

Article

A New Gorgonian *Paraplexaura binyuani* sp. nov. (Cnidaria, Octocorallia, Acanthogorgiidae) from the Huaguang Atoll, Xisha Islands, South China Sea [†]

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Abstract

A new shallow-water gorgonian coral species in the family Acanthogorgiidae, *Paraplexaura binyuani* sp. nov., is described from a specimen collected at Huaguang Atoll in the South China Sea at a depth of 22 m. The new species is distinguished from its congeners by abundant polyp sclerites, predominantly flattened rods, and by the coenenchyme bearing numerous large spindles reaching up to 0.6 mm in length, which are approximately two to three times longer than those reported for most described species of *Paraplexaura*. Phylogenomic analyses based on ultraconserved elements (UCEs) recover *Paraplexaura* as monophyletic and place *P. binyuani* sp. nov. as sister to *P. cryptotheca*, consistent with its morphological distinctiveness and supporting its recognition as a separate species.

Keywords: Malacalcyonacea; shallow-water coral; taxonomy; morphology; ultraconserved elements

1. Introduction

As habitat-forming suspension feeders, octocorals contribute three-dimensional structure to benthic habitats, increasing substrate complexity and supporting diverse associated assemblages [1–3]. Within the family Acanthogorgiidae, the genus *Paraplexaura* Kükenthal, 1909 is characterized by flabellate colonies, fully retractile polyps, and a coenenchyme typically dominated by irregularly shaped sclerites, spindles, and capstans [4–6]. Five species are currently regarded as valid: *P. asper* (Moroff, 1902), *P. cryptotheca* (Nutting, 1910), *P. debora* (Grasshoff, 2000), *P. pulchra* (Nutting, 1910), and *P. reticuloides* (Nutting, 1910) [7]. However, extensive overlap in colony morphology and sclerite forms, which are often homoplastic across Acanthogorgiidae, has long hindered species-level taxonomy within *Paraplexaura* [8]. In addition, pronounced phenotypic plasticity in colony form across ontogeny and environmental gradients can further obscure species boundaries, emphasizing the value of independent molecular evidence [9,10]. As a result, boundaries among several nominal species remain uncertain, particularly in regions such as the northern South China Sea where molecular data remains extremely limited [11,12].



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During a biodiversity survey of shallow reef habitats at Huaguang Atoll on the Chinese margin of the South China Sea, we collected a specimen attributable to *Paraplexaura* that could not be confidently assigned to any described species based on morphology alone. To resolve the taxonomic uncertainty noted above, we integrate quantitative sclerite morphology, particularly the combination of abundant, slightly flattened polyp rods and large coenenchymal spindles, with phylogenomic evidence from ultraconserved elements (UCEs). Using these data, we diagnose the material, evaluate its phylogenetic placement within Acanthogorgiidae, and recognize it as a new species, *Paraplexaura binyuani* sp. nov.

2. Materials and Methods

2.1. Specimen Collection and Morphological Examinations

In this study, *P. binyuani* sp. nov. was collected by SCUBA diving from the shallow waters at Huaguang Atoll (16°10'35" N, 111°33'58" E), South China Sea, at 22 m depth, on 26 May 2025. The specimen was photographed in situ using a Nikon D850 digital camera (Nikon Corporation, Tokyo, Japan) with an underwater housing, preserved in 99% ethanol. The specimen (hereafter designated as holotype of *Paraplexaura binyuani* sp. nov.) was deposited in the Institute of Marine Drugs, Guangxi University of Chinese Medicine (<https://www.gxtcmu.edu.cn/hyywyjy>, accessed on 8 March 2026), with identifier GXTCMU-2025-HT005. Terminology used in the descriptions followed Bayer et al. [13]. Sclerites were examined separately from the polyps, calyx region and from the outer and inner coenenchyme. The preparation of polyps and sclerites for Scanning Electron Microscopy (SEM) followed standard short digestion protocols [14].

2.2. DNA Extraction and Sequencing

Genomic DNA was extracted from ethanol-preserved tissues using the TIANamp Marine Animals DNA Kit (Tiagen Biotech Co., Ltd., Beijing, China) following the manufacturer's protocol. Samples were subjected to untargeted shotgun genomic library preparation and sequencing (i.e., whole-genome shotgun sequencing; no UCE or other target-enrichment capture was performed). DNA quantity and quality were assessed using a Qubit fluorometer (Thermo Fisher Scientific, Waltham, MA, USA) and NanoDrop spectrophotometer (Thermo Fisher Scientific, Waltham, MA, USA). Approximately 0.2 µg of genomic DNA per specimen was fragmented to ~350 bp with a Covaris LE220R-plus (Covaris, Woburn, MA, USA) and used for library preparation, including end repair, A-tailing, adapter ligation, and PCR amplification. Libraries were purified with AMPure XP beads, evaluated on an Agilent 5400 system, and quantified by real-time PCR. After phosphorylation and cyclization, DNA nanoballs were generated through rolling circle amplification, and sequencing was performed on a DNBSEQ-T7 platform (150 bp paired-end) at Novogene (Beijing, China). For the newly sequenced specimens generated in this study ($n = 12$), each specimen yielded approximately 6 Gb of clean data.

2.3. UCE Recovery and Phylogenetic Analyses

Genomic data were compiled from two sources: newly sequenced specimens generated in this study and publicly available datasets downloaded from the Sequence Read Archive (SRA). All SRA datasets were downloaded as raw sequencing reads and processed using the same trimming, locus recovery, alignment, and filtering pipeline as the newly sequenced specimens. Two *Euplexaura* species were designated as the outgroup based on their phylogenetic position inferred in McFadden et al. [15].

Raw reads were first quality-trimmed with fastp v1.0.1 [16] under default parameters (-q 15, -u 40, -n 5, -l 15 bp). Target loci were recovered in silico as UCEs and exon regions from shotgun sequencing data using sequences from a previously published octocoral bait

set [17] (29,181 probes targeting 3023 loci) as reference loci in GeneMiner2 [18], rather than for experimental hybridization enrichment.

