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A new soft coral species, *Aquaumbra aranea* sp. nov. (Octocorallia: Malacalcyonacea: Aquaumbridae), from Fiordland, Aotearoa (New Zealand)

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Abstract

We describe *Aquaumbra aranea* **sp. nov.** Korfhage & Freiwald, a new species of soft coral discovered in Fiordland, Aotearoa (New Zealand). This new species represents an extension of this previously monotypic genus *Aquaumbra* Breedy, van Ofwegen & Vagas, 2012. The discovery expands the known morphological and geographic diversity of the genus and its family Aquaumbridae. *Aquaumbra aranea* **sp. nov.** is morphologically distinguished from *Aquaumbra klapferi* Breedy, van Ofwegen & Vargas, 2012 and the sister genera *Elbeenus* Alderslade, 2002 by having a distinct sclerite composition and the presence of diverse sclerites. Its characteristic spider-web-like surface reticulation further differentiates it from the previously described species. Although *mtMutS* does not distinguish *A. aranea* **sp. nov.** from *A. klapferi*, and 28S rDNA provides only limited resolution, this pattern is consistent with previous findings in Octocorallia, where commonly used markers often fail to discriminate closely related species due to low substitution rates and limited resolution. We therefore interpret the observed morphological differentiations as taxonomically significant and sufficient to justify species recognition. Our findings underscore the potential for additional biodiscovery in coastal habitats in the Southwest Pacific.

Key words: Species delimitation, *mtMutS*, 28S rDNA, species description, integrative taxonomy

Introduction

The marine realm of New Zealand is rich in biodiversity and characterized by a high proportion of endemic species (Costello 2024). Corals are an integral part of this unique fauna and can also serve as foundation species that enhance habitat complexity through their three-dimensional growth forms (Rowden *et al.* 2020, Tracey & Hjorvarsdottir 2019). Octocorallia may play a particularly significant role in temperate and deep-sea environments by forming dense aggregations that form or enhance local biodiversity hotspots and mediate benthic-pelagic coupling, forming the basis for invertebrate and fish habitats (Goode *et al.* 2021, Nodder *et al.* 2012, O'Hara *et al.* 2008). Despite their ecological relevance, the taxonomic knowledge of New Zealand's coral fauna remains incomplete. Recent assessments indicate that the region is home to 799 currently recognized species of Anthozoa, of which approximately 335 remain undescribed. Notably, five anthozoan genera and over 111 species are considered endemic, highlighting both the region's high degree of diversification and the need for continued systematic exploration (Cairns *et al.* 2009, Macpherson *et al.* 2023). Within Octocorallia, especially many deep-sea species and shallow, inshore species from temperate waters are known only from a handful of records or individual specimens, possibly indicating limited sampling, low population density, and potentially narrow distribution ranges (Cairns 2012, 2016, 2021).

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This underlines the importance of targeted biodiversity surveys to continue to uncover the true extent of octocoral diversity.

During the *CoralNewZ* research voyage (Cold-water Coral Biology & Geology off Aotearoa New Zealand) in January 2025 on the German Research Vessel (RV) SONNE, a previously undocumented octocoral species belonging to the genus *Aquaumbra* Breedy, van Ofwegen & Vargas, 2012 was discovered. Until now, this family comprised two genera, each with one described species, *Aquaumbra klapferi* Breedy, van Ofwegen & Vargas, 2012 and *E. lauramartinae* Alderslade, 2002. These species were known from the seamounts surrounding Isla del Coco in the eastern tropical Pacific (Breedy *et al.* 2012) and the western side of Uchelbeluu Reef, Koror, Palau (Alderslade 2002), respectively. Further collections, identified to family level only, comprise the West Florida Slope, Gulf of Mexico, North Atlantic with two additional colonies (Quattrini *et al.* 2014). A more recent study documented a specimen of *Aquaumbra* from the southern Red Sea off Saudi Arabia at a depth of 115 m (Macrina *et al.* 2025), which we refer to here as *Aquaumbra* sp. 4. In the current study, new collections were conducted in the fjord systems in southwestern New Zealand, considerably extending the known range of the family and suggesting a broader biogeographic connection. The newly collected specimens were genetically highly similar to *Aquaumbra*, yet differ markedly from the type species in terms of sclerite morphology and complement, polyp arrangement, and colony architecture. We formally describe this novel species, based on detailed analyses using light and scanning electron microscopy, supplemented by molecular data and *in situ* photographic documentation. With this contribution, we not only expand the taxonomic and geographic scope of the family Aquaumbridae but also shed light on the hidden diversity of New Zealand's octocoral fauna. Our findings underscore the urgency of continued taxonomic and ecological research in these vulnerable marine ecosystems. They also highlight the importance of traditional taxonomic methods, as well as the development of new molecular markers, since traditional molecular barcoding approaches can be limited in their ability to distinguish closely related octocoral species.

Material and Methods

Specimen Collection

Two coral specimens were collected in January 2025 during the *CoralNewZ* research voyage *(Cold-water Coral Biology & Geology off Aotearoa New Zealand*) aboard the RV SONNE (SO309) using the University of Bremen Center for Marine Environmental Sciences MARUM Remotely Operated Vehicle (ROV) *Squid 2000*. The collection sites were located in Acheron Passage and Dusky Sound, Fiordland (Te Moana o Atawhenua) Marine Area, southwestern Aotearoa New Zealand, at a depth of 209 and 112 meters (Figure 1). The holotype was recorded from a vertical rock face within the fjord system, whereas the paratype was collected from a small hard-substrate plateau with a thin sediment cover (Figure 2a & 3a). Sampling was carried out using the ROV's manipulator arm, and the specimens were carefully placed into a rotary collection box. Upon recovery on deck, the colonies were photographed, and tissue samples were taken for both morphological and molecular analyses. Tissue samples were preserved in 96% undenatured ethanol and stored at 4°C to ensure high-quality DNA preservation and prevent damage to sclerites. Specimens are deposited at the Earth Sciences New Zealand (formerly National Institute of Water & Atmospheric Research, NIWA) National Invertebrate Collection in Wellington, New Zealand and tissue vouchers at the German Centre for Marine Biodiversity Research (DZMB), Senckenberg am Meer, Hamburg, Germany.

Morphological Analysis

Specimens were photographed using a macro photography station. Polyps were dissected and treated with potassium hydroxide (1 M) to facilitate the examination of sclerite arrangement. Sclerites from different parts of the colony (polyps, outer and inner stem, and base) were obtained by dissolving the organic tissue in sodium hypochlorite, followed by repeated rinsing in distilled water. The samples were then treated with hydrogen peroxide to remove residual organic material, subjected to additional washing steps, and air-dried. Cleaned sclerites were mounted on aluminum stubs using conductive carbon adhesive pads and sputter-coated with gold. Scanning electron microscopy (SEM) was performed at 10 kV at Senckenberg am Meer, Department of Marine Research, Wilhelmshaven, Germany. Morphological terminology conforms to Bayer *et al.* (1983).

