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Maria E. A. Santos<sup>1,2</sup>, Hiroki Kise<sup>2</sup>, Chloé Julie Lois Fourreau<sup>2</sup>, Bogdan Kiriukhin<sup>3</sup>, Marcelo Visentini Kitahara<sup>4</sup>, David Michael Baker<sup>5</sup>, Robert J. Toonen<sup>1</sup>, Pi Jen Liu<sup>6</sup>, Arthur Chang<sup>6</sup>, Ting-Hsuan Tu<sup>6</sup>, Widiastuti<sup>7</sup>, Kadek Miko Purnama Agustini<sup>7</sup>, Brian W. Bowen<sup>1</sup>, James D. Reimer<sup>2,8</sup>

1 ToBo Lab, Hawai'i Institute of Marine Biology, University of Hawai'i at Mānoa, Hawai'i, USA

2 Molecular Ecology and Invertebrate Systematics Laboratory, University of the Ryukyus, Okinawa, Japan

3 AquaBioSafe Laboratory, University of Tyumen, Tyumen, Russia

4 Center for Marine Biology, University of São Paulo, São Paulo, Brazil

5 The Swire Institute of Marine Science, University of Hong Kong, Hong Kong, Hong Kong

6 Graduate Institute of Marine Biology, National Dong Hwa University, Checheng, Taiwan

7 Graduate School of Marine Science, Universitas Udayana, Bali, Indonesia

8 Tropical Biosphere Research Center, University of the Ryukyus, Okinawa, Japan

Corresponding author: Maria E. A. Santos ([santos.mariaea@gmail.com](mailto:santos.mariaea@gmail.com))

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## Abstract

Biogeographic patterns for marine fishes and scleractinian stony corals are well-established, but it is still unclear whether these patterns apply to the understudied marine invertebrates. Here we investigate the distribution of zoantharians (=zoanthids), an order of cnidarians that are distributed globally from tropical coral reefs to deep temperate oceans. We examined the available literature, along with new records and morphological and DNA sequence data, to establish their first global biogeographical assessment. Two striking results emerged that contrast with previously known marine biogeographical patterns. The first was that several zoantharian genera are cosmopolitan, inhabiting most biogeographic provinces within and between ocean basins. Although the highest diversity was observed in the Indo-Pacific Ocean (IPO), concordant with biogeographic assays of reef fishes and stony corals, the distribution of genera was not significantly different between the Atlantic (ATO) and the IPO. Secondly, there were multiple sibling species complexes between the ATO and the IPO. At species and population scales, a long pelagic larval duration, asexual reproduction modes, and rafting abilities, may at least partly explain the low levels of genetic differences between ocean basins. As some zoantharian species can play a significant role in phase shifts, filling knowledge gaps on species distributions is essential to support monitoring of reef ecosystems.

## Highlights

- Our study revealed that several Zoantharia genera, and most families, are globally distributed.
- This is highly distinct from the pattern previously observed for common reef animals, such as stony corals and fishes, where the Indo-Pacific Ocean has several times the number of families/genera compared to the Atlantic Ocean.
- Some zoantharian species, especially in the genera *Palythoa* and *Zoanthus*, have dispersal strategies that allow for broad distributions within ocean basins, while the vicariant events of the rise of the Isthmus of Panama and the appearance of the Benguela upwelling likely prompted the speciation of sibling lineages between the oceans.

## Keywords

Biogeographical Barriers, Marine Provinces, Niche, Sibling Species, Vicariance, Zoanthids

## Introduction

Understanding the processes that produce and maintain biodiversity is one of the main goals of evolutionary biologists. Parapatry has been suggested as one of the key speciation mechanisms in the marine realm, occurring when divergence in alternate habitats can continue in the face of ongoing gene flow (Gavrilets et al. 2000). Most biogeographic barriers in the marine realm are soft and species with extensive larval dispersal abilities may readily traverse such barriers (Rocha and Bowen 2008). For instance, widespread marine species usually have larvae that are transported by sea currents across great ocean distances, with some dispersing for more than 5000 km from the central to eastern Pacific during El Niño episodes (Lessios and Robertson 2006). However, physical barriers cannot be crossed by marine taxa and may lead to allopatric speciation via vicariant isolation (Coyne and Orr 2004).

One relatively recent vicariant isolation event was the rise of the Isthmus of the Panama, which removed the tropical connection between the Atlantic and Pacific basins (~3.5 mya; O'Dea et al. 2016). This event led to the evolution of sibling species pairs in several marine groups, including fishes and sea urchins (Jordan 1908; Bernardi et al. 2008; Lessios 2008). However, no such clear pattern has been observed for benthic cnidarians such as scleractinian stony corals (Fukami et al. 2004) or *Millepora* fire corals (Arrigoni et al. 2018). Some stony coral genera have a high genetic divergence between ocean basins among genera/families. However, zoantharians (= zoanthids; Cnidaria; Anthozoa; Zoantharia), hexacorals related to stony corals, are an exception to this pattern as several sibling species (or species complexes) inhabit distinct ocean basins yet share highly similar DNA sequences (Reimer et al. 2010; Reimer et al. 2012a; Santos et al. 2016; Dudoit et al. 2022). To date, no detailed investigations of these zoantharian sibling species across the order have been performed, and their diversity and overall distributions remain uncertain. Zoantharians are among the most abundant non-calcifying hexacorals in shallow-water ecosystems, with colonies of some species able to cover dozens of square meters in tropical and temperate regions (Burnett et al. 1997; Oigman-Pszczol et al. 2004), and there is also high diversity known from deep to abyssal waters (Carlgren 1901; Reimer et al. 2007a).

Although biogeographical patterns of many shallow-water reef groups such as fishes and stony corals are relatively well-known (Randall 1998; Briggs and Bowen 2012; Veron et al. 2015; Cowman et al. 2017), zoantharians and many other marine invertebrates are understudied in most regions (Knowlton 2001), and this extends especially into deeper waters (Reimer et al. 2019). An exception to that is the zoantharian distribution across Atlantic subtropical and tropical provinces (Santos et al. 2016, 2019), which have some biogeographic partitions similar to reef fishes (Floeter et al. 2008), stony corals (Veron et al. 2015), and fire corals (De Souza et al. 2017). Examples of this concordance among organismal groups include both range limits and biodiversity patterns: 1) Thermohaline properties of

South Atlantic water masses may limit the southern distribution of tropical zoantharians in this region (Santos et al. 2016), and 2) the Caribbean province is the zoantharian biodiversity center of the Atlantic, while oceanic islands have the lowest species richness (Santos et al. 2019). In contrast to prevailing biogeographic patterns, a lower endemism rate among provinces was observed in Atlantic Zoantharia compared to other common reef groups. The most widespread species were *Palythoa caribaeorum* Duchassaing & Michelotti, 1860, *P. grandiflora* (Verrill, 1900), and *Zoanthus sociatus* (Ellis, 1768), all with amphiatlantic distributions (Santos et al. 2019). Despite these basin-wide efforts, no study has connected the biogeographic patterns of zoantharians on a global scale.