In GeneMiner2, UCEs locus recovery follows a reference-guided analytical framework, similar to that implemented in HybPiper [19], in which reads corresponding to target loci are first identified using k-mer based filtering, thereby restricting subsequent assembly to the intended genomic regions prior to contig construction. Filtered reads were assembled independently for each locus using a reference-guided, local de novo assembly strategy implemented in GeneMiner2; no whole-sample or genome-wide de novo assembly was conducted. For each target locus, GeneMiner2 constructs local de Bruijn graphs from locus-specific reads and applies a greedy extension procedure that prioritizes paths supported by read depth, consistency in k-mer positions relative to the reference, and strand orientation. Putative contigs are subsequently evaluated by mapping high-quality internal read segments to assess assembly reliability. GeneMiner2 was run with the parameters -kf 27 (k-mer length used for read filtering and locus identification), -tm longest (retaining, for each target locus, the longest assembled contig among alternative graph paths), -min-depth 2 (minimum read depth required for locus retention, following depth-handling logic analogous to the single-cell mode in SPAdes) [20] with the k-mer setting chosen to balance locus recovery and per-locus missing data.

Recovered loci were aligned independently by locus and subsequently filtered using AMAS v 1.0 [21] to construct concatenated data matrices retaining loci present in at least 50% of the sampled taxa. Maximum-likelihood (ML) phylogenies were reconstructed with IQ-TREE v3.0.1 [22] with initial data partitions defined by locus and best-fit substitution models and partition-merging schemes selected using ModelFinder [23] under the greedy search strategy (-m MFP). Node support was assessed using 1000 ultrafast bootstrap replicates (UFBoot) [24] and 1000 SH-like approximate likelihood ratio test (SH-aLRT) replicates [25]. Final trees were visualized and annotated using the Interactive Tree Of Life (iTOL) v6 [26]. Accession numbers and sequencing statistics for newly sequenced specimens were provided in Supplementary Table S1.

3. Results

3.1. Taxonomy

Phylum Cnidaria Hatschek, 1888.

Subphylum Anthozoa Ehrenberg, 1834.

Class Octocorallia Haeckel, 1866.

Order Malacalcyonacea McFadden, van Ofwegen & Quattrini, 2022.

Family Acanthogorgiidae Gray, 1859.

Genus *Paraplexaura* Kükenthal, 1909.

Diagnosis. (after Kükenthal 1909; Fabricius and Alderslade 2001) [1,4] Colony flabellate to subflabellate, planar, sparsely to moderately branched, never reticulate; branches relatively thick, lateral branches arising at nearly right angles and often curved upwards. Polyps monomorphic and fully retractile; calyces low or inconspicuous. Coenenchymal sclerites with tuberculate bases and low rounded mounds or thorny projections, and spindles, branched forms, capstans, and capstan derivatives. Calycular sclerites thornscales. Polyp sclerites variable in shape and number, sometimes absent, or present as a few flat rods to numerous elongate spindles.

Type species. *Paraplexaura asper* (Moroff, 1902), by monotypy.

Distribution. Indo-West Pacific. In a depth range of 13–90 m (Table 1).

Paraplexaura binyuani sp. nov.

(Figures 1 and 2, Table 1).

Zoobank ID: urn:lsid:zoobank.org:act:D22DB3CE-A79A-4570-8A02-D826E4E075A4.

Table 1. Comparison of morphological characters of *Paraplexaura* species.

Species	<i>P. binyuani</i> sp. nov.	<i>P. asper</i>	<i>P. cryptotheca</i>	<i>P. debora</i>	<i>P. pulchra</i>	<i>P. reticuloides</i>
Branching	planar	flabellate	flabellate	planar	irregular	flabellate
Colony color	purplish red	yellow	pale brown	brown	bright crimson	bright orange
Polyp sclerites	presence	absence	presence	presence	presence	absence
Sclerites	Surface layer of coenenchyme (mm)	irregularly shaped sclerites: up to 0.5	irregularly shaped sclerites: up to 0.9	irregularly shaped sclerites: up to 0.5	cockscomb thornscales, laterally flattened: up to 0.4	irregularly shaped sclerites: up to 0.4
	Inner layer of coenenchyme (mm)	spindles: up to 0.6, capstans: up to 0.12	spindles: up to 0.4, capstans: up to 0.1	spindles: up to 0.3, capstans: up to 0.1	spindles: up to 0.3, capstans: up to 0.1	spindles: up to 0.3, capstans: up to 0.1
	Calyx (mm)	thornscales: up to 0.3	thornscales: up to 0.3	thornscales: up to 0.2	thornscales: up to 0.3	thornscales: up to 0.2
Distribution	South China Sea	Sagami Bay	North Sulawesi; near New Guinea; Kei Islands; Aru Islands; South China Sea	Sinai coast; Ras Umm Sidd; South China Sea	Kei Islands; Tual Anchorage; South China Sea	Aru Islands; Flores Sea; South China Sea
References	this publication	[27,28]	[29,30]; this publication	[6]; this publication	[29,30]; this publication	[29,30]; this publication

Material examined. Holotype. GXTCMU-2025-HT005 (=HGJ023), CHINA-Hainan Prov. Xisha Islands, Huaguang Atoll; 16°10'35" N, 111°33'58" E; depth of 22 m; 26 May 2025.

Diagnosis. Colony deep purplish red in life. Branching dichotomous to irregular, largely confined to a single plane. Polyps fully retractile, forming only very low, indistinct calycular elevations. Polyp sclerites abundant, predominantly flattened rods, colorless to weakly translucent. Coenenchymal sclerites orange to orange-red, dominated by irregularly shaped sclerites and spindles, with capstans rare. Calycular sclerites yellowish orange, predominantly thornscales.

