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A phylogenetic revision of the monotypic genus *Moolabalia* Alderslade, 2001, an *incertae sedis* soft coral genus from Queensland

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Abstract

Moolabalia Alderslade, 2001 was originally described as a monotypic genus of stoloniferous soft corals within the family Clavulariidae from south-east Queensland. The type species of the genus, *Moolabalia nevillecolemani* Alderslade, 2001, was described using only morphological data, and no genetic data have been available for the species. Recent molecular studies, however, have demonstrated that many octocoral groups, including Clavulariidae, are polyphyletic, and therefore genera that were described without molecular data are generally classified as *incertae sedis*. Here, we test the phylogenetic position of the genus *Moolabalia* within Octocorallia using molecular data from freshly collected topotypes and 26 other species (28 samples) from 23 octocoral genera. Of the 28 samples, 25 were used in previous studies, and 3 were added in this study. These data confirm that *Moolabalia* belongs to Xeniidae rather than Clavulariidae. Our study is the first to obtain genetic material from topotypes of *M. nevillecolemani* and to genetically determine the phylogenetic position of the genus within Octocorallia. In addition, we added field images missing from the original description of *Moolabalia*, which have led to it being confused with a blue-polyped species of *Sarcothelia* (Xeniidae).

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No new species are described in this paper.

Introduction

Moolabalia is a stoloniferous soft coral genus originally described by Alderslade (2001) within the family Clavulariidae, with *Moolabalia nevillecolemani* Alderslade, 2001 being the type species of the genus. The species was described on the basis of two specimens collected by Neville Coleman in 1998 off Mooloolaba, Queens-

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land, Australia. The genus and species were determined based on morphology alone, but the rampant polyphyly of taxa within the Clavulariidae evident in recent molecular studies (e.g., McFadden & Ofwegen 2012) suggests that all previous morphology-based taxonomic decisions need to be revisited. *Moolabalia* is one of eight genera of former Clavulariidae currently considered to be *incertae sedis* due to a lack of sequence data, and the only one from Queensland, Australia (McFadden et al. 2022). Solving the phylogenetic position of the group within Octocorallia will allow all known stoloniferous taxa from Queensland to be included in comprehensive phylogenies and further our understanding of the biodiversity and distribution of soft coral taxa from the region.

Unfortunately, the original description of *M. nevillecolemani* did not describe the color of living colonies and therefore the species cannot be unequivocally identified in the field. The holotype, paratype and relevant collector notes are catalogued at the Museum and Art Gallery of the Northern Territory (NTM), while original photo slides taken by the collector (Neville Coleman) were acquired by the Queensland Museum in 2016, and represent the primary reference on the gross morphology of living colonies. Collector notes from NTM and linked to the record of the type material of *M. nevillecolemani* state that the *in-situ* photo of the holotype is labelled 'Alcy 628'. Additional information from the same record includes a general reference collection coordinate (26°41'S 153°07'E), and a brief note that says 'blue-polyped' (Gavin Dally, personal communication). Therefore, based on the original collector notes, *Moolabalia* is assumed to have blue polyps. However, a slide labelled 'Alcy 628' could not be found in the QM or NTM collections.

Other slides taken by Neville Coleman and catalogued at QM show blue-polyped specimens in the field that are labelled '*Moolabalia nevillecolemani*' by the collector (slide 197 and slide 279; Fig. 1). These slides also suggest the blue-polyped species is what the collector and Alderslade considered to be *Moolabalia*, and therefore what Alderslade later described in 2001. Online records from Atlas of Living Australia (ALA; https://www.ala.org.au) and iNaturalist (https://inaturalist.lu/) further suggest the blue-polyped species is widely recognised to be *Moolabalia*. We are not aware of the presence of the species in any additional book and/or field guide. Without the missing 'Alcy 628' photo slide of the type, the true living appearance of the species has been assumed to be with blue polyps. Below, we show that this is an incorrect assumption.

Here, we aim to resolve the phylogenetic position of the genus *Moolabalia* within Octocorallia using an integrative taxonomic approach combining a phylogenetic analysis of genomic data obtained from freshly collected specimens from the type locality (topotypes; see Bridge et al. 2024) with a morphological re-examination of the holotype of the species *Moolabalia nevillecolemani.* In doing so, we also aim to validate the gross morphology of living colonies, by providing in-situ images of freshly collected specimens that we examine and compare to the type material.

Methods

Data collection

Both the holotype and paratype of *M. nevillecolemani* Alderslade, 2001 are deposited at the Museum and Art Gallery of the Northern Territory (NTM), Darwin, Australia. In this study, we only examined the holotype, since the paratype was registered as a fragment of the holotype itself. The holotype was fixed in ethanol when originally collected in 1996 and is now preserved in 70% ethanol. We compared the holotype with freshly collected specimens from the type locality (e.g., topotypes). Freshly collected specimens were fixed in 100% ethanol, and have been curated and deposited at Queensland Museum, Collection and Research Centre (QM CRC; see systematic account below).

For the collection of topotype material, the species was assumed to have blue polyps (see introduction). While collecting, however, we observed two distinct morphologies growing next to each other; one with blue polyps and a second morph with larger but grey polyps (Fig. 2B & C). Vouchers of both morphologies were collected, including three of the grey and three specimens of the blue-polyped species.