Due to their wide distribution, zoantharians provide opportunities to examine evolution at large geographical scales (Swain 2010; Santos et al. 2019, 2024). The order has nine families and is subdivided into the suborders Brachycnemina and Macrocnemina (Fig. 1). Most species of Brachycnemina are associated with the Symbiodiniaceae microalgae (Muscantine and Hand 1958; LaJeunesse et al. 2018), also known as zooxanthellae, and are restricted to shallow waters. On the other hand, macrocnemians have a broader distribution into the deep sea and polar regions, and are mostly azooxanthellate (Swain 2010). Additionally, several Macrocnemina genera, and one Brachycnemina genus (*Acrozoanthus*), display epizoid symbioses, in which the polyps attach to other benthic invertebrates, including crabs, hydroids, octocorals, sponges, or tubes of polychaete worms (West 1979; Sinniger et al. 2010; Swain 2010; Kise et al. 2023). These associations are often obligatory, and the zoantharian species is only found associated with a specific genus or family of invertebrate hosts. For example, *Umimayanthus chanpuru* Montenegro, Sinniger & Reimer, 2015 is always associated with sponges, while *Epizoanthus illoricatus* Tischbierek, 1930 is only found growing on eunicid worm tubes.

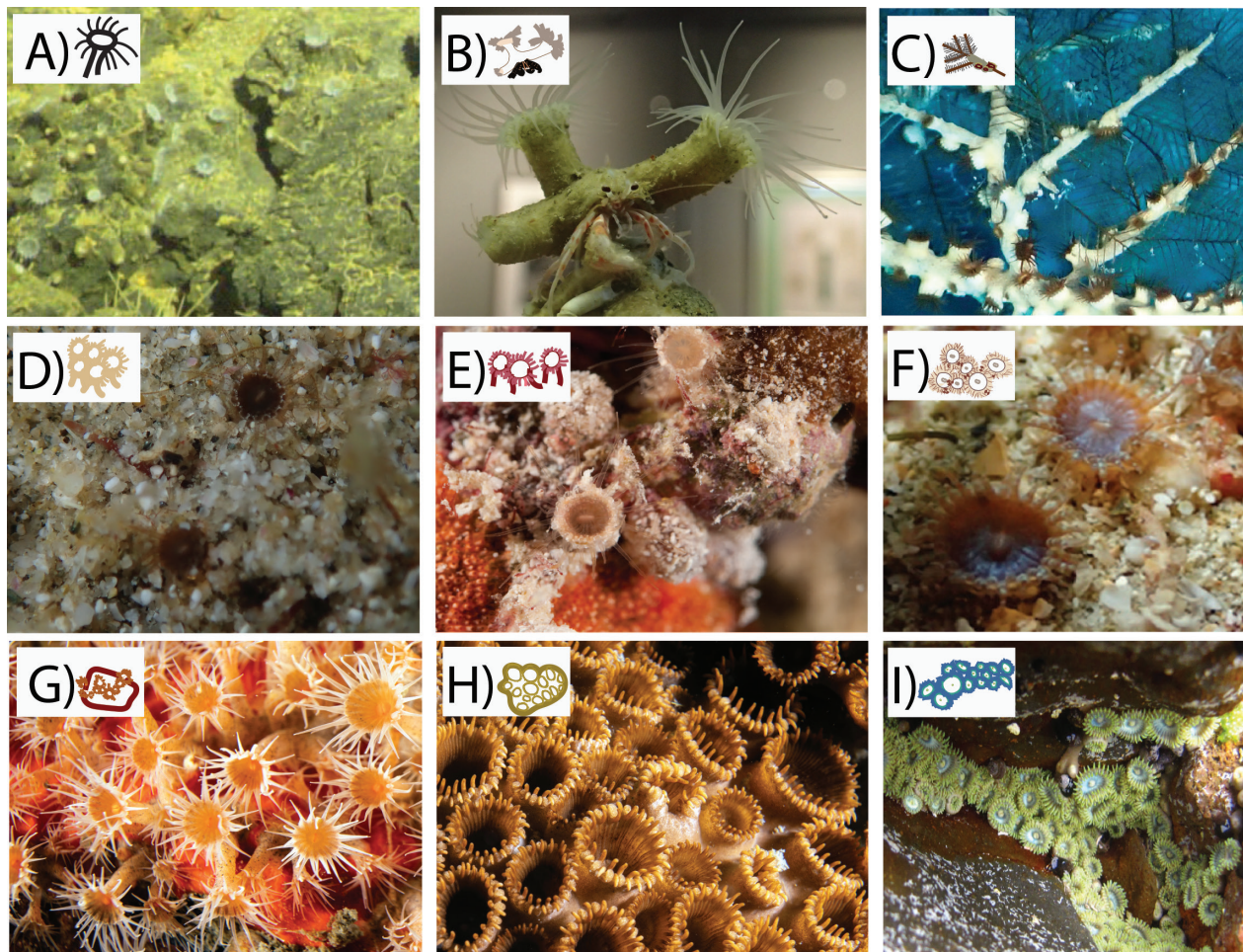
Herein, we used morphological and molecular data combined with a comprehensive literature review to investigate the global biogeography of Zoantharia. We also aimed to indicate which are the zoantharian sibling species complex between the Atlantic (ATO) and the Indo-Pacific (IPO) ocean basins. We then discussed hypotheses of how ecological traits influence dispersal and evolution of zoantharians in (primarily) shallow and (where possible) deep waters, illuminating the processes that led to these biogeographical patterns.

## Methods

### Shallow water and deep-sea surveys

Surveys were conducted using snorkeling or SCUBA diving at depths of 0 to 40 m in five regions: Yucatan, Mexico (2013), Hong Kong, Hong Kong SAR (2015 and 2024), Cebu, Philippines (2017), South Africa (2019), Bali, Indonesia (2019 and 2024) and Kenting, Taiwan (2024). Whenever possible,





**Figure 1.** Representatives of the nine zoantharian families. Abyssoanthidae (A. *Abyssoanthus convallis* Reimer & Sinniger, 2010); Epizoanthidae (B. *Epizoanthus paguricola* Roule, 1900 associated with a hermit crab), Hydrozoanthidae (C. *Hydrozoanthus gracilis* (Lwowsky, 1913) with hydrozoan), Microzoanthidae (D. *Microzoanthus* sp.), Nanozoanthidae (E. *Nanozoanthus*), Neozoanthidae (F. *Neozoanthus uchina* Reimer, Irei & Fujii, 2012), Parazoanthidae (G. *Parazoanthus swiftii* (Duchassaing de Fombressin & Michelotti, 1860) symbiotic with sponges), Sphenopidae (H. *Palythoa tuberculosa* (Esper, 1805)), and Zoanthidae (I. *Zoanthus sociatus* (Ellis, 1768)). Image credits: JD Reimer (A and E), T Moritaki (B), MEA Santos (C, F, and I), T Fujii (D), and MV Kitahara (G and H).

we followed the roving observer technique to observe as many species as possible (Schmitt et al. 2002). Additionally, *in situ* high-resolution images were taken, and a small fragment of the colony was collected (non-lethal sampling) and preserved in 90–99% ethanol for further analyses (Suppl. material 1). We also examined zoantharian specimens deposited at the Bernice Pauahi Bishop Museum (BPBM) in O’ahu, Hawai’i. To improve the understanding of deep-sea (>200 m) zoantharians, we investigated specimens deposited at the Smithsonian National Museum of Natural History (SNMNH) collected by the Okeanos 2016 expedition in the Pacific Ocean, and at the National Museum of Rio de Janeiro (MNRJ) collected in Brazilian waters (Suppl. material 1).