Description. The holotype is incomplete, consisting of a single detached branch fragment lacking the basal holdfast, measuring approximately 16.9 cm in length and 4.2 cm in width. Branching is dichotomous to irregular, with branches gently curved upward and predominantly confined to a single plane. The mean distance between adjacent branches is approximately 13 mm. Terminal branchlets are short and blunt, about 16 mm in length and 5 mm in width (Figure 1B). Polyps are fully retracted into the coenenchyme, leaving a shallow, recessed orifice with only a very low, inconspicuous surface elevation. Contracted polyps measure approximately 0.48 mm in length and 0.31 mm in width. Polyps are densely but irregularly distributed along branch surfaces, becoming sparser on thicker branches and more closely spaced on thinner distal branches, with a mean inter-polyp distance about 2.1 mm (Figure 1B–E). Both polyps and coenenchyme are densely armed with sclerites. Polyp sclerites consist predominantly of abundant, flattened rods, not arranged into a distinct collaret and points, measuring approximately 0.05–0.2 mm in length and 0.02–0.05 mm in width (Figure 2A). The surface layer of the coenenchyme contains numerous irregularly shaped sclerites with unilateral spinose bodies, measuring approximately 0.2–0.5 mm in length and 0.15–0.35 mm in width (Figure 2B). Inner layer of coenenchyme is dominated by abundant large spindles, straight or slightly curved, monaxial, and pointed at both ends, measuring approximately 0.2–0.6 mm in length and 0.05–0.2 mm

in width (Figure 2C), together with smaller capstans characterized by two whorls of tubercles or warts and terminal tufts, measuring approximately 0.05–0.12 mm in length and 0.03–0.07 mm in width (Figure 2D). The calyces are armed with thornscales bearing a central or marginal spinelike to digitiform process, measuring approximately 0.1–0.2 mm in length and 0.06–0.16 mm in width (Figure 2E).

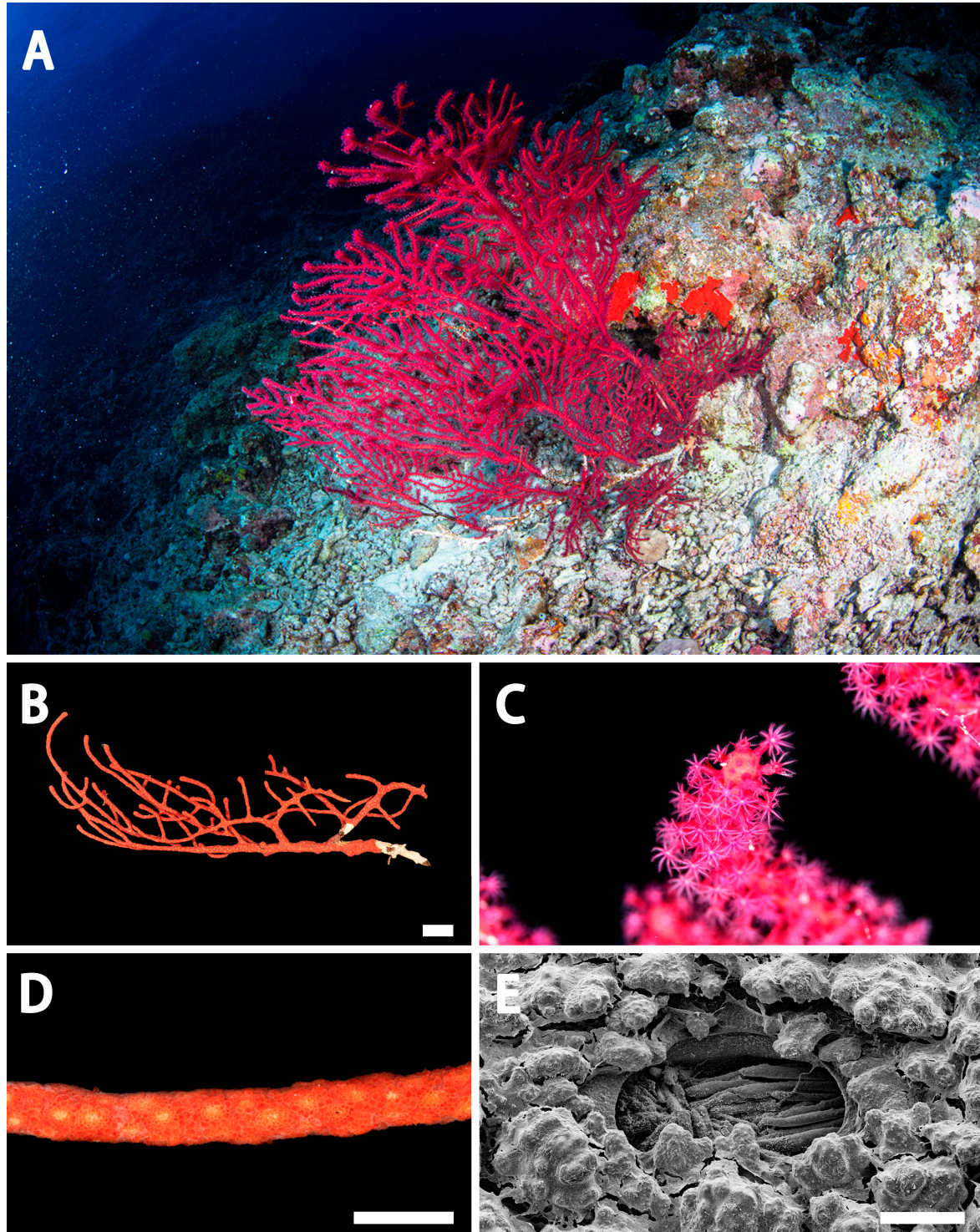


Figure 1. The external morphology and polyps of *Paraplexaura binyuani* sp. nov. Holotype, GXTCMU-2025-HT005. (A,C) *in situ*; (B) After collection; (D) Frontal view of a branch; (E) Polyps under SEM. Scale bars indicate 1 cm in (B), 5 mm in (D), 100 μ m in (E).