DNA extraction and phylogenomic analyses

DNA was extracted from the holotype of *Moolabalia nevillecolemani* (NTM C012744), four topotypes (blue-polyped QM G340749 and QM G340750; grey-polyped QM G340751 and QM G340754) and from the holotype of *Ezziona dinesenae* (Alderslade 2001; NTM C11950) using the Qiagen DNEasy Blood and Tissue Kit following the manufacturer's recommended protocol. The DNA samples were quantified using a Qubit fluorometer, and the quality checked with a NanoDrop spectrophotometer. We sent the DNA sample from the holotype for targeted capture sequencing to Arbor Biosystems for library preparation, target-enrichment and sequencing (Ann Arbor, MI, USA), following myBaits Custom DNA-Seq protocol v.5.03 (see https://arborbiosci.com/) using the octocoral v2 baitset (Erickson et al. 2021).

For three samples (NTM C11950, QM G340749 and QM G340751), DNA was sent to the Australian Genome Research Facility (AGRF) for library preparation and genome skimming (e.g., low coverage shotgun-sequencing). Library preparation was carried out via adapter ligation, using the Illumina DNA kit Prep-M for inputs between 1 to 500 ng (see https://www.agrf.org.au/).

In this study, we analysed our sequences along with UCE sequences from 25 octocoral specimens published in previous studies to reconstruct a broader picture of the position of the genus *Moolabalia* within Octocorallia

(McFadden et al. 2022; Borghi et al. 2026; Table 1). We downloaded the published data from GenBank (BioProjects PRJNA588468, PRJNA822352, PRJNA413622 and PRJNA1259156). A full list is available in the supplementary material (Table 1). We obtained targeted capture data (725 UCEs) from the holotype of *M. nevillecolemani*, but due to poor sequence quality we removed them from the analyses. We also added genome skimming data obtained from the newly collected topotype specimens QM G340749 and QM G340751 (blue-polyped and grey-polyped '*Moolabalia*' respectively), and from the holotype of *Ezziona dinesenae* (NTM C11950). In the absence of reliable DNA data for the holotype of *M. nevillecolemani*, we used the topotypes to determine the taxonomic placement of the genus within Octocorallia. We processed paired end reads for both previously sequenced UCE samples, and newly sequenced targeted capture and genome skimming data using the Phyluce v1.7.2 pipeline) with some variations. Briefly, reads were quality controlled and de novo assembled using fastp v0.32.2 (Chen et al. 2018) and SPAdes v3.15.5 (Bankevich *et al.* 2012) respectively outside of Phyluce. The resulting assembled contigs were then mapped and corrected using the dedicated workflows within phyluce (https://phyluce.readthedocs.io/en/latest/daily-use/daily-use-4-workflows.html) before being matched to the octocoral v2 baitset using Phyluce (Erickson et al. 2021). We then extracted matched contigs to individual loci FASTA file. Before alignment, target-captured and genome skimmed data were processed in phyluce separately, and then combined. Alignment was done using the standalone version of MAFFT v7.505 (Katoh et al. 2002). Loci were internally trimmed using Gblocks (Castresana 2000) and alignment matrices were filtered for loci represented by at least 60% of the total number of samples.

Phylogenetic reconstruction was done using maximum likelihood in IQ-TREE v2.2.2.2 (Minh et al. 2020), implementing the ModelFinder algorithm to select the best substitution model and partitioning scheme for the set of loci (Kalyaanamoorthy et al. 2017).

Analysis of DNA barcoding data

Morphological assessments hinted at the possibility of *Moolabalia* to belong to Xeniidae rather than Clavulariidae. Within the Xeniidae, however, only a handful of genera have targeted capture sequence available. To further investigate the systematics of genera within that family, we analyzed a concatenated barcode consisting of two mitochondrial genes (COX1 and mtMutS) and the nuclear 28S rDNA. This multilocus barcode has been extensively used to discover new genera and species of xeniids (Benayahu et al. 2021; Benayahu et al. 2022). We added 5 sequences to an alignment of ~60 xeniid samples previously analysed by McFadden et al. (2019), Benayahu et al. (2021) and Benayahu et al. (2022) (Table 2). The mitochondrial and nuclear gene fragments (mtMutS and 28S respectively) of two blue (QM G340749 and QM G340750) and two grey-morph specimens (QM G340751 and QM G340754) were amplified by polymerase chain reaction and Sanger sequenced following published protocols (McFadden et al. 2014a,b). The mitochondrial COX1 of one blue (QM G340749) and one grey morph (QM G340751) were obtained by running Mitofinder v1.4.2 (Allio et al. 2020) on the genome skimmed data (Allio et al. 2020; Quattrini et al. 2024). Similarly, Mitofinder was used to obtain both mitochondrial COX1 and mtMutS from the holotype of *Ezziona dinesenae* NTM C11950.

New sequences and previously published data were aligned using the L-INS-i method in MAFFT v7.505 (Katoh et al. 2002). The mitochondrial and nuclear gene alignments were then concatenated in Phyluce using the phyluce_align_concatenate_alignments command. Phylogenetic reconstruction was done using maximum likelihood in IQ-TREE v2.2.2.2 (Minh et al. 2020), implementing the GTR+I+G model of evolution.

Morphological analysis

The type material was morphologically re-examined under an Olympus SZ70 dissection microscope and photographed with a Canon EOS 90D. Gross morphology was compared to the freshly collected specimens. Briefly, we noted details in the gross morphology, such as the length of the polyps and tentacles, and measured the size of different sclerite shapes found across the colony. When possible, each feature was measured a minimum of three and maximum 30 times, and the mean ($\bar{x}$), standard deviation (s) and range calculated. We obtained sclerites from two main anatomical regions, including the polyp and tentacles combined and the stolon. The tissue from these sections was independently dissolved in 4% sodium hypochlorite (household bleach), rinsed twice in de-ionised water and finally two more times in 95% ethanol. The cleaned sclerites were then mounted on stubs, coated with Pd/Au, and analysed under a Hitachi TM4000Plus or TM1000 Scanning Electron Microscope (SEM).