## Literature review and biogeographical analyses

We compiled records of Zoantharia for global marine biogeographical provinces (Suppl. material 2). We followed

the provinces as described in Briggs and Bowen (2012) because this work has a special focus on reef ecosystems, and the provinces defined by >10% endemism align well with phylogeographic breaks recovered in fishes and crustaceans (Bowen et al. 2016; Iacchi et al. 2016). Due to the high number of inadvertent Zoantharia species re-descriptions combined with a lack of surveys focusing on this group (Burnett et al. 1997; Hibino et al. 2013a, b; Santos et al. 2019), data were analyzed at the taxonomic level of families and genera, and not to species level. We then summarized the relationship among global biogeographical provinces based on the number of shared zoantharian taxa common to the pair of areas using Jaccard dissimilarity index (Jaccard 1908) and Unweighted Pair Group Method with Arithmetic Mean (Sneath and Sokal 1973). We also applied a non-metric multidimensional scaling analysis (nMDS) of the dissimilarity distances to plot similarities in zoantharian composition by ocean basin (ATO or IPO) and seawater temperature (tropical or temperate). Statistical differences were tested with pairwise Adonis

(Martinez Arbizu 2020) with the package *vegan* 2.6-10 (Oksanen et al. 2025). Due to the patchiness of deep-sea data (Reimer and Sinniger 2010; Carreiro-Silva et al. 2017; Reimer et al. 2019b), we focused analyses of the biogeography and sibling species complexes only in the shallow-water data.

## Morphology, phylogenetic analyses, and sibling species complexes

Morphology was used to identify zoantharian specimens to the lowest taxonomic level possible using the following characters: number of tentacles, size range of oral disk, oral disk color, and form of the polyp as ‘liberae’, ‘intermediae’, or ‘immersae’ (Pax 1910; West 1979; Burnett et al. 1997; Reimer 2010; Reimer et al. 2013). Additionally, we retrieved molecular sequences from NCBI for the most common markers for Zoantharia: mitochondrial cytochrome oxidase subunit I (COI) and 16S ribosomal DNA (16S rDNA), and the nuclear ribosomal internal transcribed spacer (ITS rDNA). The sequences and species are listed in Suppl. material 3. We selected mainly sequences from previous authors’ publications, and for which we were confident in species identifications (e.g. had voucher specimens). Sequences were aligned using Geneious v8.1 (Kearse et al. 2012), using the global alignment tool with free-end gaps and default settings. A concatenated alignment was generated and missing data was replaced with “N” (excluding gaps). All output alignments were visually inspected and manually curated, totaling 120 sequences and 3,219 sites. Phylogenetic reconstructions were performed using this concatenated alignment for maximum-likelihood (ML; 1000 bootstrap replicates) in Geneious v8.1, with the GTR model of nucleotide substitution as selected using TOPALi v2.5 (Milne et al. 2009). The newick dataset is available at the Figshare repository (<https://doi.org/10.6084/m9.figshare.30811127>). We defined a sibling species complex in the phylogeny as sister clades composed of at least one ATO and one IPO species (or species’ group) that had a similar overall morphology (partial or total overlap of at least three out of the four following traits: number of tentacles, size range of oral disk, oral disk color, and form of the polyp). Morphological characters for described species and distribution data were compiled from the literature and newly collected specimens (Suppl. material 4).

## Results

### Biogeography of zoantharians

Our results revealed that 6 out of the 8 Zoantharia families reported in shallow-waters were cosmopolitan (Figs 2, 3; Suppl. material 2), with the exception of Nanozoanthidae and Neozoanthidae, which, so far, only have been reported in the IPO (but see Discussion; they

are most likely also distributed in the ATO). The diversity center for Zoantharia in shallow waters was the INP province in the Central IPO (Fig. 2A, B). Within the ATO, CAR was the province with the highest diversity. However, a different pattern is observed for deep waters (Fig. 2C, D) where the most diverse provinces were SNJ (7 genera), LUS (6), and HAW (5).

With the exception of the families Abysozoanthidae, Epizoanthidae, and Parazoanthidae, zoantharians were restricted to shallow waters (Fig. 3). Parazoanthidae was the most diverse family (16 genera) and the most widely distributed, with reports across 19 provinces (Figs 3, 4). Of the 31 Zoantharia genera, 14 were found only in shallow waters, 11 only in deep waters, and 6 across both depth zones (Suppl. material 2). Among the 20 genera observed in shallow waters, 6 were so far only reported to the IPO and one to the ATO.

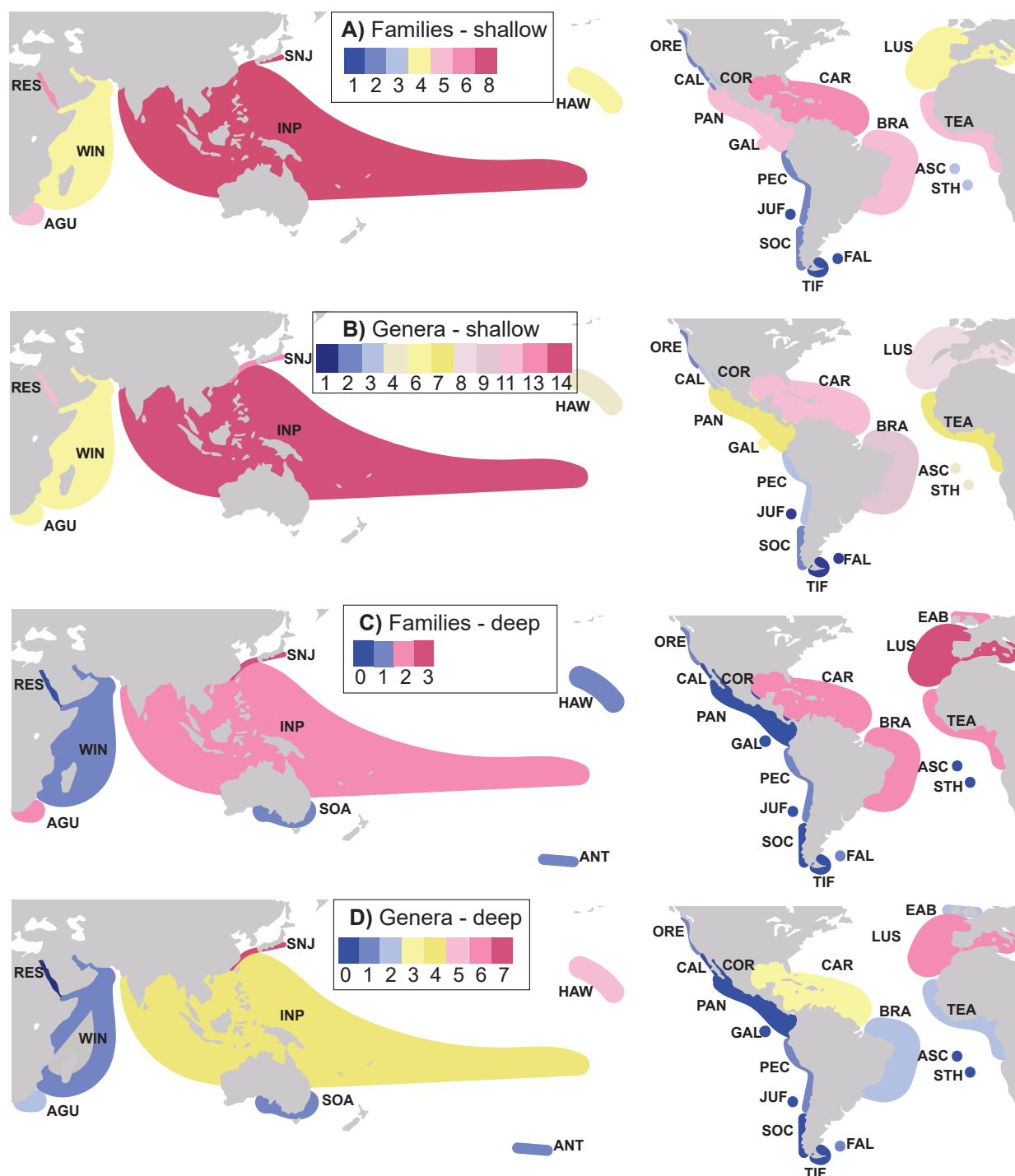
The clustering of shallow biogeographical provinces retrieved two main groups; one with all warm global provinces, in addition to the temperate provinces AGU, COR, and LUS, and the other with the remaining temperate/polar provinces (Fig. 4). Adonis analyses showed no significant differences in the composition of genera and families between the ATO and IPO, yet tropical and temperate provinces had significant differences (Suppl. material 5).