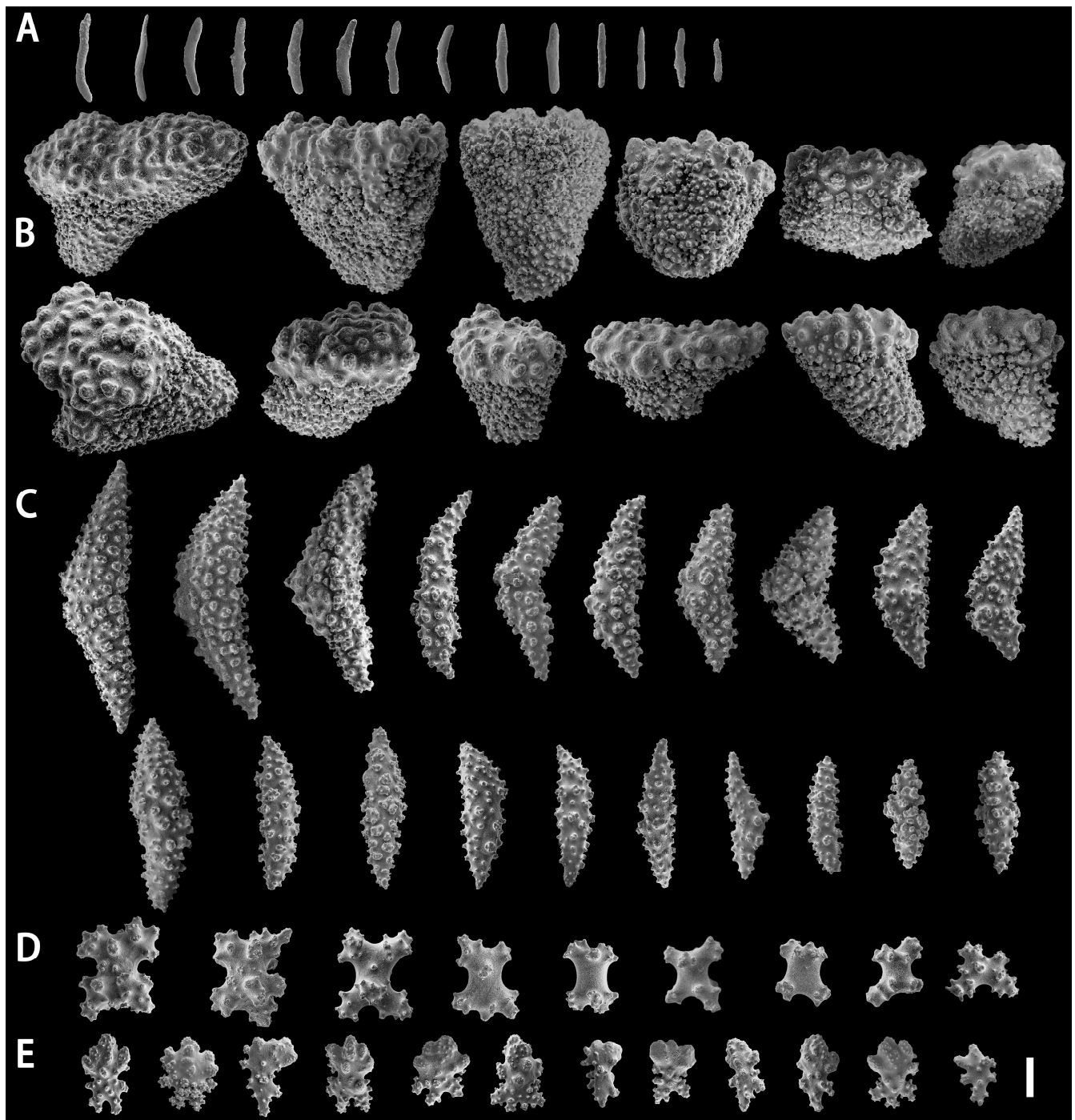


Figure 2. The sclerites of *Paraplexaura binyuani* sp. nov. (A) Polyp sclerites; (B) Irregularly shaped sclerites; (C) Spindles; (D) Capstans; (E) Thornscales. Scale bars indicate 0.1 mm in (A,B,C,E); 0.05 mm in (D).

Type locality. The subtidal zone of Huaguang Atoll with water depth of 22 m.

Etymology. The new species is named after Dr. Binyuan He, principal investigator of the Guangxi Academy of Oceanography, and for his great contribution to benthos research of Guangxi. The Chinese name of the new species is “斌源似丛柳珊瑚”

Distribution and habitat. Known only from the subtidal zone of the Huaguang Atoll on the Chinese coast of the South China Sea with a water depth of 22 m. Colony attached to a rocky substrate.

Color. Purplish red *in situ* (Figure 1A), becoming brown after fixation in ethanol (Figure 1B). Sclerites colorless to yellowish brown and red.

3.2. Molecular Results

We recovered 2771 UCE loci from 19 specimens, including 12 newly sequenced in this study and 7 retrieved from the Sequence Read Archive (SRA); in the phylogenetic tree, samples labeled with SRR accession numbers indicate SRA derived data, whereas boldfaced labels denote specimens newly sequenced in this study. The newly generated dataset comprised one *Paraplexaura binyuani* sp. nov. (HGJ023) (Figure 1B); one *P. pulchra* (Nutting, 1910) (ND39) (Figure 3A); one *P. reticuloides* (Nutting, 1910) (HGJ049) (Figure 3B); one *P. debora* Grasshoff, 2000 (QLY004) (Figure 3C); two *P. cryptotheca* (Nutting, 1910) (HGJ050, HGJ052) (Figure 4A,B); and one *Euplexaura paricladus* Wright & Studer, 1889 (HGJ018) (Figure 4C); one *Bebryce indica* Thomson, 1905 (HGJ053) (Figure 4D); one *Villogorgia intricata* (Gray, 1869) (HGJ030) (Figure 5A); and one *Menella praelonga* (Ridley, 1884) (WZD035) (Figure 5B); one *Echinogorgia ramosa* (Thomson & Henderson, 1905) (WZD036) (Figure 5C); one *Echinomuricea peterseni* Hedlund, 1890 (HGJ045) (Figure 5D). Complete collection information and voucher deposition details for all specimens used in this study are provided in Table 2. Each sample yielded 1037–2191 loci (mean $\pm$ SD = 18.46 $\pm$ 272 loci). The 50% taxon-occupancy matrix contained 1941 loci (191,049 bp), of which 25,041 sites (13.1%) were parsimony-informative.

The maximum-likelihood (ML) analysis recovered a well-resolved phylogeny for the sampled ingroup taxa of Acanthogorgiidae (Figure 6), rooted with *Euplexaura* (HGJ018 and SRR18587834) as outgroups. Within the ingroup, two maximally supported major lineages were recovered (node support values are shown as SH-aLRT (%) / ultrafast bootstrap (%); 100/100): (i) a clade comprising the sister pairs *Villogorgia* + *Paracis* and *Bebryce* + *Thesea* (all relevant nodes 100/100), and (ii) a lineage in which *Placogorgia* + *Paramuricea* formed a clade (100/100) that was sister to a clade comprising *Acanthogorgia* (monophyletic; 100/100) and a monophyletic group formed by *Menella*, *Echinogorgia*, *Echinomuricea*, and *Paraplexaura* (100/100). Within this four-genus clade, *Menella praelonga* was recovered as the earliest diverging lineage (99.9/99), followed by *Echinogorgia ramosa*; *Echinomuricea peterseni* was resolved as sister to *Paraplexaura* with maximal support (100/100). *Paraplexaura* was monophyletic (100/100), with *P. pulchra* sister to all remaining congeners (100/100). The remaining *Paraplexaura* were divided into two subclades: *P. reticuloides* + *P. debora* (99.6/99) and *P. binyuani* sp. nov. + *P. cryptotheca* (100/100), with the two *P. cryptotheca* specimens forming a strongly supported pair (100/100).