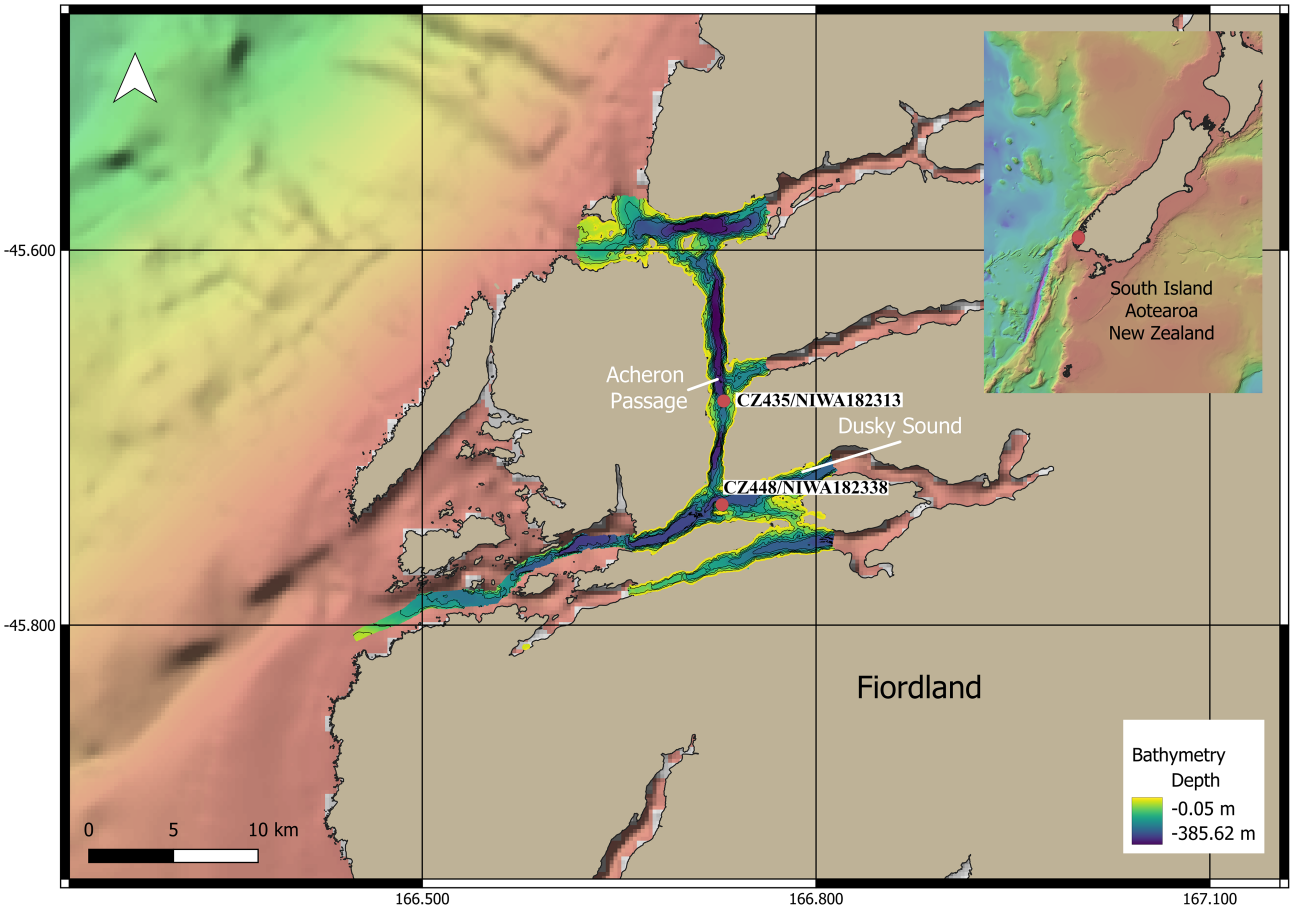

FIGURE 1. Map with the sampling locations of the *Aquaumbra aranea* **sp. nov.** specimens.

Molecular Analysis

DNA was extracted from individual polyps using the E.Z.N.A.® Mollusc & Insect DNA Kit (Omega Bio-tek, Norcross, GA), following the manufacturer's protocol. For each extraction, a single polyp was carefully excised using a sterile tweezer. Samples were lysed using overnight incubations at 37 °C. Polymerase chain reactions (PCRs) were carried out in 25 µl reaction volumes, each containing 12.5 µl AccuStart™ II PCR SuperMix (QuantaBio, Beverly, MA), 9.5 µl nuclease-free water, and 10 pmol of each forward and reverse primer. Target regions included an ~870 bp fragment of the mitochondrial *mtMutS* gene, amplified using primers ND42599F (France & Hoover 2002) and MUT3458R (Sánchez *et al.* 2003), and a ~800 bp fragment of the nuclear *28S* rDNA gene, using the octocoral-specific DNA primers 28S-Far and 28S-Rar published by McFadden and van Ofwegen (2013). PCR protocols followed Korfhage *et al.* (2022). Amplification success was confirmed by gel electrophoresis and excess primers and dNTPs were removed before sequencing using 4 µl ExoSAP-IT™ Express (ThermoFisher Scientific), following the manufacturer's instructions. Purified products were submitted to Macrogen Europe (Amsterdam, Netherlands) for bidirectional Sanger DNA sequencing.

Sequence chromatograms were assembled and trimmed in Geneious 2025.1.3. The protein-coding *mtMutS* sequences were first translated into amino acid sequences by using translation table 4 (mold, protozoan, and coelenterate mitochondrial code) to confirm the absence of internal stop codons and aid alignment. All subsequent analyses were conducted on nucleotide sequences. Additional reference sequences were obtained from GenBank and incorporated into the dataset. Reference sequences were selected based on the highest-scoring hits from NCBI BLAST searches using default parameters and supplemented with closely related taxa identified by McFadden et al. (2022). Alignments were performed separately for each marker using the L-INS-i algorithm in MAFFT v7 (Katoh *et al.* 2002). Alignments were manually trimmed to 757 bp (*mtMutS*) and 738 bp (*28S rDNA*) to ensure comparability across taxa. For both *mtMutS* and *28S rDNA* datasets, maximum likelihood (ML) and Bayesian phylogenetic analyses