### Phylogeny and sibling species complexes

The phylogenetic reconstruction confirmed that the suborder Brachynemina is monophyletic (families Neozoanthidae, Sphenopidae, and Zoanthidae), while the suborder Macrocnemina (families Epizoanthidae, Hydrozoanthidae, Microzoanthidae, Nanozoanthidae, and Parazoanthidae) is paraphyletic with the family Hydrozoanthidae residing within brachycnemic zoantharians (Fig. 5). Although the family Abysozoanthidae is not assigned to any suborder, species were phylogenetically within Macrocnemina. At least four shallow-water families had sibling species complexes (Suppl. material 4).

In the suborder Brachynemina, three genera from two families had species reported in ATO and IPO. These three genera had sibling species groups: *Palythoa* from the family Sphenopidae, and *Zoanthus* and most likely *Isaurus* (discussed below) from Zoanthidae (Fig. 6; Suppl. material 4). The suborder Macrocnemina had at least two sibling species groups, one from the family Hydrozoanthidae and another from Parazoanthidae. With the exception of *Hydrozoanthus antumbrosus* (Swain 2009), which has so far only been reported in the CAR, zoantharian sibling species had extensive distributions including at least two biogeographic provinces. The sibling pair *P. caribaeorum* (ATO) and *P. tuberculosa* (Esper, 1805) (IPO) had the most extensive distribution among zoantharians analyzed herein, with reports across all tropical and subtropical provinces (Fig. 6, Suppl. material 4).





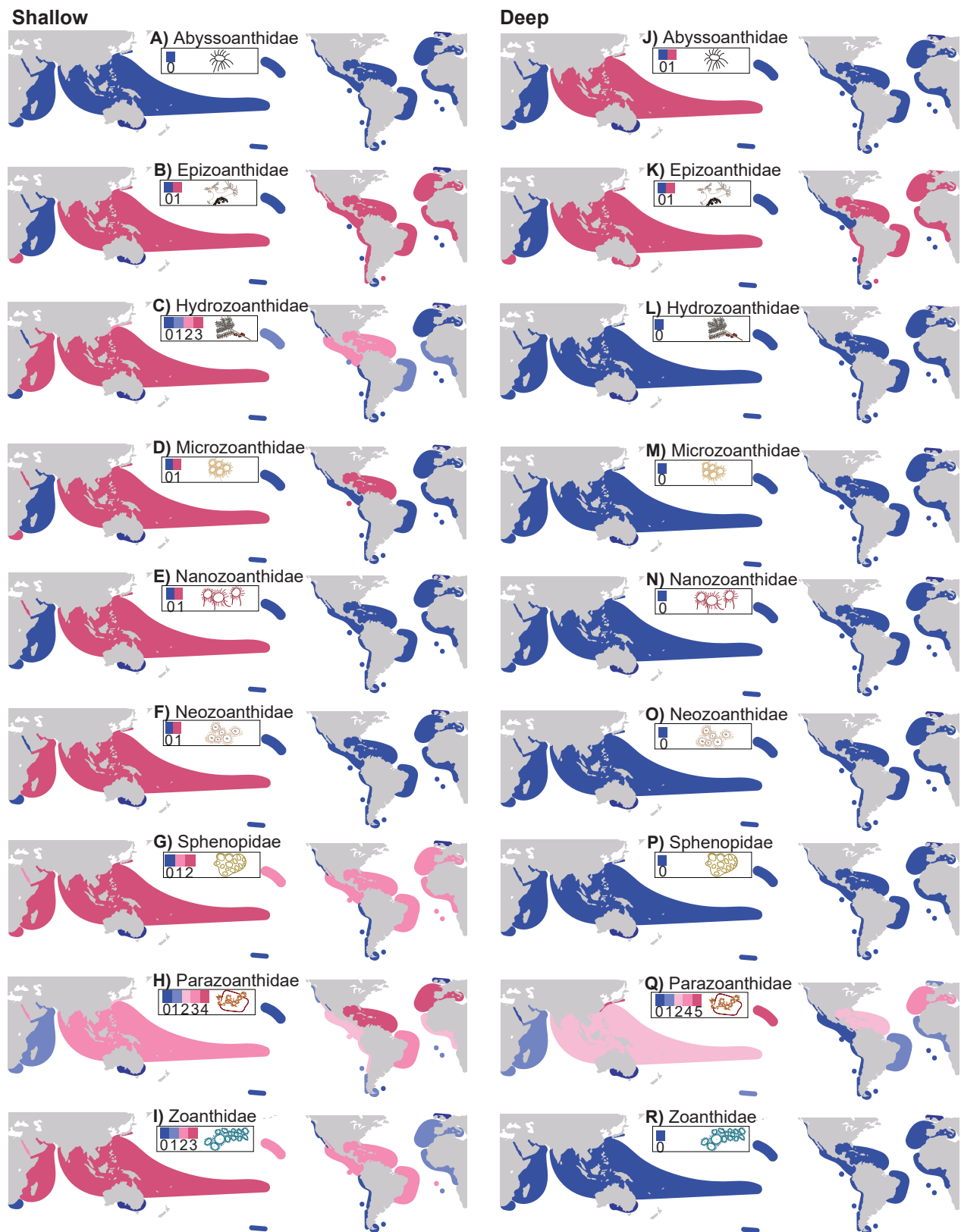
**Figure 2.** Global distribution of zoantharians. Total number of families and genera in shallow (A and B) and deep waters (C and D). Colors represent the number of families/genera reported for each province. Subtropical and tropical provinces were Ascension (ASC), Brazilian (BRA), Caribbean (CAR), Lusitania (LUS), Saint Helena (STH), Tropical Eastern Atlantic (TEA), Galapagos (GAL), Hawaiian (HAW), Indo-Polynesian (INP), Red Sea (RES), Sino-Japanese (SNJ) and Western Indian Ocean (WIN), while in temperate/polar waters were Agulhas Province (AGU), Antarctic Province (ANT), California (CAL), Cortez (COR), Easter Atlantic Boreal (EAB), Falkland Islands (FAL), Juan Fernandez (JUF), Oregon (ORE), Panamanian (PAN), Peru-Chilean (PEC), Southeastern Australian (SOA), Southern Chile (SOC), and Tierra del Fuego (TIF).