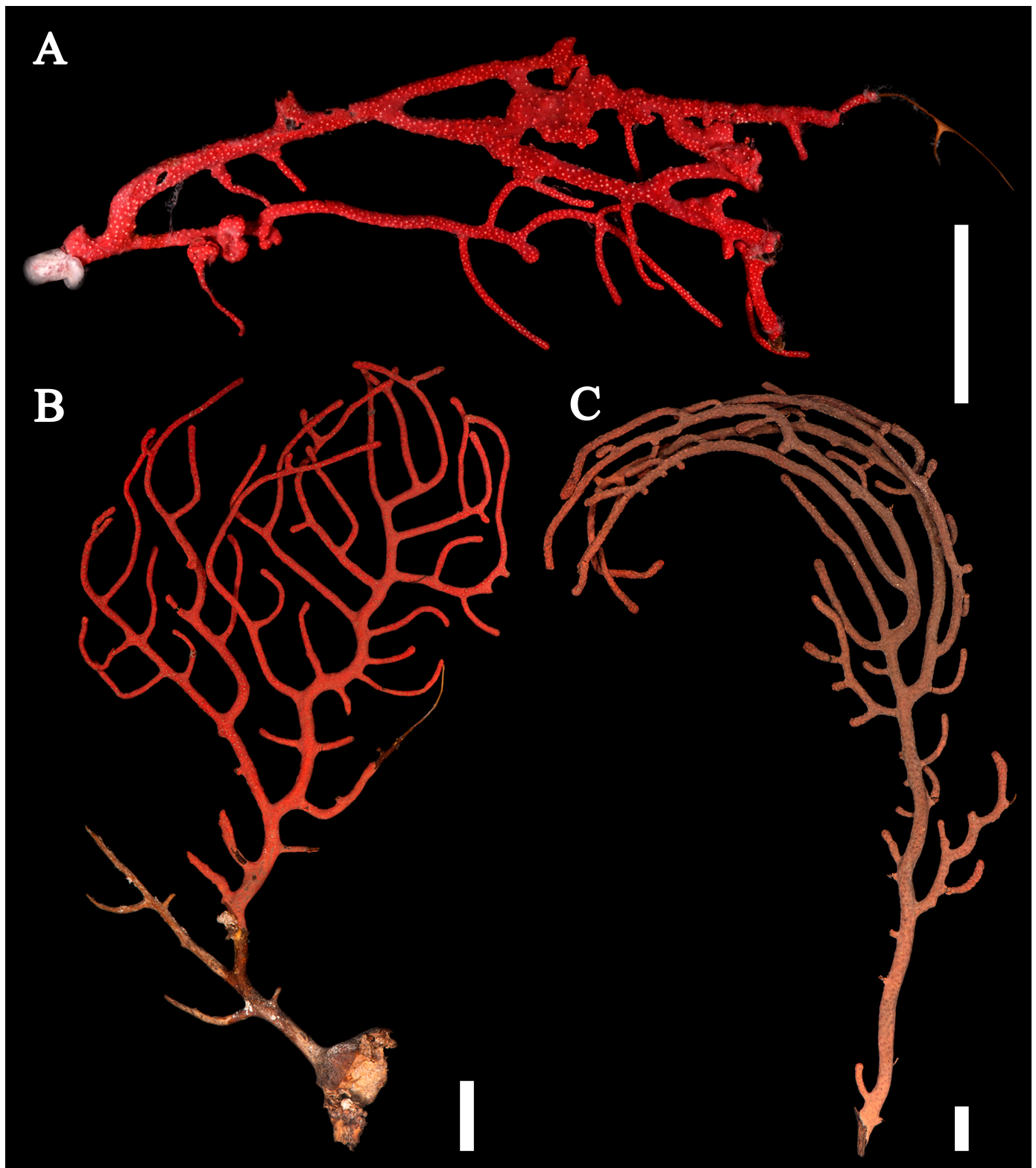


Figure 3. Photographs of the corresponding *Paraplexaura* colonies. (A) *Paraplexaura pulchra* (Nutting, 1910) (ND39); (B) *Paraplexaura reticuloides* (Nutting, 1910) (HGJ049); (C) *Paraplexaura debora* Grasshoff, 2000 (QLY004). Scale bars = 1 cm (same scale for all photographs).

