisheries Aquat. Sci. 69, 842–853.

Muths, D., Tessier, E., Gouws, G., Bourjea, J., 2015. Genetic structure of the reef grouper *Epinephelus merra* in the West Indian Ocean appears congruent with biogeographic and oceanographic boundaries. Mar. Ecol. 36, 447-461. doi: 10.1111/maec.12153

Muths, D., Tessier, E., Gouws, G., Craig, M., Mwale, M., Mwaluma, J., Mwandya, A., Bourjea, J., 2011. Restricted dispersal of the reef fish *Myripristis berndti* at the scale of the SW Indian Ocean. Mar. Ecol. Prog. Ser. 443: 167–180.

Myers, A.A., Giller, P.S., 1988. Process, pattern and scale in biogeography. Pp. 3-12 *in* A.A. Myers and P.S. Giller, editors. Analytical biogeography. Chapman & Hall, London.

Nelson, G.J., Platnick, N., 1981. Systematics and biogeography: cladistics and vicariance. Columbia University Press, New York.

Nicolè, S., Negrisolo, E., Eccher, G., Mantovani, R., Patarnello, T., Erickson, D.L., Kress W.J., Barcaccia, G., 2012. DNA barcoding as a reliable method for the authentication of commercial seafood products. Food Technol. Biotechnol. 50, 387-398.

Obura, D., 2012. The diversity and biogeography of western Indian Ocean reef-building corals. PLoS One 7, e45013. doi:10.1371/journal.pone.0045013

Parravicini, V., Kulbicki, M., Bellwood, D.R., Friedlander, A.M., Arias-Gonzalez, J.E., Chabanet, P., Floeter, S.R., Myers, R., Vigliola, L., D'Agata, S., Mouillot, D., 2013. Global patterns and predictors of tropical reef fish species richness. Ecography 36, 1254-1262.

Pellissier, L., Leprieur, F., Parravicini, V., Cowman, P.F., Kulbicki, M., Litsios, G., Olsen, S.M., Wisz, M.S., Bellwood, D.R., Mouillot, D., 2014. Quaternary coral reef refugia preserved fish diversity. Science 344, 1016-1019.

Phillips, B.F., Matsuda, H., 2011. A global review of spiny lobster aquaculture. In: Fotedar , R., Phillips, B.F., (eds.), Recent advances and new species in aquaculture. Wiley-Blackwell, Hoboken NJ, pp. 22–84.

Rice, W.R., 1989. Analyzing tables of statistical tests. Evolution 43, 223–225.

Ricklefs, R.E., 1987. Community diversity: relative roles of local and regional processes. Science 235, 167-171.

Ricklefs, R.E., Schluter, D., 1993. Species diversity in ecological communities: historical and geographical perspectives. University of Chicago Press, Chicago.

Rousset, F., 1997. Genetic differentiation and estimation of gene flow from *F*-statistics under isolation by distance. Genetics 145, 1219-1228.

Sanciangco, J.C., Carpenter, K.E., Etnoyer, P.J., Moretzsohn, F., 2013. Habitat availability and heterogeneity and the Indo-Pacific warm pool as predictors of marine species richness in the tropical Indo-Pacific. PLoS One 8, e56245. doi:10.1371/journal.pone.0056245

Santini, F., Winterbottom, R., 2002. Historical biogeography of Indo-western Pacific coral reef biota: is the Indonesian region a centre of origin? J. Biogeogr. 29, 189–205.

Scheltema, R.S., 1968. Dispersal of larvae by equatorial currents and its importance to the zoogeography of shoal-water tropical species. Nature 217, 1159–1162.

Schoelinck, C., Hinsinger, D.D., Dettaï, A., Cruaud, C., Justine, J.-L., 2014. A phylogenetic re-analysis of groupers with applications for ciguatera fish poisoning. PLoS One 9, e98198. doi: 10.1371/journal.pone.0098198

Selkoe, K.A., Toonen, R.J., 2011. Marine connectivity: a new look at pelagic larval duration and genetic metrics of dispersal. Mar. Ecol. Prog. Ser. 436, 291-305. doi: 10.3354/meps09238

Senevirathna, J., Munasinghe, D., 2014. Genetic diversity and population structure of *Panulirus homarus* populations of Southern Sri Lanka and South India revealed by the mitochondrial COI gene region. Proc. Int. Conf. Food, Biol. Med. Sci., Jan. 28-29, 2014, Bangkok, pp. 10-13.

Sims, C.A., Riginos, C., Blomberg, S.P., Huelsken, T., Drew, J., Grutter, A.S., 2014. Cleaning up the biogeography of *Labroides dimidiatus* using phylogenetics and morphometrics. Coral Reefs 33, 223–233.  doi 10.1007/s00338-013-1093-2

Slatkin, M., 1985. Gene flow in natural populations. Annu. Rev. Ecol. Syst. 16, 393-430.

Smith, M.M., Heemstra, P.C., (eds.) 1986.  Smith's sea fishes, Macmillan Publ. Co., Johannesburg, 1047 p., 144 pls.

Spalding, M.D., Fox, H.E., Allen, G.R., Davidson, N., Ferdana, Z.A., Finlayson, M., Halpern, B.S., Jorge, M.A., Lombana, A., Lourie, S.A., Martin, K.D., McManus, E., Molnar, J., Recchia, C.A., Robertson, J., 2007. Marine ecoregions of the world: a bioregionalization of coastal and shelf areas. BioScience 57, 573–583.

Tamura, K., 1992. Estimation of the number of nucleotide substitutions when there are strong transition-transversion and G+C content biases. Mol. Biol. Evol. 678-687.

Tamura, K., Nei, M., 1993. Estimation of the number of nucleotide substitutions in the control region of mitochondrial DNA in humans and chimpanzees. Mol. Biol. Evol. 19, 512-526.

Tamura, K., Stecher, G., Peterson, D., Filipski, A., Kumar, S., 2013. MEGA6: Molecular Evolutionary Genetics Analysis version 6.0. Mol. Biol. Evol. 30, 2725–2729.

Treml, E.A., Roberts, J.J., Chao, Y., Halpin, P.N., Possingham, H.P., Riginos, C., 2012. Reproductive output and duration of the pelagic larval stage determine seascape-wide connectivity of marine populations. Integr. Comp. Biol. 52, 525–537. doi:10.1093/icb/ics101

Veron, J., Stafford-Smith, M., DeVantier, L., & Turak, E., 2015. Overview of distribution patterns of zooxanthellate Scleractinia. Frontiers Mar. Sci. 1, 81.

Vogler, C., Benzie, J., Barber, P.H., Erdmann, M.V., Ambariyanto, Sheppard, C., Tenggardjaja, K., Gerard, K., Woerheide, G., 2012. Phylogeography of the Crown-of-Thorns starfish in the Indian Ocean. PLoS One 7, e43499.

Ward, R.D., Zemlak, T.S., Innes, B.H., Last, P.R., Hebert, P.D.N., 2005. DNA barcoding Australia's fish species. Phil. Trans.R. Soc. B 360, 1847-1857.

Whitney, N.M., Robbins, W.D., Schultz, J.K., Bowen, B.W., Holland, K.N., 2012. Oceanic dispersal in a sedentary reef shark (*Triaenodon obesus*): genetic evidence for extensive connectivity without a pelagic larval stage. J. Biogeogr. 39, 1144-1156.

Winters, K.L., van Herwerden, L., Choat, J.H., Robertson, D.R., 2010.  Phylogeography of the Indo-Pacific parrotfish *Scarus psittacus*: isolation generates distinctive peripheral populations in two oceans. Mar. Biol. 157, 1679-1691. doi: 10.1007/s00227-010-1442-4

Woodland, D.J., 1990. Revision of the fish family Siganidae with description of two new species and comments on distribution and biology. Indo Pac. Fishes, B. Pauahi Bishop Mus., Honolulu 19, 1-136.

Wörheide, G., Epp, L.S., Macis, L., 2008. Deep genetic divergences among Indo-Pacific populations of the coral reef sponge *Leucetta chagosensis* (Leucettidae): founder effects, vicariance, or both? BMC Evol. Biol. 8, 24. doi:10.1186/1471-2148-8-24

Wright, S., 1942. Isolation by distance. Genetics 28, 114–138.

Zemlak, T.S ., Ward, R.D., Connell, A.D., Holmes, B.H., Hebert, P.D.N., 2009. DNA barcoding reveals overlooked marine fishes. Mol. Ecol. Resour. 9 (Suppl. 1), 237–242. doi: 10.1111/j.1755-0998.2009.02649.x

Zhang, J., 2011. Species identification of marine fishes in China with DNA barcoding. Evid. Based Complement. Alternat. Med. 2011, 978253. doi:  10.1155/2011/978253

Zhuang, X., Qu, M., Zhang, X., Ding, S., 2013.  A comprehensive description and evolutionary analysis of 22 grouper  (Perciformes, Epinephelidae) mitochondrial genomes with emphasis on two novel genome organizations. PLoS One 8, e73561.

CAPTIONS TO FIGURES

**Fig. 1.** Reef fish species richness and endemism in the Indian Ocean. Abbreviations for provinces as following: *AND* Andaman-Cocos (Keeling)–Christmas; *EAF* Eastern Africa; *EI* Eastern India-Thailand-Malaysia; *LMC* Lakshadweep–Maldives–Chagos; *NAU* Northern Australia; *NWI* Northwestern Indian Ocean; *SCI* Spencer Gulf; *SWI* Southwestern Indian Ocean; *WAU* Western Australia; *WII* Western Indian Ocean Islands. **A.** Delimitation of biogeographic provinces with total number of reef fish species per province. *Circle area* proportional to number of species. **B.** Number of species with limited geographic range in each biogeographic province. *Circle area* proportional to total number of species with limited geographic range. *Inset*: categories of endemism according to number of checklists where a species occurs (see Materials and Methods). *Numbers*, from top to bottom: local, provincial, and regional endemics.

**Fig. 2.** Phylogeographic structure of humbug damselfish *Dascyllus abudafur* and *D. aruanus*. Includes cytochrome *b* gene sequence data from Liu et al. (2014)*.* **A.** Median Joining parsimony network (Bandelt et al., 1999) of the partial cytochrome *b* gene sequences of 268 individuals from various localities in the Indo-West Pacific , including the WIO (*black*), the rest of the Indian Ocean (*grey*), and the Western Pacific (*white*). Haplotype sequences trimmed to 949 bp, starting at nucleotide site homologous to site no. 14475 of the mitochondrial DNA (= no. 46 of the cytochrome *b* gene) of *Abudefduf vaigiensis* (GENBANK no. NC_009064). *Scale bar*: one mutational step. **B.** Sampling locations.

**Fig. 3.** Phylogeographic structure of areolate grouper *Epinephelus areolatus*. Includes *CO1* gene sequence data from Ward et al. (2005), Asgharian et al. (2011), He et al. (2013), Zhuang et al. (2013), Alcantara and Yambot (2014), Schoelinck et al. (2014), and GENBANK. **A.** Median Joining parsimony network (Bandelt et al. 1999) of the *CO1* gene sequences of 37 individuals from various localities in the Indo-West Pacific, including the WIO (*black*), the rest of the Indian Ocean (*grey*), and the Western Pacific (*white*). Haplotype sequences trimmed to 547 bp, starting at nucleotide site no. 111 of the *CO1* gene in this species (GENBANK no. NC_020785). *Scale bar*: one mutational step; *number*: number of mutations separating the three main haplogroups; *cross*: sampling site unknown (Nicolè et al., 2012). Haplotypes sampled in Western Australia are distinguished by symbol *Wa*. **B.** Known sampling locations. *Wa* Western Australia.

**Fig. 4.** Phylogeographic structure of blacktip grouper *Epinephelus fasciatus*. Includes *CO1* gene sequence data from Ward et al. (2005), Lakra et al. (2011), Hubert et al. (2012), Alcantara and Yambot (2014), Schoelinck et al. (2014), CRYOBANK, and GENBANK. **A.** Median Joining parsimony network (Bandelt et al. 1999) of the *CO1* gene sequences of 31 individuals from various localities in the Indo-West Pacific, including the WIO (*black*), the rest of the Indian Ocean (*grey*), and the Western Pacific (*white*). Haplotype sequences trimmed to 508 bp, starting at nucleotide site homologous to site no. 133 of the *CO1* gene of *E. fuscoguttatus* (GENBANK no. HQ174849). *Scale bar*: one mutational step; *numbers*: numbers of mutations separating the three main haplogroups. The single haplotype sampled in the Red Sea is distinguished by symbol *Rs*. **B.** Sampling locations. *Rs* Red Sea.

**Fig. 5.** Phylogeographic structure of honeycomb grouper *Epinephelus merra*. Includes cytochrome *b* gene sequence data from Muths et al. (2015), and GENBANK. **A.** Median Joining parsimony network (Bandelt et al. 1999) of the cytochrome *b* gene sequences of 487 individuals from various localities in the Indo-West Pacific, including the WIO (*black*), the rest of the Indian Ocean (*grey*), and the Western Pacific (*white*). Haplotype sequences trimmed to 803 bp, starting at nucleotide site homologous to site no. 61 of the cytochrome *b* gene of *E. costae* (GENBANK no. DQ197951). *Scale bar*: one mutational step; *number* indicates the number of mutations separating the two main haplogroups. **B.** Sampling locations.

**Fig. 6.** Phylogeographic structure of bluspotted cornetfish *Fistularia commersonii*. Includes *CO1* gene sequence data from Zhang (2011), Hubert et al. (2012), Jackson et al. (2015), and GENBANK. **A.** Median Joining parsimony network (Bandelt et al. 1999) of the *CO1* gene sequences of 113 individuals from various localities in the Indo-West Pacific, including the WIO (*black*), the rest of the Indian Ocean (*grey*), and the Western Pacific (*white*). Haplotype sequences trimmed to 474 bp, starting at nucleotide site no. 201 of the gene (GENBANK no. NC_010274; Kawahara et al., 2008). *Cross* indicates additional sequence of Kawahara et al. (2008), of unknown origin. *Scale bar*: one mutational step. *Re*, *Bc* haplotypes sampled in, respectively, Reunion Island and Baja California. **B.** Sampling locations, excluding La Paz, Baja California. *Re* Reunion Island.

**Fig. 7.** Phylogeographic structure of bluestripe snapper *Lutjanus kasmira*. Sequence data from Muths et al. (2012). **A.** Median Joining parsimony network (Bandelt et al., 1999) of the cytochrome *b* gene sequences of samples (total $N$ = 935) from various localities in the Indo-West Pacific , including the WIO (*black*), the rest of the Indian Ocean (*grey*), and the Western Pacific (*white*). Haplotype sequences trimmed to 475 bp, starting at nucleotide site homologous to site no. 14667 of the complete mitochondrial DNA of the species (= no. 274 of the cytochrome *b* gene) (GENBANK no. NC_011578). *Scale bar*: one mutational step. **B.** Sampling locations.

**Fig. 8.** Phylogeographic structure of spiny lobster *Panulirus homarus.* Includes *CO1* gene sequence data from Jeena (2013), Lavery et al. (2014), and Senevirathna and Munasinghe (2014); other data retrieved from GENBANK. **A.** Median Joining parsimony network (Bandelt et al., 1999) of the partial *CO1* gene sequences of samples from various localities in the Indo-West Pacific , including the WIO (*black*), other localities in the Indian Ocean (*grey*), and the Western Pacific (*white*). Haplotype sequences (total $N$ = 98) were trimmed to a common length of 547 bp, starting at nucleotide site homologous to site no. 135 of the mitochondrial DNA (= no. 135 of the *CO1* gene) of *P. ornatus* (GENBANK no. NC_014854). *Scale bar*: one mutational step; *numbers* indicates the number of mutations separating the two main haplogroups. **B.** Sampling locations.

**Fig. 9.** Phylogeographic structure of crescent grunter *Terapon jarbua.* Includes *CO1* gene sequence data from Asgharian et al. (2011), Lakra et al. (2011), Lavergne et al. (2014), and GENBANK. **A.** Median Joining parsimony network (Bandelt et al., 1999) of the *CO1* gene sequences of samples from various localities in the Indo-West Pacific , including the WIO (*black*), other localities in the Indian Ocean (*grey*), and the Western Pacific (*white*). Haplotype sequences trimmed to 551 bp,