Results

We obtained 725 UCEs from the holotype of *Moolabalia nevillecolemani*. However, they were excluded in the analyses due to poor sequence quality. From the genome skimming dataset, we obtained 1078 and 1028 UCEs for the grey and blue-morph species respectively. For the targeted capture analysis, the numbers of trimmed reads and assembled contigs are given in Table 1. The 60% data matrix included 2,689 loci, for a total length of 10,108,498 nucleotides, and 366 alignments.

Phylogenetic analysis of UCE data with a 60% data matrix shows that both the blue and the grey morph topotypes of *Moolabalia nevillecolemani* fall within Xeniidae, but in different places. Maximum likelihood of concatenated mitochondrial and nuclear barcoding genes recovered a similar tree topology to previously published data (Benayahu et al. 2022). The grey morph (pre-

Table 1. GenBank accession numbers for all targeted capture samples included in the analysis. Samples newly sequenced in this study are under the BioProject PRJNA1259156. (**) UCEs extracted from genome skimming data. Holotypes are shaded grey.

Sample ID	Classification	Museum	Latitude and Longitude	SRA acc.	# trimmed reads	# loci
S012	*Moolabalia nevillecolemani*	NTM C012744	26°41'S,153°07'E	SAMN48354706	14013108	725
S201	*Sarcothelia* sp.	QM G340749	26°39'01.0"S,153°12'27.9"E	SAMN48354707	37801590	1078**
S202	*Moolabalia nevillecolemani*	QM G340751	26°39'01.0"S,153°12'27.9"E	SAMN48354708	74985406	1028**
C11950	*Ezziona dinesenae*	NTM C11950	18°14'S,146°54'E	SAMN60209297	11106974	1020**
S141	*Knopia octoconta-canalis*	NTM C015392	See Borghi et al. 2026	SAMN48354709	54224010	1003**
S028	*Knopia octoconta-canalis*	QMT G84389	See Borghi et al. 2026	SAMN50550381	13503508	1101
S120	*Hanabira yukibana*	QMT G84473	See Borghi et al. 2026	SAMN48354710	68550632	1416**
S024	*Clavularia koellikeri*	QMT G84393	See Borghi et al. 2026	SAMN48354711	1991320	1028
S021	*Clavularia koellikeri*	QMT G84408	See Borghi et al. 2026	SAMN48354712	12169534	804
S035	*Clavularia koellikeri*	QMT G84394	See Borghi et al. 2026	SAMN48354713	11311194	888
S115	*Clavularia koellikeri*	QMT G84462	See Borghi et al. 2026	SAMN48354714	63956592	1226**
S001	*Carijoa cf. riisei*	QMT G84927	See Borghi et al. 2026	SAMN48354715	3590774	1324
ANT68	*Solenocaulon sp.*	RMNH.COEL.40033	See McFadden et al. 2022	SRR10443767	9584496	860
ANT72	*Melithaea erythraea*	Co37709	See McFadden et al. 2022	SRR10443764	3958700	600
ANT62	*Alertigorgia orientalis*	NTM C014528	See McFadden et al. 2022	SRR10443774	4156006	398
ANT108	*Azoriella bayeri*	RMNH.COEL.40806	See McFadden et al. 2022	SRR10443675	2456006	331
ANT101	*Malacacanthus capensis*	CASIZ 222387	See McFadden et al. 2022	SRR10443825	9139848	572
ANT70	*Nidalia simpsoni*	RMNH.COEL.40975	See McFadden et al. 2022	SRR10443765	8773082	774
OCT042	*Hicksonia tohrui*	Co38221	See McFadden et al. 2022	SRR27744982	4537450	1722
OCT041	*Altumia delicata*	Co37427	See McFadden et al. 2022	SRR27744981	2902078	1340
ANT109	*Acanthoaxis wirtzi*	RMNH.COEL.39502	See McFadden et al. 2022	SRR10443664	11184266	1187
OCT043	*Cryptophyton goddardi*	USNM 1516882	See McFadden et al. 2022	SRR27744983	4719166	1497
ANT36	*Tubipora sp.*	Co34116	See McFadden et al. 2022	SRR6178958	2717108	233
ANT50	*Paratelesto sp.*	RMNH.COEL.40019	See McFadden et al. 2022	SRR10443786	9429700	496
ANT99	*Arula petunia*	RMNH.COEL.40188	See McFadden et al. 2022	SRR10443734	9044516	1127
ANT73	*Acrossota amboinensis*	USNM 1516854	See McFadden et al. 2022	SRR10443763	7692088	654
OCT077	*Sympodium caeruleum*	Co34185	See McFadden et al. 2022	SRR10443693	1925208	395
ANT115	*Protodendron repens*	Co35118	See McFadden et al. 2022	SRR10443791	1830273	421
ANT25	*Coelogorgia palmosa*	NTM C014914	See McFadden et al. 2022	SRR6178990	4946043	579

sumed to be *Moolabalia nevillecolemani*, see taxonomic account below) falls within the Xeniidae, sister to the genera *Ezziona* and *Latissimia* (Figure 3B). The blue morph specimens are also Xeniidae, but fall within the *Sarcothelia* group, sister to the genus *Quattuoria*, potentially as an undescribed species of *Sarcothelia*.

Table 2. Xeniidae specimens and DNA barcoding data included in the phylogenetic analysis. Holotypes are shaded grey.

