Urodacus, *Acanthodillo*, and *Conothele* from the Eramurra Solar Salt Project area: A comparison with Pilbara congeners

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INTRODUCTION

To clarify the taxonomic and distributional status of three potential short-range endemic invertebrate species recorded from the Eramurra Solar Salt Project area, southwest of Karratha, Western Australia, Stephen Van Leeuwen of Curtin University engaged the Western Australian Museum (WAM) to perform a morphological and molecular assessment of these species using available specimens. The taxa of interest are *Urodacus* sp. indet. 'eramurra' (a scorpion), *Acanthodillo* sp. indet. B 'eramurra' (an isopod) and *Conothele* ‘MYG726’ (a mygalomorph spider). This report presents the identity and reviews the taxonomic status of the available specimens of *U.* sp. indet. 'eramurra', *A.* sp. indet. B. 'eramurra', and *C.* ‘MYG726’. The molecular systematics of *U*. sp. indet. 'eramurra' and *Acanthodillo* sp. indet. B ‘erramurra’ are reviewed based on a comparison of molecular (COI barcode) characters with reference to congeneric specimens collected at other sites in the Pilbara bioregion of Western Australia.

METHODS

In February 2025, WAM collection staff examined the single specimen of *Urodacus* sp. indet. 'eramurra', two specimens of *Acanthodillo* sp. indet. B. 'eramurra', and single specimen of *Conothele* ‘MYG726’ held in the WAM collection. Leg tissue was subsampled from the *Urodacus* and *Acanthodillo* specimens for genetic barcode analysis. Specimen information is provided in Appendix 1. In addition to the three taxa of interest recorded from the project area, other specimens were selected to serve as comparative material from locations outside the project area. Specifically, representatives of *Acanthodillo* from near-coastal sites in the Mardie area and east to near Port Hedland, as well as the central Pilbara, were subsampled for genetic analysis. Preference was given to the most recently collected specimens to maximise the likelihood of successful amplification of the target barcoding gene region. Specimens were photographed using a Leica M205c microscope paired with a Leica DMC5000 camera. Image stacks were captured at multiple focal planes using the LAS X software suite and combined with the automontage feature to produce high-resolution composite images.

DNA extraction, amplification and sequence preparation was carried out in the WAM Genetic Resources laboratory. A 658 bp region of the mitochondrial cytochrome oxidase I (COI) gene was targeted, amplified and sequenced using primers LCO1490:HCO2198 (Folmer *et al.* 1994) or dgLCO1490:dgHCO2198: (Meyer *et al.* 2005). Bidirectional sequencing was carried out at the Australian Genomic Research Facility (AGRF) Perth node. Sequences were compared to the NCBI GenBank database (www.ncbi.nlm.nih.gov/genbank/, accessed 25th March 2025) using BLAST search to find similar nucleotide sequences. These sequences, along with unpublished COI sequences in WAM reference libraries, were included in subsequent analyses. Pairwise genetic distances (% sequence divergence) between the query and the most similar reference sequences, were estimated using a GTR GAMMA model of evolution (RAxML, Stamatakis 2014) implemented in Geneious Prime 2025.0.3. For visualisation purposes, maximum-likelihood gene trees were constructed using a GTR GAMMA model of evolution and 100 bootstraps.

RESULTS AND DISCUSSION

High-quality COI barcode sequences were successfully obtained from the scorpion sample and from ten out of the fifteen isopod samples (Table 1). Four isopod samples failed to amplify DNA, so new leg tissue subsamples were collected from these specimens; of these, three were successfully amplified and sequenced. Five isopod samples either failed to sequence or were identified as human sequences (suggesting possible contamination during the specimen or sample handling stages), though negative results were obtained from DNA extraction and amplification reagent controls.

Urodacus sp. 'eramurra'

Molecular assessment confirms the specimen WAM T152484 identified as *Urodacus sp.* 'eramurra' (Table 1; Figure 1) is not conspecific with available sequences of other species of *Urodacus*. The closest match to the molecular data was with a specimen collected from ca. 72 km NNE of Munjina roadhouse (WAM T123624, identified as *U.* sp. SCO033). This specimen is a juvenile so morphological comparisons are unreliable, as juveniles and adult females lack the morphological features found in males that are used to diagnose species. However, to provide comparisons, images of both species are shown here (Figure 3).