starting at nucleotide site homologous to site no. 5591 of the mitochondrial DNA (= no. 109 of the *CO1* gene) of *Crenimugil crenilabis* (GᴇɴBᴀɴᴋ no. NC_017884). *Scale bar*: one mutational step; *numbers* indicate the numbers of mutations separating the three main haplogroups. Haplotypes sampled in the Red Sea and Juan de Nova are distinguished by symbols *Rs* and *Jn*, respectively. **B.** Sampling locations. *Rs* Red Sea; *Jn* Juan de Nova.
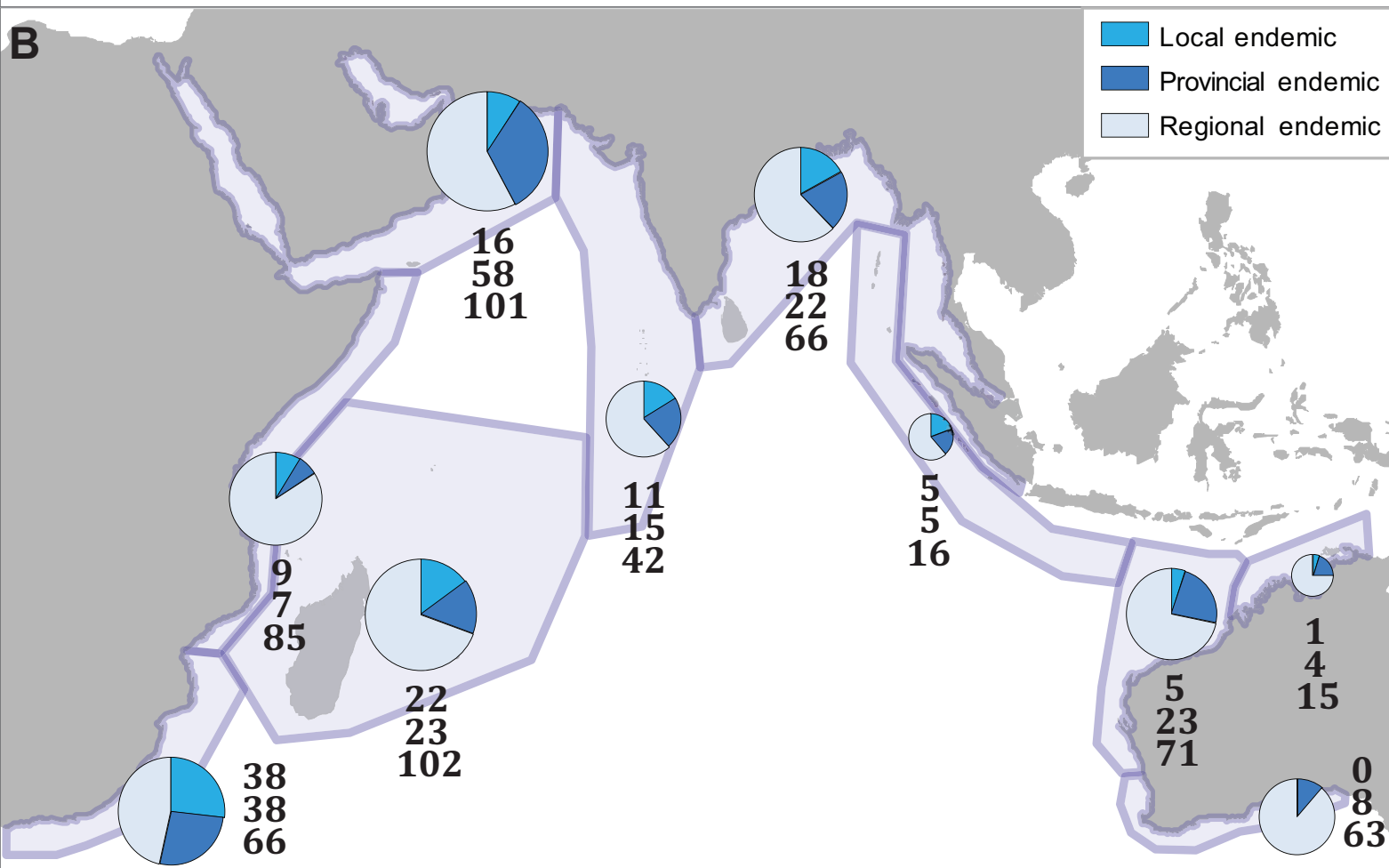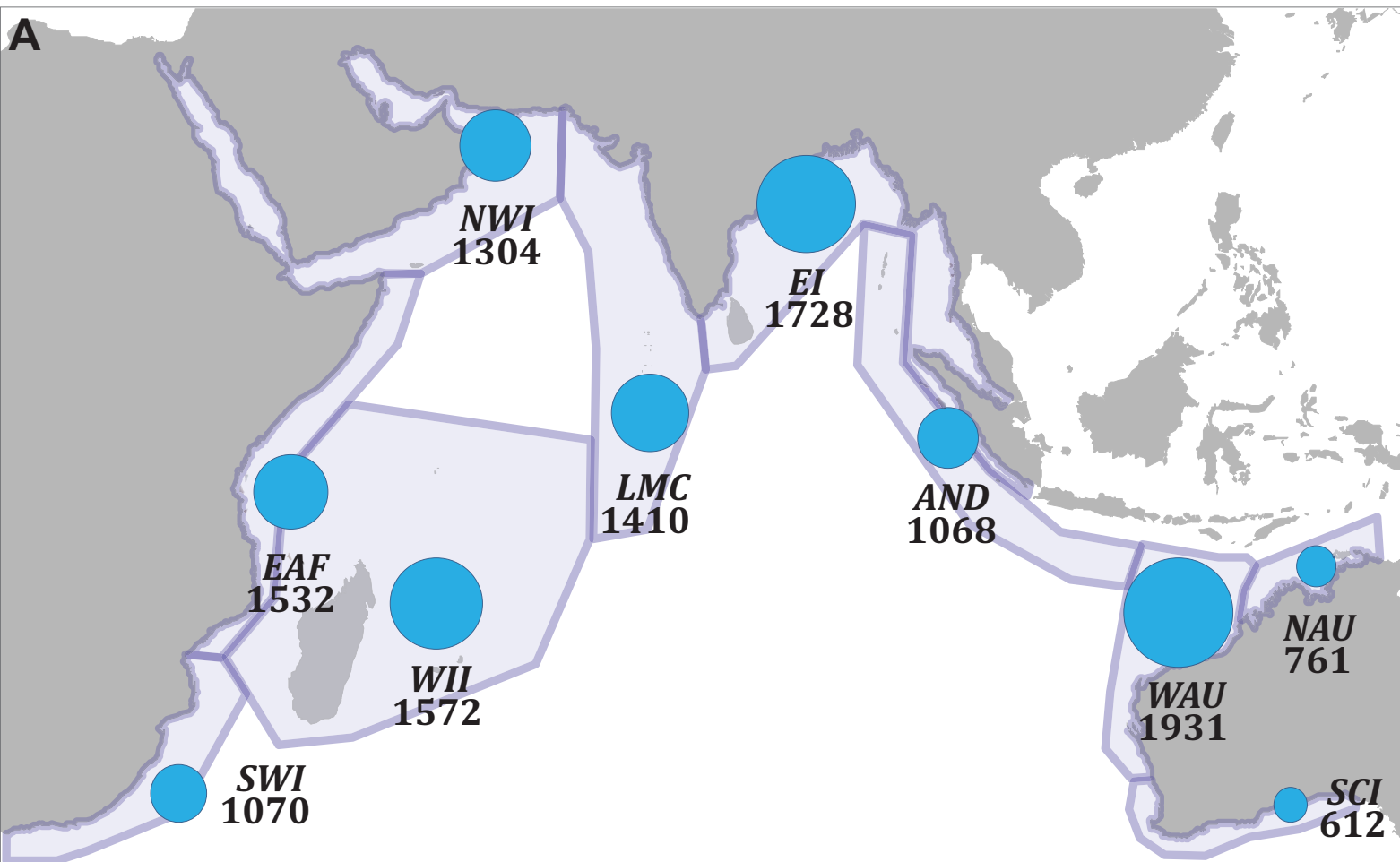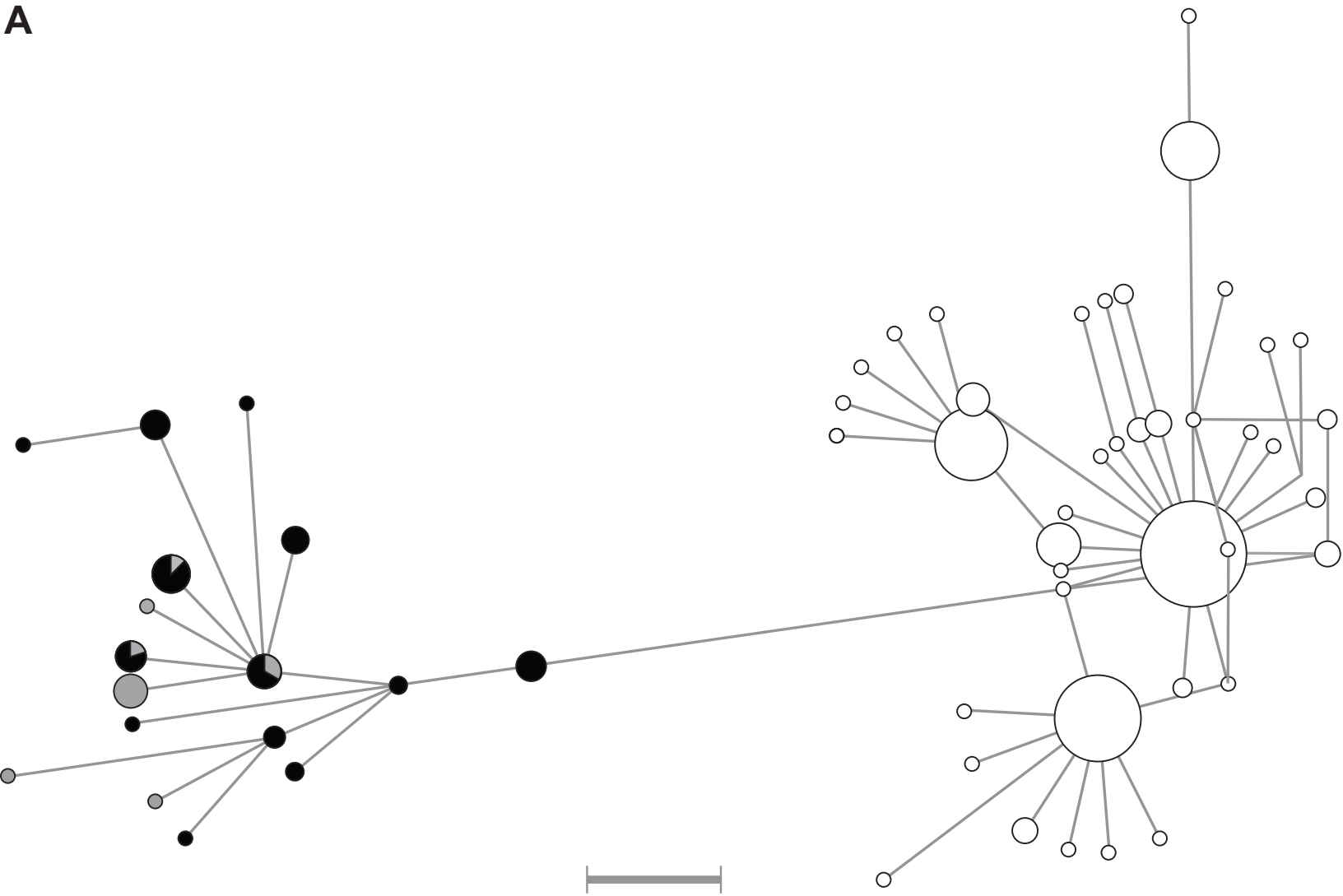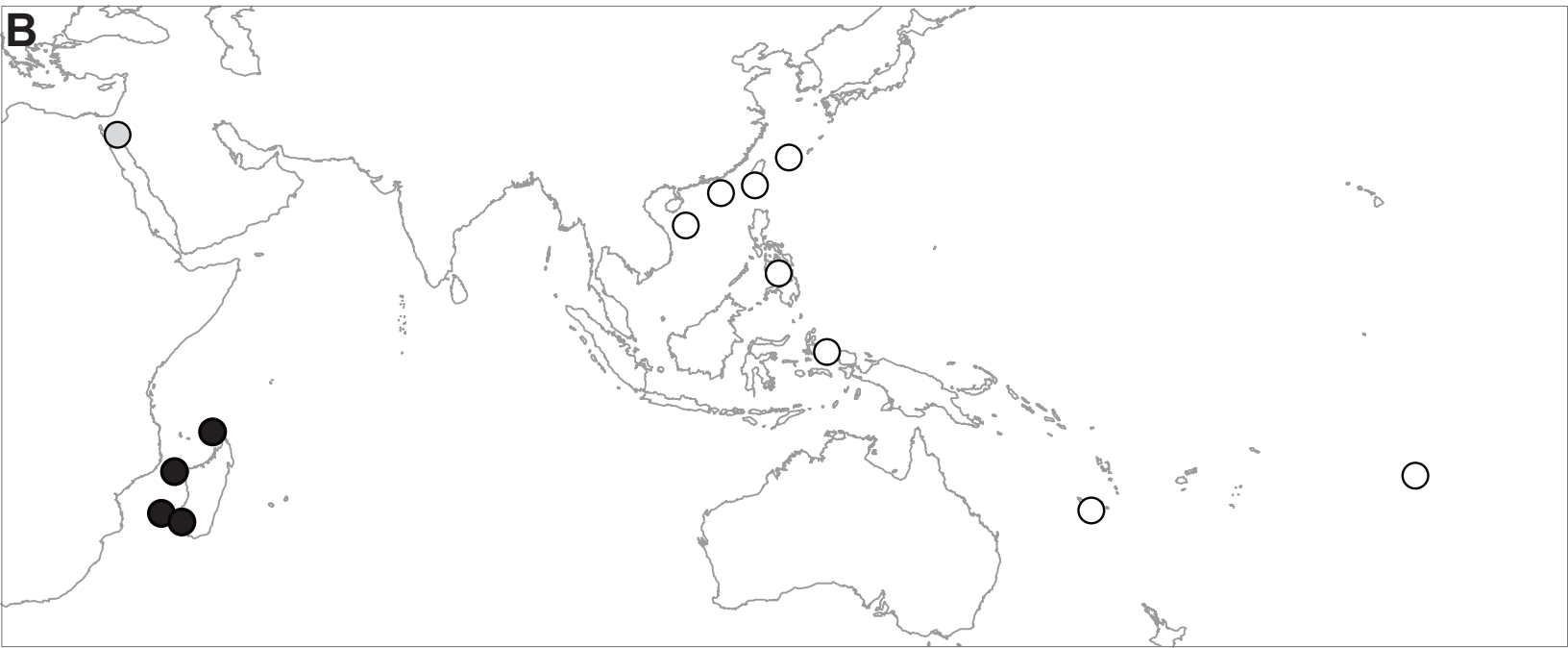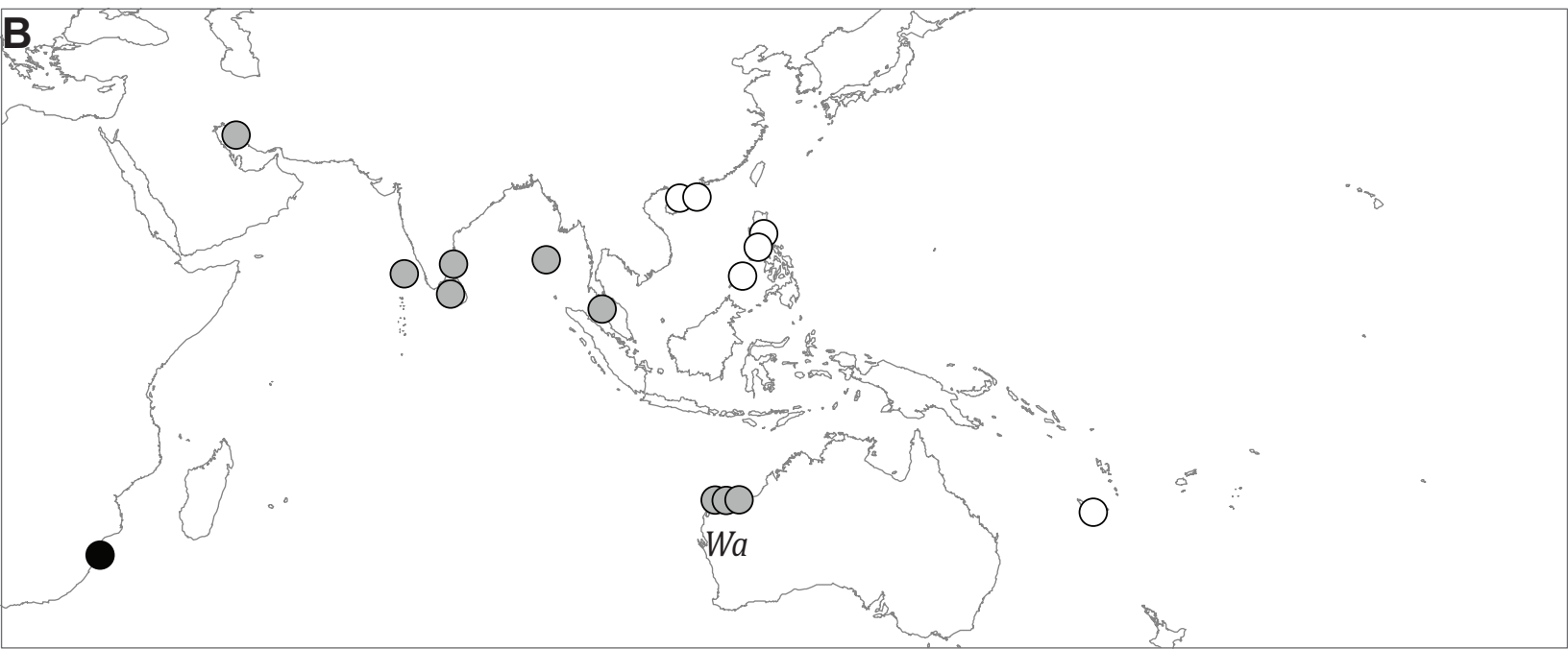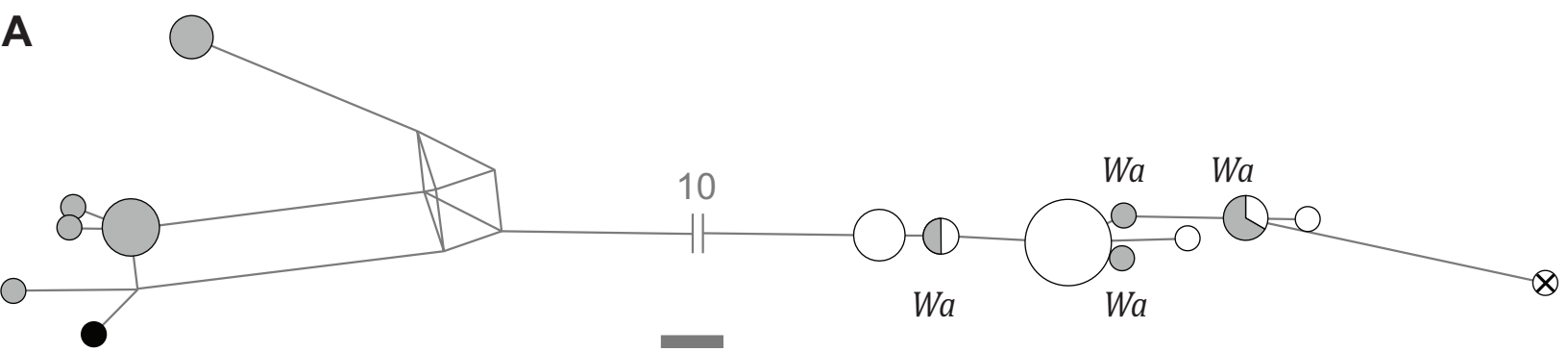
**Figure 1 Borsa et al**

**Figure 2 Borsa et al**

**Figure 3 Borsa et al**



A

10

*Wa*   *Wa*

*Wa*

*Wa*   *Wa*

B

*Wa*

**Figure 4 Borsa et al**



A

B

*Rs*

14

40

*Rs*
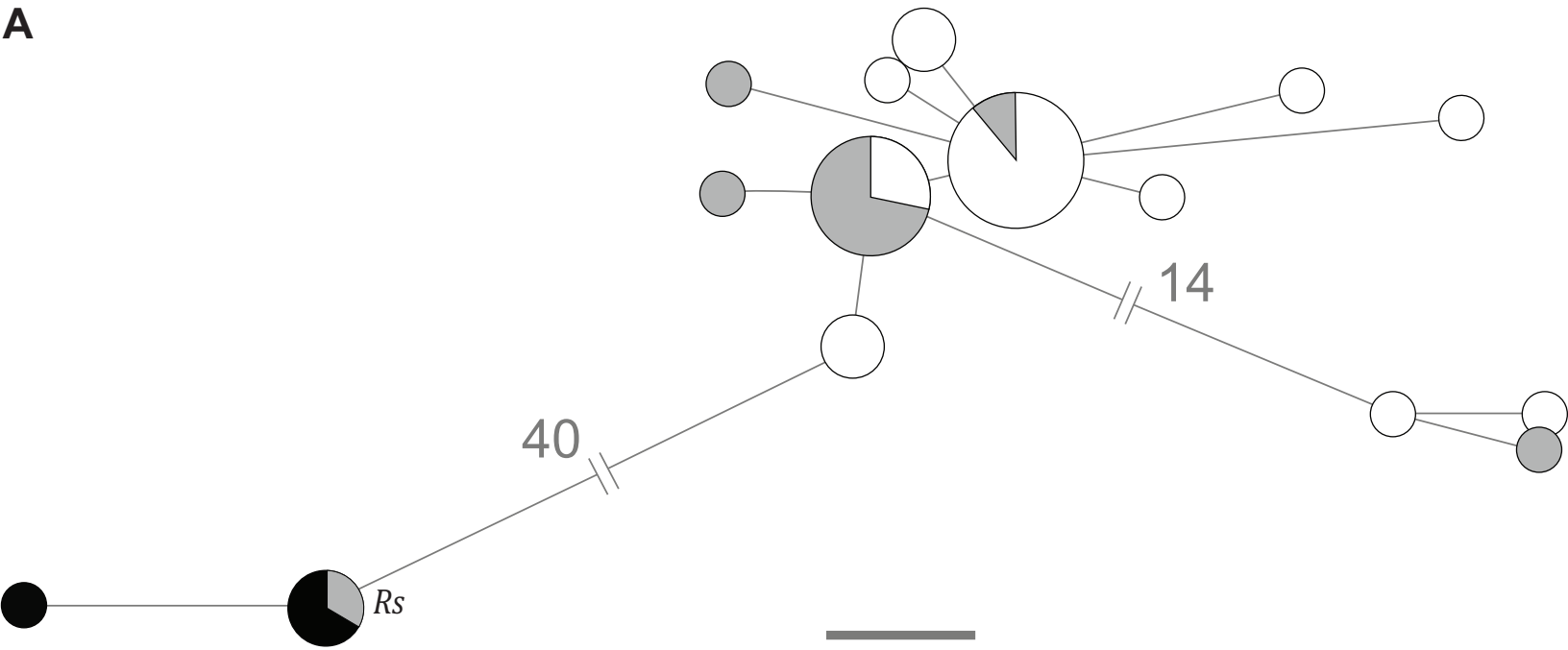
**Figure 5 Borsa et al**

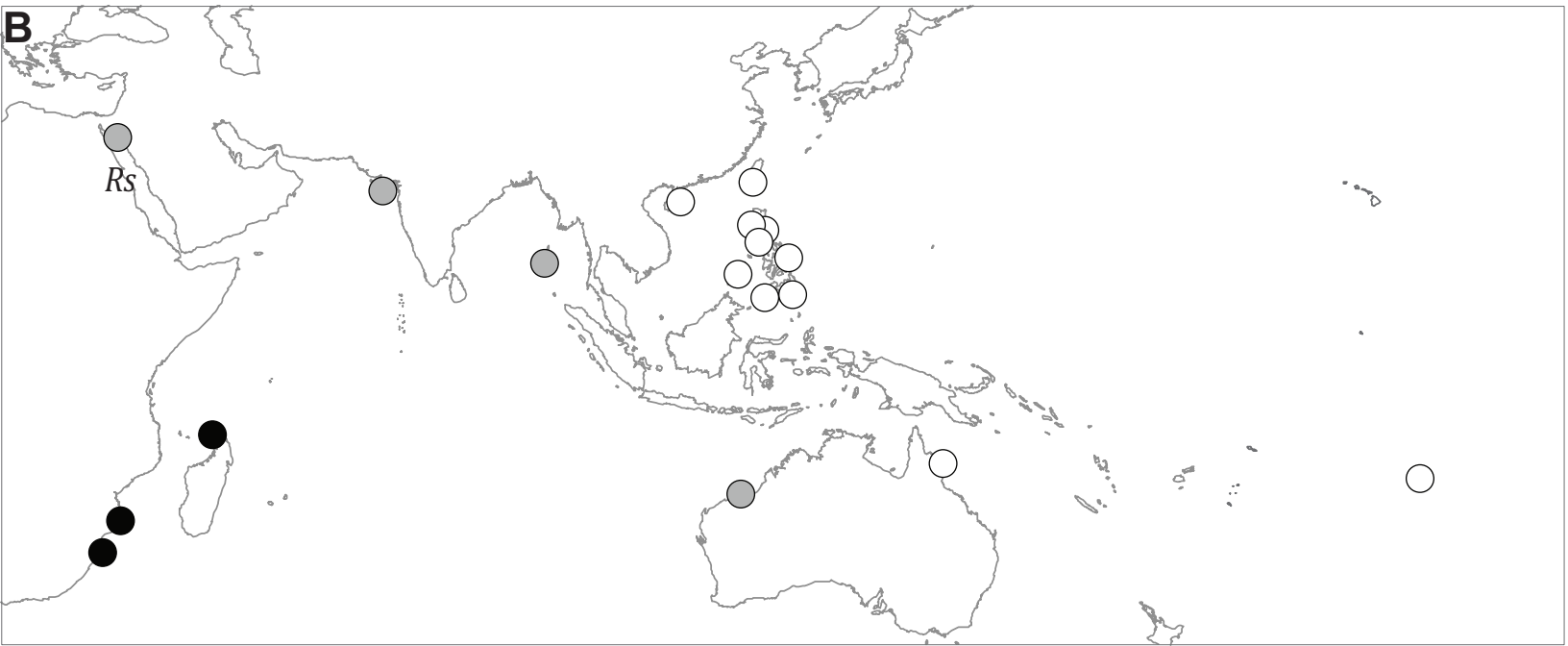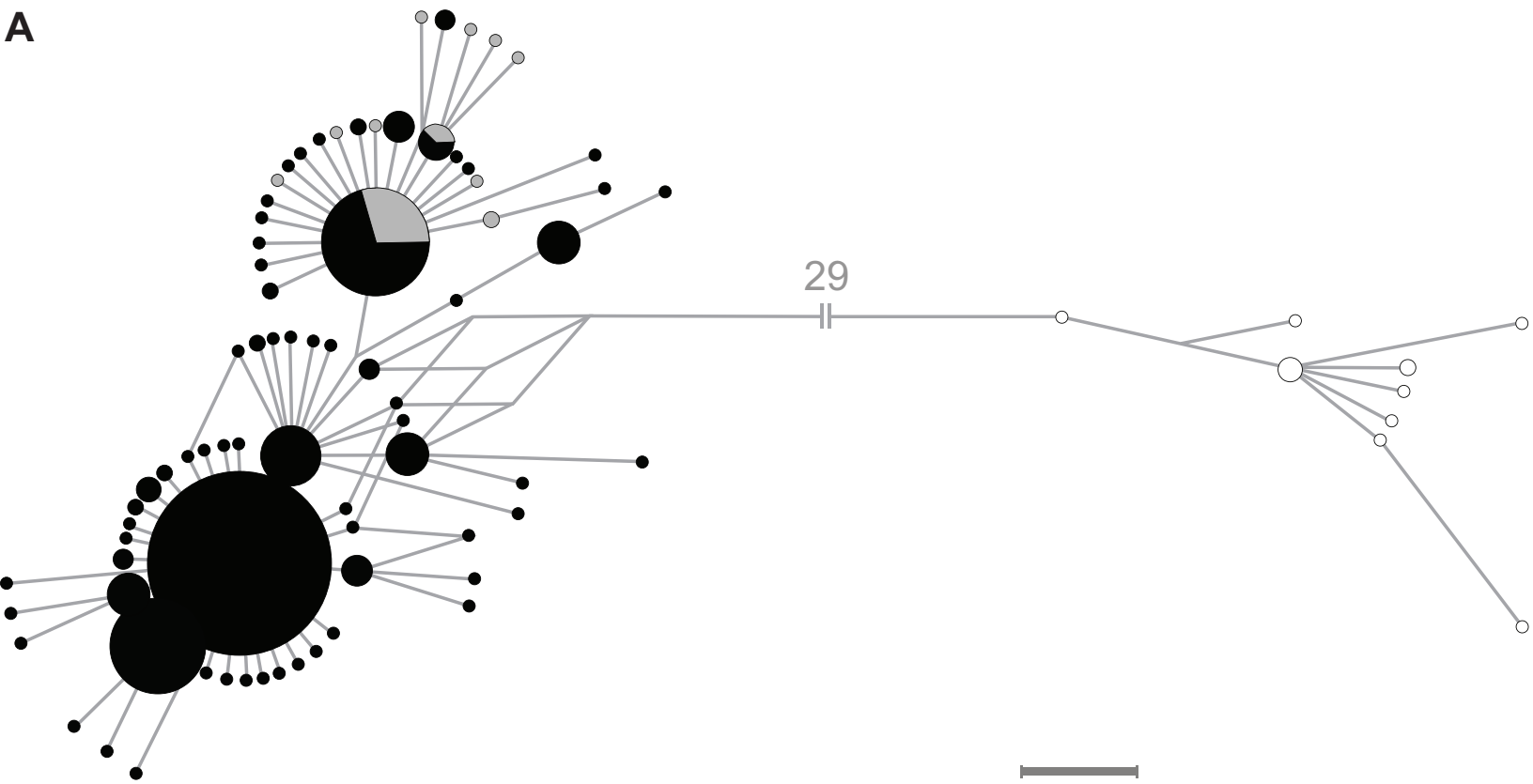**Figure 6 Borsa et al**