were conducted. The optimal nucleotide substitution model for each dataset was determined using ModelFinder in IQ-TREE (Nguyen *et al.*, 2015). The best-fit substitution model for the *mtMutS* dataset was K3Pu+F+G4 based on the Bayesian Information Criterion (BIC), whereas TIM3+F+I+R2 was selected for the *28S rDNA* dataset. As neither model is implemented in BEAST v2.7.7 (Bouckaert *et al.* 2019), we approximated the *mtMutS* dataset using the HKY+F+G4 model and the *28S rDNA* dataset using the GTR+F+I+Γ model, which represent the closest available substitution schemes in BEAST. Bayesian analyses were performed using BEAST v2.7.7. XML input files were generated in BEAUti v2.7.7, applying a Yule speciation prior (Yule 1925), a chain length of 10 million generations, sampling every 1,000 generations, and a log relaxed clock model. Analyses were initiated with a random number seed. Convergence diagnostics and Effective Sample Size (ESS) values were assessed using Tracer v1.7 (Rambaut *et al.* 2018), ensuring that all ESS values exceeded 200. Maximum clade credibility (MCC) trees were summarized in TreeAnnotator v1.7 (Drummond & Rambaut 2007) after discarding the first 10% of trees as burn-in. ML trees were reconstructed with IQ-TREE using 1,000 ultrafast bootstrap replicates to assess branch support. Sequences generated in this study were deposited in GenBank under accession numbers PX215760–PX215761 (*mtMutS*) and PX215174–PX215175 (*28S rDNA*).

Results

Systematic Account

Class Octocorallia Haeckel, 1866

Order Malacalcyonacea McFadden, van Ofwegen, & Quattrini, 2022

Family Aquaumbridae Breedy, van Ofwegen & Vargas, 2012

Genus *Aquaumbra* Breedy, van Ofwegen & Vargas, 2012

Diagnosis (amended)

Soft corals forming flaccid, arborescent colonies arising from a basal stalk; lobes transparent and jelly-like. Polyps with points; collaret present but sometimes weakly developed. Sclerites colorless, predominantly elongate in form, including rods, needles, sticks, spindles, or irregular bodies. Coenenchymal sclerites present in the stalk and may occur in branches; sclerite shape and distribution within the colony are variable among species, being either uniform throughout the colony or differentiated between polyp and coenenchymal regions.

Aquaumbra aranea Korfhage & Freiwald, sp. nov.

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Figures 2–5

Material examined

Holotype: NIWA182313 (DZMB field number: CZ435), Acheron Passage, Fiordland (Te Moana o Atawhenua) Marine Area, Aotearoa New Zealand, 45°40'49.9"S, 166°43'46.6"E, 209 m, R/V SONNE, MARUM ROV Squid 2000 dive 108 (GeoB26356-1), collected January 30, 2025.

Paratype: NIWA182338 (DZMB field number: CZ448), Acheron Passage, Fiordland (Te Moana o Atawhenua) Marine Area, Aotearoa New Zealand, 45°44'08.9"S, 166°43'42.2"E, 112 m, R/V SONNE, MARUM ROV Squid 2000 dive 109 (GeoB26361-1), collected January 31, 2025.

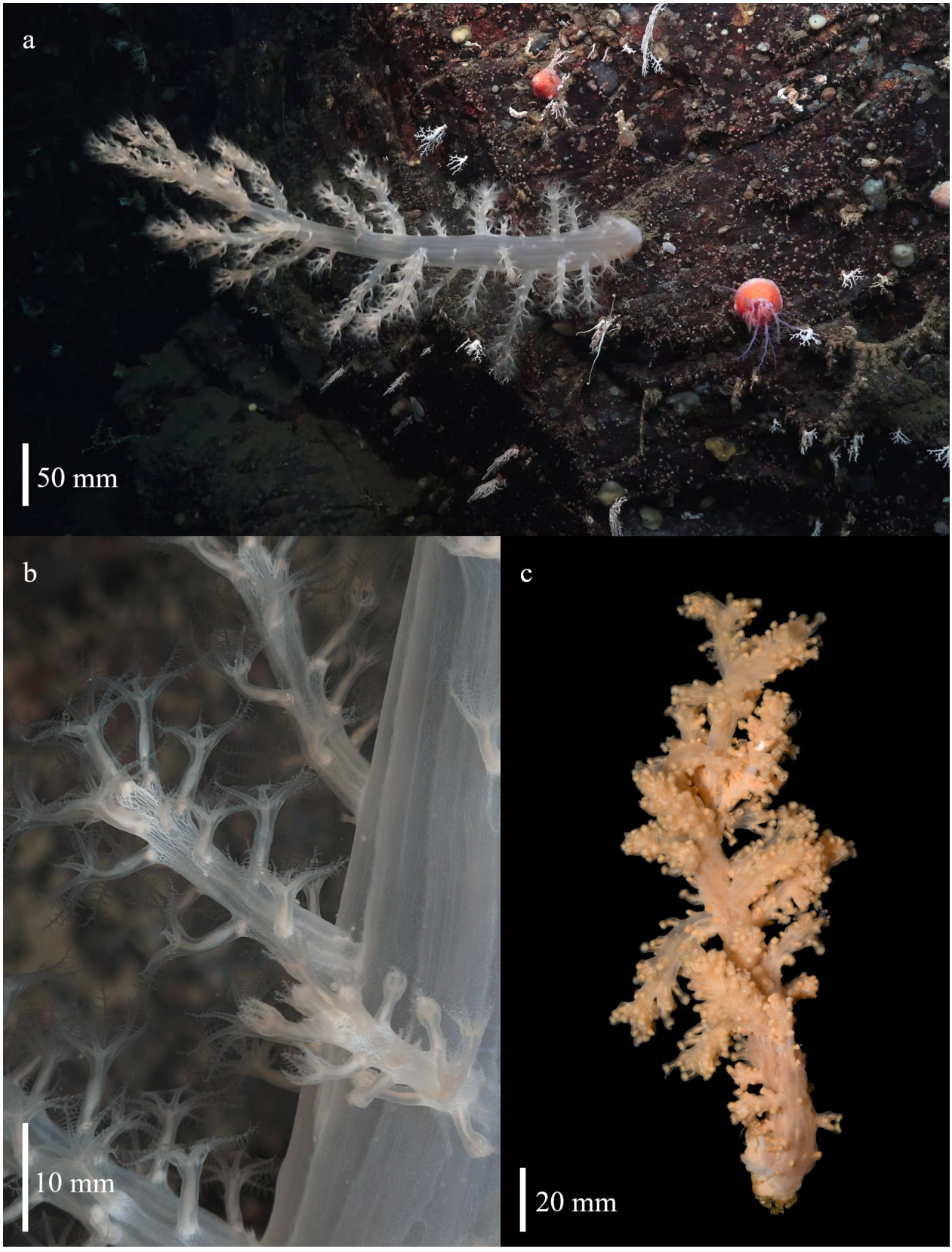

FIGURE 2. Holotype (CZ435/ NIWA182313) of *Aquaumbra aranea* **sp. nov.**; a, colony in situ; b, stem with branches and single polyps at the stem; c, colony on deck (a-b: MARUM, ROV Team Squid 2000, University of Bremen; c: Peter Marriott, ESNZ).