Sample ID	Classification	Museum number	MutS	COX1	28S
C11950	*Ezziona dinesenae*	NTM C11950	PZ194706	PZ195135	PZ196224
S201/ MOL49	*Sarcothelia sp.*	QM G340749	PZ194705	PZ195133	PZ196226
S202/ MOL51	*Moolabalia nevillecolemani*	QM G340751	PZ194704	PZ195134	PZ196227
MOL50	*Sarcothelia sp.*	QM G340750	PZ194702	NA	PZ196223
MOL54	*Moolabalia nevillecolemani*	QM G340754	PZ194703	NA	PZ196225

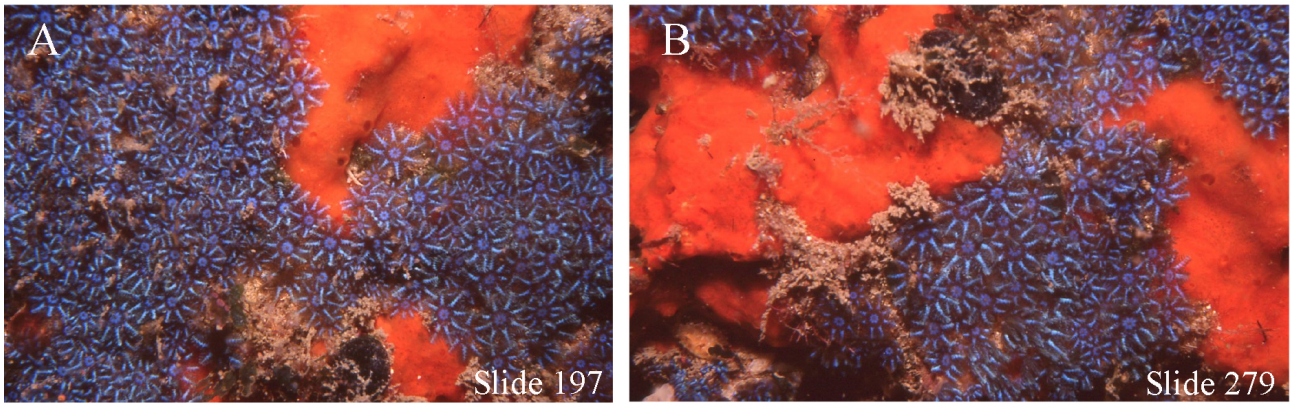

Figure 1. Original collector's slides of additional living colonies (not type material) photographed in the field and labelled as *Moolabalia nevillecolemani*. (**A**) slide number 197 and (**B**) 279, preserved at Queensland Museum (QM). The slide of the holotype is lost (referred to as 'Alcy 628').

Discussion

This study resolves the phylogenetic position of the genus *Moolabalia* within Octocorallia, removing the taxon from the list of *incertae sedis* octocorals (McFadden et al. 2022). The genus is here placed within the Xeniidae, and shows further the genus-level morphological diversity within that family.

The genus *Moolabalia* was previously placed in Clavulariidae, but the presence of *Xenia*-like sclerites was noted (Alderslade 2001). Alderslade placed the genus within Clavulariidae based solely on the thin perisarc which covers most of the colony, a feature typically found in other stoloniferous octocorals in the genera *Clavularia* and *Carijoa*. Octocorals that share this morphological feature, however, are polyphyletic. For instance, the genus *Carijoa* was recently transferred to the newly described family Carijoidae based on molecular evidence (McFadden et al. 2022), suggesting the perisarc may not be as taxonomically informative as previously thought. Other families of former Clavulariidae that have perisarcs are Cerveridae McFadden, van Ofwegen & Quattrini, 2024 and Cornulariidae Dana, 1846, further showing how the presence of the perisarc is not informative to even family-level diagnostics (McFadden et al. 2022). Alderslade (2001) also stated that the sclerites of *Moolabalia* are unlike any other known from Clavulariidae. However, he decided to place *Moolabalia* in Clavulariidae because the sclerites formed by euhedral crystals that are observed in the stolon share similarities with the description of sclerites in *Clavularia ochracea* provided by Weinberg (1978). Members of the family Clavulariidae exhibit great variability in sclerite shapes and diversity (McFadden et al. 2022). Within the Clavulariidae clade, the genera *Clavularia* Blainville, 1830 and *Hanabira* Lau, Stokvis, Imahara & Reimer, 2019 lack fine sculpturing features in smaller sclerites (Lau et al. 2019), while the genus *Knopia* is characterised by small and abundant platelets constructed from calcite rods (Alderslade and McFadden 2007). *Moolabalia* Alderslade, 2001 has tentacle sclerites similar in general appearance to those of *Knopia*, but they differ in the sculpturing on their surface.