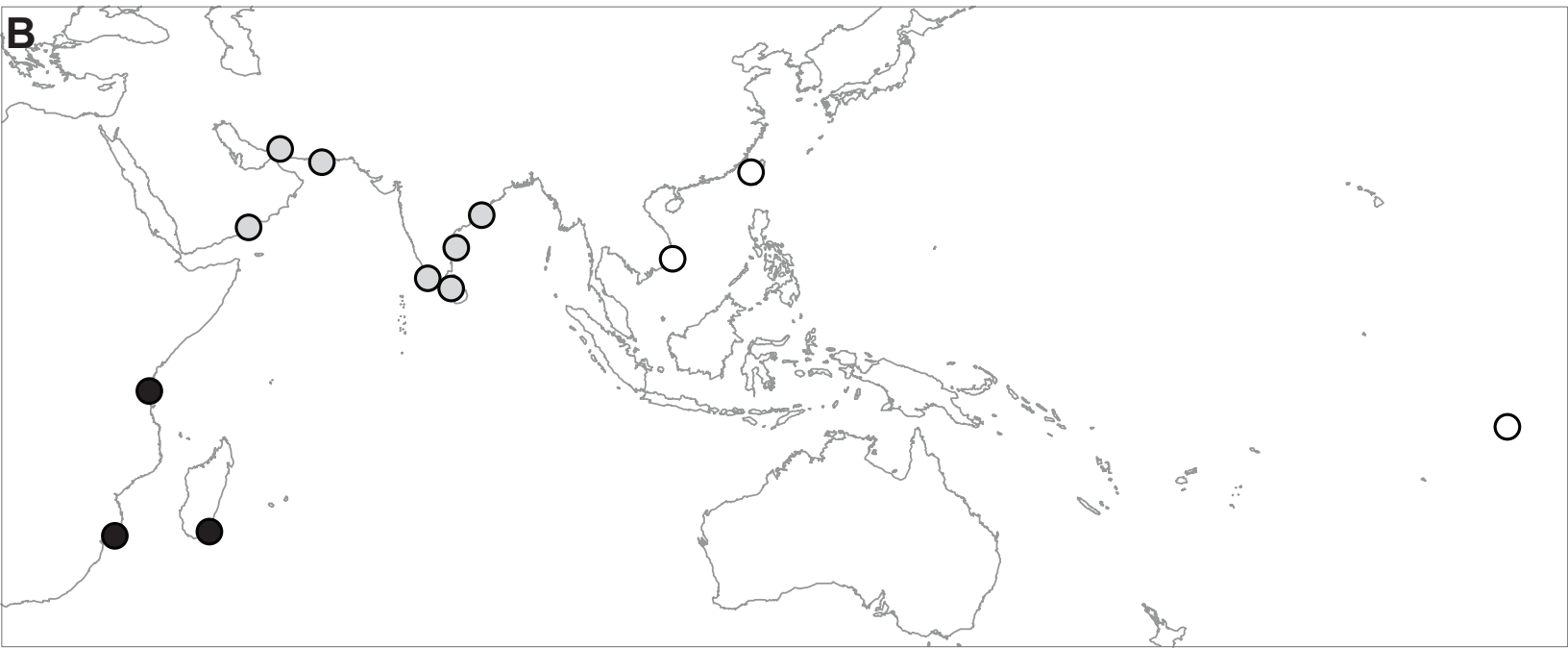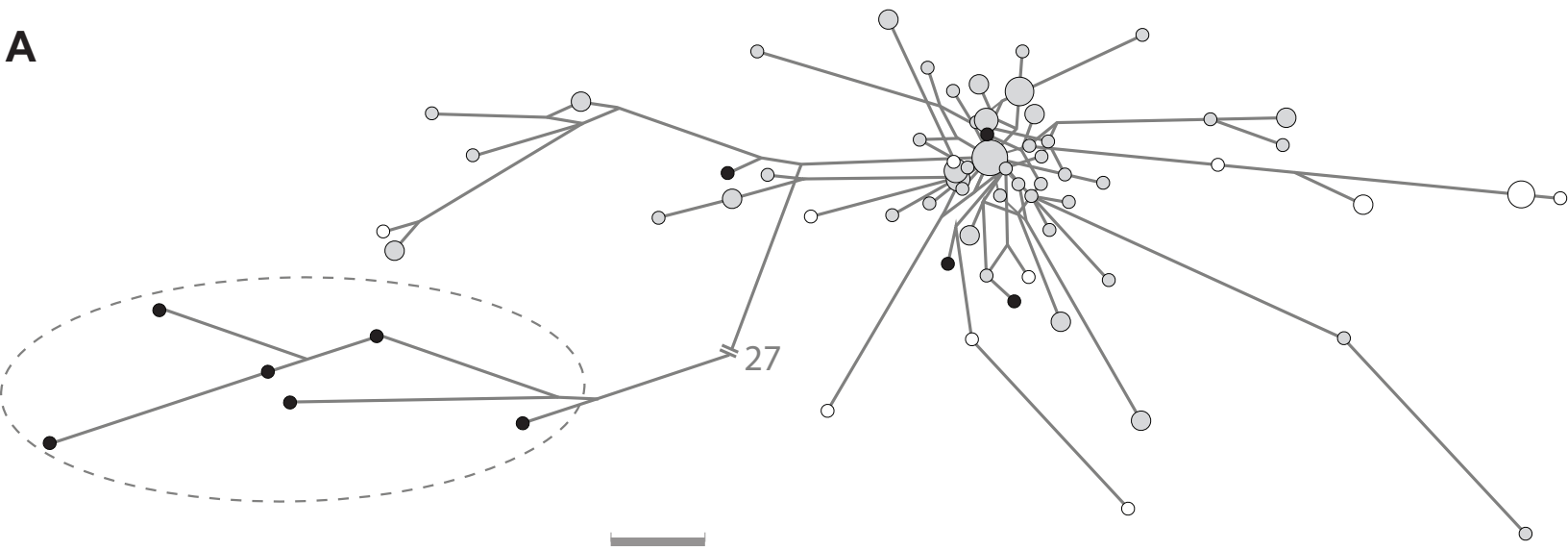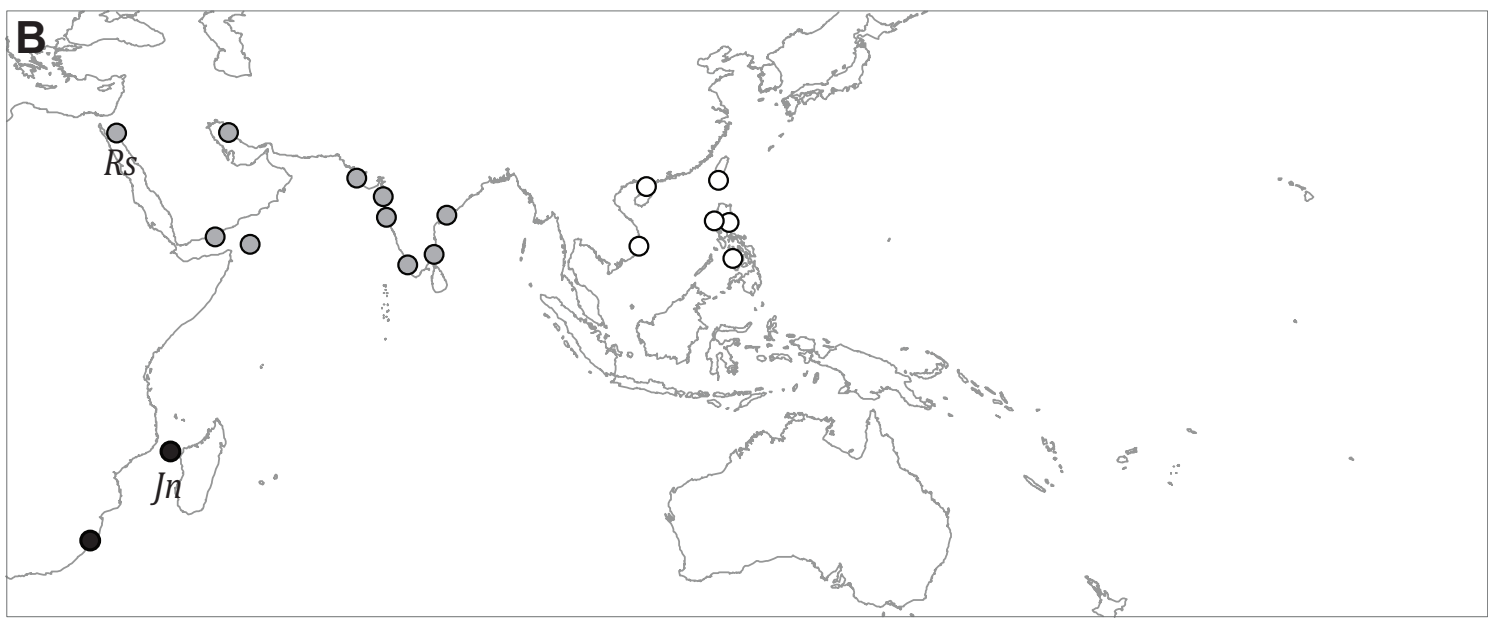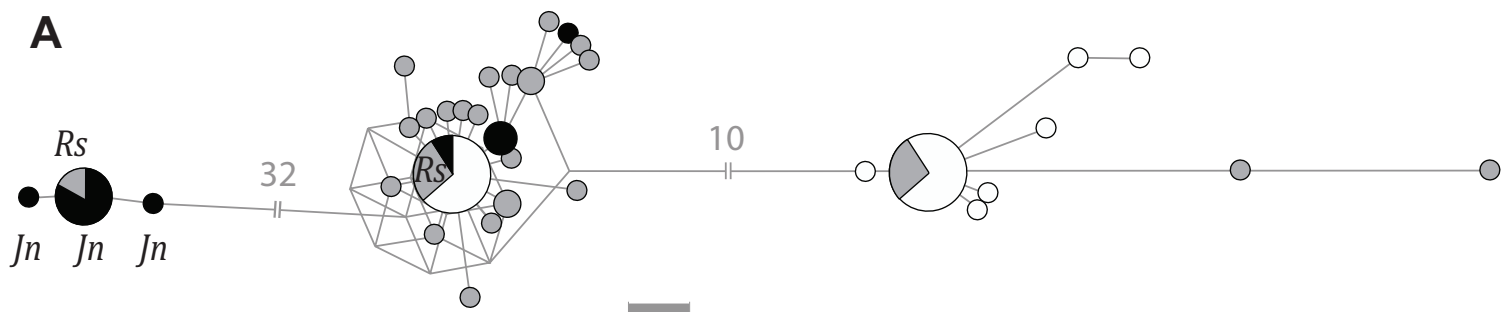**Figure 7 Borsa et al**
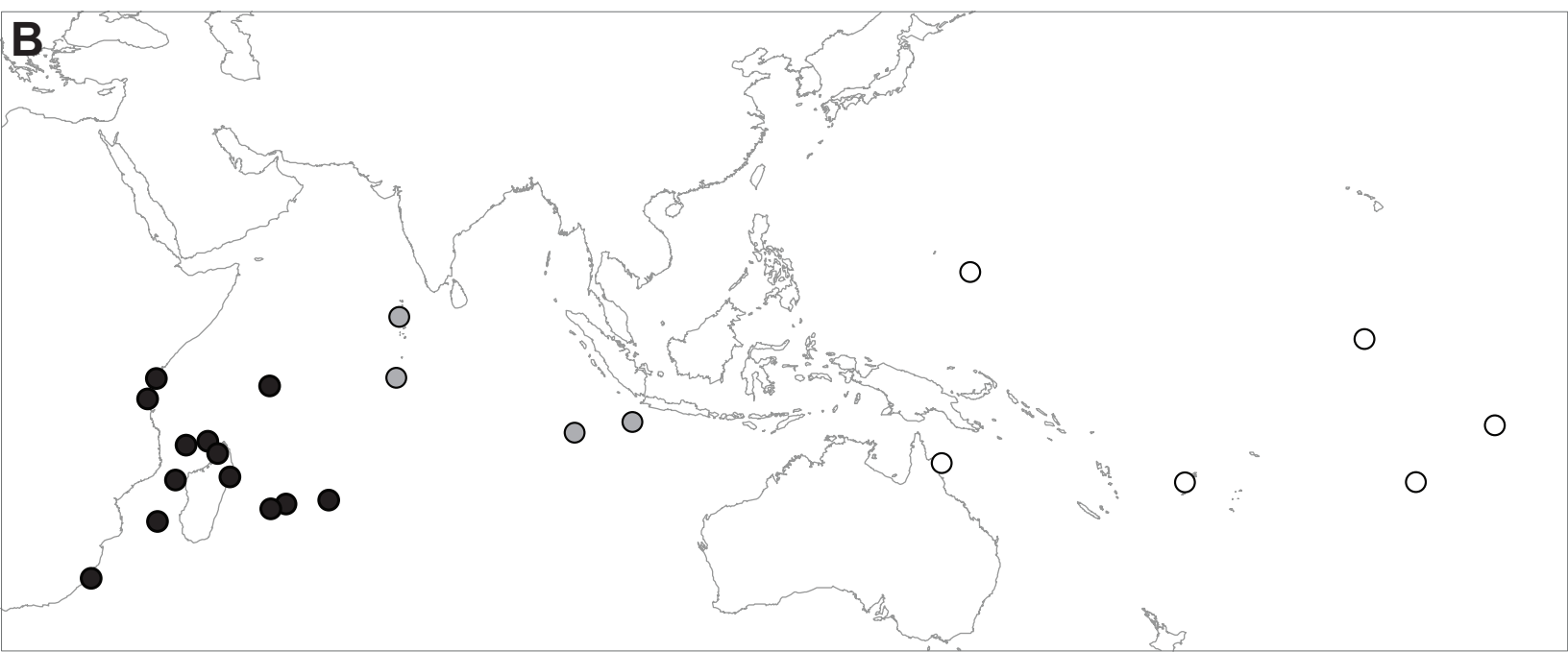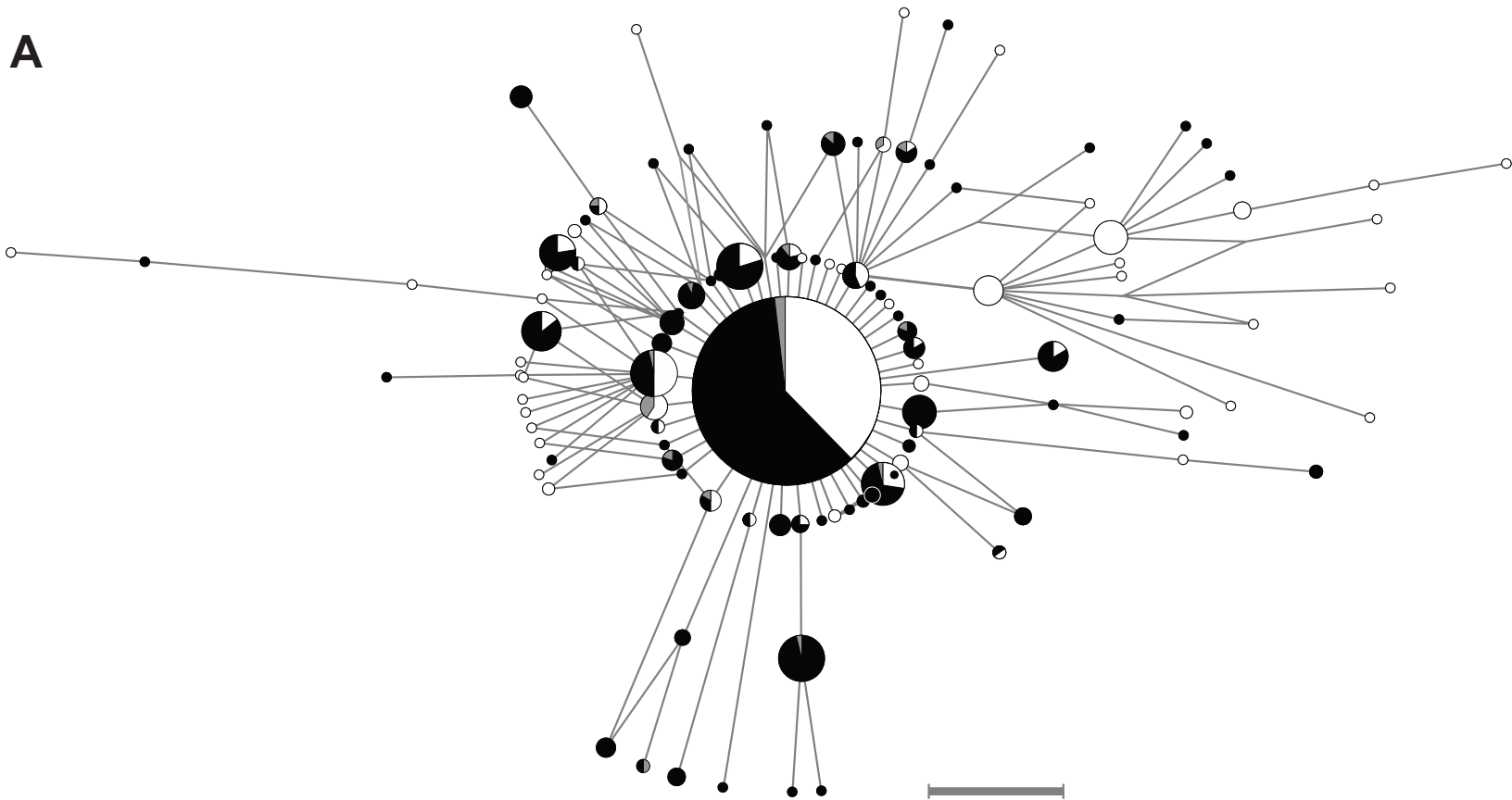
**Figure 8 Borsa et al**

**Figure 9 Borsa et al**

*Supplementary material to:*

**Comparative phylogeography of the western Indian Ocean reef fauna**

*P. Borsa, J.-D. Durand, W.-J. Chen, N. Hubert, D. Muths, G. Mou-Tham, M. Kulbicki*

Tables S1-S8 and Figs. S1-S14 here appended

**Table S1** References for lists of reef fish species by locality/country in the Indian Ocean. Localities arranged by alphabetical order. *General* references for species lists not restricted to a particular geographic region

| Region, |
| --- |
| Reference |

**Arabian Gulf**

Kuronuma, K., Abe, Y., 1986. Fishes of the Arabian Gulf. Kuwait Inst. Sci. Res.

Randall, J.E., Downing, N., McCarthy, J.B., Stanaland, E., Tarr, A.B., 1994. Fifty-one new records of fishes from the Arabian Gulf. Fauna of Saudi Arabia, 14, 220-258.

**Australia**

Paxton, J.R., Hoese, D.F., Allen, G.R., Hanley, J.E., 1989. Zoological catalogue of Australia, vol. 7. Pisces, Petromyzontidae to Carangidae. Australian Government Publishing Service, Canberra, xii+665 pp.

Russell, B.C., Larson, H.K., Hutchins, J.B., Allen, G.R., Reef fishes of the Sahul Shelf. Unpublished report Museum and Art Gallery of the Northern Territory - Darwin- 33 p.

Sainsbury, K.J., Kailola, P.J. and Leyland, G.G. (1985). Continental shelf fishes of northern and north-western Australia. An illustrated guide. CSIRO, Australia.

**Chagos**

Winterbottom, R., Emery, A.R., Holm, E., 1989. An annotated checklist of the fishes of Chagos Archipelago, central Indian Ocean.Roy. Ontario Mus. Life Sci. Contr. 145, 1-226.

Winterbottom, R., Anderson, R.C., 1997. A revised checklist of the epipelagic and shore fishes of the Chagos Archipelago, central Indian Ocean. Ichth. Bull., J.L.B. Smith Inst. Ichthyol. 66, 1-28.

**Christmas**

Allen, G.R., Steene, R.C., 1988. - The Fishes of Christmas Island, Indian Oceanic Australian National Parks Service, Special Publ., 2, 81 p.

Allen, G.R., Steene, R.C., 1979. The fishes of Christmas Island, Indian Ocean. Australian National Parks and Wildlife Service, Special Publication 2, 1-81.

Allen, G.R., Steene, R., Orchard, M., 2007. Fishes of Christmas Island, second edition. Christmas Island Natural History Association, Christmas Island, 284 pp.

Hobbs, J.P.A., Ayling, A.M., Choat, J. H., Gilligan, J.J., McDonald, C.A., Neilson, J., Newman, S.J., 2010. New records of marine fishes illustrate the biogeographic importance of Christmas Island, Indian Ocean. Zootaxa 2422, 63–68

**Cocos**

Allen, G.R., Smith-Vaniz, W.F., 1994. Fishes of the Cocos (Keeling) islands. Atoll Res. Bull. 412, 21 pp.

**E. Africa**

MASDEA data base 2011

Obura, D., 2004. Biodiversity surveys of the coral reefs of Mnazi Bay - Ruvuma Estuary Marine Park. IUCN EARO Publication.

**Iles Eparses**

Chabanet, P., Durville, P., 2005. Reef fish inventory of the Juan de Nova natural park (Western Indian Ocean). Western Indian Ocean J.Mar.Sci. 4, 145-162

Chabanet, P., Tessier, E., Durville, P., Mulochau, T., René, F., 2002. Peuplement ichtyologique des bancs de Geyser et Zélée (Océan Indien Occidental). Cybium 26, 11-26.

Durville, P., Chabanet, P., Quod, J.-P., 2003. Visual census of the reef fishes in the natural reserve of the Glorieuses Islands (Western Indian Ocean). Western Indian Ocean J. Mar. Sci. 2, 95-104.

Fricke, R., Durville, P. , Bernardi, G., Borsa, P., Mou-Tham, G., Chabanet, P., 2013. Checklist of the shore fishes of Europa Island, Mozambique Channel, southwestern Indian Ocean, including 297 new records. Stuttgarter Beiträge zur Naturkunde A, Neue Serie 6, 247-276.

Wickel, J., Jamon, A., 2010. Inventaire taxonomique actualisé des poissons marins de l'île de Mayotte et des bancs récifaux de Geyser-Zélée, Canal de Mozambique. Liste révisée des espèces et élaboration d'une base de données fonctionnelle.IFRECOR report  97 pp.

**India**

Misra, K.S., 1969. The fauna of India and the adjacent countries. Pisces Elasmobranchii and Holocephali. Delhi, Manager Publication. 276 pp.

Ramesh, R., Nammalwar, P., Gowri, V.S., 2008. Database on coastal information of Tamil Nadu Institute for ocean management. Anna University Chennai - 600 025, 132 pp.

**Kenya**

Bock, K.R., 1972. Preliminary checklist of lagoonal fishes of Diani, Kenya. Journal of East African Natural History Society and National Museum 137, 1-6.

**Madagascar**

Allen, G.R., 2005. Reef fi shes of Northwestern Madagascar. In: McKenna, S., G.R. Allen and H. Randrianasolo (eds.). A Rapid Marine Biodiversity Assessment of the Coral reefs of Northwest Madagascar. RAP Bulletin of Biological Assessment 31. Conservation International, Washington DC, USA. Pp. 39-48.

Gillibrand, C.J., Harris, A.R., Mara, E., 2007. Inventory and Spatial Assemblage Study of Reef Fish in the Area of Andavadoaka, South-West Madagascar (Western Indian Ocean). Western Indian Ocean J. Mar. Sci. Vol. 6, No. 2, pp. 183-197

Harding, S., Randriamanantsoa, B., Hardy, T., Curd, A.2006 Coral Reef Monitoring and Biodiversity Assessment to support the planning of a proposed MPA at Andavadoaka. 100 pp.

McKenna, S.A, Allen, G.R. (eds.), 2003. A Rapid Marine Biodiversity Assessment of Northwest Madagascar. Bulletin of the Rapid Assessment Program 31, Conservation International, Washington, DC.

Obura D., Di Carlo, G., Rabearisoa, A., Oliver, T. (eds.), 2011. A rapid marine biodiversity assessment of the coral reefs of northeast Madagascar. RAP Bulletin of Biological Assessment 61. Conservation International. Arlington, VA.

Samoilys and Randriamanantsoa Reef fishes of northeast Madagascar in Obura, D.O. and Oliver,T. (2011) A Rapid Marine Biodiversity Assessment of the Coral Reefs of Northeast Madagascar....

Maldives

Anderson, R.C., Randall, J.E., Kuiter, R.H., 1998. Additions to the fish fauna of the Maldive Islands. Part 2: New records of fishes from the Maldive Islands, with notes on other species. – Ichthyological Bulletin of the J. L. B. Smith Institute of Ichthyology 67, 20-32, pls. 1-4.

Kuiter, R.H., 1998. Photo Guide to Fishes of the Maldives. Atoll Editions, Apollo Bay, Australia, 257 pp.

Randall, J.E., Anderson, R.C., 1981. Annotated checklist of the epipelagic and shorefishes of the Maldive Islands.Ichth. Bull., J.L.B. Smith Inst. Ichthyol. 59: 1-47.

Randall, J.E., Anderson, R.C., 1993. Annotated checklist of the epipelagic and shore fishes of the Maldive Islands. Ichthyol. Bull., 59,1-47.