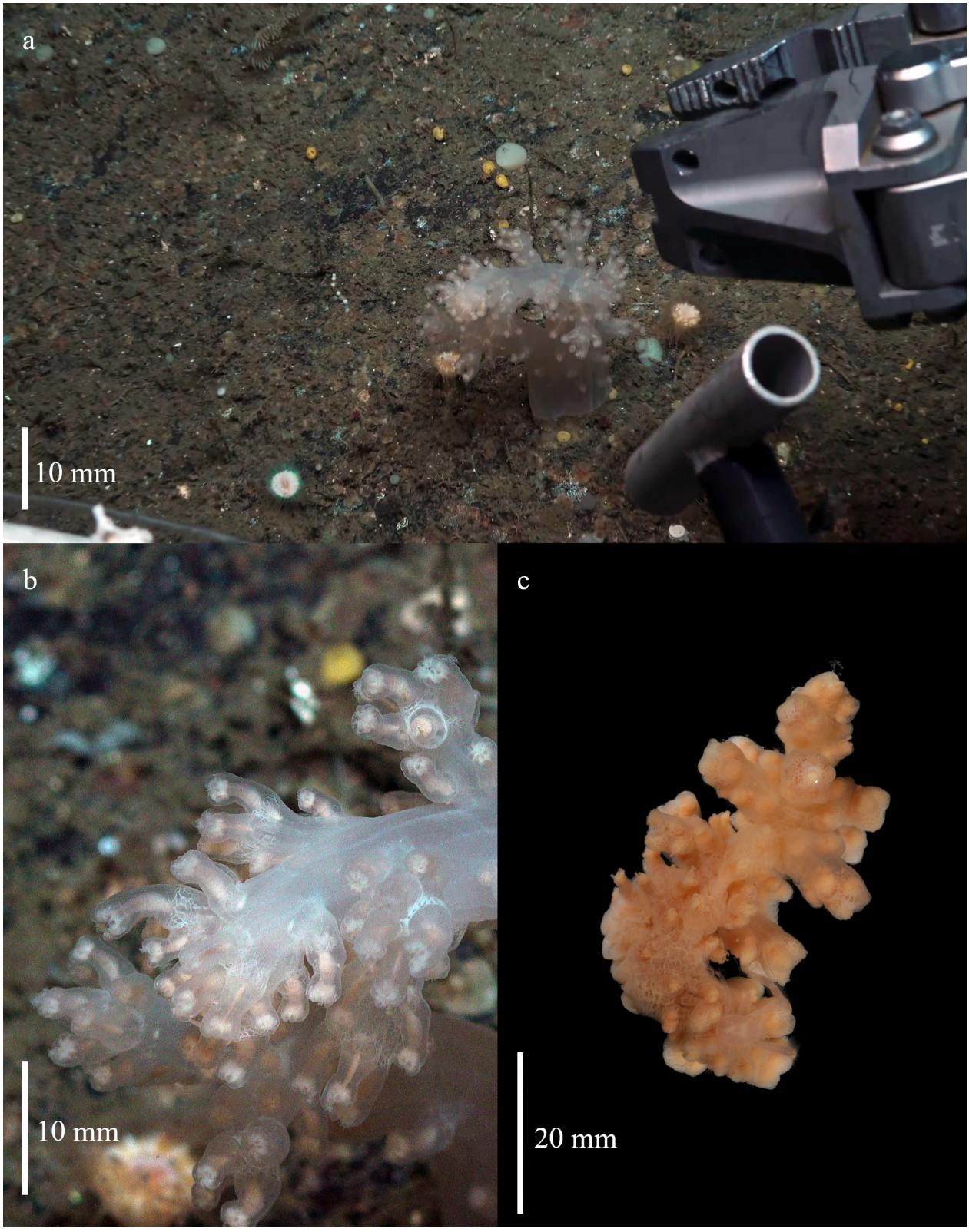

FIGURE 3. Paratype (CZ448/ NIWA 182338) of *Aquaumbra aranea* **sp. nov.**: a, colony in situ; b, branch with polyps; c, colony on deck with associated decapod *Uroptychus tomentosus* Baba, 1974 (NIWA 182339); (a-b: MARUM, ROV Team Squid 2000, University of Bremen).