The small platelets from the tentacles of *Moolabalia* bear a closer resemblance to the sclerites found in many other Xeniidae (see Benayahu et al. 2022) (e.g., *Sansibia* Alderslade, 2000, *Quattuoria* Benayahu et al., 2022, *Ovabunda* Alderslade, 2001 and *Latissimia* Benayahu, Ekins & McFadden, 2022), although sclerites in *Moolabalia* Alderslade, 2001 are never fractured. Sclerites of similar shape to the ones found in the tentacles of *Moolabalia* can also be found in the species *Ezziona dinesenae* Alderslade, 2001. The genus *Ezziona* was described together with *Moolabalia* in 2001, but speci-

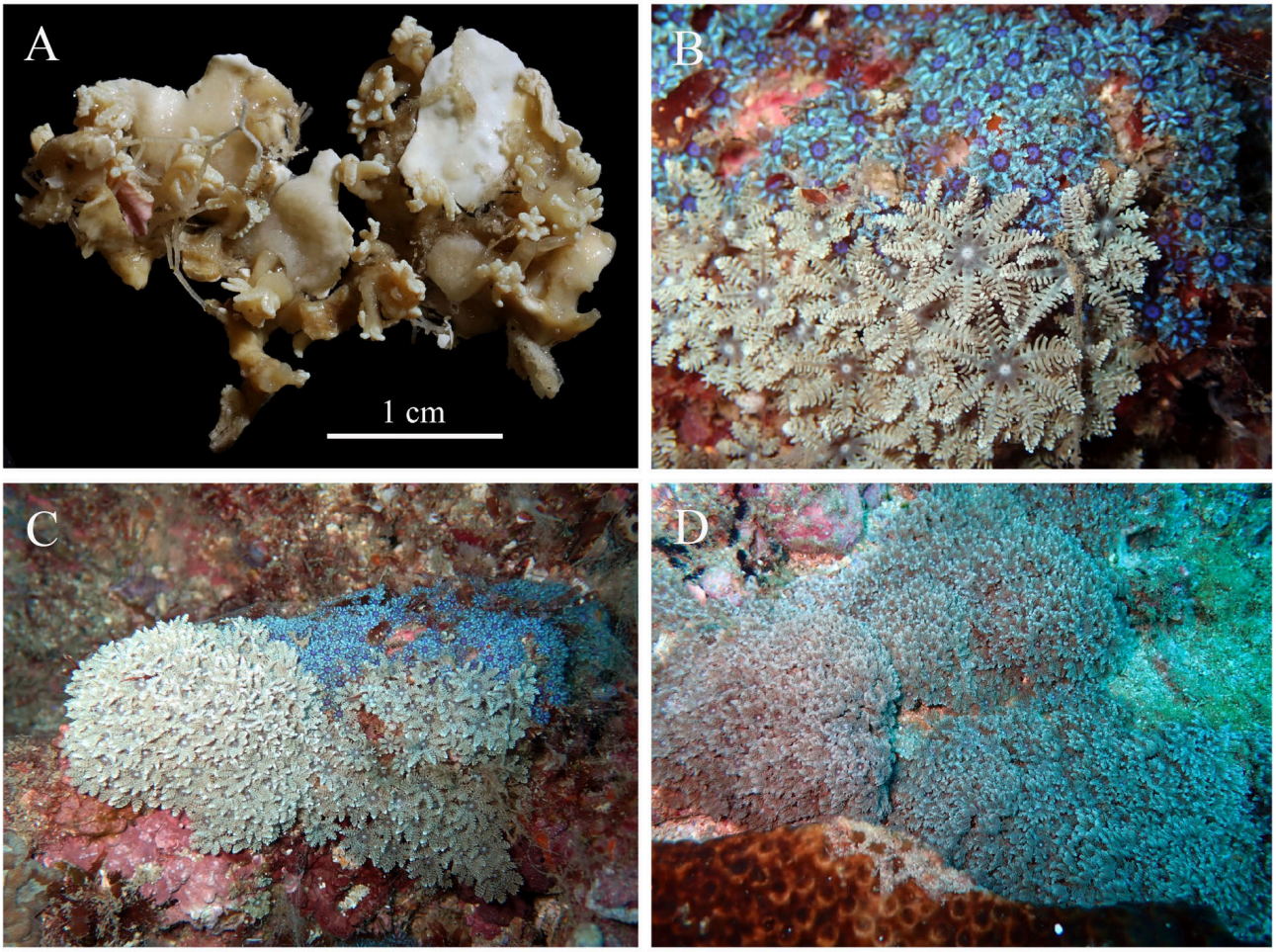

Figure 2. *Moolabalia nevillecolemani* Alderslade, 2001; (**A**) Image of the holotype (NTM C012744) deposited and curated at the Museum and Art Gallery of the Northern Territory (NTM) in Darwin (Photo taken by Stefano Borghi). Living colonies from the type locality, which were collected and used as topotypes; (**B** and **C**) QM G340750 (blue) and QM G340754 (grey) and (**D**) QM G340751 (grey). The grey colonies are *Moolabalia nevillecolemani*, while the blue colonies are of a potentially undescribed *Sarcothelia* species (Photos taken by Dr. Merrick Ekins).

mens were collected from the outer reefs in the Central Great Barrier Reef. The sclerites in *Ezziona* are constructed by radially-arranged dendritic rods, which is a typical microstructure feature found in xeniids, including *Moolabalia* (Alderslade 2001). Similarly to sclerites in *Moolabalia*, *Ezziona* has sclerites with irregular outline, but never fractured. Our maximum likelihood analyses which also include genetic data from the holotype of *E. dinesenae* support the two genera to be distinct within the Xeniidae. The sclerites from the stolons of *Moolabalia* remain unique among xeniids, and a potentially informative morphological feature that defines the genus.

Alderslade (2001) noted that the diversity in sclerite shapes in the Xeniidae is understudied. However, recent work revised the diagnosis of the Xeniidae, and showed that sclerites can differ significantly between genera. For instance, the genus *Protodendron* was recently transferred to Xeniidae based on molecular evidence, despite its sclerites being distinct from the ones found in other Xeniidae (McFadden et al. 2022). These observations, together with our results, corroborate that gross morphology and sclerite microstructures alone are often not reliable diagnostic characters in familial- to species-level identifications, especially in the absence of extensive morphological assessments. An integrative taxonomic approach combining the morphological re-examination of type material and molecular data is necessary to confirm taxonomic assignments.