Mascarene Islands

Fricke, R., 1999. Fishes of the Mascarene Islands (Réunion, Mauritius, and Rodrigues). An annotated checklist, with descriptions of new species. Koeltz Scientific Books, Koenigstein, viii+759 pp.

Letourneur, Y., Chabanet, P., Durville, P., Taquet, M., Teissier, E., Parmentier, M., Quéro, J.-C., Pothin, K., 2004. An updated checklist of the marine fish fauna of Reunion Island, South-Western Indian Ocean. Cybium 28, 199-216.

Anderson, R.C., 2005. Developing Marine Reserves for Biodiversity Conservation and Sustainable Fisheries in Rodrigues. Impacts of Marine Reserves in Rodrigues: Report of a training visit to Shoals Rodrigues, 26 pp.

Heemstra, E., Heemstra, P.C., Smale, M.J., Hooper, T., Pelicier, D., 2004. Preliminary checklist of coastal fishes from the Mauritian island of Rodrigues. Journal of Natural History 38, 3315-3344.

Mozambique

Davidson, J., N. Hill, L. Muaves, S. Mucaves, I. Silva, A. Guissamulo and A. Shaw. 2006. Vamizi Island Mozambique: Marine Ecological Assessment October 2006. ZSL/Maluane Report.

Pereira, M.A.M., 2000. Preliminary Checklist of Reef-associated Fishes of Mozambique.Maputo, MICOA. 21 pp.

Samoilys, M.A., Silva, I., Ndagala, J., Muciva, S., Macharia, D., in press. A rapid assessment of coral reefs in Cabo Delgado, northern Mozambique. CORDIO Report.

Nicobar

Rajaram, R., Nedumaran, T., 2009. Ichthyofaunal diversity in Great Nicobar Biosphere Reserve, Bay of Bengal. Journal of Threatened Taxa 1, 166-169.

Rao, D.V., Devi, K., Rajan, P.T., 2000. An account of ichthhyofauna of Niconar and Andaman islands, Bay of Bengal. Records of the Zoological Survey of India Occ. Paper 178, 1-434

NW Australia

Blaber, S.J.M., Salini, J.P., Brewer, D.T., 1990. A checklist of fEshes from Albatross Bay and the Embley estuary, North-eastern Gulf of Carpentaria. CSIRO Marine Lab. Report 210: 22 pp.

Oman

Al-Jufaili, S.M., Hermosa, G., Al-Shuaily, S.S., Al Mujaini, A., 2010. Oman Fish biodiversity JKAU: Mar. Sci. 21, 3-51.

Randall, J. E., 1995. Coastal fishes of Oman. University of Hawaii Press, Honolulu.

Red Sea

Baranes, A., Golani, D., 1993. An annotated list of deep-sea fishes collected in the northern Red Sea, Gulf of Aqaba. Israel Journal of Zoology. 39, 299-336.

Bonfil, R. ,Abdallah, M., 2004. Field Identification Guide to the Sharks and Rays of the Red Sea and Gulf of Adan. FAO of the UN, Rome. 71pp +xii plates.

Dor, M., 1984. CLOFRES - Checklist of the Fishes of the Red Sea. Israel Academy of Sciences and Humanities, Jerusalem, xxii+437 pp.

Golani, D., Bogorodsky, S.V., 2012. The fishes of the Red Sea -Reappraisal and Updated Checklist

Khalaf, M., 2004. Fish Fauna of the Jordanian Coast, Gulf of Aqaba, Red Sea JKAU Marine Sci. 15, 23-50.

Randall, J.E. 1994. Twenty two new records of fishes from the Red Sea. Fauna of Saudi Arabia, 14, 259-275.

Seychelles

Smith, J.L.B., Smith, M.M., 1963. The Fishes of Seychelles. 215 p. Grahamstown: Rhodes Univ., Department Ichthyology

Smith, J.L.B., Smith, M.M., 1963. The fishes of Seychelles, i-viii + 1-215, 98 pls; Grahamstown (Department of Ichthyology, Rhodes University).

Socotra

Kemp, J.M., 1998. Zoogeography of the coral reef fishes of the Socotra archipelago J. Biogeogr. 25, 919–933.

South Africa

Heemstra, P.C., Heemstra, E., 2004. Coastal fishes of southern Africa. South African Institute for Aquatic Biodiversity (SAIAB) and National Inquiry Service Center (NISC), Grahamstown, 488 pp.

Smith, M.M., Heemstra, P.C. (eds.), 1986. Smith's sea fishes. Macmillan, Johannesburg, 1047 p., 144 pls.

Smith, M.M., Heemstra, P.C., 2003. Smith's sea fishes. Struik Publishers.

Wood, A.D., Brouwer, S.L., Cowley, P.D., Harrison, T.D. An updated check list of the ichtyofaunal species assemblage of te Tsitsikamma national Park,South Africa. Koedoe 43, 88-95.

Smith, M.M., 1980. Marine fishes of Maputaland. In : Studies on the ecology of Maputaland. Bruton M.N. and Cooper K.H. (eds). Rhodes University, Grahamstown and Wildlife Society. Durban : 164-187.

Van des Elst, R.P., 1988. Shelf ichtyofauna of Natal. In: Coastal ocean studies off Natal. South Africa. Schumann E.H. (ed.). Springer. Berlin: 209-225.

Tanzania

Lugendo, B.R., Nagelkerken, Y., Jiddawi, N., Mgaya, Y.N., van der Velde, G., 2007. Fish community composition of a tropical nonestuarine embayment in Zanzibar, Tanzania. Fisheries Sci. 73, 1213–1223.

Thailand

Chavalit Vidthayanon, A., Siraprapha Premcharoen, B., 2002. The status of estuarine fish diversity in Thailand. Marine and Freshwater Research 53, 471-478.

Allen, G.R., Stone, G.S. (eds.) 2005. Rapid assessment survey of tsunami-affected reefs of Thailand, final technical report. New England Aquarium Technical Report 02-05

Satapoomin, U., 2000. A preliminary checklist of coral reef fishes of the Gulf of Thailand, South China Sea. The Raffles Bulletin of Zoology 48,31-53

W. Australia

Allen, G.R., 2000. Fishes of the Montebello Islands. In Berry, P.F. and Wells, F.E. (eds.), Survey of the marine fauna and habitats of the Montebello Islands, Western Australia. Records of the Western Australian Museum Supplement No. 59: 47-57.J

Allen, G.R., 1993. Fishes of Ashmore and Cartier Island, pp. 67-91 In: Berry, P.F. (ed.) Marine faunal survey of Ashmore Reef and Cartier Island, north-western Australia. Records of the Western Australian Museum, Supplement 44.

Allen, G.R., 1996. New records of reef and shore fishes from north-western Australia. Records of the Western Australian Museum, 18(1): 109-112.

Allen, G.R., Russell, B.C., 1986. Part VII. Fishes, pp 79-103 In: Berry, P.F. (ed.) Faunal Surveys of the Rowley Shoals, Scott Reef, and Seringapatam Reef, north-western Australia. Records of the Western Australian Museum, Supplement 25.

Berry, P.F., 1993. Historical background, description of the physical environments of Ashmore Reef and Cartier Island and notes on exploited species. Pp 1-11 In: Berry, P.F. (ed.)Marine faunal survey of Ashmore Reef and Cartier Island, north-western Australia. Records of the Western Australian Museum, Supplement 44.

Hutchins, J.B., 2003 Checklist of marine fishes of the Dampier Archipelago, Western Australia in F.E. Wells, D.I. Walker and D.S. Jones (eds) 2003. The Marine Flora and Fauna of Dampier, Western Australia. Western Australian Museum, Perth.455-478

Hutchins, J.B., 1998. Survey of the fishes of Ashmore Reef. Report prepared for Parks Australia North, Western Australian Museum of Natural Science, August 1998.

Hutchins, J.B., Williams, D.McB., Newman, S.J., Cappo, M., Speare, P,. 1995. New records of fishes for the Rowley Shoals and Scott/Seringapatam reefs, off north-western Australia. Records of the Western Australian Museum 17: 119-123.

Russell, B.C., Hanley, J.R. (eds.) 1993. The Biological Resources and Heritage Values of the Cartier and Hibernia Reef Systems, Timor Sea. Report of the Northern Territory Museum Cartier and Hibernia Reefs Expedition, May 1992. Australian National Parks and Wildlife Service, Canberra.

General

Al-Absy, A.H., 1988. Review of the goatfishes (Pisces: Perciformes: Mullidae) in the Gulf of Aqaba, Red Sea, Fauna of Saudi Arabia, 9: 152-168.

Allen, G.R., 2002. Descriptions of two new species of damselfishes (Pomacentridae: Pomacentrus) from Madagascar. Journal of Ichthyology and Aquatic Biology 6, 45-52.

Allen, G.R., Cross, N., Allen, C., Gomon, M., 2006. Labridae: Wrasses. Zoological Catalogue of Australia. Volume 35. Fishes.

Allen, G.R., Randall, J.E., 1980. A review of the damselfishes (Teleostei: Pomacentridae) of the Red Sea. Israel Journal of Zoology, 29, 1-98.

Allen, G.R., Steene, R., 1988. Reef Fishes of the Indian Ocean. A Pictorial Guide to the common reef fishes of the Indian Ocean. T.F.H. Publications, Neptune City, N.J., 240 pp.

Allen, G.R., Steene, R., Allen, M., 1998. Guide to Angelfishes and Butterflyfishes, Odyssey Press. Baranes, A. and Golani, D. (1993) An annotated list on deep-sea fishes collected in the northern Red Sea, Gulf of Aqaba, Israel J. Zool., 39: 299-336.

Anderson, M.E., Heemstra, P.C., 2003. Review of the glassfishes (Perciformes: Ambassidae) of the western Indian Ocean. Cybium, 27, 199-209.

Carpenter, K.E., Krupp, F., Jones, D.A., Zajonz, U., 1997. FAO species identification guide for fishery purposes. The living marine resources of Kuwait, Eastern Saudi Arabia, Bahrain, Qatar and the United Arab Emirates. FAO, Rome 293 pp. 17 colour plates

Carpenter, K.E., Allen, G.R., 1989. FAO species catalogue. Emperor fishes and large-eye breams of the world (family Lethrinidae). An annotated and illustrated catalogue of Lethrinidae species known to date. FAO Fisheries Synopsis. No. 125. Vol. 9. Rome FAO. 118 pp.

Chakrabarty, P., Sparks, J.S., 2008. Diagnoses for Leiognathus Lacepède 1802, Equula Cuvier 1815, Equulites Fowler 1904, Eubleekeria Fowler 1904, and a new Ponyfish genus (Teleostei: Leiognathidae). Novitates,3623, 1-11.

Debelius, H., 1993. Indian Ocean tropical fish guide, 321 pp. Aquaprint Verlags GmbH, Neu Isenberg, Germany.

Fischer, W., Bianchi, G. (eds.) FAO species identification sheets for fishery purposes. Western Indian Ocean (Fishing Area 51). Volume 4. FAO, Rome.

Fraser, T.H., 2008. Cardinalfishes of the genus Nectamia (Apogonidae, Perciformes) from the Indo-Pacific region with descriptions of four new species. Zootaxa 1691, 1-52.

Fraser, T.H., Randall, J.E., Lachner, E.A., 1999. A review of the Red Sea cardinalfishes of the Apogon bandanensis complex, with a description of a new species. Special Publication, J.L.B. Smith Institute of Ichthyology 63, 1-13.

Gill, A.C., 2004. Revision of the Indo-Pacific dottyback fish subfamily Preudochromidae (Perciformes: Pseudochromidae). Smithiana Monograph, 1-213.

Gill, A.C., Edwards, A.J., 2004. Revision of the Indian Ocean Dottyback fish genera Chlidichthys and Pectinochromis (Perciformes: Pseudochromidae: Pseudoplesiopinae). Smithiana, Publication in Aquatic Biodiversity 3, 46 pp.

Gill, A.C., Fricke, R., 2001. Revision of the western Indian Ocean fish subfamily Anisochrominae (Perciformes, Pseudochromidae). – Bulletin of the Natural History Museum London (Zoology) 67, 191-207.

Gon, O., Randall, J.E., 2003a. A review of the Cardinalfishes (Perciformes: Apogonidae) of the Red Sea. Smithiana Bulletin (The South African Institute for Aquatic Biodiversity. Grahamstown) 1, 1-46.

Gon, O, Randall, J.E., 2003b. Revision of the Indo-Pacific Cardinalfishes genus Archamia (Perciformes: Apogonidae) with description of a new species. Indo-Pacific Fishes, 35, 1-49 + III plates.

Heemstra, P.C., Randall, J.E., 1993. Groupers of the World (Family Serranidae, Subfamily Epinephelinae). An annotated and illustrated catalogue of the grouper. FAO Fisheries Synopsis 125. FAO, Rome. 382 pp.

Heemstra, P.C., Randall, J.E., 2009. A review of the anthiine fish genus Plectranthias (Perciformes: Serranidae) of the western Indian Ocean, with description of a new species, and a key to the apecies. Smithiana Bulletin, 10, 3-17.

Herler, J., Hilgers, H., 2005. A synopsis of coral and coral-rock associated gobies (Pisces: Gobiidae) from Gulf of Aqaba, northern Red Sea. Aqua 10, 103-132.

Holleman, W., 2005. A review of the triplefin fish genus Enneapterygius (Blennioidei: Tripterygiidae) in the western Indian Ocean, with descriptions of four new species. Smithiana, Publications in Aquatic Biodiversity, 5, 1-25 + 2 plates.

Holleman, W., 2007. Fishes of the genus Helcogramma (Blennioidei: Tripterygiidae) in the western Indian Ocean, including Sri Lanka, with descriptions of four new species. – Smithiana, Publications in Aquatic Biodiversity, Bulletin 7: 51-81.

Hutchins, J.B., 1997. Review of the monacanthid fish genus Paramonacanthus, with descriptions of three new species. Records of the Western Australia Museum (Suppl.) 54, 1-57.

Inoue, T., Nakabo, T., 2006. The Saurida undosquamis group (Aulopiformes: Synodontidae), with description of a new species from southern Japan. Ichthyological Research, 53, 379-397.

Jaafar, Z., Randall, J.E., 2009. A pictorial review and key to the shrimp gobies of the genus Amblyeleotris of the Red Sea, with description of a new species. Smithiana Bulletin 10, 23-29.

Knapp, L.W., 1996. Review of the genus Coeciella Whitley (Teleostei: Platycephalidae) with the description of three new species. Proceedings of the Biological Society of Washington, 109, 17-33.

Kuiter, R.H., Tonozuka, T., 2001. Pictorial guide to Indonesian reef fishes. Part 2. Fusiliers - Dragonets, Caesionidae - Callionymidae. Zoonetics, Australia. 304-622 p.

Kuiter, R.H., 1998. Pipefishes of the syngnathid genus Dunckerocampus (Sygnathiformes: Syngnathidae), with a description of a new species from the Indian Ocean. – Aqua, Journal of Ichthyology and Aquatic Biology 3: 81-84.

Kuiter, R.H., Randall, J.E. ,1981. Three look-alike Indo-Pacific labrid fishes, Halichoeres margaritaceus, H. nebulosus and H. miniatus. Revue française d'Aquariologie 8, 13-18.

Kuiter, R.H., 2002. Fairy and rainbow wrasses and their relatives. A comprehensive guide to selected Labroids. Chorleywood, Herts: TMC Publishing. 208 pp.

Kuiter, R.H., 2000. Seahorses, pipefishes and their relatives. TMC Publishing, Chorleywood, UK.

Lachner, E.A., Karnella, S.J., 1978. Fishes of the genus Eviota of the Red Sea with descriptions of three new species (Teleostei: Gobiidae). – Smithsonian Contributions to Zoology 286: 1-23.

Lachner, E.A., Karnella, S.J., 1980. Fishes of the Indo-Pacific genus Eviota with descriptions of eight new species (Teleostei: Gobiidae). – Smithsonian Contributions to Zoology 315: i-iii + 1-127.

Larson, H.K., 1990. A revision of the commensal gobiid fish genera Pleurosicya and Luposicya (Gobiidae), with descriptions of eight new species of Pleurosicya and discussion of related genera. Beagle, Records of the Northern Territory Museum , 7(1): 1-53.

Lourie, S.A., Foster, S.J., Cooper, E.W.T., Vincent, A.C.J., 2004. A Guide to the Identification of Seahorses. Project Seahorse and TRAFFIC North America. 114 pp.

Markle , D.F., Olney, J.E., 1990. Systematics of the Pearlfishes (Pisces: Carapidae). Bulletin of Marine Science, 47, 269-410

McCosker, J.E., 1998. A revision of the snake-eel genus Callechelys (Anguilliformes: Ophichthidae) with the description of two new Indo-Pacific species and a new Callechelyin genus. Proceedings of the California Academy of Sciences, 50(7),185-215.

Menon, A.G.K., 1977. A systematic monograph of the tongue soles of the genus Cynoglossus Hamilton-Buchanan (Pisces: Cynoglossidae). Smithsonian Contribution to Zoology, 238, 1-129.

Mooi, R.D., 1995. Revision, phylogeny and discussion of biology and biogeography of the fish genus Plesiops (Perciformes: Plesiopidae). Royal Ontario Museum of Life Sciences Contributions, 159. IV+107 pp.

Parin, N.V., Collette, B.B., Shcherbachev, Y.N., 1980. Beloniformes fishes of the world oceans. Trudy Okeanologii Instituta anUSSR, 97, 1-173.

Randall, J.E., 1978. A revision of the Indo-Pacific labrid genus Macropharyngodon, with descriptions of five new species. Pacific Science, 28(4), 742-770.

Randall, J.E., 1982. A review of the labrid fish Genus Hologymnosus. Revue française d'Aquaecologie, 9(1): 13-20.

Randall, J.E., 1983. Red Sea Fishes. IMMEL, London, 192 p, 465 col. Figs.

Randall, J.E., 1986. Sharks of Arabia. IMMEL, London, 148 p.

Randall, J.E., 1999. Revision of the Indo-Pacific labrid fishes of the genus Coris, with description of five new species. Indo-Pacific Fishes, 29, 1-74.

Randall, J.E., 2001b. Five new Indo-Pacific gobiid fishes of the genus Coryphopterus. Zoological Studies. 40, 206-225.

Randall, J.E., 2001c. Surgeonfishes of Hawai'i and the World. Mutual Publishing and Bishop Museum Press, Hawai'i. 123 pp.

Randall, J.E., 2004. Revision of the goatfish genus Parupeneus (Perciformes: Mullidae), with descriptions of two new species. – Indo-Pacific Fishes 36: 1-64, pls. 1-16.

Randall, J.E., Baldwin, C.C., 1997. Revision of the serranid fishes of the subtribe Pseudogrammina, with descriptions of five new species. Indo-Pacific Fishes, 26. 56 pp.

Randall, J.E., Bruce, R.W., 1982. The parrotfishes of the subfamily Scarinae of the western Indian Ocean, with descriptions of three new species. Ichthyological Bulletin of the J.L.B. Smith Institute of Ichthyology, 47, 1- 39 pp.

Randall, J.E., Clements, K.D., 2001. Second revision of the surgeonfish genus Ctenochaetus (Perciformes: Acanthuridae), with descriptions of two new species. – Indo-Pacific Fishes 32: 1-33, pls. 1-6.

Randall, J.E., Gon, O., 2006. Review of the soles of the genus Aseraggodes of the western Indian Ocean, with descriptions of three new species. – Israel Journal of Zoology 51: 165-190.

Randall, J.E., Heemstra, P.C., 1985. A review of the squirrelfishes of the subfamily Holocentrinae from the western Indian Ocean and Red Sea. – Ichthyological Bulletin of the J. L. B. Smith Institute of Ichthyology 49: 1-27, 2 pls.

Randall, J.E., Earle, J.L., 2002. Review of Hawaiian razorfishes of the genus Iniistius (Perciformes: Labridae). Pacific Science, 56, 389-402.

Randall, J.E., Eschmeyer, W.N., 2001. Revision of the Indo-Pacific scorpionfish genus Scorpaenopsis, with descriptions of eight new species. Indo-Pacific Fishes, 34, 1-79.

Randall, J.E., Golani, D., 1995. Review of the moray eels (Anguilliformes: Muraenidae) of the Red Sea. Bulletin of Marine Science, 56, 849-880.

Randall, J.E., Gon, O., 2005. Review of the soles of the genus Aseraggodes of the western Indian Ocean, with descriptions of three new species. Israel Journal of Zoology, 51, 165-190.

Randall, J.E., Goren, M., 1993. A review of the gobioid fishes of the Maldive Islands. Ichthyological Bulletin, 58, 1-37.

Randall, J.E., Heemstra, P.C., 1991. Revision of Indo-Pacific groupers (Perciformes: Serranidae: Epinephelinae), with descriptions of five new species. Indo-Pacific Fishes, 20, 1-332.

Randall, J.E., Hoese, D.F., 1986. Revision of the Indo-Pacific genus Plectropomus (Percifermes: Serranidae). Indo-Pacific Fishes

Randall, J.E., Smith, M.M., 1982. A review of the labrid fishes of the genus Halichoeres of the western Indian Ocean, with descriptions of six new species. Ichthyological Bulletin of the J.L.B. Smith Institute of Ichthyology, 45, 1-26.

Randall, J.E., Shao, K.-T., Chen, J.-P., 2003. A review of the Indo-Pacific gobiid fish genus Ctenogobiops, with descriptions of two new species. Zoological Studies, 42, 506-515.

Randall, J.E., Shimizu, T., Yamakawa, T., 1982. A revision of the holocentrid fish genus Ostichthys, with descriptions of four new species and a related new genus. Japanese Journal of Ichthyology, 29, 1-26.

Randall, J.E., Williams, J.T. & Rocha, L.A. (2008). The Indo-Pacific tetraodontid fish Canthigaster coronata, a complex of three species. Smithiana, Publications in Aquatic Biodiversity, 9, 3-13.

Ringer, V.G., Williams, J.T., 1994. The Indo-Pacific blenniid fish genus Istiblennius reappraised: a revision of Istiblennius, Blenniella, and Paralticus, new genus. – Smithsonian Contributions to Zoology 565, i-iv + 1-193.

Russell, B.C., Golani, D., 1993. A review of the fish genus Parascolopsis (Nemipteridae) of the western Indian Ocean, with description of a new species from the northern Red Sea. Israel Journal of Zoology 39,337-347.

Russell, B.C., 1985. Revision of the Indo-Pacific labrid fish genus Suezichthys, with descriptions of four new species. Indo-Pacific Fishes, 2, 1-21.

Schwarzhans, W., Møller, P.R., 2007. Review of the Dinematichthyini (Teleostei: Bythitidae) of the Indo-west Pacific. Part III. Beaglichthys, Brosmolus, Monothrix and eight new genera with description of 20 new species. – The Beagle, Records of the Museums and Art Galleries of the Northern Territory 23, 29-110.

Schwarzhans, W., Møller, P.R., Nielsen, J.G., 2005. Review of the Dinematichthyini (Teleostei: Bythitidae) of the Indo-West Pacific. Part I. Diancistrus and two new genera with 26 new species. – The Beagle, Records of the Museums and Art Galleries of the Northern Territory 21: 73-163.

Smith-Vaniz, W.F., 1989. Revision of the jawfish genus Stalix (Pisces: Opistognathidae), with descriptions of four new species. Proceedings of the Academy of Natural Sciences Philadelphia, v. 141, 375-407.

Smith-Vaniz, W.F., 2010. New species of Indo-Pacific jawfishes (Opisthognathus: Opistognathidae) from the western Indian Ocean and Red Sea. – Smithiana, Publications in Aquatic Biodiversity, Bulletin 12: 39-54.

Smith-Vaniz, W.F., 1987. The saber-toothed blennies, tribe Nemophini (Pisces: Blenniidae): an update. Proceedings of the Academy of Natural Sciences Philadelphia, 139, 1-52.

Springer, V.G., Williams, J.T. , 1994. The Indo-West Pacific blenniid fish genus Istiblenius reappraised: a revision of Istiblennius, Blenniella, and Paralticus, new genus. Smithsonian Contributions to Zoology 565, 1-193.