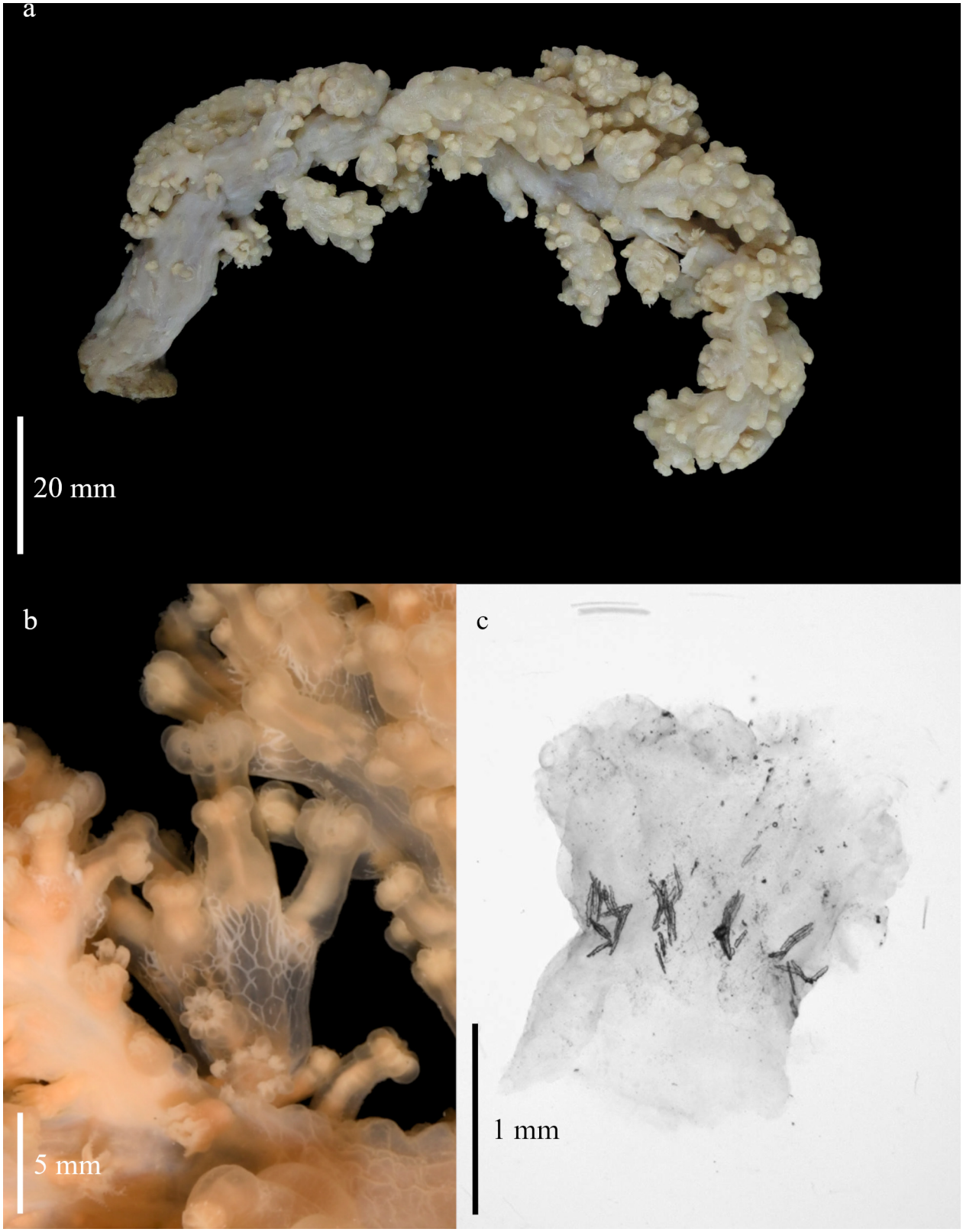

FIGURE 4. Holotype of *Aquaumbra aranea* **sp. nov.** (CZ435/ NIWA182313), a, preserved holotype; b, spider-web-like surface structures of the coenenchyme, live specimen; c, sclerite arrangement of polyps.

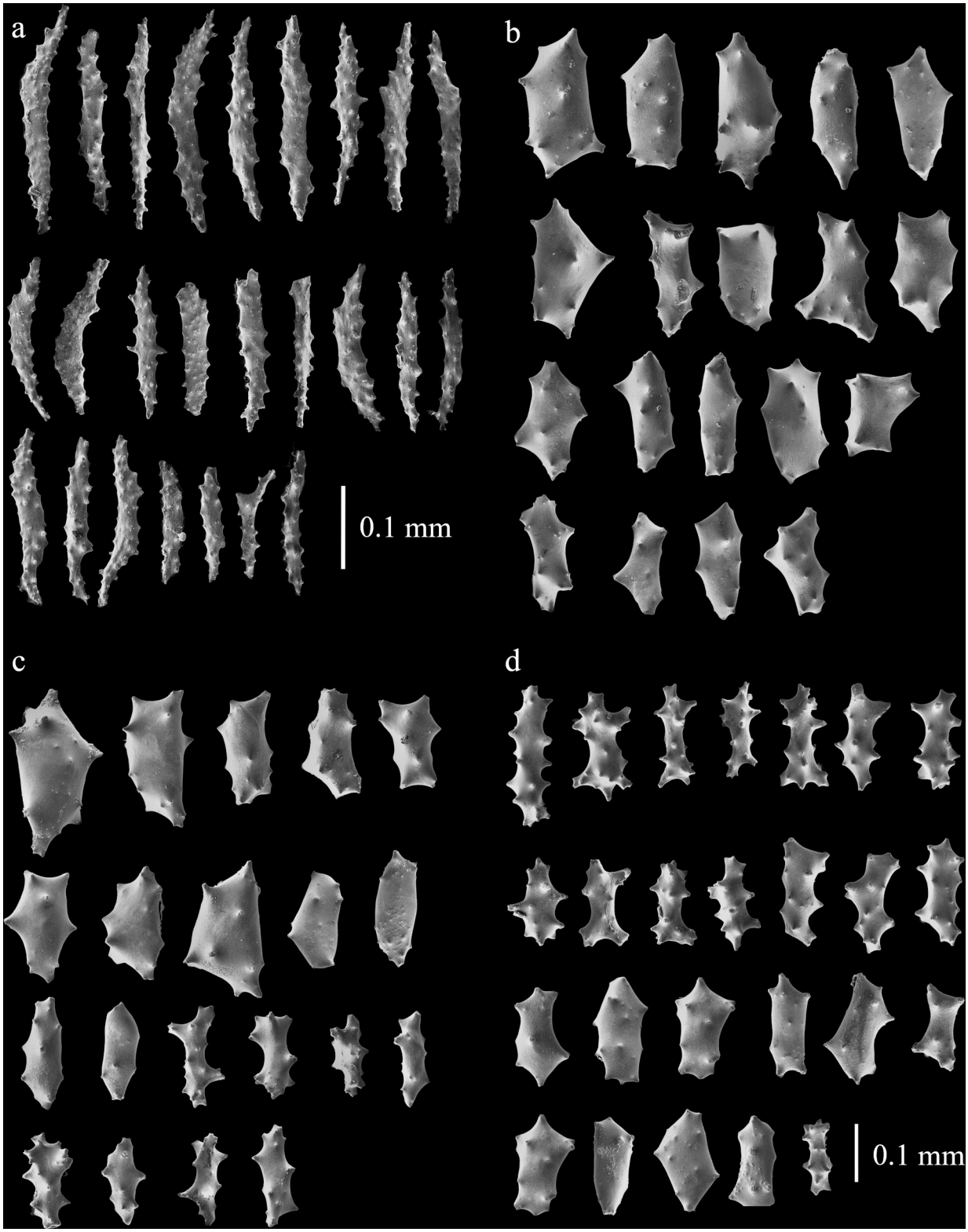

FIGURE 5. Sclerites of holotype (CZ435/NIWA 182313) of *Aquaumbra aranea* **sp. nov.**; a, curved spindles from the points with rounded or cone-shaped tubercles; b, irregular bodies of the outer stem; c-d, irregular bodies, rods and some derivatives of capstans from the inner stem (c) and the base (d); Scale bars = 0.1 mm.

Diagnosis

Expanded colonies are erect and arborescent with a flaccid, translucent to faint orange-brown coenenchyme. Contracted colonies are lobate. There is a short basal stalk from which extends a single main stem that gives rise to branches distributed all around. These branches may rebranch. There is no axis. Polyps are monomorphic, contractile but non-retractile, arranged all around the branches, often clustered distally. Solitary polyps occur sparingly on the stalk and main stem. Points formed by varying numbers of slender sclerites, longitudinally or obliquely arranged. Collaret weakly developed or entirely absent. Sclerites are colourless. Point sclerites are curved spindles. The sclerites of the outer stem are irregular bodies. In the inner stem and base, rods and some derivatives of capstans occur in addition to irregular bodies.