## Discussion

### Global marine biogeography

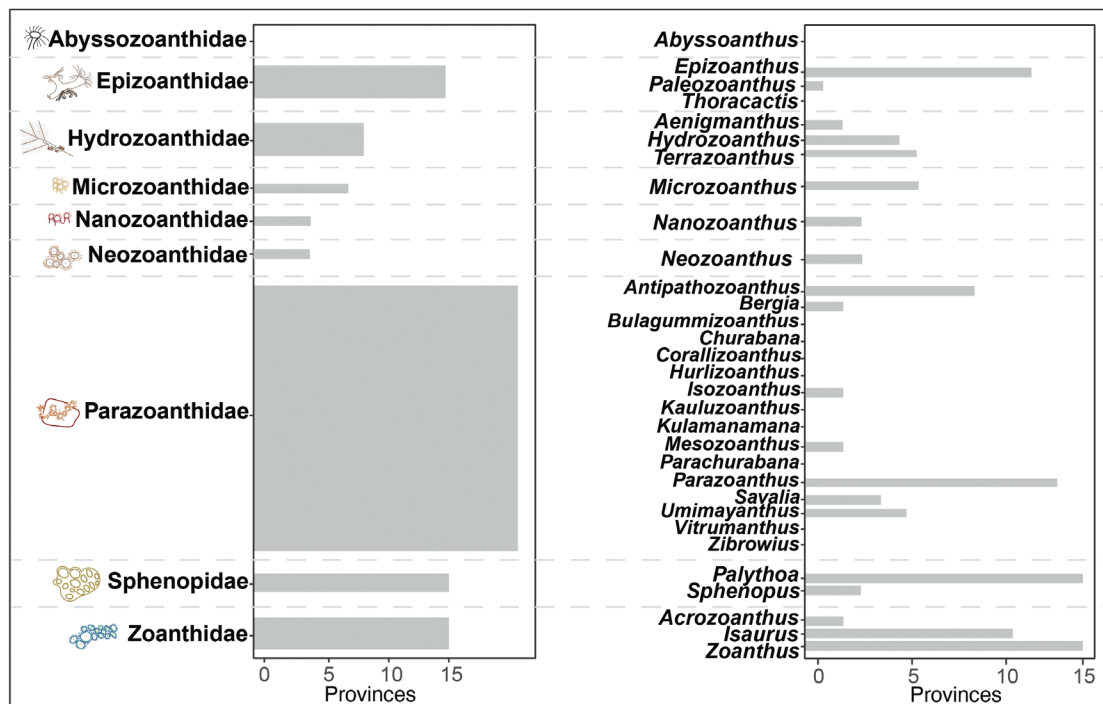
We observed a higher diversity of Zoantharia in shallow waters in the IPO compared to the ATO, with the global

hotspot in the INP province (Fig. 2A, B), similarly to global patterns observed for marine fishes, corals, and macroinvertebrates (Roberts et al. 2002; Bowen et al. 2013; Briggs and Bowen 2013; Veron et al. 2015). Nevertheless, the composition of genera and families between the IPO and ATO was not significantly different (Fig. 4 and Suppl.

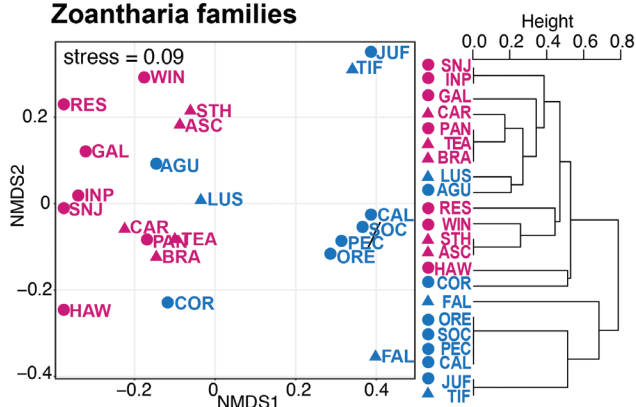


**Figure 3.** Global distribution of zoantharians for each family in shallow (A–I) and deep (J–R) waters. Colors represent the number of families/genera reported for each province. Subtropical and tropical provinces were Ascension (ASC), Brazilian (BRA), Caribbean (CAR), Lusitania (LUS), Saint Helena (STH), Tropical Eastern Atlantic (TEA), Galapagos (GAL), Hawaiian (HAW), Indo-Polynesian (INP), Red Sea (RES), Sino-Japanese (SNJ) and Western Indian Ocean (WIN), while in temperate/polar waters were Agulhas Province (AGU), Antarctic Province (ANT), California (CAL), Cortez (COR), Easter Atlantic Boreal (EAB), Falkland Islands (FAL), Juan Fernandez (JUF), Oregon (ORE), Panamanian (PAN), Peru-Chilean (PEC), Southeastern Australian (SOA), Southern Chile (SOC), and Tierra del Fuego (TIF).

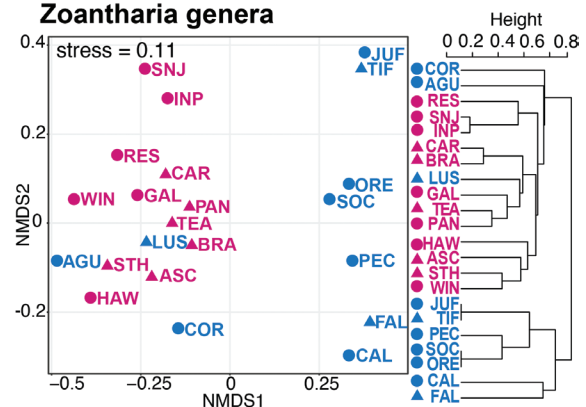
## A) Number of biogeographical provinces for each family and genera (shallow waters)



## B) Relationship of provinces for Zoantharia families



## C) Relationship of provinces for Zoantharia genera



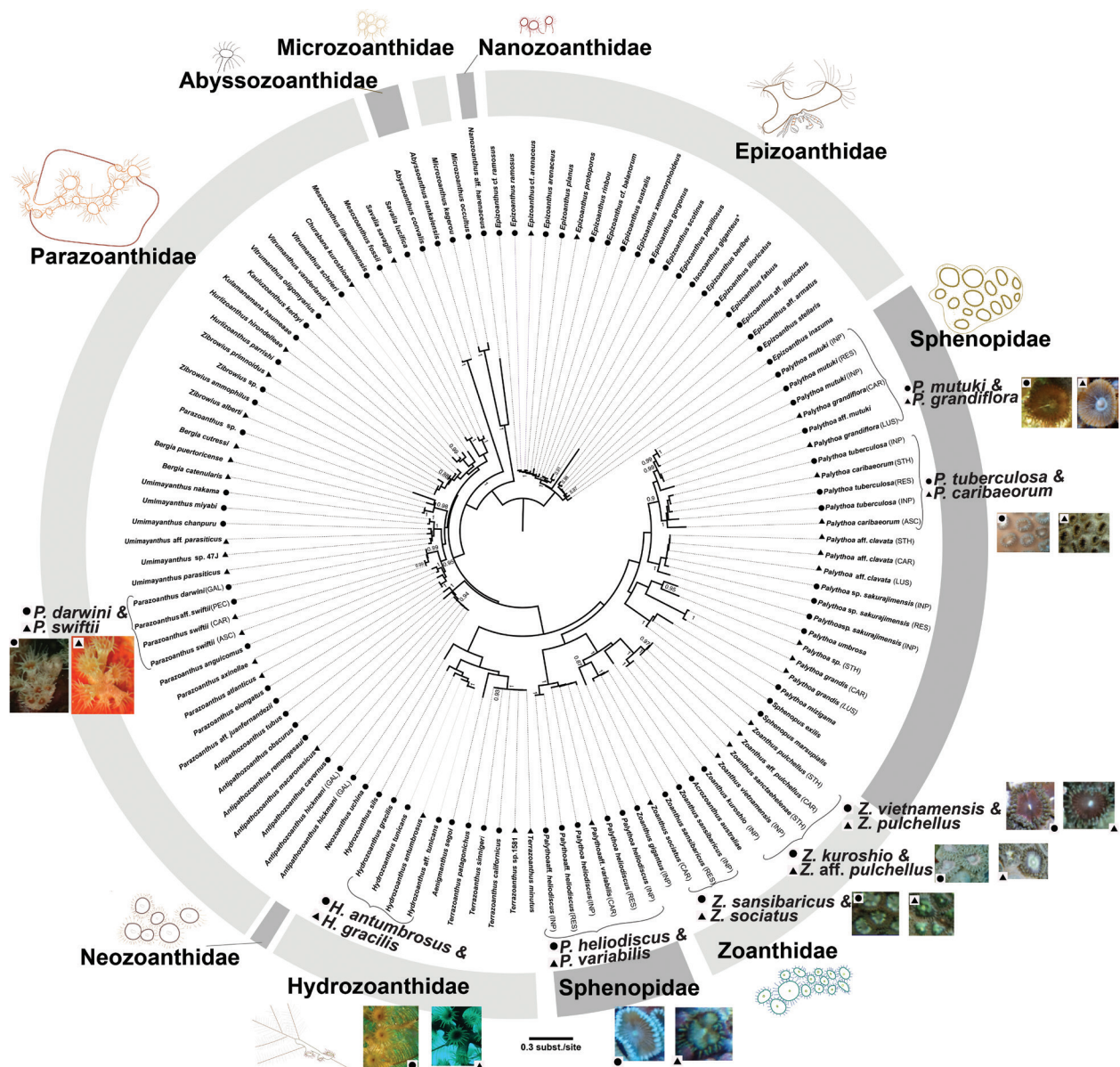
**Figure 4.** Relationship of the global biogeographical provinces based on Zoantharia distribution in shallow waters. Total number of provinces records for (A) each family (left) and genera (right). The thickness of the barplot for each family is proportional to its number of genera. Taxa with no records in shallow waters were reported only in the deep sea. The relationship among biogeographical provinces was summarized for families (B) and genera (C), based on a non-metric multidimensional scaling analysis (left) and Jaccard dissimilarity index and Unweighted Pair Group Method with Arithmetic Mean (right). Tropical/subtropical provinces are shown in pink, and temperate/polar provinces in blue. Provinces from the Atlantic Ocean are indicated by a triangle, and from the Indo-Pacific by a circle. Subtropical and tropical provinces were Ascension (ASC), Brazilian (BRA), Caribbean (CAR), Lusitania (LUS), Saint Helena (STH), Tropical Eastern Atlantic (TEA), Galapagos (GAL), Hawaiian (HAW), Indo-Polynesian (INP), Red Sea (RES), Sino-Japanese (SNJ) and Western Indian Ocean (WIN), while in temperate/polar waters they were Agulhas Province (AGU), Antarctic Province (ANT), California (CAL), Cortez (COR), Easter Atlantic Boreal (EAB), Falkland Islands (FAL), Juan Fernandez (JUF), Oregon (ORE), Panamanian (PAN), Peru-Chilean (PEC), Southeastern Australian (SOA), Southern Chile (SOC), and Tierra del Fuego (TIF).