Uiblein, F., 2011. Taxonomic review of western Indian Ocean goatfishes of the genus Mulloidichthys (Family Mullidae), with description of a new species and remarks on colour and body form variation in Indo-West Pacific species. – Smithsiana, Publications in Aquatic Biodiversity Bulletin 13, 51-73.

Winterbottom, R., 1995. Red Sea gobiid fishes of the genus Trimma, with the description of two new species. Revue française d'Aquariologie 22, 93-98.

**Table S2** Total number of species (*N*) and number of species with a limited geographic range for each biogeographic region. *Local*, *provincial* and *regional* ranges are defined in the main text. *All* sum of the numbers of species with limited range (also expressed as % of *N*)

| Province [a] | | *N* | No. species with limited geographic range | | | |
|---|---|---|---|---|---|---|
| Name | Abbreviation | | Local | Provincial | Regional | All |
| Andaman - Cocos - Christmas | AND | 1068 | 5 | 5 | 16 | 26  (2.4%) |
| Eastern African coast | EAF | 1532 | 9 | 7 | 85 | 101   (6.6%) |
| East India – Thailand - Malaysia | EI | 1728 | 18 | 22 | 66 | 106   (6.1%) |
| Maldives – Laccadives - Chagos | MLC | 1410 | 11 | 15 | 42 | 68  (4.8%) |
| Northern Australia | NAU | 761 | 1 | 4 | 15 | 20  (2.6%) |
| Northwestern Indian Ocean | NWI | 1304 | 16 | 58 | 101 | 175 (13.4%) |
| Spencer Gulf Province | SCI | 612 | 0 | 8 | 63 | 71 (11.6%) |
| Southwestern Indian Ocean | SWI | 1070 | 38 | 38 | 66 | 142 (13.3%) |
| Western Australia | WAU | 1931 | 5 | 23 | 71 | 99  (5.1%) |
| Western Indian Ocean Islands | WII | 1572 | 22 | 23 | 102 | 147  (9.4%) |
| Western Indian Ocean [b] | WIO | 1826 | 27 | 23 | 155 | 205 (11.2%) |

[a]  delimited according to Kulbicki et al. (2013)
[b]  defined by merging EAF and WII provinces

**Table S3** Population-pairwise $\phi_{ST}$ estimates (Excoffier et al., 1992) for *Dascyllus abudafur / D. aruanus*. *Abbreviations for samples*: as in Borsa et al. (2014). Sample names arranged from West to East. WIO samples are EU, JN, MD and GL; the other Indian-Ocean sample is RS; Pacific-Ocean samples are PI, DS, TW, LL, SK, RA, MA, NC and SI. Table cells are toned grey, whose intensity is positively correlated with value of $\phi_{ST}$ estimate (ARLEQUIN 3.5; Excoffier and Lischer, 2010). Probability of $\phi_{ST}$ value under null hypothesis of genetic homogeneity estimated from 1,000 random permutations under ARLEQUIN. * $P<0.05$; ** $P<0.01$; *** $P<0.001$

| Sample | Sample | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | RS | EU | JN | MD | GL | PI | DS | TW | LL | SK | RA | MA | NC |
| EU | 0.354*** | | | | | | | | | | | | |
| JN | 0.369*** | -0.039 | | | | | | | | | | | |
| MD | 0.353*** | -0.028 | -0.080 | | | | | | | | | | |
| GL | 0.386*** | 0.000 | -0.015 | 0.052 | | | | | | | | | |
| PI | 0.803*** | 0.703*** | 0.744*** | 0.735*** | 0.650*** | | | | | | | | |
| DS | 0.800*** | 0.713*** | 0.744*** | 0.739*** | 0.668*** | 0.102* | | | | | | | |
| TW | 0.811*** | 0.735*** | 0.771*** | 0.759*** | 0.708*** | 0.061 | -0.020 | | | | | | |
| LL | 0.779*** | 0.703*** | 0.729*** | 0.723*** | 0.668*** | 0.026 | -0.006 | -0.016 | | | | | |
| SK | 0.767*** | 0.685*** | 0.708*** | 0.705*** | 0.637*** | 0.032 | 0.021 | 0.015 | -0.010 | | | | |
| RA | 0.770*** | 0.693*** | 0.719*** | 0.711*** | 0.651*** | 0.079 | 0.180** | 0.142** | 0.090** | 0.029 | | | |
| MA | 0.785*** | 0.676*** | 0.680** | 0.703*** | 0.560** | 0.202* | 0.126 | 0.146* | 0.104 | 0.014 | 0.042 | | |
| NC | 0.694*** | 0.621*** | 0.625*** | 0.632*** | 0.563*** | 0.117** | 0.060 | 0.085* | 0.068* | 0.020 | 0.079* | -0.050 | |
| SI | 0.859*** | 0.802*** | 0.836*** | 0.824*** | 0.783*** | 0.556*** | 0.549*** | 0.552*** | 0.500*** | 0.513*** | 0.547*** | 0.625*** | 0.466*** |

**Table S4** Population-pairwise $\phi_{ST}$ estimates (Excoffier et al., 1992) for *Epinephelus merra*, computed using ARLEQUIN 3.5 (Excoffier and Lischer, 2010). *Abbreviations for samples*: NCA, New Caledonia; MRU, Moruroa atoll, Gambier archipelago; else same locations and same 9bbreviations as in Muths et al. (2014). Sample names arranged from West to East. WIO samples are EUR, GEY, GLO, JDN, KEN, MAD, MAY, MOH, MOR, REU, ROD, SEY and TAN; the other Indian-Ocean sample is MAL; Pacific-Ocean samples are NCA and MRU. Table cells are toned grey, with intensity of grey tone positively correlated with value of $\phi_{ST}$ estimate. Probability of $\phi_{ST}$ value under null hypothesis of genetic homogeneity estimated from 1,000 random permutations under ARLEQUIN. * $P<0.05$; ** $P<0.01$; *** $P<0.001$

| Sample | Sample | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | TAN | KEN | EUR | JDN | MOR | MOH | MAY | GEY | GLO | MAD | SEY | REU | MAU | ROD | MAL | NCA |
| KEN | 0.007 | | | | | | | | | | | | | | | |
| EUR | -0.032 | 0.020 | | | | | | | | | | | | | | |
| JDN | -0.030 | 0.065 | 0.005 | | | | | | | | | | | | | |
| MOR | 0.018 | 0.214** | 0.046* | 0.020 | | | | | | | | | | | | |
| MOH | -0.033 | 0.031 | -0.013 | -0.015 | 0.039* | | | | | | | | | | | |
| MAY | -0.026 | 0.170 | 0.010 | -0.019 | -0.060 | 0.003 | | | | | | | | | | |
| GEY | -0.032 | 0.080 | 0.002 | -0.013 | 0.015 | -0.007 | -0.033 | | | | | | | | | |
| GLO | -0.033 | 0.084* | 0.000 | -0.012 | 0.007 | -0.008 | -0.038 | -0.016 | | | | | | | | |
| MAD | 0.077* | 0.307*** | 0.090** | 0.055* | 0.003 | 0.083** | -0.057 | 0.034* | 0.036* | | | | | | | |
| SEY | -0.050 | 0.057 | -0.006 | -0.017 | 0.022 | -0.011 | -0.026 | -0.020 | -0.017 | 0.056* | | | | | | |
| REU | 0.015 | 0.198** | 0.059* | 0.033 | 0.005 | 0.057* | -0.053 | 0.011 | 0.018 | -0.011 | 0.009 | | | | | |
| MAU | -0.026 | 0.109* | 0.009 | -0.009 | 0.000 | 0.004 | -0.051 | -0.012 | -0.011 | 0.015 | -0.018 | 0.004 | | | | |
| ROD | 0.102* | 0.344*** | 0.128*** | 0.086** | 0.022 | 0.120*** | -0.031 | 0.068** | 0.063** | 0.002 | 0.075* | -0.006 | 0.042* | | | |
| MAL | 0.189** | 0.006 | 0.161*** | 0.222*** | 0.369*** | 0.178*** | 0.356*** | 0.240*** | 0.242*** | 0.445*** | 0.230*** | 0.368*** | 0.274*** | 0.480*** | | |
| NCA | -0.016 | 0.069 | 0.024 | 0.026 | 0.050 | 0.025 | -0.005 | 0.016 | 0.018 | 0.093* | 0.025 | 0.054 | 0.023 | 0.138** | 0.247** | |
| MRU | -0.072 | -0.140 | -0.029 | 0.023 | 0.199 | 0.003 | 0.224 | 0.043 | 0.042 | 0.336* | 0.018 | 0.168 | 0.060 | 0.371 | 0.076 | -0.201 |

**Table S5** Population-pairwise $\phi_{ST}$ estimates (Excoffier et al., 1992) for *Lutjanus kasmira*, computed using Arlequin 3.5 (Excoffier and Lischer, 2010). Samples Christmas Island (*CHR*), Cocos-Keeling (*COC*), Diego Garcia (*DIE*), Fiji (*FIJ*), Guam (*GUA*), Kiritimati (*KIR*), Lizard Island (*LIZ*), Marquesas (*MAR*), Moorea (*MOO*), Okinawa (*OKI*), Seychelles (*SEC*) and Sodwana Bay (*SOD*) from Gaither et al. (2010); *other abbreviations*: *NOS*, Nosy Be (Muths et al., 2012), else as in Muths et al. (2014). Sample names arranged from West to East. WIO samples are SOD, TAN, KEN, EUR, JDN, MOR, MOH, MAY, GEY, GLO, NOS, MAD, SEC, SEY, REU, MAU and ROD; the other Indian-Ocean samples are DIE, MAL, COC and CHR; Pacific-Ocean samples are OKI, LIZ, GUA, FIJ, KIR, MOO and MAR. Table cells are toned grey, with intensity of grey tone positively correlated with value of $\phi_{ST}$ estimate. Probability of $\phi_{ST}$ value under null hypothesis of genetic homogeneity estimated from 1,000 random permutations under Arlequin. * $P<0.05$; ** $P<0.01$; *** $P<0.001$

| Sample | SOD | TAN | KEN | EUR | JDN | MOR | MOH | MAY | GEY | GLO | NOS | MAD | SEC | SEY |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| TAN | 0.016 | | | | | | | | | | | | | |
| KEN | -0.016 | 0.002 | | | | | | | | | | | | |
| EUR | -0.006 | 0.021 | -0.011 | | | | | | | | | | | |
| JDN | 0.000 | 0.006 | -0.007 | -0.003 | | | | | | | | | | |
| MOR | -0.005 | 0.000 | 0.000 | -0.002 | -0.011 | | | | | | | | | |
| MOH | 0.001 | 0.009 | 0.009 | 0.001 | -0.010 | -0.013 | | | | | | | | |
| MAY | -0.009 | 0.007 | -0.012 | -0.008 | -0.005 | -0.005 | 0.003 | | | | | | | |
| GEY | 0.008 | 0.014 | 0.005 | 0.005 | -0.010 | -0.008 | -0.005 | 0.000 | | | | | | |
| GLO | -0.005 | 0.002 | -0.007 | -0.006 | -0.013 | -0.014 | -0.011 | -0.006 | -0.009 | | | | | |
| NOS | -0.006 | -0.010 | 0.002 | 0.011 | -0.006 | -0.013 | -0.011 | 0.003 | 0.000 | -0.006 | | | | |
| MAD | -0.014 | -0.003 | 0.008 | -0.004 | -0.014 | -0.023 | -0.027 | -0.007 | -0.003 | -0.019 | -0.028 | | | |
| SEC | -0.007 | 0.000 | -0.026 | -0.004 | -0.021 | -0.020 | -0.015 | -0.010 | -0.021 | -0.020 | -0.014 | -0.017 | | |
| SEY | -0.011 | -0.028 | -0.017 | 0.009 | -0.017 | -0.019 | -0.010 | -0.006 | 0.003 | -0.014 | -0.028 | -0.026 | -0.031 | |
| RUN | 0.004 | 0.010 | -0.008 | 0.008 | -0.012 | -0.001 | 0.001 | 0.003 | 0.000 | -0.001 | -0.002 | -0.008 | -0.010 | -0.010 |
| MAU | 0.042* | 0.061* | 0.051* | 0.053** | 0.055*** | 0.047** | 0.058*** | 0.037** | 0.037** | 0.051** | 0.055*** | 0.046** | 0.043 | 0.054* | 0.061* |
| ROD | -0.005 | 0.019 | 0.002 | 0.003 | 0.002 | 0.004 | 0.006 | -0.002 | 0.015 | 0.008 | 0.004 | 0.005 | 0.004 | 0.009 |
| DIE | -0.006 | -0.002 | 0.002 | 0.014 | -0.001 | -0.011 | -0.004 | 0.001 | 0.002 | -0.003 | -0.023 | -0.024 | -0.016 | -0.026 |
| MAL | -0.014 | -0.016 | -0.035 | -0.015 | -0.012 | -0.018 | -0.004 | -0.022 | -0.008 | -0.018 | -0.006 | -0.011 | -0.022 | -0.028 |
| COC | 0.003 | 0.002 | 0.006 | 0.000 | -0.003 | -0.001 | -0.001 | 0.001 | -0.001 | -0.003 | 0.002 | -0.009 | 0.002 | 0.009 |
| CHR | 0.011 | 0.023 | 0.006 | 0.024 | 0.007 | 0.006 | 0.019 | 0.005 | 0.011 | 0.010 | 0.010 | 0.023 | -0.006 | -0.002 |
| OKI | -0.303 | -0.292 | -0.331 | -0.317 | -0.317 | -0.308 | -0.313 | -0.305 | -0.311 | -0.317 | -0.298 | -0.305 | -0.327 | -0.315 |
| LIZ | -0.066 | -0.058 | -0.069 | -0.054 | -0.070 | -0.073 | -0.057 | -0.076 | -0.051 | -0.069 | -0.064 | -0.026 | -0.071 | -0.082 |
| GUA | 0.016* | 0.030* | 0.015 | 0.014* | 0.006 | 0.011 | 0.015* | 0.007 | 0.012 | 0.009 | 0.023** | 0.021 | 0.012 | 0.026* |
| FIJ | 0.023** | 0.026 | 0.019 | 0.015* | 0.004 | 0.007 | 0.012 | 0.010 | 0.009 | 0.005 | 0.021* | 0.030 | 0.007 | 0.024 |
| KIR | 0.032*** | 0.039* | 0.024 | 0.032*** | 0.015* | 0.021** | 0.027** | 0.018* | 0.023* | 0.021*** | 0.034*** | 0.030 | 0.018 | 0.028* |
| MOO | 0.040*** | 0.066** | 0.046* | 0.031*** | 0.036*** | 0.033 | 0.036*** | 0.028 | 0.036** | 0.035*** | 0.047 | 0.026* | 0.042** | 0.063 |
| MAR | 0.546*** | 0.569*** | 0.538*** | 0.590*** | 0.571*** | 0.560*** | 0.586*** | 0.548*** | 0.584*** | 0.575*** | 0.551*** | 0.578*** | 0.539*** | 0.515*** |

| Sample | RUN | MAU | ROD | DIE | MAL | COC | CHR | OKI | LIZ | GUA | FIJ | KIR | MOO |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| MAU | 0.039* | | | | | | | | | | | | |
| ROD | 0.003 | 0.038* | | | | | | | | | | | |
| DIE | 0.003 | 0.034* | 0.006 | | | | | | | | | | |
| MAL | -0.003 | 0.050* | 0.000 | -0.005 | | | | | | | | | |
| COC | 0.003 | 0.039* | 0.008 | 0.007 | -0.007 | | | | | | | | |
| CHR | -0.009 | 0.045 | 0.009 | 0.007 | 0.001 | 0.018 | | | | | | | |
| OKI | -0.312 | -0.224 | -0.292 | -0.292 | -0.327 | -0.328 | -0.297 | | | | | | |
| LIZ | -0.081 | -0.009 | -0.067 | -0.062 | -0.087 | -0.064 | -0.090 | -0.290 | | | | | |
| GUA | 0.005 | 0.064*** | 0.012 | 0.029** | 0.007 | 0.003 | -0.004 | -0.307 | -0.101 | | | | |
| FIJ | 0.004 | 0.070** | 0.021* | 0.028** | 0.007 | 0.001 | -0.007 | -0.311 | -0.092 | -0.010 | | | |
| KIR | 0.014* | 0.077*** | 0.031** | 0.039*** | 0.012 | 0.021* | -0.007 | -0.282 | -0.100 | -0.007 | -0.005 | | |
| MOO | 0.036 | 0.048*** | 0.043 | 0.046*** | 0.037** | 0.028** | 0.028** | 0.047* | -0.021 | 0.042*** | 0.043*** | 0.054*** | |
| MAR | 0.553*** | 0.606*** | 0.581*** | 0.528*** | 0.529*** | 0.612*** | 0.560*** | 0.499** | 0.551*** | 0.611*** | 0.618*** | 0.587*** | 0.627*** |

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**Table S6** Population-pairwise $\phi_{ST}$ estimates (Excoffier et al., 1992) for *Panulirus homarus*, computed using ARLEQUIN 3.5 (Excoffier and Lischer, 2010). Samples were constituted as following. *WIO* included samples Za and Tn of Lavery et al. (2014) excluding 3 haplotypes of Za assigned to *P. h. rubellus*; *NWIO* included samples Om, L and Ch of Lavery et al. (2014); *Kollam* included sample QLN of Jeena (2013); *SriLanka* included samples JSPHK and JSPHW of Senevirathna and Munasinghe (2014) (GENBANK nos. KC959890, KC959891 and KF548571) and sequences nos. KF715528-KF715550 and KF715552 from GENBANK; *Chennai* is sample CHE of Jeena (2013); *Visakhapatnam* included sample VSK of Jeena (2013) and sequence no. JN418937 from GENBANK; *SChinaSea* included samples Vn and Tw of Lavery et al. (2014) and sequences nos. JN542716 and JN591360 from GENBANK; *Marquesas* is sample M of Lavery et al. (2014). Sample names arranged from West to East. Indian-Ocean samples other than WIO are: NWIO, Kollam, SriLanka, Chennai and Visakhapatnam; Pacific-Ocean samples are SChinaSea and Marquesas. Table cells are toned grey, with intensity of grey tone positively correlated with value of $\phi_{ST}$ estimate. Probability of $\phi_{ST}$ value under null hypothesis of genetic homogeneity estimated from 1,000 random permutations under ARLEQUIN. * $P<0.05$; ** $P<0.01$; *** $P<0.001$

| Sample | Sample | | | | | | |
|---|---|---|---|---|---|---|---|
| | WIO | NWIO | Kollam | SriLanka | Chennai | Visakhapatnam | SChinaSea |
| NWIO | 0.284*** | | | | | | |
| Kollam | -0.025 | 0.022 | | | | | |
| SriLanka | -0.014 | 0.041 | -0.037 | | | | |
| Chennai | -0.013 | 0.127** | -0.033 | -0.036 | | | |
| Visakhapatnam | 0.068 | 0.064** | -0.011 | 0.016 | 0.022 | | |
| SChinaSea | -0.059 | 0.176*** | 0.024 | 0.035 | 0.034 | 0.059 | |
| Marquesas | 0.621** | 0.749*** | 0.610*** | 0.525*** | 0.619*** | 0.639*** | 0.531*** |

**Table S7** Population-pairwise $\phi_{ST}$ estimates (Excoffier et al., 1992) for *Terapon jarbua*, computed using ARLEQUIN 3.5 (Excoffier and Lischer, 2010) on the basis of partial *CO1* gene sequences. Samples were constituted as following. *Safrica* included four individual sequences from Kwazulu-Natal (GENBANK nos. JF494663-JF494666); *RedSea* included two individual sequences from the Gulf of Eilat (GENBANK nos. KJ466137, KJ466138); *Eparses* included seven new sequences from Juan de Nova; *Yemen* included all samples from Al-Mukalla and Socotra in Lavergne et al. (2014) (GENBANK nos. JQ342095-JQ342111); *Gulf* included three individual sequences from Bushehr, Persian Gulf (Asgharian et al., 2011) (GENBANK nos. HQ149959-HQ149961); *Windia* included a sequence published by Lakra et al. (2011) (GENBANK no. FJ237549) and three individual sequences fom the western coast of the Indian peninsula (GENBANK nos. KC774674, KF268188 and KF268189); *Eindia* included four individual sequences from the eastern coast of the Indian peninsula (GENBANK nos. FJ265859, JX260979, KC241987 and KC417308); *SchinaSea* included two sequences from off southeastern China (GenBank nos. EU871691, EU871692), three new sequences from around Nha Trang, Vietnam and 10 new sequences from around Kenting, Taiwan; *Philippines* included four individual sequences from the Philippines archipelago (GenBank nos. JN021254, JN021255, KC970423, KF009671). Sample names arranged from West to East. WIO samples are Safrica and RedSea; Indian-Ocean samples other than WIO are: RedSea, Yemen, Gulf, Windia and Eindia; Pacific-Ocean samples are SchinaSea and Philippines. Table cells are toned grey, with intensity of grey tone positively correlated with value of $\phi_{ST}$ estimate. Probability of $\phi_{ST}$ value under null hypothesis of genetic homogeneity estimated from 1,000 random permutations under ARLEQUIN. * $P<0.05$; ** $P<0.01$; *** $P<0.001$

| Sample | Sample | | | | | | | |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| | Safrica | RedSea | Eparses | Yemen | Gulf | Windia | Eindia | SchinaSea |
| RedSea | -0.336 | | | | | | | |
| Eparses | -0.197 | -0.267 | | | | | | |
| Yemen | 0.655** | 0.363 | 0.613*** | | | | | |
| Gulf | 0.571 | 0.205 | 0.517* | -0.113 | | | | |
| Windia | 0.543 | 0.149 | 0.500* | 0.084 | 0.067 | | | |
| Eindia | 0.508 | 0.099 | 0.472* | 0.057 | -0.044 | -0.243 | | |
| SchinaSea | 0.676*** | 0.423 | 0.628*** | 0.081* | 0.004 | -0.030 | -0.045 | |
| Philippines | 0.565* | 0.204 | 0.506* | 0.279** | 0.329 | -0.101 | -0.088 | 0.056 |