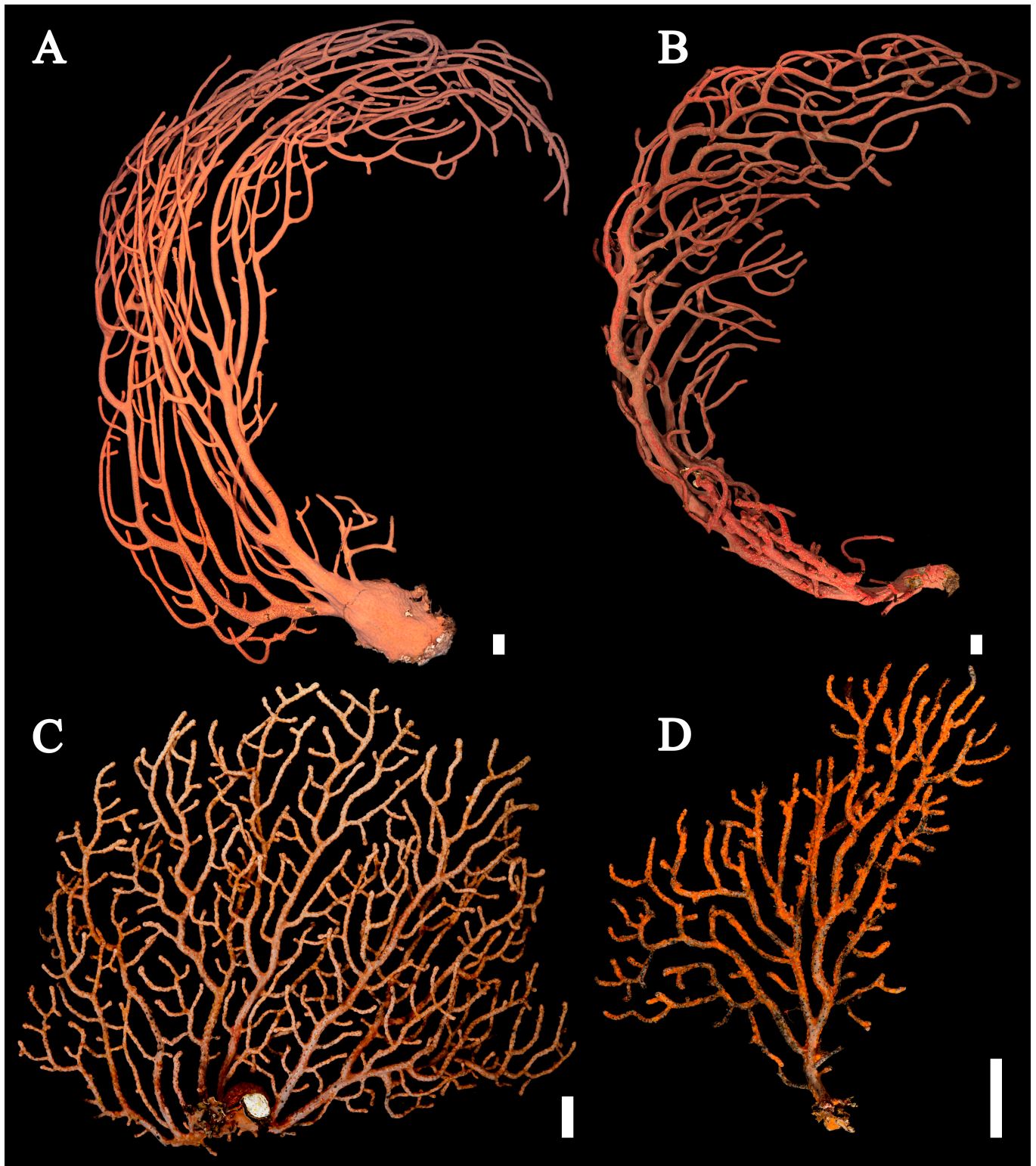


Figure 4. Photographs of the corresponding octocoral colonies. (A,B) *Paraplexaura cryptotheca* (Nutting, 1910) (HGJ050, HGJ052); (C) *Euplexaura parviclados* Wright & Studer, 1889 (HGJ018); (D) *Bebryce indica* Thomson, 1905 (HGJ053). Scale bars = 1 cm (same scale for all photographs).

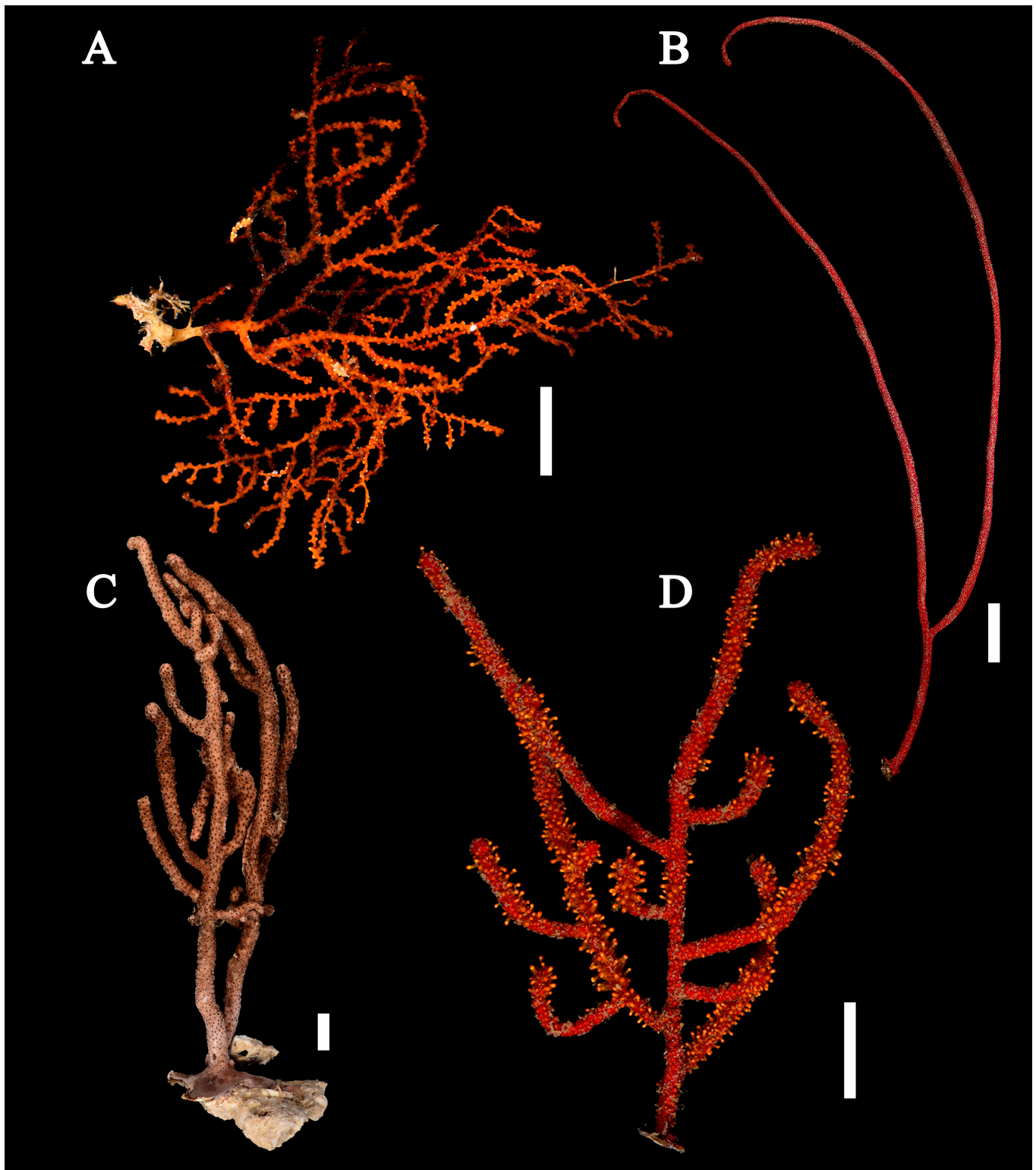


Figure 5. Photographs of the corresponding octocoral colonies. (A) *Villogorgia intricata* (Gray, 1869) (HGJ030); (B) *Menella praelonga* (Ridley, 1884) (WZD035); (C) *Echinogorgia ramosa* (Thomson & Henderson, 1905) (WZD036); (D) *Echinomuricea peterseni* Hedlund, 1890 (HGJ045). Scale bars = 1 cm (same scale for all photographs).