material 5), contrasting with prevailing biogeographical patterns that indicate strong vicariance between these ocean basins (Cowman and Bellwood 2013; Costello et al. 2017). Most, if not all, zoantharian families had a global distribution in shallow waters, which is remarkable and distinct from most other common marine animals.

We hypothesize that low or moderate genetic diversity may partially explain this pattern of low divergence

between ocean basins. Anomalous low mutation rates have been observed in a diversity of taxa including plants (Wolf et al. 1987; Xu et al. 2019), cnidarians (Tseng et al. 2005) and vertebrates (Avice et al. 1992; Feng et al. 2017). A low mtDNA mutation rate may prevail in most anthozoan orders, including stony corals and zoantharians (Shearer et al. 2002; Huang et al. 2008). Likewise, hybridization and incomplete lineage sorting may obscure





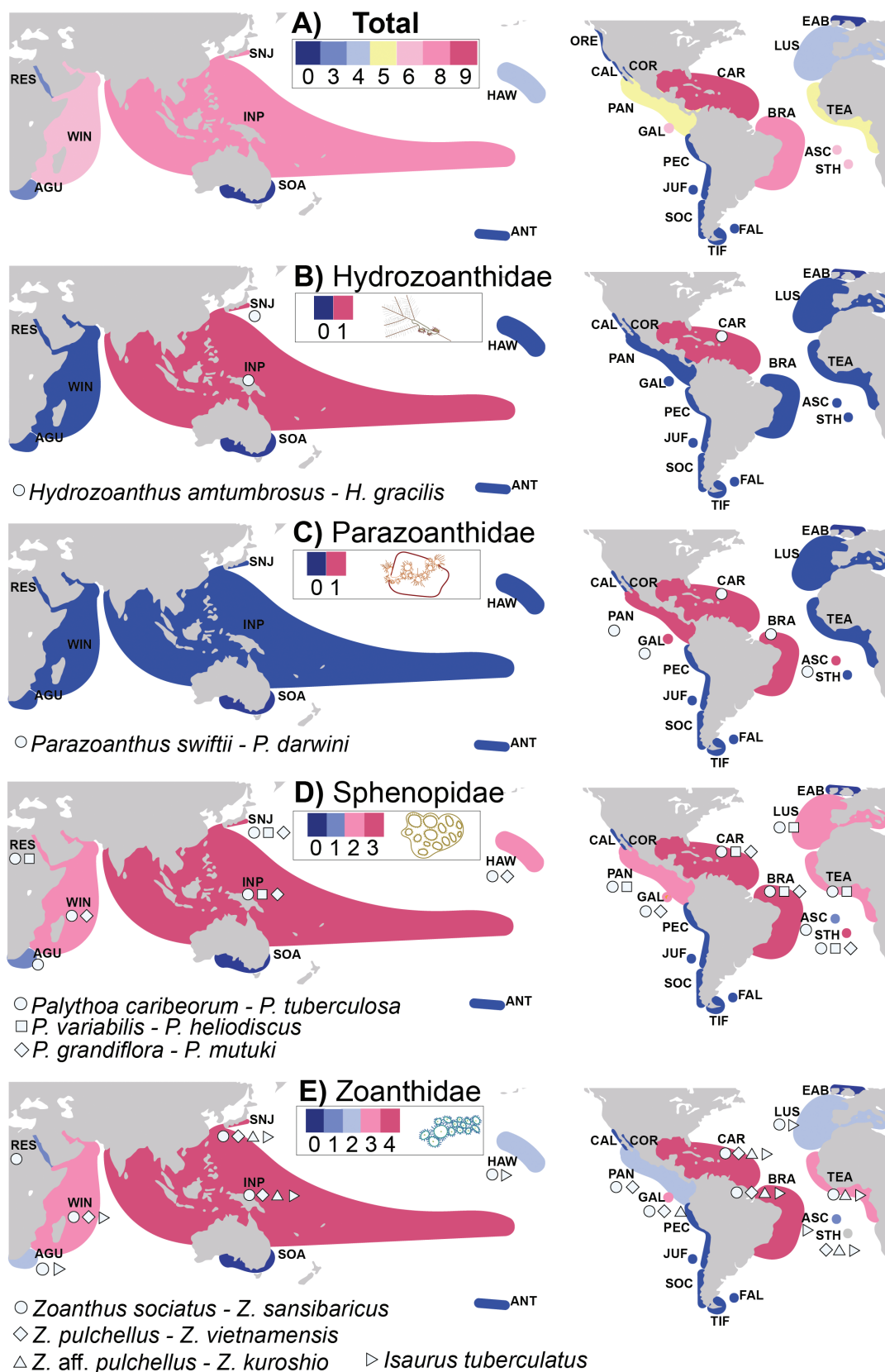
**Figure 5.** Phylogeny of the order Zoantharia. Phylogenetic tree obtained from a concatenated alignment of the mitochondrial markers of COI, 16S-rDNA, and the nuclear ITS-rDNA. Values at nodes represent ML bootstrap values >75%, respectively. Species distributed in the Atlantic Ocean are indicated by a triangle, and in the Indo-Pacific Ocean by a circle. Sibling species complexes are indicated with curly brackets. \*Family Parazoanthidae.

evolutionary relationships for many *Palythoa* and *Zoanthus* lineages (Reimer et al. 2007b; Shiroma and Reimer 2010; Mizuyama et al. 2018), as well as for some stony coral species (Vollmer and Palumbi 2002; Johnston et al. 2017; Terraneo et al. 2025). Additionally, many Zoantharia lineages have evolved high ecological plasticity, adapting to distinct habitats/environment settings. For instance, endosymbiosis with Symbiodiniaceae and epizoisism have been gained and lost multiple times in several distinct genera/families (Swain 2010; Kise et al. 2023). However, genomic studies of zoantharians are still scarce (Fourreau et al. 2023; Yoshioka et al. 2024), hampering our ability to compare their gene repertoire with other groups such as stony corals. For example, the evolutionary mechanisms that promote a lower mutation rate in zoantharian

lineages, and/or facilitate generalist ecological strategies. Therefore, further research on this topic is needed to shed light on the puzzling evolution of Zoantharia and the apparent unusual low levels of DNA evolutionary rates between the IPO and ATO.