Description

The preserved holotype is 15.9 cm (Fig. 4a). Branching is mainly to the first order, but a few branches are beginning to divide. Polyps, which are contractile but not retractile, are evenly distributed all around the branches and lobes. Toward the distal ends of the branches, they occur closer together. A few isolated polyps are present on the main stem and the stalk. The polyps measured 2.32–4.89 mm in length and 1.84–2.67 mm in width at the base of the polyp body (n = 15). In situ, the holotype exhibited an arborescent growth form, with a short stalk that continued as main branch through to the distal part of the colony (Fig. 2a). On deck, the partially contracted colony (Fig. 2c) was 19.8 cm tall with a maximum width of 9.2 cm. The stalk, which was 15 mm in diameter at its base, extended as a single main stem throughout the colony. Many of the branches had contracted to form lobes. Branching originated approximately 20 mm above the holdfast, initially forming short lateral branches. Further along the stem the more inflated branches were about 30.97–60.98 mm long. The live polyps measured 4.71–8.36 mm in length and 2.22–3.96 mm in width at the base of the polyp body (n = 15).

Polyp sclerites are essentially only present as points where they are irregularly arranged, obliquely or longitudinally, in small groups (Fig. 5c). If a collaret is present at all, it is very weakly developed. Sclerites are absent from the tentacles and the polyp body (Fig. 4c). The point sclerites are curved spindles, 0.15 to 0.28 mm long and 0.02 to 0.03 mm wide (n = 16) with rounded or cone-shaped tubercles (Fig. 5a). Sclerites from the outer stem comprise mainly small irregular bodies (Fig. 5b). The sclerites of the inner stem and the base of the colony are also irregular bodies, but also include rods and some derivatives of capstans (Fig. 5c–d). The sclerites are ornamented with sparse, rounded or cone-shaped tubercles. The most common sclerites measure 0.14–0.34 mm in length and 0.04–0.09 mm in width (n = 35). Sclerites are absent from the branches.

Variations. The paratype shows clear branching to the second order.

Colour. The live state of the coenenchyme is transparent to translucent, with a faint orange-brown to ocher pigmentation that becomes distinctly more saturated when contracted. The live colony on deck was light brown with a faint orange. The coloration of the polyps was similar to that of the colony, though sometimes slightly more intense.

Remarks

The new species differs from *A. klapferi* and *E. lauramartinae* by the distinctly different morphology of the sclerites in both the basal stalk, as well as the outer and inner stem. In *A. klapferi*, the sclerites are predominantly rods and needles of similar shape, whereas the sclerites of *E. lauramartinae* comprise large spindles (exceeding 6 mm in length) and rods. In contrast, *A. aranea* **sp. nov.** possesses a heterogeneous assemblage of sclerites with irregular shapes of the stem and the base sclerites. These sclerites distinguish *A. aranea* **sp. nov.** from *A. klapferi* by cone-shaped tubercles. In addition, *A. aranea* **sp. nov.** exhibits a less pronounced armature in the anthocodia, further distinguishing it from *A. klapferi*. A notable external feature is the spider-web-like pattern covering the entire colony surface, which is particularly prominent at the base of the polyps. This network appears to represent a canal system originating from the base of the gastric cavity and is most consistent with solenia. However, definitive confirmation would require histological examinations, which were beyond the scope of the present species description. Furthermore, *A. aranea* **sp. nov.** has a weakly developed collaret, in contrast to the more prominent collarets observed in *A. klapferi* and *E. lauramartinae*.

The paratype was found in association with a crustacean identified as *Uroptychus tomentosus* Baba, 1974 (NIWA 182339), which was collected together with the colony (Fig. 3c).

Etymology

The species name *aranea* is the Latin word for spider is used here as a noun in apposition. The name was chosen to describe the unique spider-web-like pattern of the colony, which becomes particularly evident around the polyps when the tissue is retracted.

Distribution

Only known from the type locality: Fiordland (Te Moana o Atawhenua) Marine Area, South Island, Southwest Pacific, Aotearoa (New Zealand).

Molecular Systematics

Sequences of *mtMutS* and *28S rDNA* were successfully obtained for both specimens. Phylogenetic analysis of the *mtMutS* sequences placed the family Aquaumbridae in a well-supported clade (bootstrap = 99%, posterior probability = 1; Fig. 6a). Within this family, the genus *Elbeenus* and the undescribed Aquaumbridae specimens from the Northwest Pacific (NWP) and the Red Sea (RS) (Aquaumbridae sp. 3 OQ607054; *Aquaumbra* sp. 4 PV731099) form distinct lineages (bootstrap = 85%, posterior probability = 0.98).