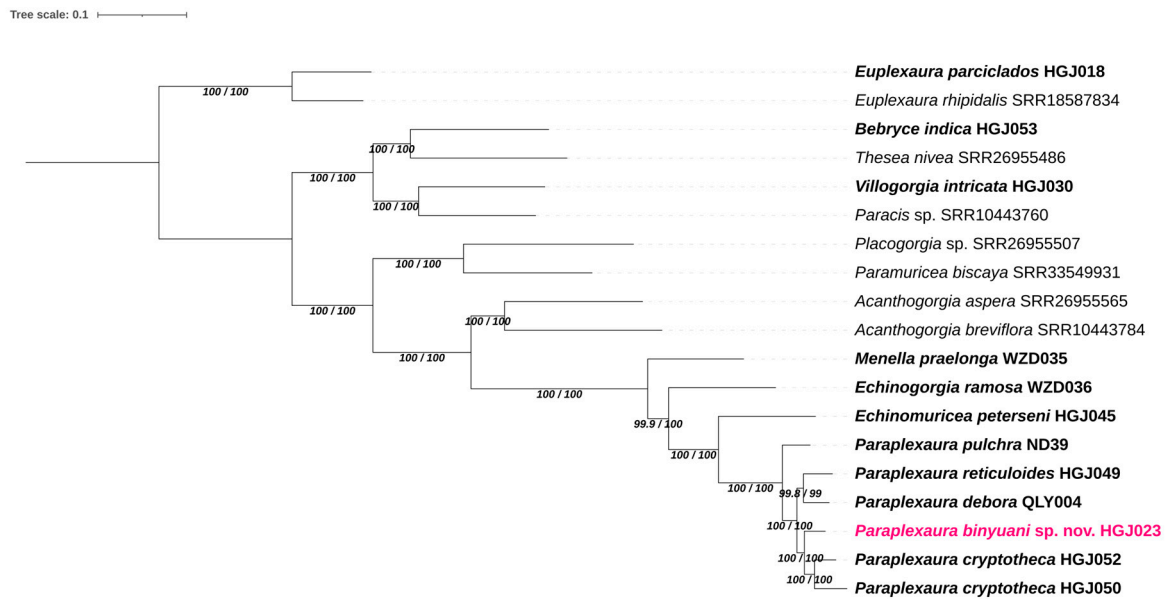


Figure 6. Phylogenetic reconstruction of sampled Acanthogorgiidae (ingroup) and Euplexauridae (outgroup) taxa based on a concatenated ultraconserved element (UCE) dataset (1941 loci; 50% taxon occupancy; 191,049 bp; $n = 19$). The best maximum-likelihood (ML) tree inferred in IQ-TREE is shown. Newly sequenced specimens generated in this study are indicated in bold, whereas samples labeled with SRR accession numbers represent data retrieved from the Sequence Read Archive (SRA). *Paraplexaura binyuani* sp. nov. is highlighted in pink. Branch support values are shown as ultrafast bootstrap (UFBoot; left) and SH-like approximate likelihood ratio test (SH-aLRT; right), respectively.

Table 2. Specimen information and voucher deposition for all specimens used in this study.

Species	Sample ID	Sampling Site	Longitude & Latitude	Sampling Date	Depth (m)	Quantity	Voucher Repository
<i>Euplexaura parciados</i>	HGJ018	Huaguang Atoll, Xisha Islands	16°15'26" N, 111°48'45" E	25 May 2025	22	1	GXTCMU
<i>Bebryce indica</i>	HGJ053	Huaguang Atoll, Xisha Islands	16°15'26" N, 111°48'45" E	25 May 2025	17	1	GXTCMU
<i>Villogorgia intricata</i>	HGJ030	Huaguang Atoll, Xisha Islands	16°16'59" N, 111°40'21" E	25 May 2025	19	1	GXTCMU
<i>Menella praelonga</i>	WZD035	Weizhou Island	21°07'32" N, 109°10'23" E	4 May 2025	10	1	GXTCMU
<i>Menella praelonga</i>	WZD038	Weizhou Island	21°07'32" N, 109°10'23" E	4 May 2025	10	1	GXTCMU
<i>Echinogorgia ramosa</i>	WZD036	Weizhou Island	21°07'32" N, 109°10'23" E	4 May 2025	15	1	GXTCMU
<i>Echinogorgia ramosa</i>	WZD049	Weizhou Island	21°05'12" N, 109°10'28" E	15 September 2025	12	1	GXTCMU
<i>Echinomuricea peterseni</i>	HGJ045	Huaguang Atoll, Xisha Islands	16°16'59" N, 111°40'21" E	25 May 2025	25	1	GXTCMU
<i>Paraplexaura pulchra</i>	ND39	Taishan Islands	26°53'12" N, 120°43'48" E	1 August 2025	20	1	GXTCMU

Table 2. Cont.