## Which processes might have driven the sibling species pattern?

There was a striking pattern in zoantharians having sibling evolutionary lineages between ocean basins (Figs 5, 6), which is far different from that observed in stony corals and fire corals (Fukami et al. 2004; Arrigoni et al. 2018). In a genetic survey of 35 marine vertebrates and invertebrates,



**Figure 6.** Global distribution of zoantharian sibling species complexes (A) and for each family (B–E). Colors represent the number of species reported for each province. Subtropical and tropical provinces were Ascension (ASC), Brazilian (BRA), Caribbean (CAR), Lusitania (LUS), Saint Helena (STH), Tropical Eastern Atlantic (TEA), Galapagos (GAL), Hawaiian (HAW), Indo-Pacific (INP), Red Sea (RES), Sino-Japanese (SNJ) and Western Indian Ocean (WIN), while in temperate/polar waters were Agulhas Province (AGU), Antarctic Province (ANT), California (CAL), Cortez (COR), Easter Atlantic Boreal (EAB), Falkland Islands (FAL), Juan Fernandez (JUF), Oregon (ORE), Panamanian (PAN), Peru-Chilean (PEC), Southeastern Australian (SOA), Southern Chile (SOC), and Tierra del Fuego (TIF).

Selkoe et al. (2014) reported that at most 50% of population dispersal could be attributed to pelagic larval duration (PLD). Research on zoantharian PLDs is limited, but an extended planktonic larval phase of more than 100 days is known for *P. tuberculosa* (Polak et al. 2011). Plankton tows also indicate long PLDs for the families Sphenopidae and Zoanthidae (Ryland et al. 2000). Asexual reproduction may promote local dispersal and increase substrate occupancy (Ryland 1997), and this trait has been described for genera such as *Palythoa*, *Parazoanthus*, and *Zoanthus* (Garrahou 1999; Acosta et al. 2005a; Acosta and González 2007). Additionally, some zoantharians have a high rafting potential (Santos and Reimer 2018). Many coastal organisms, including stony corals and reef fishes, are able to disperse for hundreds to thousands of kilometers attached to drift material such as volcanic pumice, seaweed, logs, or man-made objects (Jokiel 1990; Hoeksema et al. 2012). Combined, a long PLD, asexual reproduction modes, and rafting, at least partly explain the apparent low levels of genetic differentiation between ocean basins and the widespread distribution of several species (Fig. 6).

The low molecular and morphological divergence observed between zoantharian sibling species may also reflect a similar use of resources (e.g., related niches). For example, *P. tuberculosa* is often the most abundant zoantharian in shallow waters of the IPO, including Okinawa (Irei et al. 2011; Yang et al. 2013), Taiwan (Reimer et al. 2011a; Reimer et al. 2017a), Malaysia (Wee et al. 2017), and Red Sea (Reimer et al. 2017b). A similar trend was observed in the ATO sibling *P. caribaeorum*, which is widespread along the Brazilian and Caribbean coasts (Suchanek and Green 1981; Acosta et al. 2005b; Santos et al. 2016; Reimer et al. 2018), the Mid-Atlantic ridge (Reimer et al. 2014; Santos et al. 2019), and the East Atlantic (Reimer et al. 2010). Both species have been reported as generalists found in diverse environments from the backreef moat to the outer reef, and from the intertidal zone to more than 20 m deep (Sebens 1982; Yang et al. 2013; Santos et al. 2016, 2019, 2021; Reimer et al. 2017b). In contrast, the siblings *P. mutuki* (Haddon & Shackleton, 1891) and *P. grandiflora* are relatively less abundant than *P. tuberculosa* and *P. caribaeorum*, respectively, and occur most commonly on intertidal reef crests or exposed habitats in both ocean basins (Oigman-Pszczol et al. 2004; Shiroma and Reimer 2010; Irei et al. 2011; Santos et al. 2016). Additional ecological studies will help to understand if sibling zoantharians share other traits, such as reproduction cycles, trophic ecology, and interaction with symbiotic partners (Santos et al. 2021).

Speciation driven by ecological differentiation is documented in marine habitats (Rocha et al. 2005; Bowen et al. 2013). However, considering that most zoantharians are widely distributed across regions, and might share similar traits, it is unlikely that these sibling species result from ecological differences between the ATO and IPO. On the other hand, processes on a geological time scale are important in allopatric evolution. Due to the high molecular and morphological similarities between the zoantharian sibling species, and the widespread species distribution

within each ocean basin, their ancestors may have had a cosmopolitan distribution before the comparatively recent separation of the tropical ocean basins, prompting the allopatric processes generating this sibling species pattern.

The vicariant rise of the Panama Isthmus, along with the cold Benguela Current in southern Africa, are the most likely barriers that lead to the sibling zoantharian pairs and/or groups. The Isthmus of Panama connects the North and South American landmasses and its rise closed the tropical exchange between the ATO and IPO via the Central American Sea approximately 3.5 mya (Keigwin 1978; O'Dea et al. 2016). The Benguela upwelling zone started approximately 2 mya and encompass the South Atlantic coast of Angola, Namibia, and South Africa (Etourneau et al. 2009; Hutchings et al. 2009), and its cold water is an environmental barrier to many tropical marine species (Floeter et al. 2008). Nevertheless, water exchange from the Indian Ocean to the South ATO still occurs due to rings and filaments of the warm Agulhas Current that occasionally intrude into the Atlantic (Lutjeharms 1996), possibly connecting reef fish populations (Cord et al. 2025). Another vicariant event that could have influenced the sibling zoantharians' speciation process was the closure of the Tethys Sea. However, this is a much older event (20 to 12 mya; Dercourt et al. 1986; Cowman and Bellwood 2013b), which would have likely resulted in higher genetic differentiation than has been observed from zoantharian siblings.

## Main gaps on biogeography of zoantharians

There is no information on the connectivity of zoantharian populations at large scales. Studies describing high-quality whole genomes of Zoantharia species will further support phylogenomic trees and population genomic analysis. Such work is crucial to clarify how biogeographical barriers affect the gene flow and evolution of species and populations. Although our study is a first attempt to characterize the morphological similarities of sibling zoantharians, we highlight that additional work on the taxonomy and ecology of these species is much needed.