Taxonomy

Sub-Phylum ANTHOZOA Ehrenberg, 1834

Class OCTOCORALLIA Haeckel, 1866

Family XENIIDAE Ehrenberg, 1828

Moolabalia Alderslade, 2001

Type species: *Moolabalia nevillecolemani* Alderslade, 2001

Diagnosis (after Alderslade 2001). Non-retractile and monomorphic polyps arising from a narrow ribbon-like stolon. Stolon and most of polyps covered by a transpar-

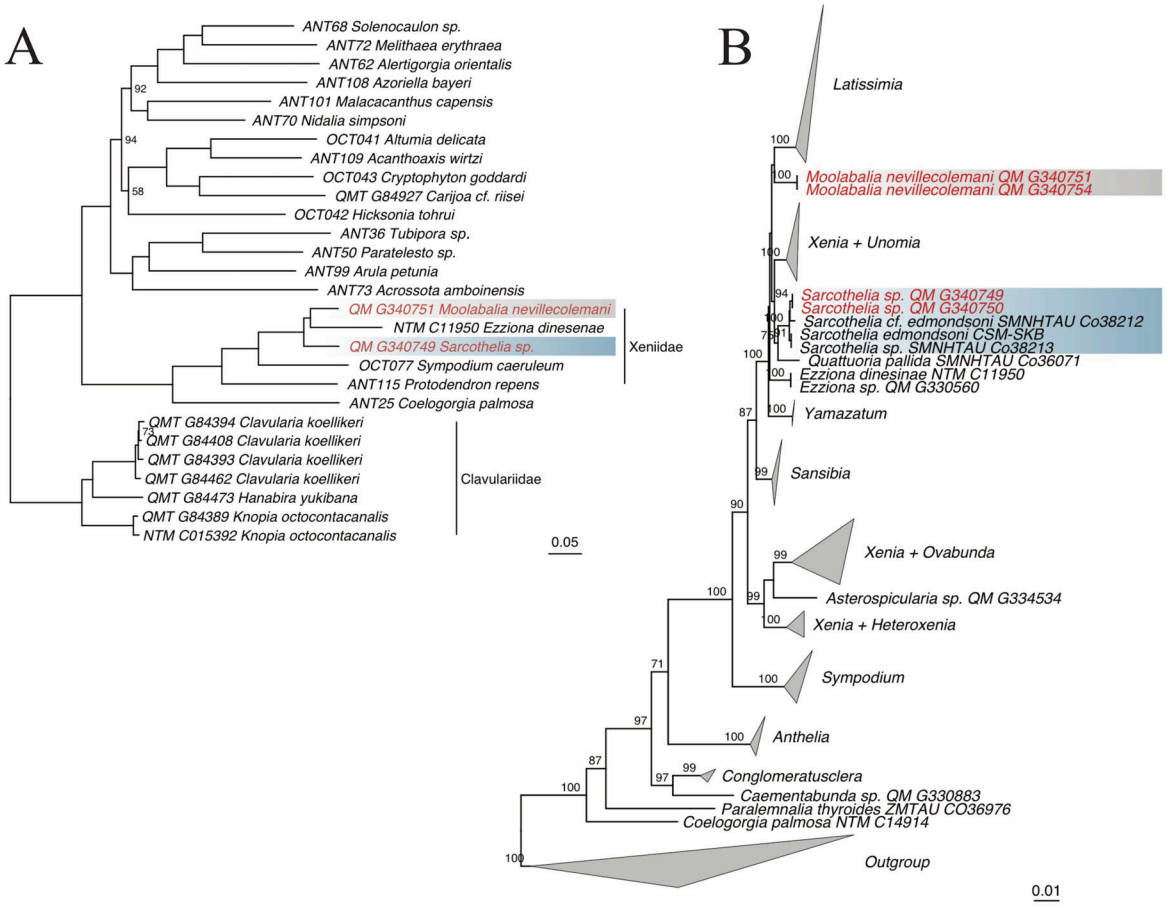

Figure 3. (**A**) Maximum likelihood phylogeny of soft corals of the order Malacalcyonacea (Octocorallia) inferred from the 60% incomplete internal-trimmed alignment matrix. Bootstrap values are plotted at the nodes when lower than 100. (**B**) Maximum likelihood phylogeny inferred from a concatenated alignment of *28S*, *mtMutS* and *COX1*. Bootstrap values are plotted at the nodes when > 70. The monotypic genus *Moolabalia* is highlighted in red within the family Clavulariidae (grey highlight). The genus *Sarcothelia* is highlighted in blue.

ent and thin perisarc. Sclerites of stolon as small ellipsoid or peanut-shaped platelets with fine sculpturing on their surface comprising calcite prisms. Sclerites of tentacles as small platelets made of dendritic, sinuous, anhedral rods. Zooxanthellate.

Moolabalia nevillecolemani Alderslade, 2001

Figures 2 and 4

Moolabalia nevillecolemani Alderslade 2001: 52–56, Fig. 31–34; McFadden et al. 2022: 67 (listed only).

Description.(After Alderslade 2001). Our morphological analysis of the type specimen agrees with the original description of the species, but a few remarks are to be made. The holotype, NTM C012744, consists of two fragments connected by the ribbon-like stolonic structure of the specimen. At its widest measurable region, the specimen measures 3.43 cm (Fig. 2). The stolon appears soft, thin and transparent. The preserved polyps are flaccid, with a transparent body, and white tentacles and pinnules. The polyp body measures between 1.56 to 3.11 mm in length ($\bar{x}$ = 2.65 mm, s = 0.07, n = 4). The tentacles range in length between 0.88 to 1.74 mm ($\bar{x}$ = 1.38 mm, s = 0.03, n = 7). The pinnules are numerous, short, bulbous and appear to be arranged in a single row.