The morphology of the adult male scorpion WAM T152484 is rather unique within the genus and has highly reduced dorsal keels on the metasomal segments (especially segment IV) and the telson has an ovoid vesicle and a short and curved aculeus (Figure 3). Specimen WAM T152484 was compared with males collected from elsewhere in the Pilbara and no adult males with matching morphology could be found. While it is likely that *U. sp.* 'eramurra' represents a short-range endemic species, there is insufficient conclusive evidence that this is the case, as the scorpion fauna of the Pilbara is poorly known.

Acanthodillo sp. indet. B 'eramurra'

Morphologically, *Acanthodillo* sp. indet. B is distinguishable from other examined specimens by the reduced development of dorsal tubercles on each body segment (Figure 4). In this genus, tubercles are typically well-developed and often acutely spiniform. The two available specimens are small, and it remains unclear whether they have reached full maturity. To assess whether the observed tubercle development is linked to maturation, and therefore variable, sequence data were analysed. The resulting sequence did not match any available to WAM, either from unpublished in-house datasets or those deposited in GenBank. Unfortunately, the second specimen of *A.* sp. indet. B (WAM C76218) did not produce a viable sequence. Importantly, the genetic data confirm that *A.* sp. indet. B, represented by WAM C76219, is not conspecific with *A.* sp. indet. A, despite both being collected from the vicinity of the Eramurra project area. In fact, *A.* sp. indet. B did not clade within a group of other *Acanthodillo* species in the analysis (Figure 2). Also, the *A.* sp. indet. A sequences fell into two separate clades (Figure 2). As with most arthropod groups, particularly those with many undescribed species, taxonomic revisions are much needed. The nearest match for *A.* sp. indet. B was to an isopod identified as Armadillidae sp. Biologic-ISOP031 (WAM C77596) collected from near Nullagine but at only 87.2% similarity (12.8% divergence), not much information can be drawn from this. That specimen is also small, ~4 mm, and lacks prominent tubercles.

Conothele 'MYG726'

A single collection of the trapdoor spider genus *Conothele* was made at Eramurra (WAM T150888), which comprised an adult female and 40 spiderlings. The female was compared with other females from the Pilbara and found to possess a unique morphology of leg III, a character that has been shown to of importance in distinguishing species of *Conothele* in Western Australia. The presence of a potential short-range endemic species of *Conothele* at Eramurra is consistent with other species of *Conothele* in Western Australia. In fact, all Western Australian species of *Conothele* are short-range endemics, and all represent new, undescribed species.

CONCLUSION

The morphological and molecular assessment presented in this report finds that the query specimens, WAM T152484 *Urodacus* sp. 'eramurra', WAM C76219 *Acanthodillo* sp. indet. B, and WAM T150888 *Conothele* 'MYG726', are not conspecific with other available specimens or COI barcode sequences from the vicinity of the Eramurra Solar Salt Project and likely represent new, undescribed species. While the query specimens are potential short-range endemics, further studies incorporating additional specimens from nearby areas and additional genetic characters are needed to improve the taxonomic and distributional framework for these species.

Table 1. Summary of molecular assessment of ***Urodacus*** and ***Acanthodillo*** tissues held in the WAM collection, based on mitochondrial COI sequences. Specimens of interest are shown in bold text.