**Table S8** Pelagic larval duration for the species investigated in the present review, or from genetically closely related, congeneric species

| Species | Pelagic larval duration (days) | Reference |
|---|---|---|
| *Cephalopholis argus* | 25-29 d | Stier et al. (2014) |
| *Chaetodon ornatissimus* | 61-64 d | Stier et al. (2014) |
| *Dascyllus aruanus* | 18.6-24.3 d | Stier et al. (2014) |
| *Epinephelus areolatus* | 18 d | Stier et al. (2014) |
| *Epinephelus merra* | 29.6 d | Stier et al. (2014) |
| *Fistularia commersonii* | 42-48 d | Stier et al. (2014) |
| *Labroides dimidiatus* | 23.2-24.7 d | Stier et al. (2014) |
| *Lethrinus nebulosus* | ≥37 d | Brothers et al. (1983) |
| *Linckia laevigata* | ≥22 d | Yamaguchi (1973) in Crandall et al. (2014) |
| *Lutjanus kasmira* | 31.0 d | Stier et al. (2014) |
| *Naso lituratus* | 65-72 d | Stier et al. (2014) |
| *Panulirus argus* | 174 ± 22 d | Goldstein et al. (2008) |
| *Panulirus homarus* | ca. 180 d | Phillips and Matsuda (2011) in Lavery et al. (2014) |
| *Scarus schlegeli* | 28-35 d | Stier et al. (2014) |
| *Tridacna maxima* | 10-19 d | Jameson (1976) |
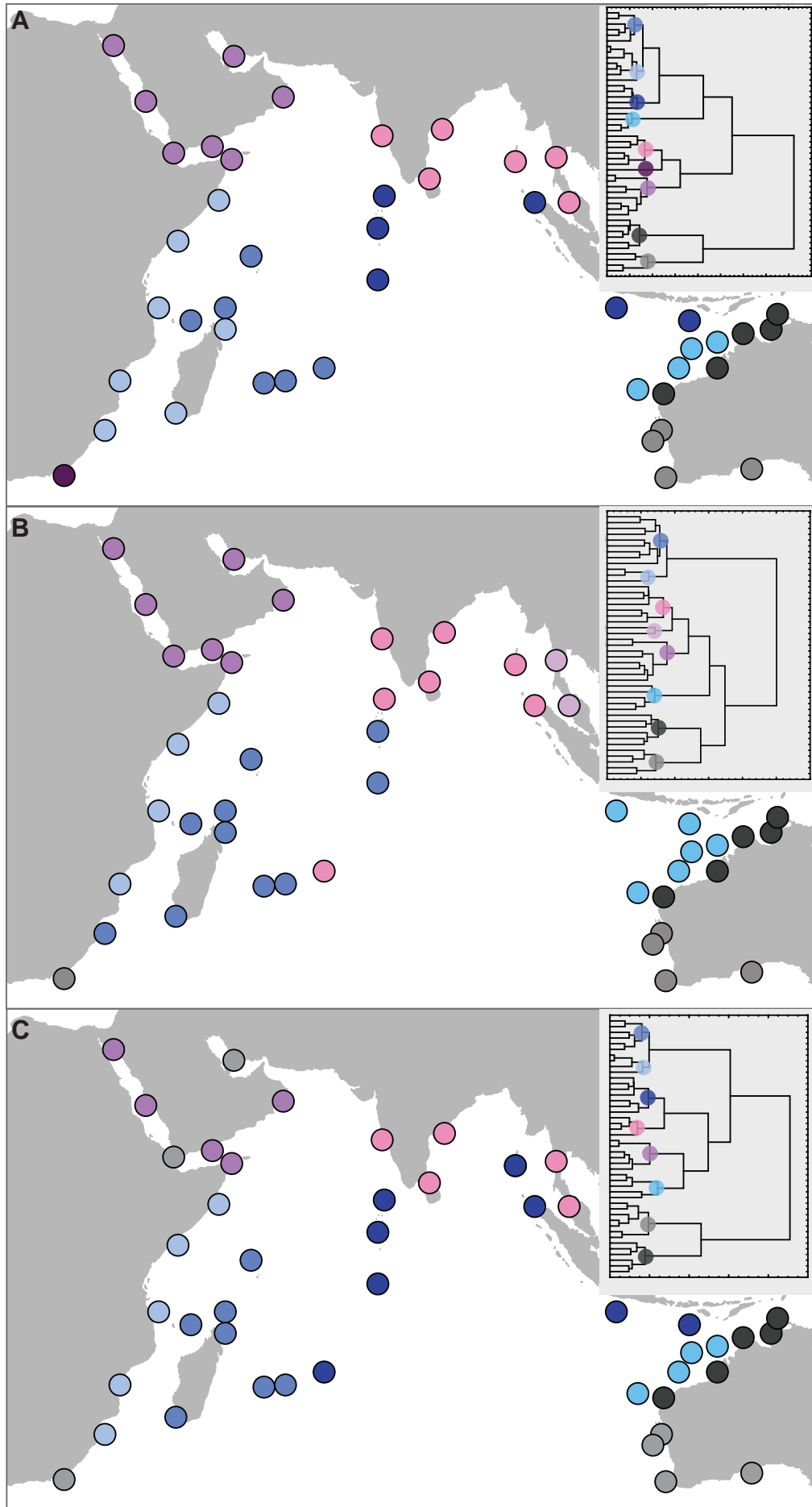
**Fig. S1** Aggregation of localities in the Indian Ocean, defined by their checklists of reef fishes (from references in Table S1). Inset: hierarchical classification based on Ward's aggregation algorithm (Legendre and Legendre, 2012) using Pearson's r coefficient (**A**), Euclidean distance (**B**), and squared Euclidean distance (**C**). Different clusters are distinguished by different colours.
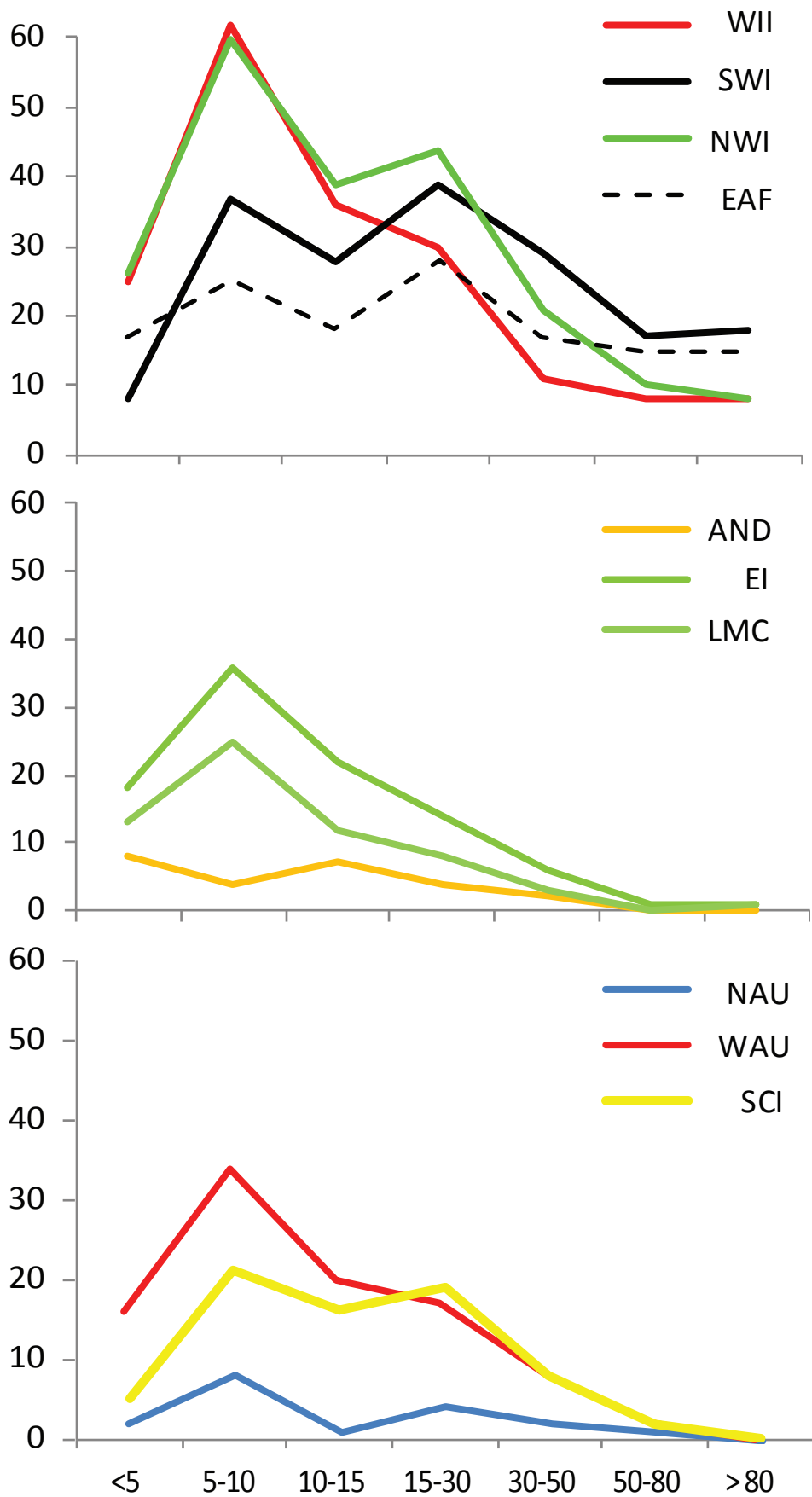
**Fig. S2** Size frequency distribution of reef fish species according by biogeographic province (see Table S2 for abbreviations and Fig. 1 of main article for province boundaries) . *Abscissa,* body size (in cm); *ordinates,* frequency (%).
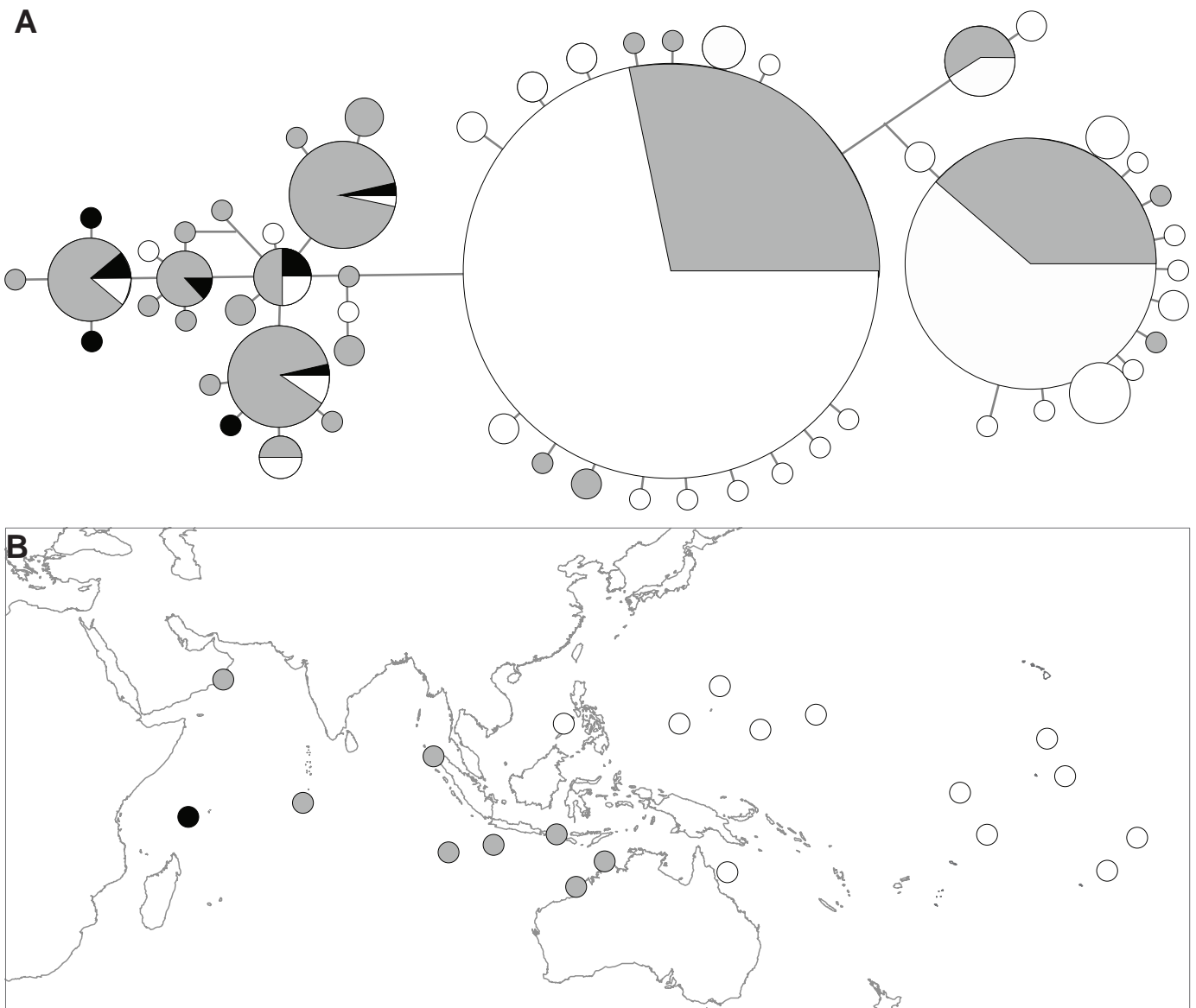
**Fig. S3** Phylogeographic structure in peacock grouper, *Cephalopholis argus* (Gaither et al., 2011). Samples encoded according to geographic origin: *black*, western Indian Ocean (WIO); *grey*, Indian Ocean; *white*, Pacific Ocean. Gaither et al.'s (2011) sample from Bali was arbitrarily placed in the Indian Ocean. **A** Parsimony network of cytochrome *b* gene haplotypes (modified from Gaither et al., 2011). Two major haplogroups were observed, with a clear Indian vs. Pacific phylogeographic partition. This indicates separate evolution between an 'Indian' and a 'Pacific' mitochondrial forms. However, the 'Indian' haplogroup also harboured haplotypes sampled in the Pacific Ocean and vice versa, suggesting either incomplete lineage sorting, or secondary overlap between the two oceans. The latter hypothesis is the one favoured by Gaither et al. (2011). Haplotypes sampled in the WIO were nested within the 'Indian' haplogroup exclusively, indicating that 'Pacific' haplotypes under Gaither et al.'s (2011) overlap hypothesis have not reached the WIO. **B** Sampling locations.
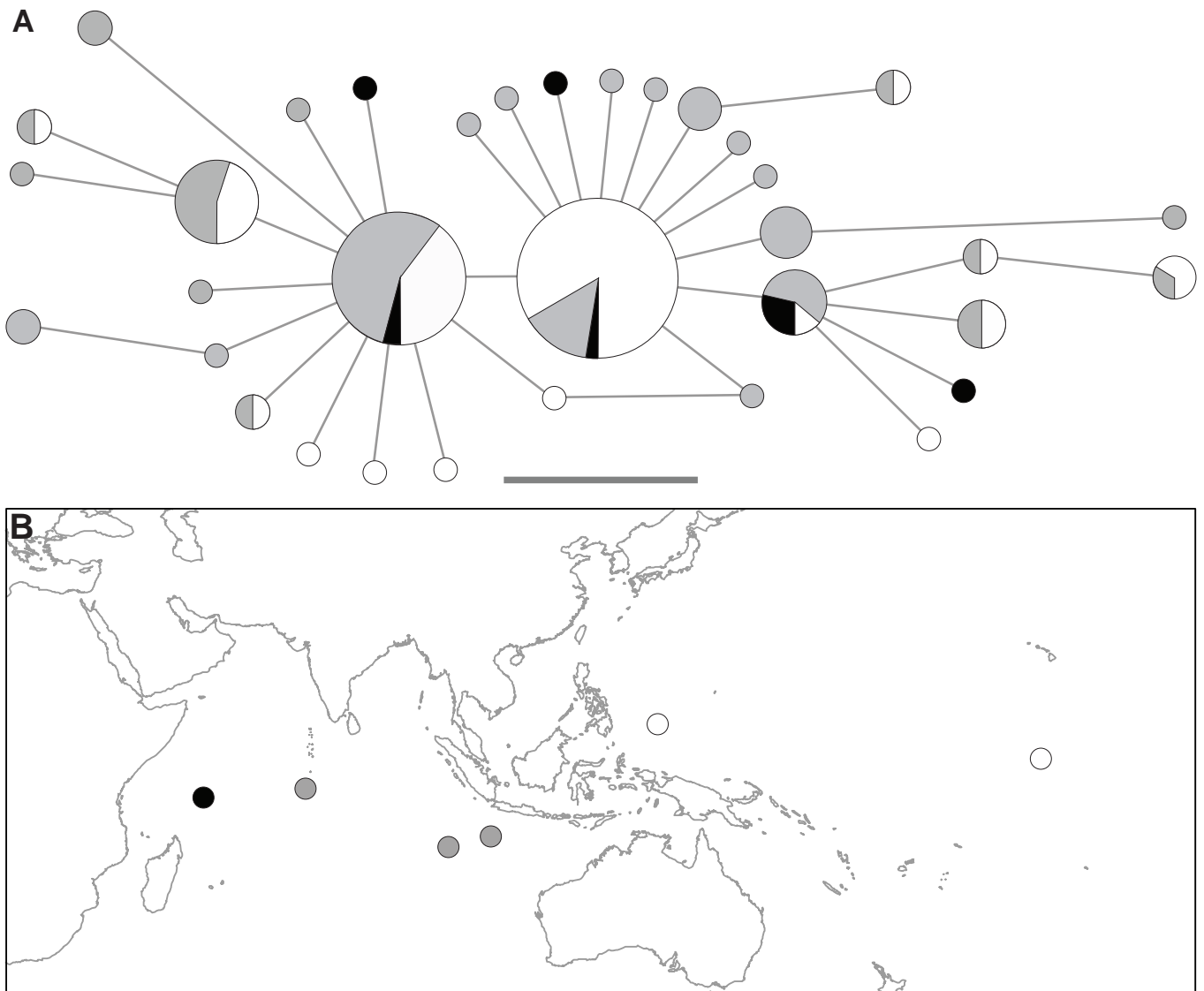
**Fig. S4** Scrawled butterflyfish, *Chaetodon meyeri*. **A** Parsimony network (redrawn from DiBattista et al., 2012) of the cytochrome *b* gene sequences of 134 individuals from various localities in the Indo-West Pacific, including the WIO (*black*), the rest of the Indian Ocean (*grey*), and the Western Pacific (*white*). *Scale bar*: one mutational step. Only moderate Indian vs. Pacific phylogeographic partition was observed, suggesting weak differentiation between populations from the two oceans. **B** Sampling locations.
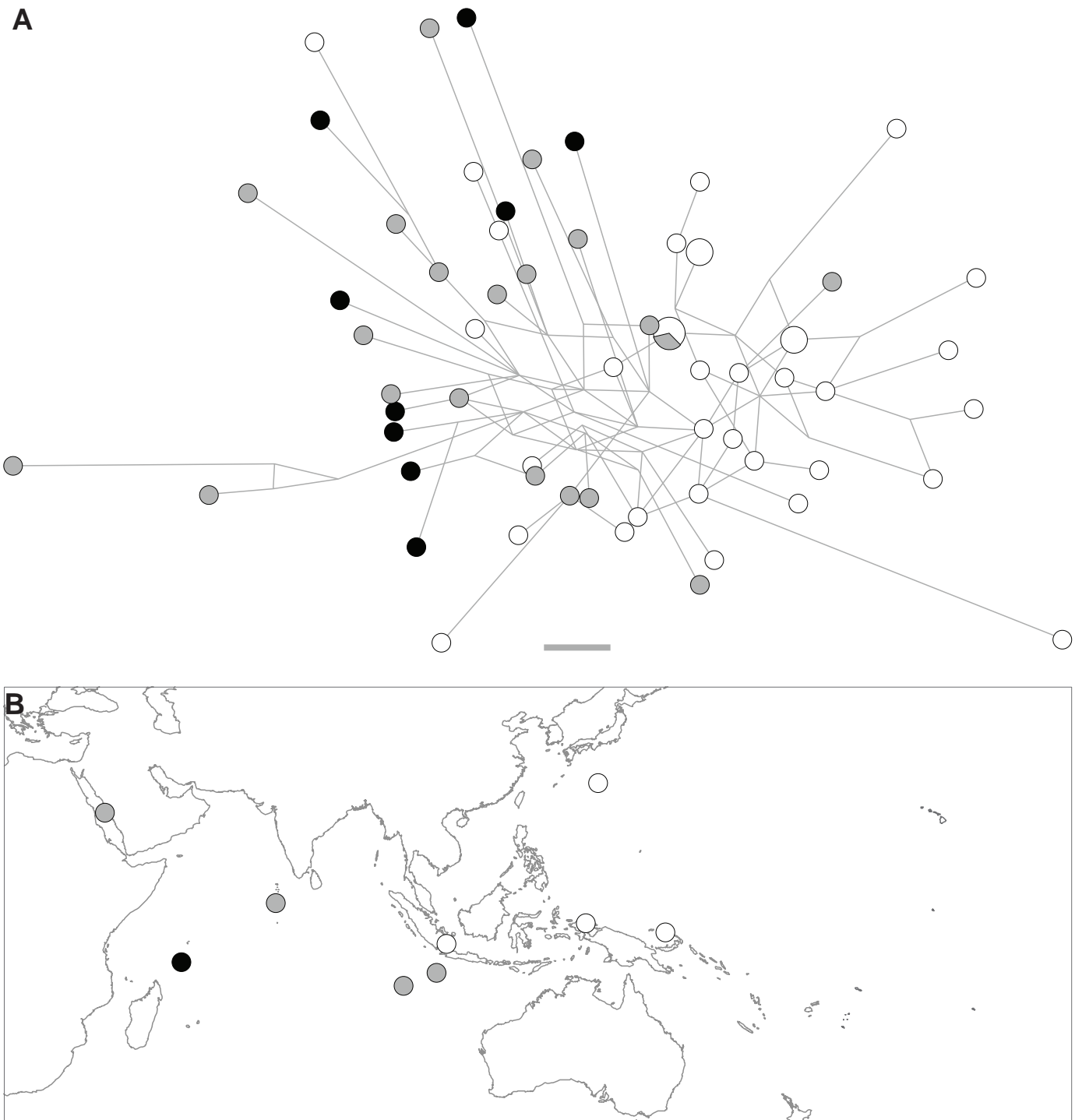
**Fig. S5** Phylogeographic structure in cleaner wrasse, *Labroides* sp. 1 (Sims et al., 2014). Samples encoded according to geographic origin: *black*, western Indian Ocean; *grey*, Indian Ocean; *white*, Pacific Ocean. **A** Median-joining parsimony network (Bandelt et al., 1999) of mitochondrial control-region haplotypes. Sixty three sequences were selected (GENBANK accession nos. EU256890-EU256903, KC151127-KC15138, KC151172-KC151184, KC151212, KC151214-KC151216, KC151219, KC151227, KC151230, KC151232, KC151234, KC151236-KC151250), aligned under BIOEDIT (Hall, 1999) and trimmed to 267 base pairs. *Scale bar*, one mutational step. Loose phylogeographic structure was inferred from the structure of the network, where Pacific haplotypes tended to cluster at one side of the network and Indian haplotypes, including those from the WIO, tended to cluster on the other side. A few haplotypes from the 'Indian' cluster were sampled in the Pacific Ocean and vice versa, suggesting either incomplete lineage sorting, or secondary gene flow between populations from the two oceans. This pattern is also compatible with isolation by distance (Wright, 1942), the hypothesis favoured by Sims et al. (2014) on the basis of observed correlation between $\phi_{ST}$ and geographic distance. **B** Sampling locations (redrawn from Sims et al., 2014).