The sclerites are diverse throughout the holotype, abundant on the tentacle, neck and stolonic sections, and rarer across the polyp body. Sclerites from the stolon (Fig. 4C) are larger than the ones found elsewhere, 0.02 to 0.04 mm in length ($\bar{x}$ = 0.03 mm, s = 0.01, n = 30). They are also quite distinct as they have irregular margins and a rough surface of organised prisms. In contrast, sclerites from the tentacles and polyp body are small platelets with smooth margins, although two different types are observed. The most common are small platelets constructed by small rods (Fig. 4A), 0.02 to 0.03 mm ($\bar{x}$= 0.02 mm, s = 0.01, n = 30). Other platelets are larger and have a more granular surface, forming an intermediate morphology between the other sclerite surface structures ($\bar{x}$= 0.03 mm, s = 0.01, n = 30) (Fig. 4B).

Material examined. Holotype: Australia. NTM C012744, two fragments, Mooloolaba, Queensland, at 16 m depth, 14th June 1998, coll. Neville Coleman. **Additional material**: Australia, QM G340751, Nurse Rock, outer Gneerings, Mooloolaba, Queensland

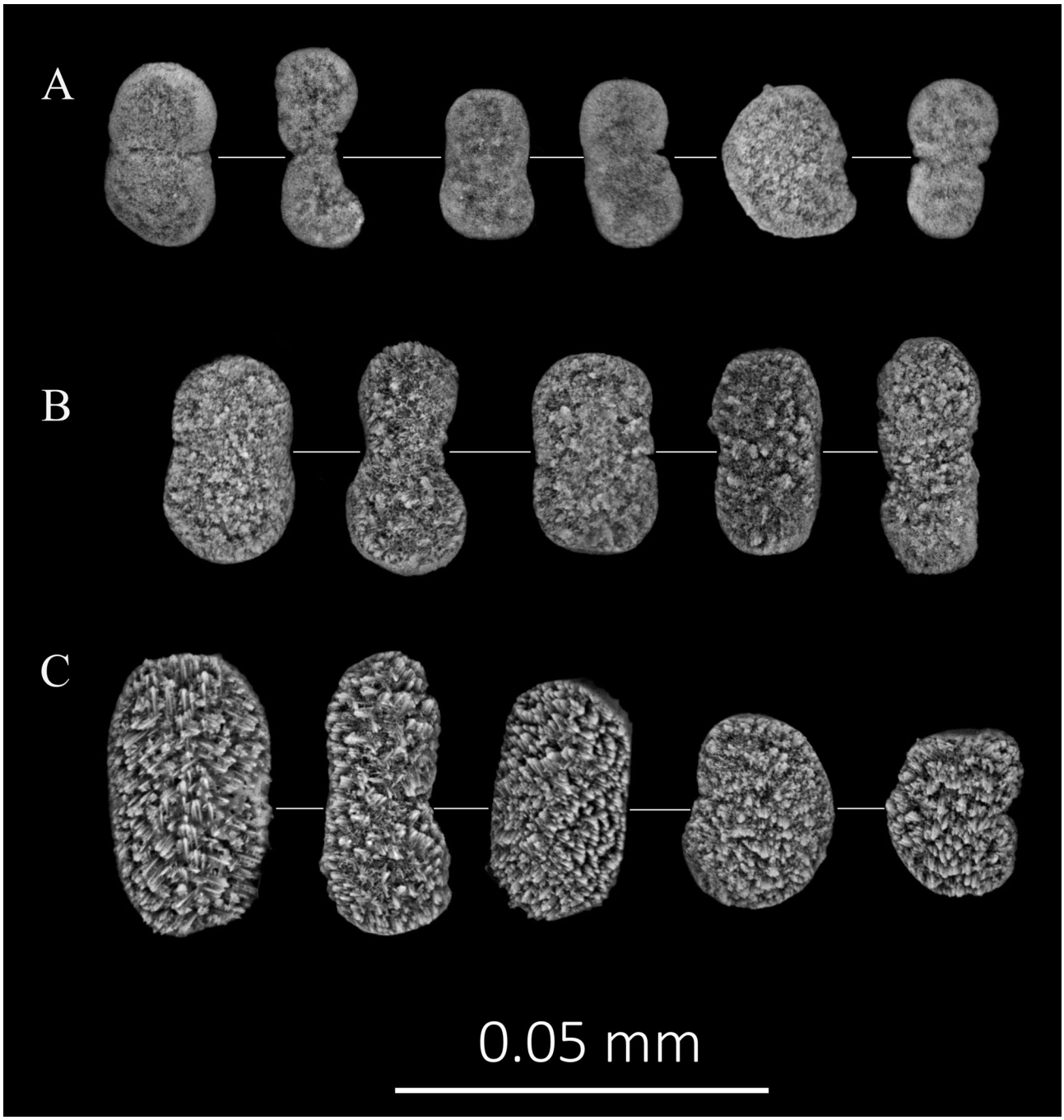

Figure 4. Scanning electron micrographs showing sclerites from the holotype (NTM C012744) from the (**A**) tentacles, (**C**) stolon and (**B**) an intermediate morphology that can be found across the entire colony. Scale bar applies to all groups.