Zoantharians are often overlooked in ecological surveys, and their distributions as reported here are still underestimated. In particular, there is a paucity of research in the African coasts (Southeastern Atlantic and Western Indian), and Polynesian archipelagos. There is also great potential for discovering additional zoantharian species within cryptic habitats, such as caves (Kise et al. 2017), rubble zones (Fujii and Reimer 2013), and turf (Vaga et al. 2021). Although deep-sea research in HAW (Sinniger et al. 2013) and LUS (Carreiro-Silva et al. 2017) provinces have reported and described several species, the high diversity at these locations could be biased due to a paucity of zoantharian research in the mesophotic and deep-sea zones across most other provinces (Reimer et al. 2019).

It is most likely that the two current IPO-endemic families, Nanozoanthidae and Neozoanthidae, are cosmopolitan. Combined with the lack of focused surveys on



Zoantharia, species of the family Nanozoanthidae are difficult to spot due to a pale/translucid color and a small polyp size (<1 mm; Fujii and Reimer 2013). Molecular data have also pointed that the species *Isozoanthus sulcatus* found off the coast of western Europe likely belongs to Nanozoanthidae (Fujii and Reimer 2013). Likewise, phylogenetic analyses indicated that the family Neozoanthidae should be reassigned to the cosmopolitan family Zoanthidae (Reimer et al. 2011b, 2012b).

At the suborder level, Brachycnemina was recovered as a monophyletic group but several phylogenetic studies have shown that Macrocnemina is a polyphyletic clade (Sinniger et al. 2005; Swain 2010; Fourreau et al. 2023). Our results also retrieved Macrocnemina as a polyphyletic group (Fig. 5). Although our tree showed Parazoanthidae and Sphenopidae (genera *Palythoa*) as non-molophyletic clades, these nodes had poor support, while previous studies have endorsed the monophyly of these families (Sinniger et al. 2005; Poliseno et al. 2019; Forreau et al. 2023). Previous studies have also called for research to determine whether: (1) the monospecific genus *Acrozoanthus* is actually within *Zoanthus* (family Zoanthidae; Reimer et al. 2011c); (2) the monospecific genus *Sphenopus* is actually within *Palythoa* (family Sphenopidae; Reimer et al. 2012c; Fujii and Reimer 2016; Poliseno et al. 2019); (3) the monospecific genus *Paleozoanthus* is actually within *Terrazoanthus* (families Epizoanthidae and Hydrozoanthidae, respectively; Low et al. 2016; Fourreau et al. 2023); (4) the monospecific genus *Thoracactis* of the family Epizoanthidae is actually within Parazoanthidae (Kise et al. 2024); (5) *Isaurus tuberculatus* Gray, 1828, originally described from the ATO and later reported across the IPO, is likely a sibling species group (yet only mitochondrial sequences had been published; Reimer et al. 2008); (6) putative *P. sp.* 'sakurajimensis' (IPO) and *P. aff. clavata* (ATO) while not formally described, are part of a sibling species clade (Fig. 5); and (7) there are additional shallow-water zoantharian species with records from both oceans (e.g., *Epizoanthus paguricola* Roule, 1900 has been recorded from ATO and New Zealand, but no molecular data are available for these specimens). Lastly, species of *Palythoa* and *Zoanthus* play a significant ecological role in phase shifts from coral to zoantharian-dominated reefs (Cruz et al. 2016; Oliveira et al. 2022). With ongoing environmental changes, such phase-shifts may become more common in coral reefs worldwide (Reimer et al. 2021). Filling knowledge gaps on the distributions and biology of zoantharians will be essential to support monitoring and management of marine ecosystems.

## Conclusions

We reported unusual low DNA divergence for zoantharian lineages between the ATO and the IPO. Additional research is needed to reveal the processes behind this pattern, such as investigating whole-genomes of representatives of Zoantharia families, which could reveal low rates of molecular evolution. At the species level, we hypothesize

that some zoantharians have evolved generalist niches to survive in distinct biogeographical provinces across a wide range of environmental conditions, such as nutritional interactions with symbionts (Santos et al. 2021). Some species, particularly in *Palythoa* and *Zoanthus*, have dispersal strategies that allow for broad distributions within ocean basins, while the vicariant events of the rise of the Isthmus of Panama and the appearance of the Benguela Current upwelling likely prompted the speciation of sibling lineages between the ATO and the IPO.

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## Author contributions

All authors have contributed equally.

## Data accessibility statement

All of the data that support the findings of this study are available in the main text or Supplementary Information.

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## Supplementary materials

### Supplementary material 1

**ESM table S1: Sampling information.** We conducted surveys using snorkeling and SCUBA diving at depths between 0–40 m following the roving technique to observe as many species as possible in the following locations: Yucantan, Mexico (2013 and 2017), Hong Kong, Hong Kong SAR (2015 and 2024), Cebu, Philippines (2017), Bali, Indonesia (2019) and Kenting, Taiwan (2024). Whenever possible, in situ high-resolution images were taken and samples were collected and preserved in 90–99% ethanol for further analyses. We also examined specimens from the Smithsonian National Museum of Natural History (SNMNH), Museu Nacional do Rio de Janeiro (MNRJ), Brazil, and Bernice Pauahi Bishop Museum (BPBM), Hawai'i (.xlsx)  
Link: <https://doi.org/10.21425/fob.19.174247.suppl1>

### Supplementary material 2

**ESM table S2: Compiled records of Zoantharia for 25 global marine biogeographical provinces for shallow and deep waters.** Subtropical and tropical provinces were Ascension (ASC), Brazilian (BRA), Caribbean (CAR), Lusitania (LUS), Saint Helena (STH), Tropical Eastern Atlantic (TEA), Galapagos (GAL), Hawaiian (HAW), Indo-Polynesian (INP), Red Sea (RES), Sino-Japanese (SJA) and Western Indian Ocean (WIN), while in temperate waters were Agulhas Province (AGU) Tierra del Fuego (TIF) and Falkland Islands (FAL), California (CAL), Cortez (COR), Juan Fernandez (JUF), Panamanian (PAN), Peru-Chilean (PEC), Southern Chile (SOC), and Southeastern Australian (SOA), and the cold temperate Antarctic (ANT), Eastern Atlantic Boreal (EAB), and Oregon (ORE) provinces (.xlsx)  
Link: <https://doi.org/10.21425/fob.19.174247.suppl2>

### Supplementary material 3

ESM table S3: GenBank accession numbers of the zoantharian sequences used in this study (.xlsx)

Link: <https://doi.org/10.21425/fob.19.174247.suppl3>

### Supplementary material 4

ESM table S4: List of zoantharian sibling species along with their associated Symbiodiniaceae, and morphological and distribution data. Morphological data examined in this study (polyp form, oral disk color, and tentacle number) are shown in bold. Subtropical and tropical provinces were Ascension (ASC), Brazilian (BRA), Caribbean (CAR), Lusitania (LUS), Saint Helena (STH), Tropical Eastern Atlantic (TEA), Galapagos (GAL), Hawaiian (HAW), Indo-Polynesian (INP), Red Sea (RES), Sino-Japanese (SNJ) and Western Indian Ocean (WIN), while in temperate warm were Agulhas Province (AGU) Tierra del Fuego (TIF) and Falkland Islands (FAL), California (CAL), Cortez (COR), Juan Fernandez (JUF), Panamanian (PAN), Peru-Chilean (PEC), Southern Chile (SOC), and Southeastern Australian (SOA), and the cold temperate/polar provinces Antarctic (ANT) and Oregon (ORE) provinces (.docx)

Link: <https://doi.org/10.21425/fob.19.174247.suppl4>

### Supplementary material 5

ESM table S5: Summary of the Adonis results for the distribution of zoantharians in shallow waters tested for Ocean (Atlantic or Indo-Pacific) and localities (Temp; tropical or temperate provinces). Test under reduced model with 999 permutations. Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1 (.xlsx)

Link: <https://doi.org/10.21425/fob.19.174247.suppl5>