Species	Sample ID	Sampling Site	Longitude & Latitude	Sampling Date	Depth(m)	Quantity	Voucher Repository
<i>Paraplexaura reticuloides</i>	HGJ049	Huaguang Atoll, Xisha Islands	16°11'58" N, 111°41'19" E	25 May 2025	50	1	GXTCMU
<i>Paraplexaura debora</i>	QLY004	Qilian Atoll, Xisha Islands	16°56'47" N, 112°20'58" E	29 May 2025	45	1	GXTCMU
<i>Paraplexaura binyuani</i> sp. nov.	HGJ023	Huaguang Atoll, Xisha Islands	16°10'35" N, 111°33'58" E	26 May 2025	22	1	GXTCMU
<i>Paraplexaura cryptotheca</i>	HGJ050	Huaguang Atoll, Xisha Islands	16°15'26" N, 111°48'45" E	25 May 2025	13	1	GXTCMU
<i>Paraplexaura cryptotheca</i>	HGJ052	Huaguang Atoll, Xisha Islands	16°15'26" N, 111°48'45" E	25 May 2025	13	1	GXTCMU

4. Discussion

The genus *Paraplexaura* Kükenthal, 1909 currently comprises five species considered valid. Species-level taxonomy within the genus has long been complicated by extensive overlap in colony forms and sclerites morphology, and by uneven geographic and molecular sampling across the Indo-West Pacific. In this context, the present study provides a quantitatively documented (SEM-based) morphological diagnosis together with a phylogenomic placement for a South China Sea specimen, providing a reference point for evaluating species boundaries in *Paraplexaura*. Among the described congeners, *P. asper*, *P. cryptotheca*, *P. pulchra*, and *P. reticuloides* have been reported from the Pacific Ocean [27–30], whereas *P. debora* was described from the Indian Ocean [6]. *Paraplexaura binyuani* sp. nov. was likewise discovered in the Pacific Ocean. Available records therefore suggest that most described species have been reported primarily from a single ocean basin; however, this apparent pattern should be interpreted cautiously given uneven sampling and limited molecular coverage across the Indo-West Pacific. *Euplexaura parviclados* (HGJ018), *Bebryce indica* (HGJ053), *Villogorgia intricata* (Gray, 1869) (HGJ030), *Menella praelonga* (WZD035), *Echinogorgia ramosa* (WZD036), *Echinomuricea peterseni* (HGJ045), *P. cryptotheca* (HGJ050), *P. debora* (QLY004), *P. pulchra* (ND39), and *P. reticuloides* (HGJ049) were provided in the Supplementary Figure S1, providing additional supporting evidence for their morphological characteristics.

Morphologically, *P. binyuani* sp. nov. is most similar to *P. cryptotheca* (Nutting, 1910) in exhibiting abundant polyp sclerites and broadly comparable coenenchymal sclerites morphologies. Nevertheless, it can be distinguished by a consistent diagnostic combination of characters, most notably the predominance of slightly flattened polyp rods and the markedly larger maximum sizes of coenenchymal spindles (Table 1). Specifically, *P. binyuani* sp. nov. possesses polyp rods reaching up to 0.12 mm in length and coenenchymal spindles up to 0.6 mm, whereas *P. cryptotheca* bears slightly bent polyp spindles not exceeding 0.15 mm and coenenchymal spindles up to 0.30 mm [28,29] (Table 1). Thus, the distinction involves not only maximum sizes but also the predominant polyp sclerites forms (flattened rods versus spindles). *Paraplexaura binyuani* sp. nov. also resembles *P. asper* (Moroff 1902) in overall coenenchymal sclerites form but differs markedly in the presence of abundant polyp sclerites and in the maximum size range of coenenchymal sclerites: *P. binyuani* sp. nov. has irregularly shaped sclerites up to 0.5 mm, whereas *P. asper* lacks polyp sclerites entirely and possesses irregularly shaped sclerites reaching up

to 0.9 mm [27,29] (Table 1). Taken together, the combination of abundant, slightly flattened polyp rods and comparatively large coenenchymal spindles provides a practical diagnostic basis for distinguishing *P. binyuani* sp. nov. from all other congeners.

Phylogenomic evidence from UCEs provides independent support for the distinctiveness of *P. binyuani* sp. nov. In particular, the UCE-based placement of the Huaguang Atoll specimen as a discrete lineage within *Paraplexaura* is congruent with the diagnostic morphological character combination documented here. The close relationship inferred between *P. binyuani* sp. nov. and *P. cryptotheca* is consistent with their overall morphological resemblance, while the distinct branch corresponding to *P. binyuani* sp. nov. supports recognition of this taxon despite the general homoplasy of colony and sclerite traits within the family. This concordance between quantitative morphology and phylogenomics reduces the likelihood that the observed diagnostic differences reflect only local intraspecific variation.

At present, *P. binyuani* sp. nov. is known only from the type locality and is represented by limited material (a single incomplete colony fragment), which precludes assessment of the full extent of intraspecific variation and limits evaluation of potential ecological or ontogenetic sources of morphological variability. Nevertheless, the proposed diagnosis is based on a consistent combination of characters spanning multiple sclerite categories and on maximum sizes that exceed reported ranges for congeners, and it is independently supported by UCE-based phylogenomic evidence. Future work should prioritize expanded sampling across adjacent reefs in the South China Sea, together with comparative phylogenomic screening of morphologically similar *Paraplexaura* populations, to evaluate geographic structure and species boundaries within the genus. In addition, examination of type material or reliably identified reference specimens, particularly of closely related congeners, will be essential to test the stability and broader applicability of the diagnostic character combination proposed here.

Supplementary Materials: The following supporting information can be downloaded at: <https://www.mdpi.com/article/10.3390/d18030166/s1>, Supplementary Table S1: Accession numbers and sequencing statistics for newly sequenced specimens. Supplementary Figure S1: Light microscope photographs of comparative specimens, including *Euplexaura parviclados* (HGJ018), *Bebryce indica* (HGJ053), *Villogorgia intricata* (HGJ030), *Menella praelonga* (WZD035), *Echinogorgia ramosa* (WZD036), *Echinomuricea peterseni* (HGJ045), *Paraplexaura cryptotheca* (HGJ050, HGJ052), *P. debora* (QLY004), *P. pulchra* (ND39), and *P. reticuloides* (HGJ049).

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Data Availability Statement: Voucher specimens are deposited in the Institute of Marine Drugs, Guangxi University of Chinese Medicine (Nanning, Guangxi, China). The holotype of *Paraplexaura binyuani* sp. nov. is GXTCMU-2025-HT005 (=HGJ023) and is available for examination. All newly generated genomic shotgun sequencing reads for the 12 specimens in this study have been deposited in the CNCB Genome Sequence Archive (GSA) under BioProject: PRJCA057506, with individual CRA accession numbers for each specimen listed in Supplementary Table S1 alongside detailed sequencing statistics. Light microscope photographs of comparative specimens are provided in Supplementary Figure S1.

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Conflicts of Interest: The authors declare no conflicts of interest.

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