(26°39'01.0"S, 153°12'27.9"E), 17m, 30th August 2024, coll. Merrick Ekins; Australia, QM G340754, Nurse Rock, outer Gneerings, Mooloolaba, Queensland (26°39'01.0"S, 153°12'27.9"E), 17m, 30th August 2024, coll. Merrick Ekins.

Variations in gross morphology. Living colonies of both grey and blue-polyped specimens were collected and morphologically examined. Sclerites of the grey-polyped specimens match the sclerites of the holotype. The blue-polyped specimens, however, had more typical Xeniidae sclerites (Fig. 5). These are small and ellipsoid platelets with smooth margins, 0.010 to 0.015 mm long ($\bar{x}$ = 0.013 mm, s = 0.001), and fine sculpturing on the surface made of calcite rods, radially arranged. The sclerites often appear fractured under SEM. These differences support the conclusion that the grey species is *Moolabalia*.

Examination of images of living colonies revealed that *Moolabalia* has pinnules arranged in two rows, 9 to 11 pinnules per row. This feature is not evident in preserved specimens nor noted in the original description, as the pinnules in ethanol are contracted and look short, bulbous and appear to be organised in a single row. Sclerite shape and size are consistent across all grey specimens examined.

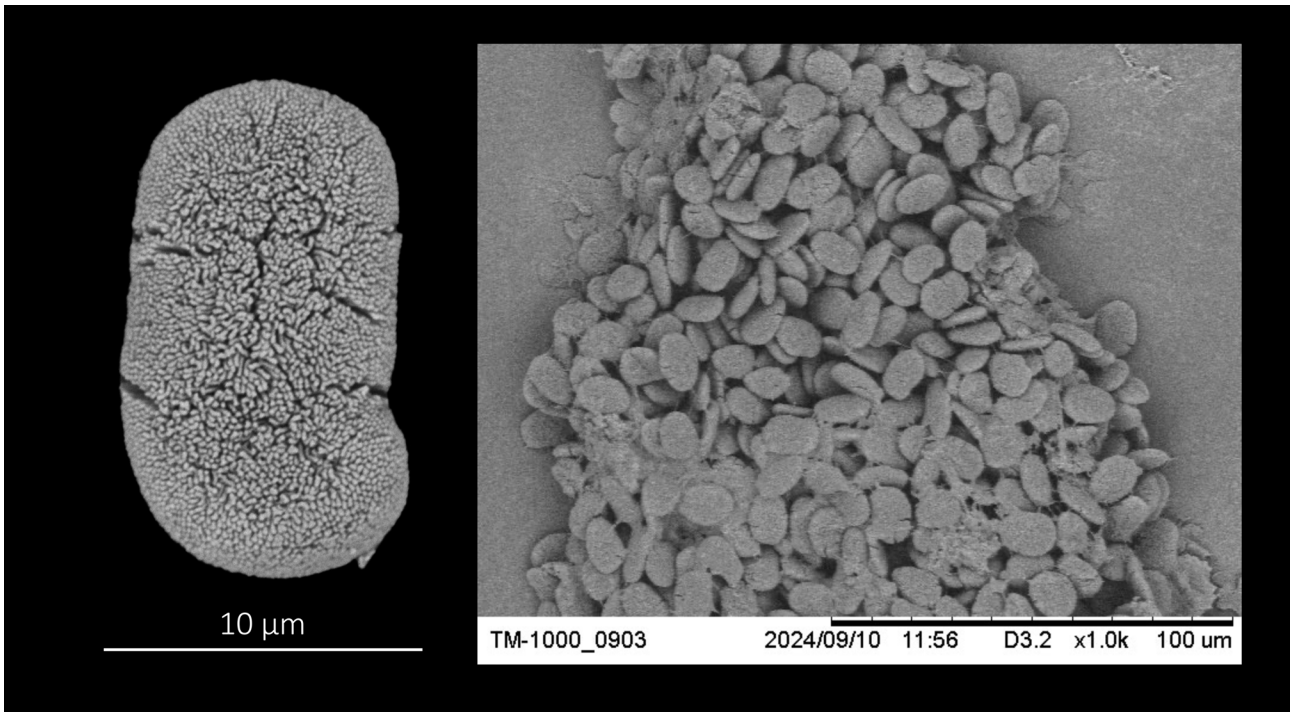

Figure 5. Scanning electron microscopy of the topotype QM G340749. Group of ellipsoid platelets (right) and close up to show the radial arrangement of calcite rods and the fractured surface typical of Xeniidae soft corals (left).

Color. The ethanol-preserved holotype has a transparent stolon and polyp body with white tentacles. Based on the *in situ* photographs of the topotypes, living colonies have grey polyps with a white oral disk (Fig. 2B-D).

Remarks. The current study is the first to address the phylogenetic position of the genus *Moolabalia* within Octocorallia using molecular evidence. Our morphological analysis corresponds to the original description of the species, although we reveal that *Moolabalia nevillecolemani* is not the blue-polyped species shown in Coleman's slides. The molecular analysis of the grey morph specimens that correspond morphologically to *Moolabalia nevillecolemani* places the species within the Xeniidae. The blue-polyped specimens are also placed within the family Xeniidae but within the *Sarcothelia* Verrill, 1928 clade, and do not resemble the *Moolabalia* holotype in sclerite morphology. The two species were observed to grow in close proximity to each other and are often collected on the same substrate. This close association may have led to photos of the blue species (*Sarcothelia*) being attributed to *Moolabalia*.

Distribution. Only known from Mooloolaba, Queensland.

Disclosures

The authors declare no conflicts of interest.

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