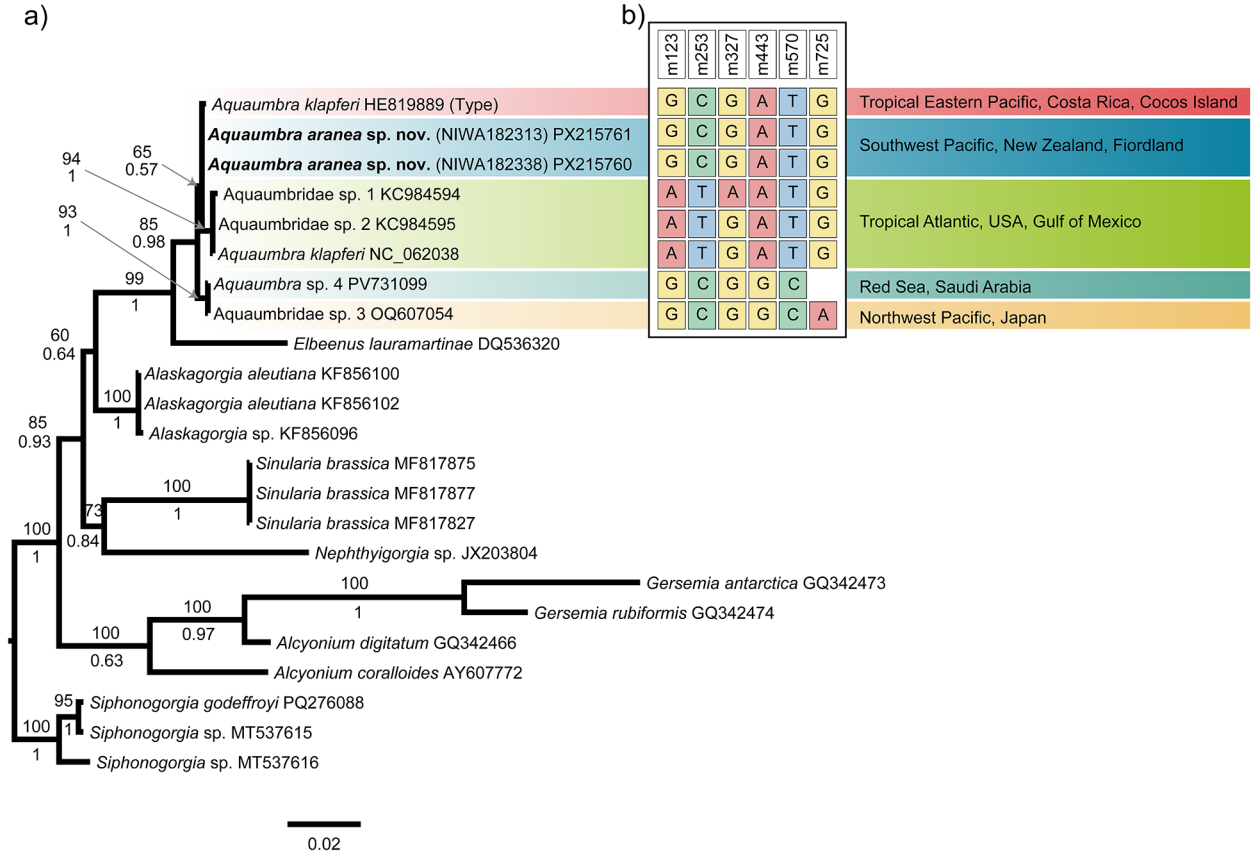

FIGURE 6. a) Maximum Likelihood tree based on *mtMutS* sequence data. Numbers above branches indicate bootstrap support values, and numbers below branches represent posterior probabilities from Bayesian inference. Newly described species are highlighted in bold. Colored bars indicate geographic origin. b) Base-pair substitutions in the alignment. Numbers above the bases indicate positions in the alignment.

TABLE 1. Pairwise uncorrected p-distances of mtMutS sequences among specimens of the family Aquaumbridae and the genus Alaskagorgia.

	HE819889	PX215761	PX215760	PV731099	KC984595	NC_062038	OQ607054	KC984594	KF856100	KF856102	KF856096	DQ536320
Aquaumbra klapferi HE819889 (Type)	-											
Aquaumbra aranea **sp. nov.** PX215761	0	-										
Aquaumbra aranea **sp. nov.** PX215760	0	0	-									
Aquaumbra sp. 4 PV731099	0.003	0.003	0.003	-								
Aquaumbridae sp. 2 KC984595	0.004	0.003	0.003	0.006	-							
Aquaumbra klapferi NC_062038	0.004	0.003	0.003	0.006	0	-						
Aquaumbridae sp. 3 OQ607054	0.004	0.004	0.004	0	0.007	0.007	-					
Aquaumbridae sp. 1 KC984594	0.005	0.004	0.004	0.007	0.001	0.001	0.008	-				
Alaskagorgia aleutiana KF856100	0.033	0.035	0.034	0.035	0.038	0.038	0.037	0.039	-			
Alaskagorgia aleutiana KF856102	0.033	0.035	0.034	0.035	0.038	0.038	0.037	0.039	0	-		
Alaskagorgia sp. KF856096	0.035	0.037	0.035	0.037	0.039	0.038	0.038	0.040	0.001	0.001	-	
Elbeenus lauramartinae DQ536320	0.036	0.035	0.036	0.039	0.039	0.039	0.039	0.040	0.059	0.059	0.0605	-

The sister clade of the NWP-RS complex comprises the type species of *A. klapferi*, our newly described species *A. aranea* **sp. nov.**, and a clade of specimens from the Gulf of Mexico (GoM). However, this relationship is not significantly supported (bootstrap = 65%, posterior probability = 0.57). Within this clade, the GoM specimen complex shows moderate to strong support (bootstrap = 94%, posterior probability = 1). One specimen within the GoM complex, assigned to *A. klapferi,* does not cluster with the type specimen of this species. Instead, the type specimen of *A. klapferi* and the colonies of *A. aranea* **sp. nov.** form an unresolved polytomy.

Comparison of base-pair substitutions (Fig. 6b) and uncorrected p-distances (Table 1) revealed no base-pair substitutions and no differences in uncorrected p-distances between *A. aranea* **sp. nov.** and *A. klapferi*. In contrast, two to three base-pair substitutions and uncorrected p-distances ranging from 0.004 to 0.005 were observed between the GoM clade and the *A. klapferi* and *A. aranea* **sp. nov.**, respectively. The NWP-RS clade also differs by two to three base-pair substitutions occurring at different positions in the alignment, resulting in uncorrected p-distances between 0.003 and 0.004. One substitution could not be assessed for *Aquaumbra* sp. 4 (PV731099) due to incomplete sequence data.

The species *E. lauramartinae* exhibited the highest number of substitutions (21 base pairs) and an uncorrected p-distance of 0.036. In contrast, representatives of the genus *Alaskagorgia* showed 24–26 substitutions but slightly lower uncorrected p-distances (0.033–0.035).

Analysis of the *28S rDNA* sequences recovered a similar overall topology, although resolution of sister relationships was limited by the lack of available sequences for *Elbeenus* and *Alaskagorgia* in GenBank (Fig. 7a). The nuclear phylogenetic tree showed moderate support for the separation of *A. aranea* **sp. nov.** and a specimen of *A. klapferi* (bootstrap = 76%, posterior probability = 0.91).

In the ML tree, Aquaumbridae was recovered as sister to *Nephthyigorgia* Kükenthal, 1910, albeit with weak bootstrap support (66%). In contrast, Bayesian inference placed Aquaumbridae as sister to a clade comprising *Sinularia* May, 1898 and *Nephthyigorgia*, with high posterior probability (0.99). Relationships within the *Sinularia-Nephthyigorgia* clade, however, remained poorly resolved (posterior probability = 0.43).

Aquaumbra klapferi and *A. aranea* **sp. nov.** differ by three base-pair substitutions in the 28S marker, whereas *A. aranea* **sp. nov.** and *Aquaumbridae* sp. 3 (OQ592056) differ by five substitutions (Fig. 7b).