WAM Registration No.	**Molecular Results**	**Specimen Identification**
Urodacus		
WAM T152484	640 bp COI sequence. The specimen is 6% divergent from its nearest relative, WAMT123624 *Urodacus* sp. SCO033 collected 150 km SSE of Port Hedland, ca. 72 km NNE of Munjina Roadhouse, and 8.1% divergent from other reference sequences.	***Urodacus sp.* 'eramurra'**
Acanthodillo		
WAM C62646	Failed to sequence	*Acanthodillo* sp. indet.
WAM C62873	658 bp COI sequence. Forms a clade with WAMC 76215 and WAM C85952 (sequence divergence <0.2%) and is more than 17% divergent from other reference sequences.	*Acanthodillo* sp. indet.
WAM C62942	Non-target (human) DNA amplified	*Acanthodillo* sp. indet.
WAM C63174	Failed to sequence	*Acanthodillo* sp. indet.
WAM C66488	658 bp COI sequence. Moderate divergence from all reference sequences. The most similar reference sequence was WAM C76217 (14% divergence) collected at Eramurra.	*Acanthodillo* sp. indet.
WAM C76215	627 bp COI sequence. Forms a clade with WAMC 62873 and WAMC 85952 (sequence divergence <0.2%) and is more than 17% divergent from other reference sequences.	*Acanthodillo* `sp. indet. A (eramurra)`
WAM C76217	648 bp COI sequence. Moderate divergence from all reference sequences. The most similar reference sequence was WAM C66488 (14% divergence) collected ca. 30km SW of Pannawonica.	*Acanthodillo* `sp. indet. A (eramurra)`
WAM C76218	Non-target (human) DNA amplified	*Acanthodillo* `sp. indet. B (eramurra)`
WAM C76219	657 bp COI sequence. Moderate divergence from all reference sequences. The most similar reference sequence was OP242130 Armadillidae sp. Biologic-ISOP031 WAM C77596 (12.8% divergence), Collected from Nullagine, WA. At least 20% divergent from other reference sequences.	***Acanthodillo* `sp. indet. B (eramurra)`**
WAM C85948	650 bp COI sequence. Forms a clade with WAMC 85953, WAMC 85951 and WAMC 85950 (sequence divergence <0.03%) and is more than 16% divergent from other reference sequences.	*Acanthodillo* `sp. indet. A (eramurra)`
WAM C85949	Failed to sequence	*Acanthodillo* sp. indet.
WAM C85950	650 bp COI sequence. Forms a clade with WAMC 85953, WAMC 85951 and WAMC 85948 (sequence divergence <0.03%) and is more than 16% divergent from other reference sequences.	*Acanthodillo* `sp. indet. A (eramurra)`
WAM C85951	650 bp COI sequence. Forms a clade with WAMC 85953, WAMC 85950 and WAMC 85948 (sequence divergence <0.03%) and is more than 16% divergent from other reference sequences.	*Acanthodillo* `sp. indet. A (eramurra)`
WAM C85952	658 bp COI sequence. Forms a clade with WAMC 62873 and WAMC 85952 (sequence divergence <0.2%) and is more than 17% divergent from other reference sequences.	*Acanthodillo* `sp. indet. A (eramurra)`
WAM C85953	650 bp COI sequence. Forms a clade with WAMC 85951, WAMC 85950 and WAMC 85948 (sequence divergence <0.03%) and is more than 16% divergent from other reference sequences.	*Acanthodillo* `sp. indet. A (eramurra)`