**Fig. S6** Longface emperor, *Lethrinus* sp. A sensu Borsa et al. (2013b). **A** Median Joining parsimony network (Bandelt et al., 1999) of the cytochrome *b* gene sequences of 16 individuals from various localities in the Indo-West Pacific, including the WIO (*black*), the rest of the Indian Ocean (*grey*), and the Western Pacific (*white*). Haplotype sequences are from Fig. 5 of Borsa et al. (2013b). Complete sequences have nos. AF381252, KC596033-KC596044, KC596046, KC596048, and KC596051 in GENBANK. *Scale bar*: one mutational step; *number* indicates the number of mutations separating the two main haplogroups. A clear Indian vs. Pacific phylogeographic partition was observed, indicating a geographic barrier between the two mitochondrial forms. The geographic barrier is located east of Bali and west of West Papua. **B** Sampling locations.
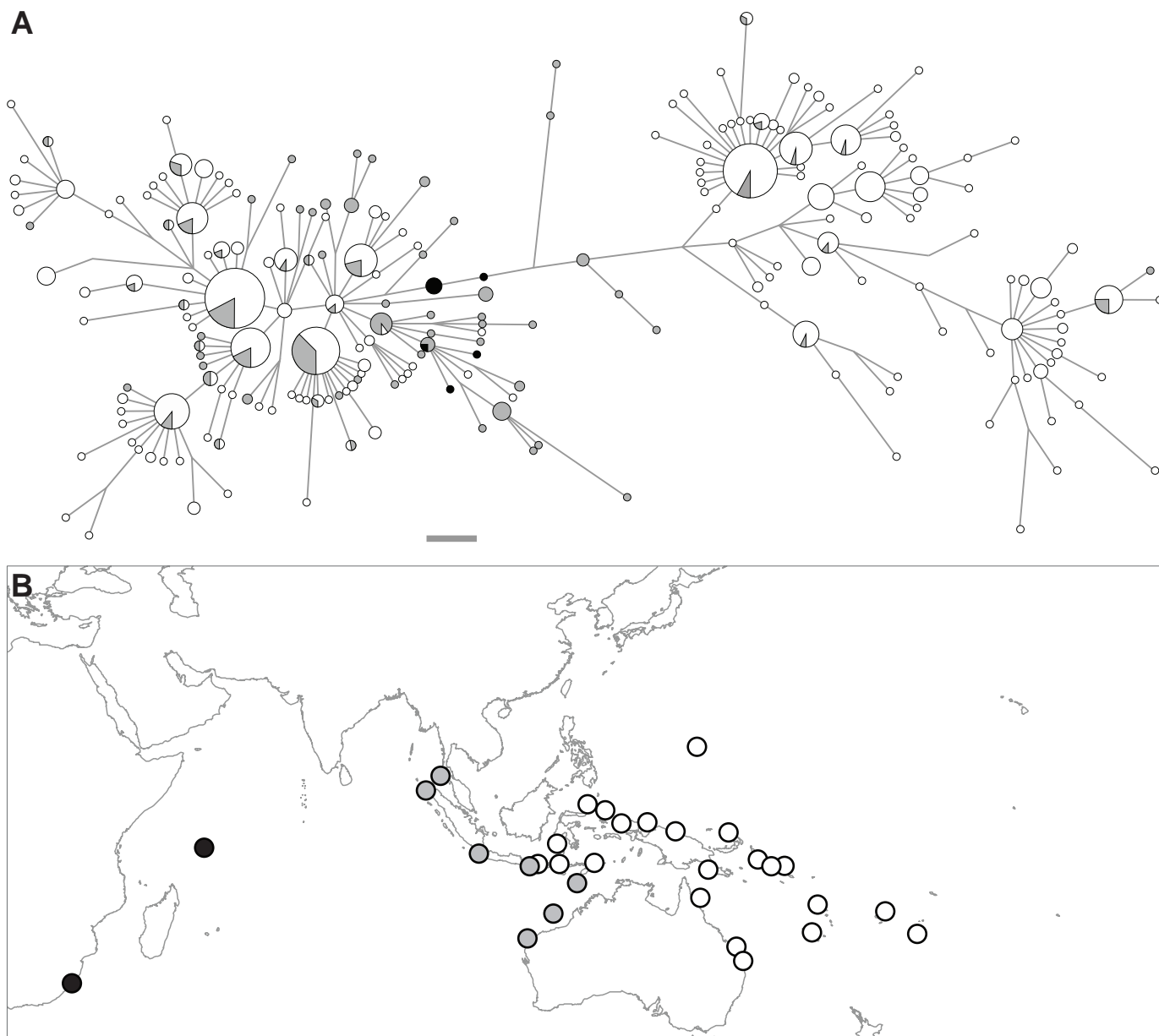
**Fig. S7** Blue sea star, *Linckia laevigata*. **A** Parsimony network (redrawn from Crandall et al., 2014) of the partial *CO1* gene sequences of 791 individuals from various localities in the Indo-West Pacific, including the WIO (*black*), the eastern Indian Ocean (*grey*), and the western Pacific Ocean (*white*). *Scale bar*: one mutational step. Two major clusters of haplotypes were observed, both including eastern Indian and Pacific haplotypes. One of the two clusters, which included a few WIO haplotypes, also had a substantially higher proportion of Indian-Ocean haplotypes than the other cluster, which was predominantly Pacific. This suggests either incomplete lineage sorting between populations from the Indian vs. Pacific oceans, or secondary admixture of haplotypes from one ocean to the other and vice versa. Interestingly, the dominant WIO haplotypes occupied a central position in the network, implying that one or the other, possibly both, of the two major haplogroups may derive from an ancestral WIO stock, or from a geographically larger region encompassing the WIO. **B** Sampling locations.
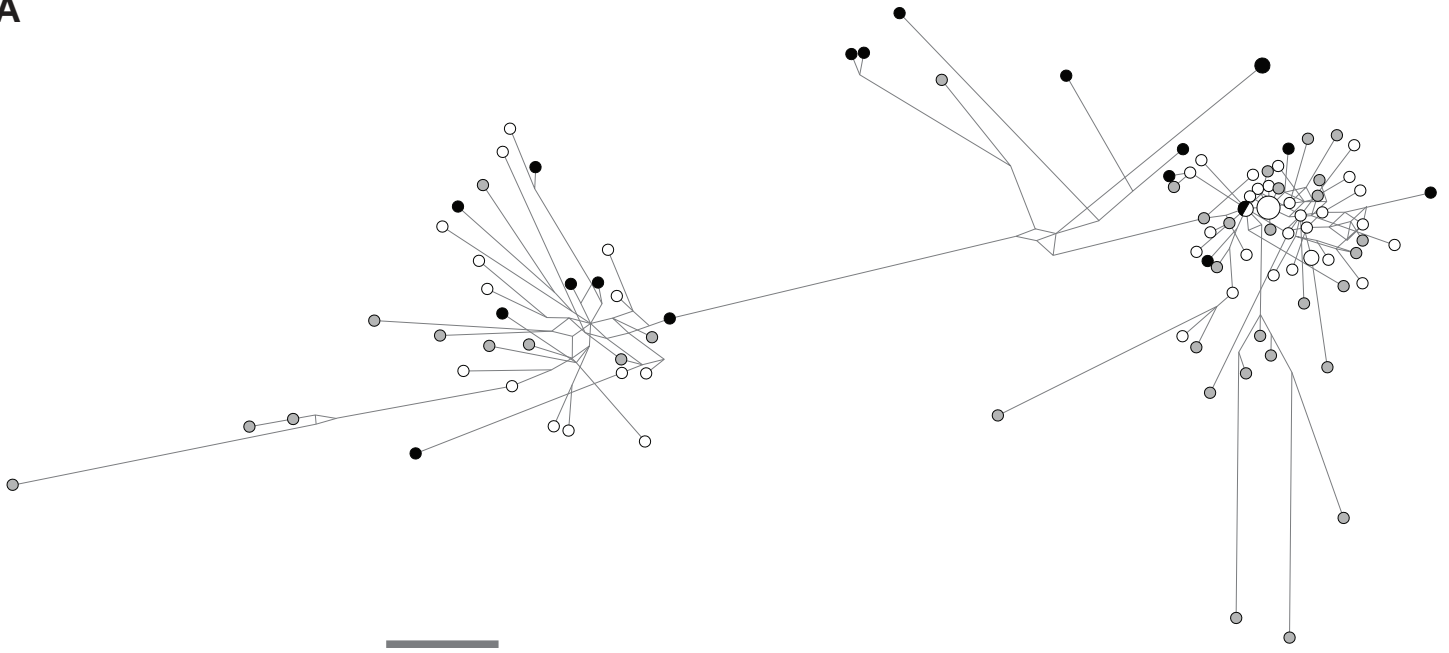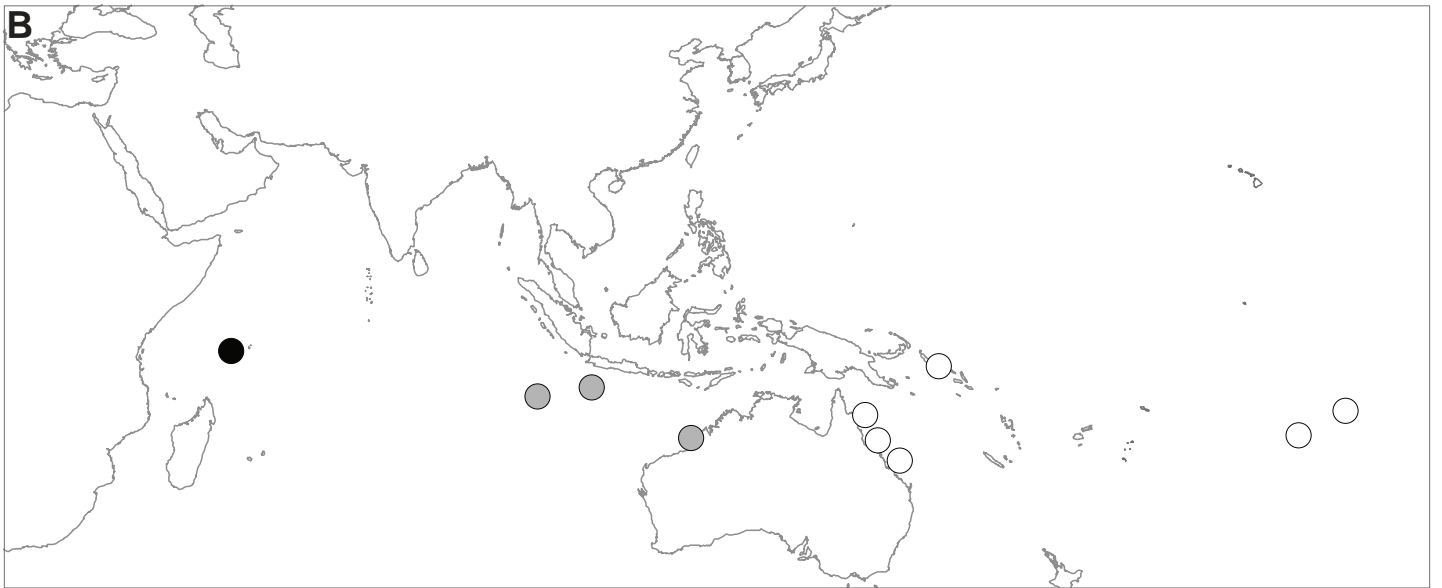
**Fig. S8** Phylogeographic structure in spotted unicornfish, *Naso brevirostris*. Samples encoded according to geographic origin: *black*, western Indian Ocean (WIO); *grey*, Indian Ocean; *white*, Pacific Ocean. **A** Median-joining parsimony network (Bandelt et al., 1999) of mitochondrial control-region haplotypes. One hundred two sequences were retrieved from GENBANK (nos. FJ216727-FJ216828) and aligned under BIOEDIT (Hall, 1999). Gaps of one to five nucleotides were inserted; sequences had a common length of 247 base pairs. Haplotypes were organized into two loose haplogroups. Each haplogroup possessed haplotypes from the WIO, the rest of the Indian Ocean, and the Pacific Ocean and no geographic differences were observed in haplogroup frequencies (Horne et al., 2008). *Scale bar*, five mutational steps. **B** Sampling locations.
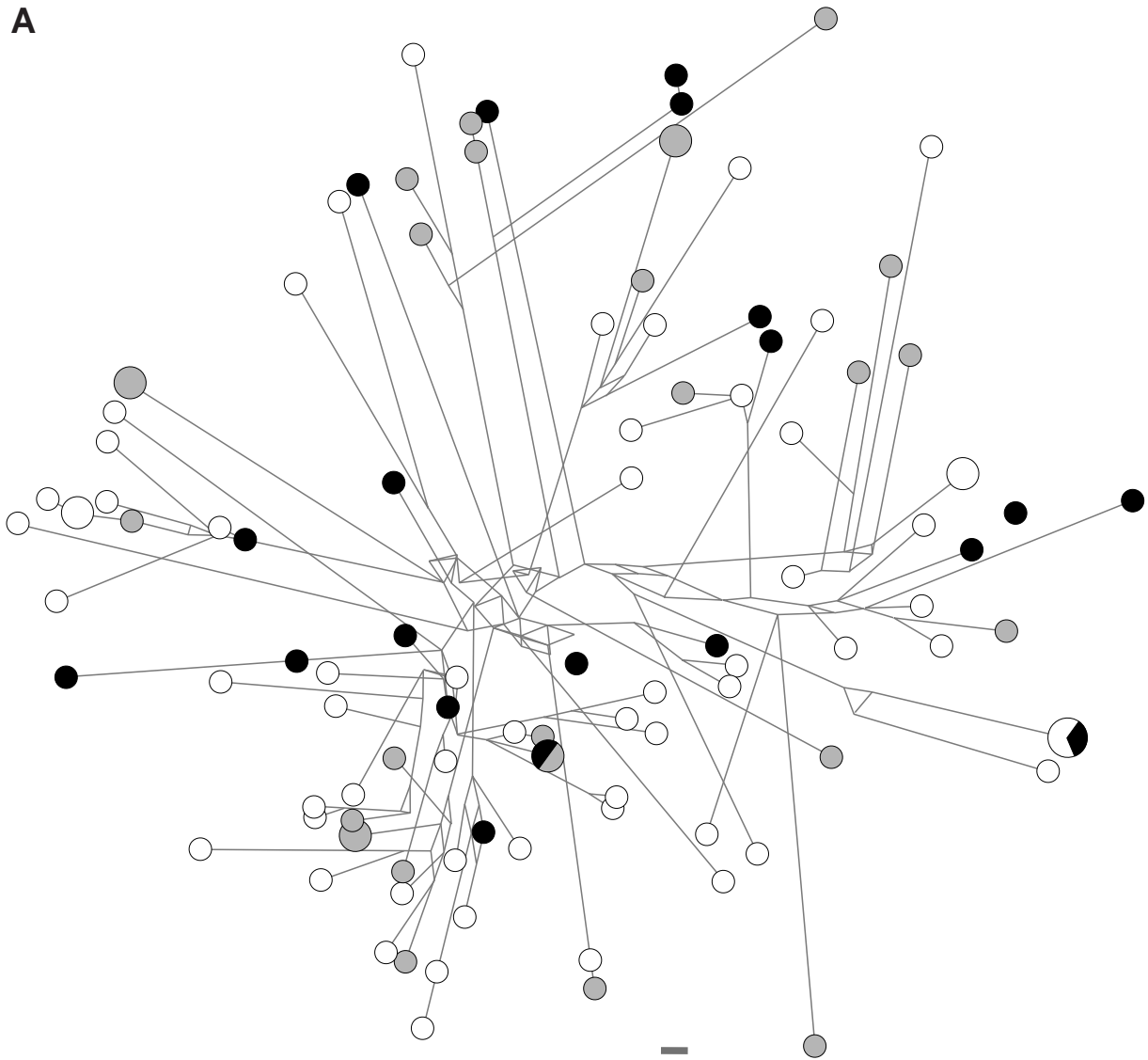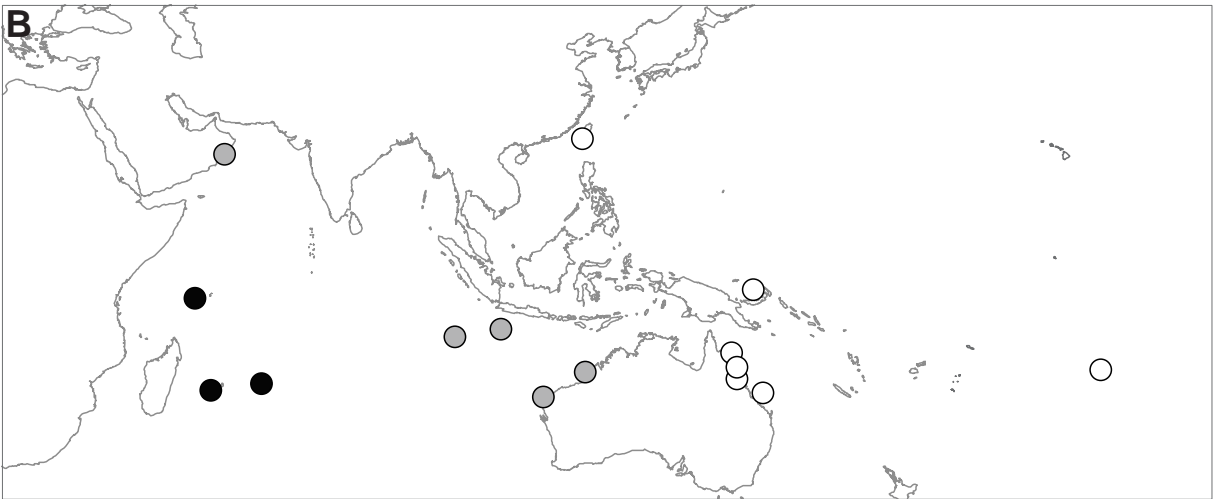
**Fig. S9** Phylogeographic structure in bluespine unicornfish, *Naso unicornis*. Samples encoded according to geographic origin: *black*, western Indian Ocean; *grey*, Indian Ocean; *white*, Pacific Ocean. **A** Median-joining parsimony network (Bandelt et al., 1999) of mitochondrial control-region haplotypes. One hundred seven sequences (Horne et al., 2008) were retrieved from GENBANK (nos. FJ216829-FJ216935) and aligned under BIOEDIT (Hall, 1999). Gaps of one to two nucleotides were inserted; sequences had a common length of 277 base pairs. No phylogeographic structure was detected, either from this network or from $\phi_{ST}$ analysis (Horne et al., 2008). *Scale bar*, one mutational step. **B** Sampling locations.
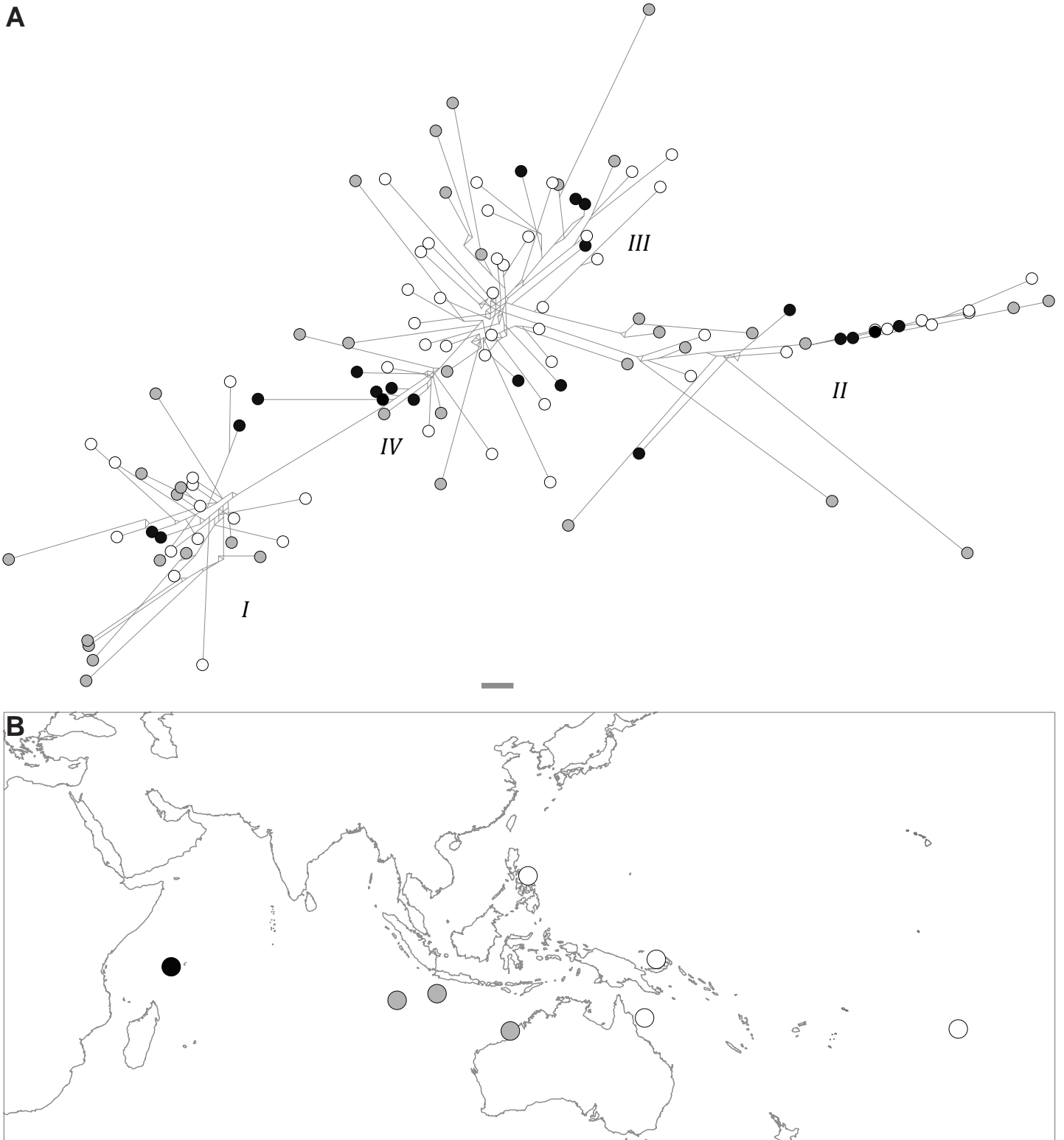
**Fig. S10** Phylogeographic structure in bignose unicornfish, *Naso vlamingii*. Samples encoded according to geographic origin: *black*, western Indian Ocean; *grey*, Indian Ocean; *white*, Pacific Ocean. **A** Median-joining parsimony network (Bandelt et al., 1999) of mitochondrial control-region haplotypes. One hundred thirteen sequences were retrieved from GENBANK (nos. DQ767974-DQ768086) and aligned under BIOEDIT (Hall, 1999). Gaps of one to five nucleotides were inserted; sequences had a common length of 354 base pairs. Haplotypes were organized into four loose haplogroups, coined "Clades I-IV" by Klanten et al. (2007) (*I-IV* here). Each haplogroup possessed haplotypes from the WIO, the rest of the Indian Ocean, and the Pacific Ocean and no geographic differences were observed in haplogroup frequencies (Klanten et al., 2007). *Scale bar*, five mutational steps. **B** Sampling locations (redrawn from Klanten et al., 2007).
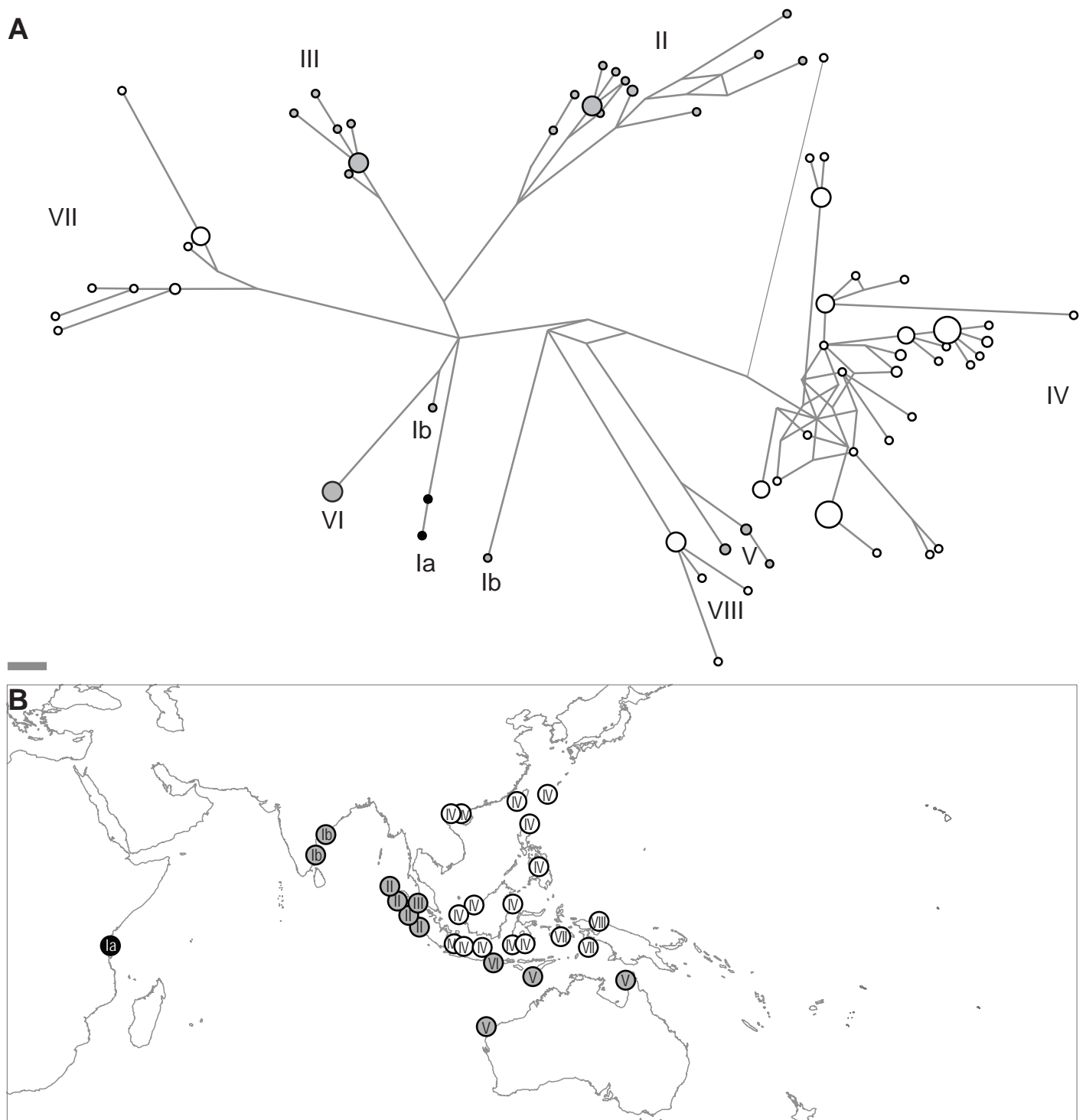
**Fig. S8** Blue-spotted maskray, *Neotrygon kuhlii*. **A** Parsimony network (edited from Arlyza et al., 2013) of the partial *CO1* gene sequences of 147 individuals from various localities in the Indo-West Pacific, including the WIO (*black*), the eastern Indian Ocean (*grey*), and the western Pacific Ocean (*white*). *Scale bar*: one mutational step. Eight distinct haplogroups were observed, including haplogroups *II-VIII* from the Coral Triangle region, and a loosely defined haplogroup (*Ia*, *Ib*) from the Indian Ocean (Arlyza et al., 2013). Coral-Sea haplotypes not represented here, as they pertain to the recently-resurrected *N. trigonoides* (see Borsa et al., 2013a). **B** Sampling locations.