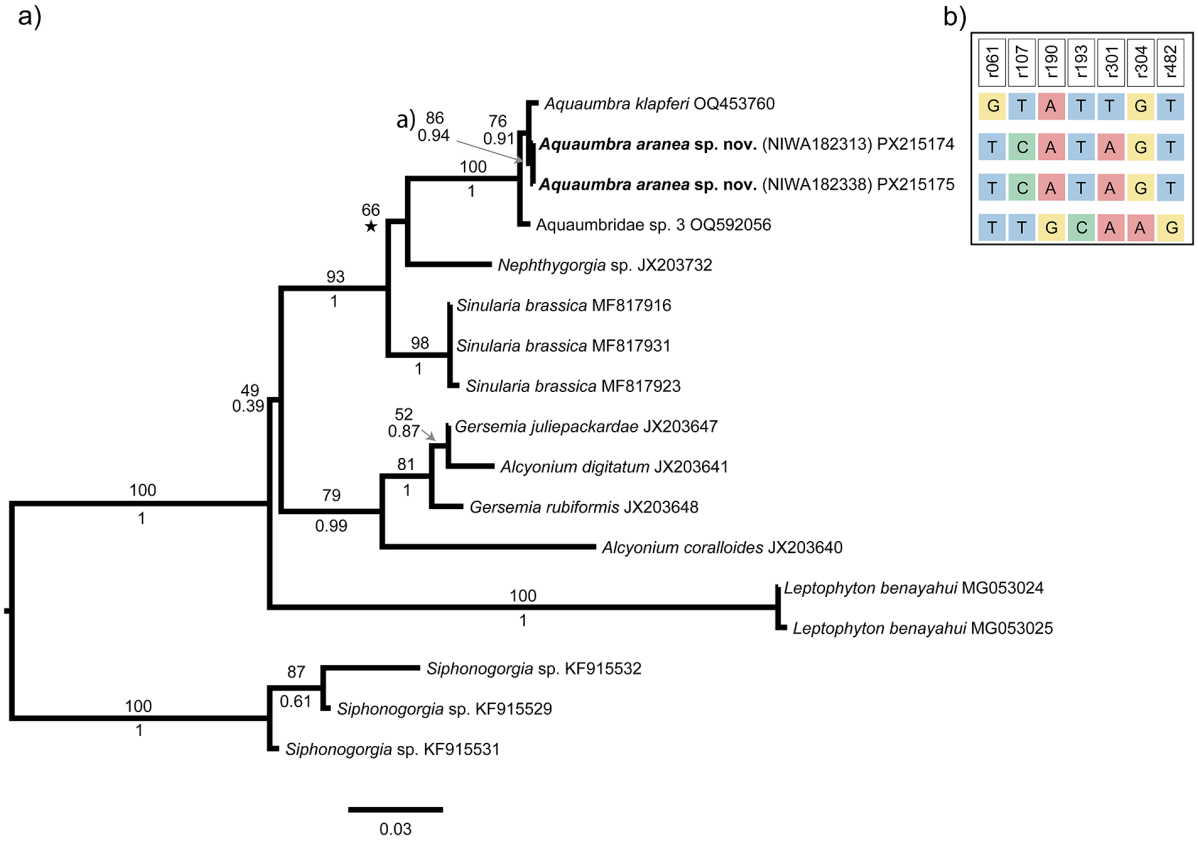

FIGURE 7. a) Maximum Likelihood tree based on *28S rDNA* sequence data. Numbers above branches indicate bootstrap support values, and numbers below branches represent posterior probabilities from Bayesian inference. Newly described species are highlighted in bold. b) Base-pair substitutions in the alignment. Numbers above the bases indicate positions in the alignment.

Discussion

The discovery of *A. aranea* **sp. nov.** expands both the morphological and geographical range of the genus *Aquaumbra*. Unlike *A. klapferi*, which is restricted to seamounts in the eastern tropical Pacific (Breedy *et al.* 2012), *A. aranea* **sp. nov.** inhabits temperate fjord systems of the Southwest Pacific, indicating that the distribution of the genus is broader than previously assumed. The presence of distinct sclerite morphologies, particularly the dominance of unusually formed sclerites, such as irregular bodies with cone-shaped tubercles, further supports the recognition of this taxon as a separate species.

According to Van Ofwegen & Schleyer (1997), the smooth rods in *Leptophyton benayahui* resemble eroded sclerites commonly encountered in formalin-preserved specimens. These structures bear some resemblance to the irregular bodies found in *A. aranea* **sp. nov.** Comparable structures have also been observed in octocorals from Arctic and Antarctic regions under unfavorable growth conditions (van Ofwegen & Schleyer 1997). Neither explanation applies to the material examined here, as all specimens were preserved in ethanol and collected from temperate environments.

The mitochondrial marker *mtMutS* did not reveal any base-pair substitutions between *A. aranea* **sp. nov.** and A. *klapferi*. Accordingly, no differences in p-distances were detected between the two species. The mitochondrial genome of octocorals exhibits a comparatively low mutation rate, which substantially limits species discrimination based on single-marker approaches (McFadden *et al.* 2011). This low mutation rate has been attributed to the presence of the *mtMutS* gene, a characteristic feature of octocorals. The gene is thought to reduce the overall mitochondrial mutation rate through a mismatch repair function, while also exhibiting low levels of sequence variation itself (Bilewitch & Degnan 2011, Muthye *et al.* 2022).

Genetic distance thresholds of approximately 0.003–0.005 for *mtMutS* have frequently been proposed for species delimitation in octocorals (McFadden *et al.* 2014, Quattrini *et al.* 2019, McFadden *et al.* 2025). While these thresholds are effective for distinguishing a large proportion of species, they do not resolve all cases. For instance, Kessel *et al.* (2022) reported p-distances below this threshold among distinct octocoral species from New Zealand fjords. In addition, previous studies have demonstrated that in several octocoral species complexes, the lack of informative sites in *mtMutS* sequences hampers molecular species delimitation, even when morphological analyses support clear species distinctions. For example, this has been reported for the genera *Ovabunda* Alderslade, 2001 and *Sclerophytum* Pratt, 1903 (McFadden *et al.* 2017; Quattrini *et al.* 2019). It is therefore plausible that widely used single markers such as *mtMutS* and *28S rDNA* are sufficient to distinguish many octocoral species, but lack the resolution required to separate more recently diverged taxa. As discussed in McFadden *et al.* (2025), more sensitive genomic approaches, such as analyses of ultra-conserved elements (UCEs) and exon loci, may provide improved resolution for recently diversified species.

Although *A. aranea* **sp. nov.** shows genetic differences from a colony identified as *A. klapferi* (NC_062038), we suspect that this specimen may have been misidentified. The specimen was collected in the GoM, whereas the type material of *A. klapferi* originates from the eastern Pacific off Costa Rica. However, this hypothesis cannot be tested, as neither the type material of *A. klapferi* nor the GoM specimens were available for examination in the present study.

The consistent and diagnostic morphological differences, particularly the unique composition and structure of sclerites, clearly distinguish *A. aranea* **sp. nov.** from *A. klapferi*. These differences cannot be explained by preservation artifacts. In addition, the marked geographic separation between temperate fjord systems of the Southwest Pacific and the eastern tropical Pacific may further support the interpretation of independent evolutionary lineages. The absence of mitochondrial differentiation in *mtMutS* does not contradict this conclusion, as this marker is known to lack resolution in octocorals, particularly among recently diverged taxa. Therefore, based on the morphological evidence presented here, we conclude that *A. aranea* **sp. nov.** represents a distinct species. The description of *A. aranea* **sp. nov.** further reveals the hidden biodiversity of New Zealand's marine ecosystems. In light of growing anthropogenic pressures on benthic habitats, documenting such species is critical for effective conservation and management.

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Data availability

All of the data that support the findings of this study are available in the main text. Sequences generated in this study were deposited in GenBank under accession numbers PX215760–PX215761 (*mtMutS*) and PX215174–PX215175 (*28S rDNA*).

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