**Fig. S12** Phylogeographic structure in common parrotfish, *Scarus psittacus*. Samples encoded according to geographic origin: *black*, western Indian Ocean; *grey*, Indian Ocean; *white*, Pacific Ocean. **A** Median-joining parsimony network (Bandelt et al., 1999) of mitochondrial control-region haplotypes. One hundred sixty nine sequences were retrieved from GENBANK (nos. AY324601, EU926978-EU927144 and JX026573), aligned under BIOEDIT (Hall, 1999) and trimmed to 270 base pairs. *Scale bar*, one mutational step. Haplotypes were organized as a quasi-star like network with a dominant central haplotype that was shared between the WIO, the central and eastern Indian Ocean, and the Pacific Ocean. $\phi_{ST}$ analysis revealed genetic differences between the WIO population from Seychelles and the eastern-Indian Ocean populations, which was thought to reflect peripheral genetic differentiation (Winters et al., 2010). **B** Sampling locations (modified from Winters et al., 2010).
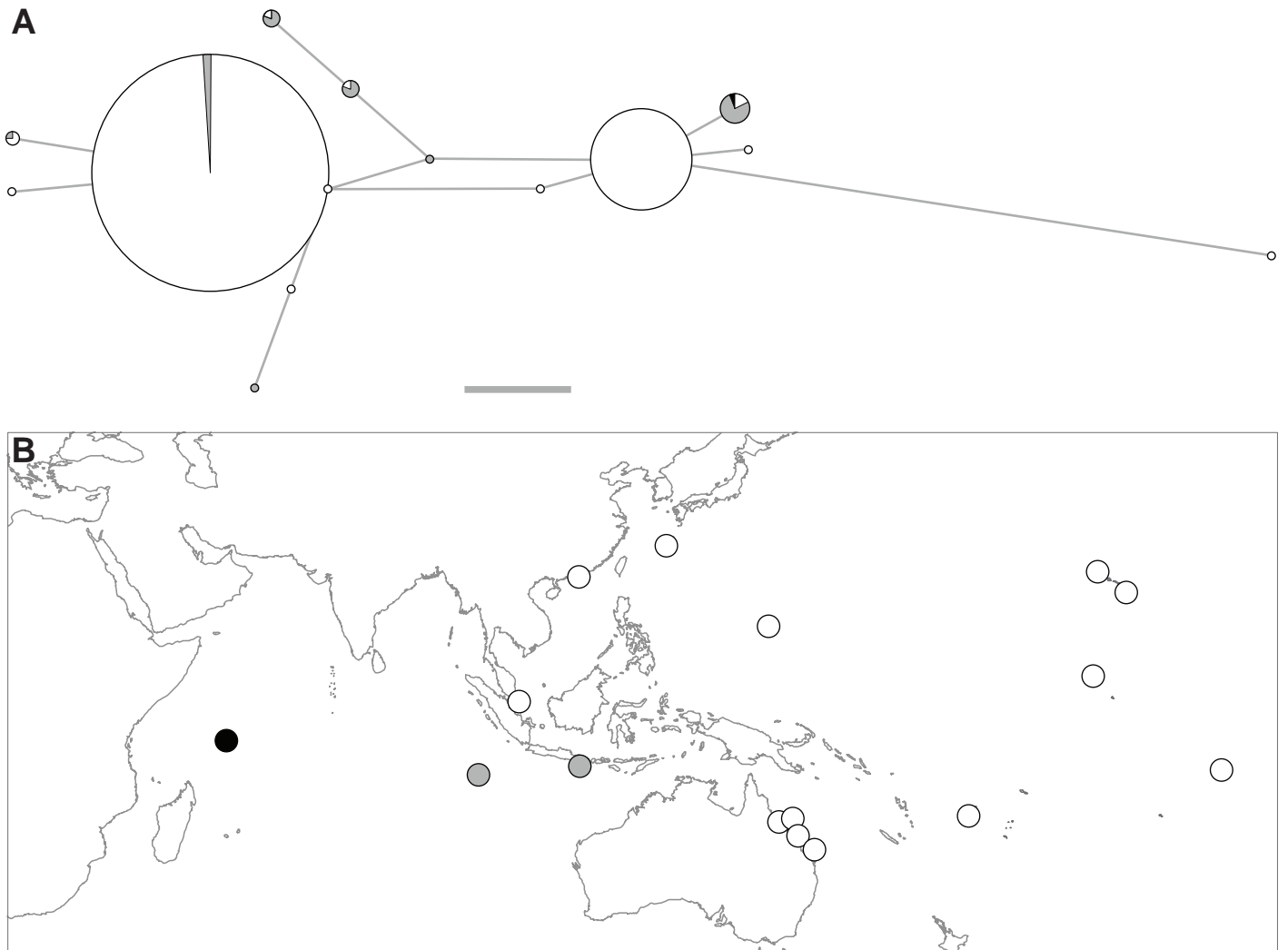
**Fig. S13** Phylogeographic structure in whitetip reef shark, *Triaenodon obesus* (Whitney et al., 2012). Samples encoded according to geographic origin: *black*, western Indian Ocean; *grey*, Indian Ocean; *white*, Pacific Ocean. **A** Median-joining parsimony network (Bandelt et al., 1999) of mitochondrial control-region haplotypes, aligned under BIOEDIT (Hall, 1999) and reduced to a common length of 881 bp. *Scale bar*, one mutational step. No obvious Indian vs. Pacific partition was visible from the network. However, this apparent lack of phylogeographic structure may be an artefact of unbalanced sampling design. $\phi_{ST}$ analysis revealed substantial genetic differentiation between populations either side of the Indo-Pacific barrier (Whitney et al., 2012). The only WIO haplotype, from the Seychelles, was identical to the haplotype dominant in the Indian Ocean. **B** Sampling locations (redrawn from Whitney et al., 2014). Two additional Pacific samples, not represented on this figure, were from Costa Rica.
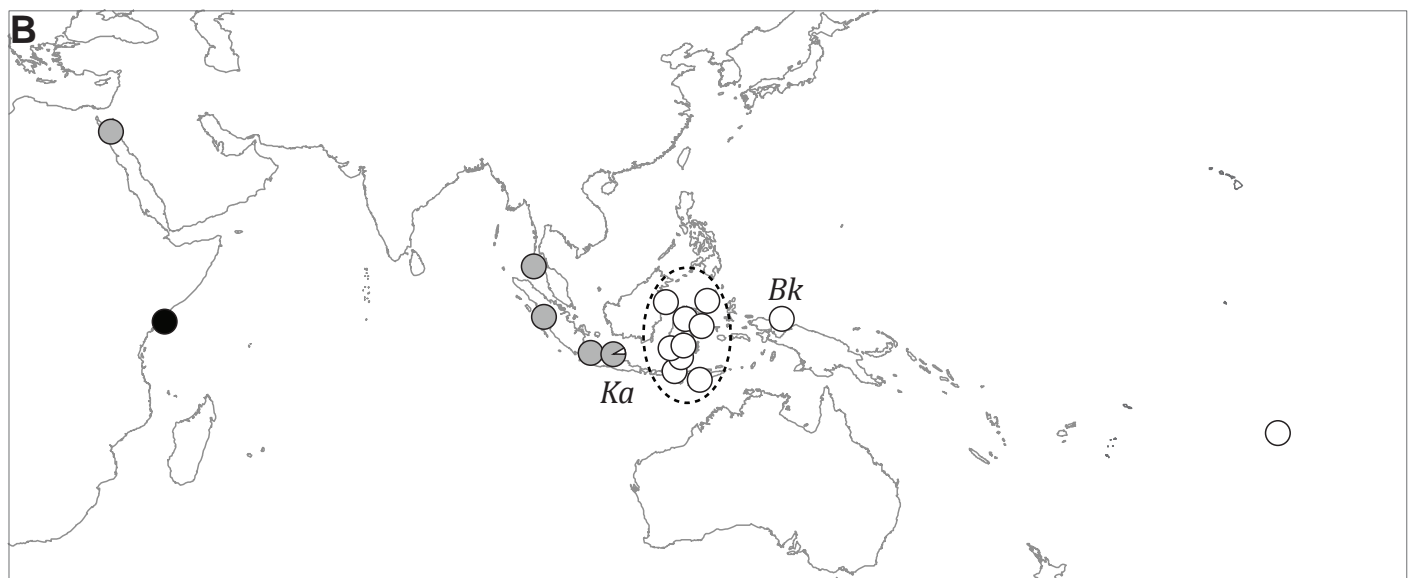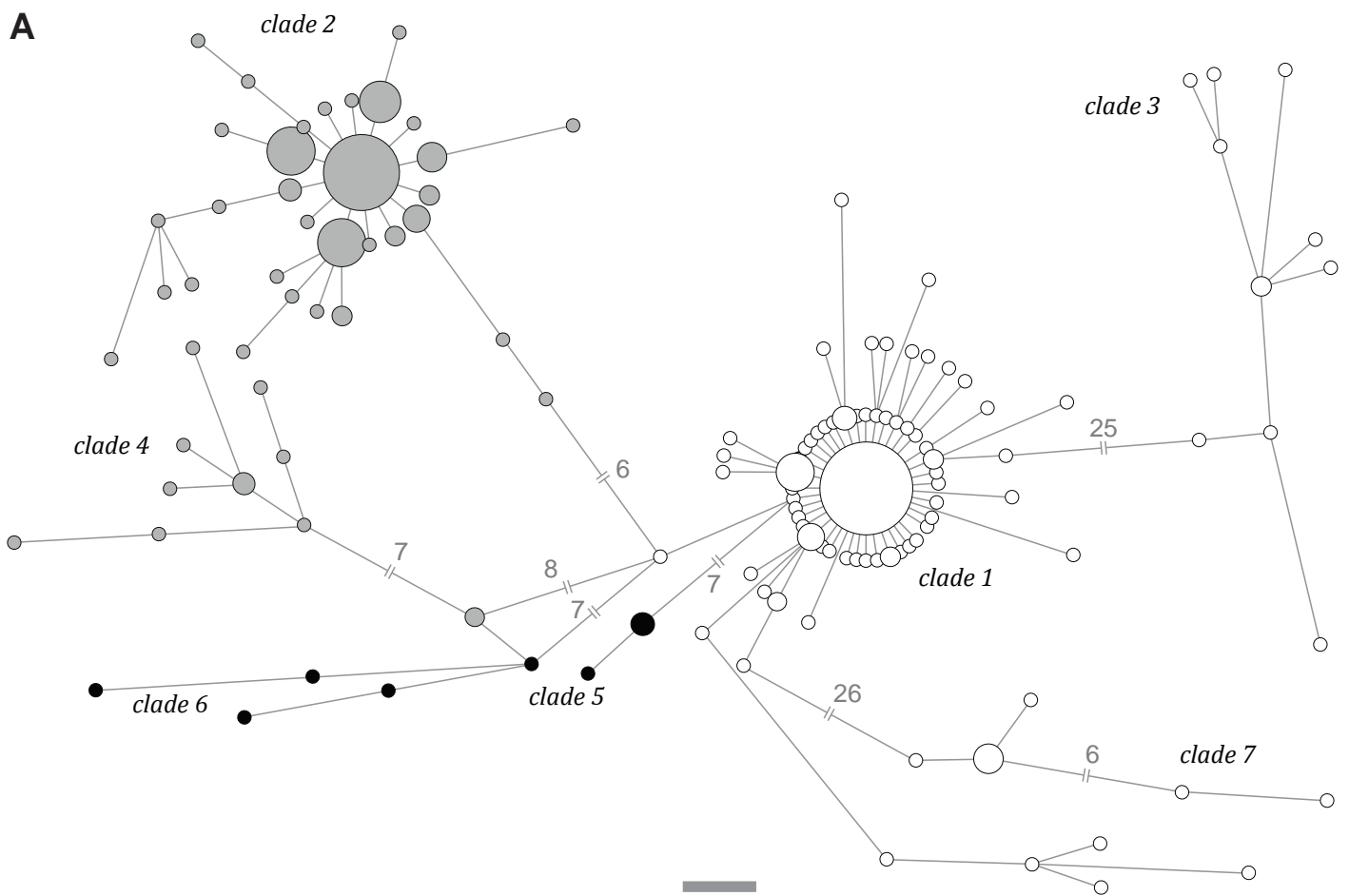
**Fig. S14** Phylogeographic structure in small giant clam, *Tridacna maxima*. Samples encoded according to geographic origin: *black*, western Indian Ocean; *grey*, Indian Ocean; *white*, Pacific Ocean. **A** Parsimony network of *CO1* haplotypes (GENBANK accession nos. FM244476-FM244619 and HE995454-HE995487; *N* = 151) (redrawn from Hui, 2012). Seven major haplogroups, coined clades 1-7 by Hui (2012) were observed, each geographically circumscribed. Clade 1 was the single one represented in samples from eastern Indonesia (dotted elipse); it was also marginally present in samples Karimunjawa (Java Sea, Indonesia) and in Biak (northern West Papua); clade 2 was exclusively present in the Andaman Sea and in western Indonesia; clade 3 was exclusively present in Biak; clade 4 was exclusive to the Red Sea; clades 5 and 6 were exclusively sampled from Kenya, WIO; clade 7 was exclusively sampled in French Polynesia. Strong phylogeographic partition was thus revealed. Maximum-likelihood phylogenetic analysis (T92+G+I; MEGA6; Tamura et al., 2013) using homologous sequences from *T. crocea*, *T. derasa*, *T. gigas*, *T. noae* and *T. squamosa* (GENBANK accession nos. EU341379, GQ166591, KJ202113, KC456023 and EU346364, respectively) as outgroups determined clades 3 and 7 to be outgroups and placed the root at the basis of a rattle comprising clade 5, clades (4+6), and the rest. *Scale bar*, one mutational step. **B** Sampling locations (from Hui, 2012). *Bk* sample Biak; *Ka* sample Karimunjawa; *dotted ellipse* delineates all samples from eastern Indonesia.

## References (other than Table S1)

Arlyza, I.S., Shen, K.-N., Durand, J.-D., Borsa, P., 2013. Mitochondrial haplotypes indicate parapatric-like phylogeographic structure in blue-spotted maskray (*Neotrygon kuhlii*) from the Coral Triangle region. J. Hered. 104, 725-733.

Asgharian, H., Sahafi, H.H., Ardalan, A.A., Shekarriz, S., Elahi, E., 2011. Cytochrome c oxidase subunit 1 barcode data of fish of the Nayband National Park in the Persian Gulf and analysis using meta-data flag several cryptic species. Mol. Ecol. Resour. 11, 461-472.

Bandelt, H.J., Forster, P., Röhl, A., 1999. Median-joining networks for inferring intraspecific phylogenies. Mol. Biol. Evol. 16, 37–48.

Borsa, .P, Arlyza, I.S., Chen, W.-J., Durand, J.-D., Meekan, M.G., Shen, K.-N., 2013a. Resurrection of New Caledonian maskray *Neotrygon trigonoides* (Myliobatoidei: Dasyatidae) from synonymy with *N. kuhlii*, based on cytochrome-oxidase I gene sequences and spotting patterns. C. R. Biol. 336, 221-232.

Borsa, P., Hsiao, D.-R., Carpenter, K.E., Chen, W.-J., 2013b. Cranial morphometrics and mitochondrial DNA sequences distinguish cryptic species of the longface emperor (*Lethrinus olivaceus*), an emblematic fish of the Indo-West Pacific coral reefs. C. R. Biol. 336, 505-514.

Brothers, E.B., Williams, D.McB., Sale, P.F., 1983. Length of larval life in twelve families of fishes at 'One Tree Lagoon', Great Barrier Reef, Australia. Mar. Biol. 76, 319-324.

Crandall, E.D., Treml, E.A., Liggins, L., Gleeson, L., Yasuda, N., Barber, P.H., Wörheide, G., Riginos, C., 2014. Return of the ghosts of dispersal past: historical spread and contemporary gene flow in the blue sea star *Linckia laevigata*. Bull. Mar. Sci. 90, 399–425.

DiBattista, J.D., Rocha, L.A., Craig, M.T., Feldheim, K.A., Bowen, B.W., 2012. Phylogeography of two closely related Indo-Pacific butterflyfishes reveals divergent evolutionary histories and discordant results from mtDNA and microsatellites. J. Hered. 103, 617–629.

Excoffier, L., Lischer, H.E.L., 2010. ARLEQUIN suite ver. 3.5: A new series of programs to perform population genetics analyses under LINUX and WINDOWS. Mol. Ecol. Resour. 10, 564-567.

Excoffier, L., Smouse, P.E., Quattro, J.M., 1992. Analysis of molecular variance inferred from metric distances among DNA haplotypes - Application to human mitochondrial-DNA restriction data. Genetics 131, 479-491.

Gaither, .M.R, Bowen, B, W., Bordenave, T.R., Rocha, L.A., Newman, S.J., Gomez, J.A., van Herwerden, L., Craig, M.T., 2011. Phylogeography of the reef fish *Cephalopholis argus* (Epinephelidae) indicates Pleistocene isolation across the Indo-Pacific Barrier with contemporary overlap in the Coral Triangle. BMC Evol. Biol. 11, 189.

Gaither, M.R., Toonen, R.J., Robertson, D.R., Planes, S., Bowen, B.W., 2010. Genetic evaluation of marine biogeographical barriers: perspectives from two widespread Indo-Pacific snappers (*Lutjanus kasmira* and *Lutjanus fulvus*). J. Biogeogr. 37, 133–147.

Goldstein, J.S., Matsuda, H., Takenouchi, T., Butler, M.J.4, 2008. The complete development of larval Caribbean spiny lobster, *Panulirus argus*, in culture. J. Crustacean Biol. 28, 306–327.

Hall, T.A., 1999. BioEdit: a user-friendly biological sequence alignment editor and analysis program for Windows 95/98/NT. Nucl. Acids Symp. Ser. 41, 95-98.

Hui, M., 2012. Connectivity and evolution of giant clams (Tridacnidae): a molecular genetic approach. PhD dissertation, Universität Bremen, Bremen, xv+85 p.

Jameson, S.C., 1976. Early life-history of giant clams *Tridacna crocea* Lamarck, *Tridacna maxima* (Röding), and *Hippopus hippopus* (Linnaeus). Pac. Sci. 30, 219–232.

Jeena, N.S., 2013. Genetic divergence in lobsters (Crustacea: Palinuridae and Scyllaridae) from the Indian EEZ. PhD dissertation, Cochin University of Science and Technology, Kochi, xviii+238 p.

Klanten, O.S., Choat, J.H., van Herwerden, L., 2007. Extreme genetic diversity and temporal rather than spatial partitioning in a widely distributed coral reef fish. Mar. Biol. 150, 659–670.

Kulbicki, M., Parravicini, V., Bellwood, D.R., Arias-Gonzàlez, E., Chabanet, P., Floeter, S.R., Friedlander, A., McPherson, J., Myers, R.E., Vigliola, L., Mouillot, D., 2013a. Global biogeography of reef fishes: A hierarchical quantitative delineation of regions. PLoS One 8, e81847.

Lakra, W.S., Verma, M.S., Goswami, M., Lal, K.K., Mohindra, V., Punia, P., Gopalakrishnan, A., Singh, K.V., Ward, R.D., Hebert, P., 2011. DNA barcoding Indian marine fishes. Mol. Ecol. Resour. 11, 60-71.

Lavery, S.D., Farhadi, A., Farahmand, H., Chan, T.-Y., Azhdehakoshpour, A., Thakur, V., Jeffs, A.G., 2014. Evolutionary divergence of geographic subspecies within the scalloped spiny lobster *Panulirus homarus* (Linnaeus 1758). PLoS One 9, e97247.

Legendre, P., Legendre, L., 2012. Numerical ecology, 3rd edn. Elsevier, Amsterdam, 1006 p.

Muths, D., Gouws, G., Mwale, M., Tessier, E., Bourjea, J., 2012. Genetic connectivity of the reef fish *Lutjanus kasmira* at the scale of the West Indian Ocean. Can. J. Fisheries Aquat. Sci. 69, 842–853.

Muths, D., Tessier, E., Gouws, G., Bourjea, J., 2014. Genetic structure of the reef grouper *Epinephelus merra* in the West Indian Ocean appears congruent with biogeographic and oceanographic boundaries. Mar. Ecol.

Phillips, B.F., Matsuda, H., 2011. A global review of spiny lobster aquaculture. In: Fotedar , R., Phillips, B.F., (eds.), Recent advances and new species in aquaculture. Wiley-Blackwell, Hoboken NJ, pp. 22–84.

Senevirathna, J., Munasinghe, D., 2014. Genetic diversity and population structure of *Panulirus homarus* populations of Southern Sri Lanka and South India revealed by the mitochondrial *COI* gene region. Proc. Int. Conf. Food, Biol. Med. Sci., Jan. 28-29, 2014, Bangkok, pp. 10-13.

Sims, C.A., Riginos, C., Blomberg, S.P., Huelsken, T., Drew, J., Grutter, A.S., 2014. Cleaning up the biogeography of *Labroides dimidiatus* using phylogenetics and morphometrics. Coral Reefs 33, 223–233.

Stier, A.C., Hein, A.W., Parravicini, V., Kulbicki, M., 2014. Larval dispersal drives trophic structure across Pacific coral reefs. Nature Comm. 5, 5575.

Tamura, K., Stecher, G., Peterson, D., Filipski A., Kumar, S., 2013. MEGA6: Molecular Evolutionary Genetics Analysis version 6.0. Mol. Biol. Evol. 30, 2725–2729.

Whitney, N.M., Robbins, W.D., Schultz, J.K., Bowen, B.W., Holland, K.N., 2012. Oceanic dispersal in a sedentary reef shark (*Triaenodon obesus*): genetic evidence for extensive connectivity without a pelagic larval stage. J. Biogeogr. 39, 1144-1156.

Winters, K.L., van Herwerden, L., Choat, J.H., Robertson, D.R., 2010. Phylogeography of the Indo-Pacific parrotfish *Scarus psittacus*: isolation generates distinctive peripheral populations in two oceans. Mar. Biol. 157, 1679-1691.

Wright, S., 1942. Isolation by distance. Genetics 28, 114–138.

Yamaguchi, M., 1973. Early life history of coral reef asteroids, with special reference to *Acanthaster planci* (L.). In: Jones, O.A., Endean, R (eds. ), Biology and geology of coral reefs. Academic Press, New York, pp. 369–389.