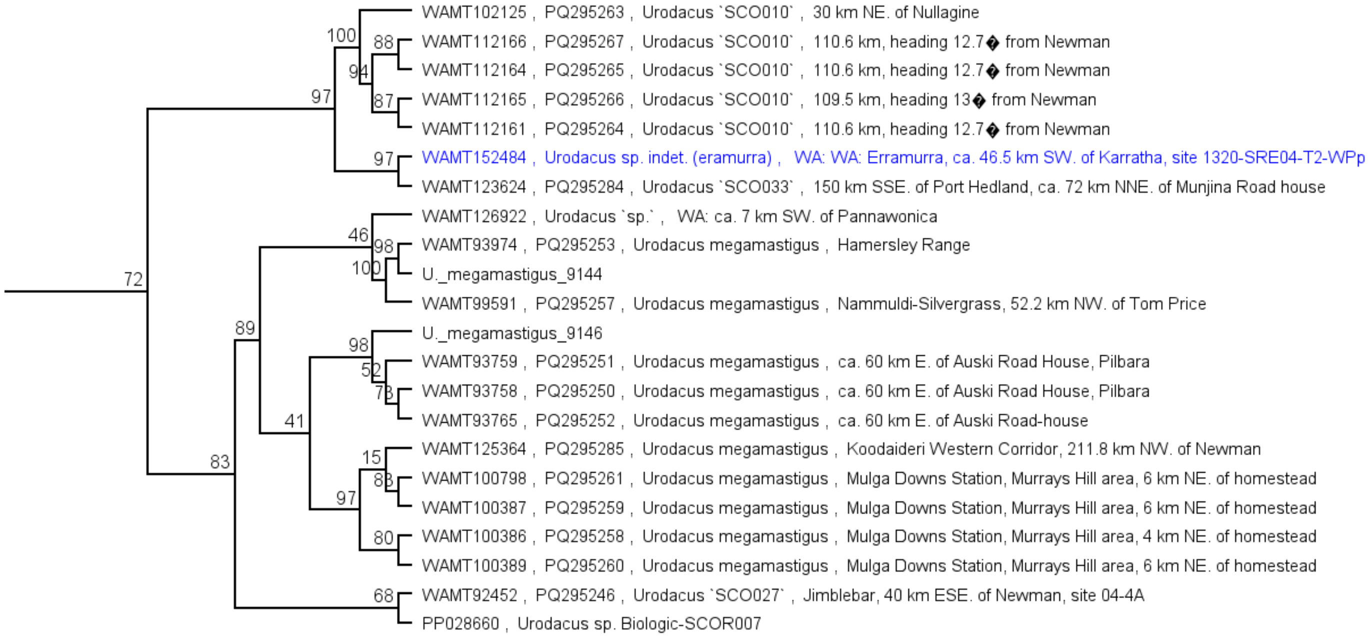

Figure 1. Excerpt of maximum likelihood gene tree of mitochondrial COI sequences from *Urodacus* vouchers. Tip labels include museum registration numbers and/or GenBank accession numbers. Query specimen is highlighted in blue text. Branch labels represent bootstrap values. This tree is intended only for visualization of molecular data and does not represent a comprehensive phylogenetic analysis.

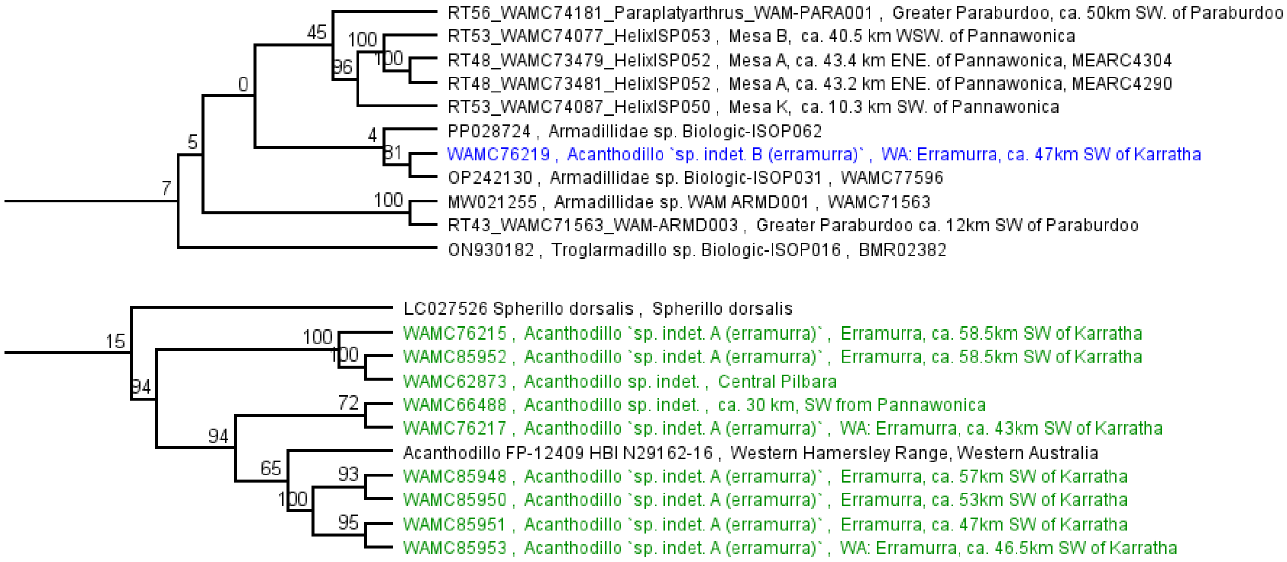

Figure 2a, b. Excerpts of maximum likelihood gene tree of mitochondrial COI sequences from Acanthodillo and related isopod genera. Tip labels indicate museum registration number, GenBank accession number, and/or Fauna Portal (FP) number. Query specimen is highlighted in blue text. Additional reference sequences generated for this report are highlighted in green text. Branch labels represent bootstrap values. Tree is for visualisation of molecular data only and does not represent a comprehensive phylogenetic analysis.

Urodacus sp. Eramurra (WAM T152484), male

Urodacus sp. SCO033 (WAM T123624), juvenile

Figure 3. Microscopic images of vouchers WAM T152484 (identified here as *Urodacus* sp. Eramurra) and WAM T123624 (identified here as *Urodacus* sp. SCO033).

Figure 4. Microscopic photograph of voucher WAM C76219 (identified here as *Acanthodillo* sp. indet. B).

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Appendix 1. Specimen information

Registration Number	Class	Order	Family	Genus	Species	Site	Latitude	Longitude	Field Number
WAM T152484	Arachnida	Pseudoscorpiones	Olpiidae	*Urodacus*	`sp. indet. (eramurra)`	WA: Eramurra, ca. 46.5 km SW. of Karratha, site 1320-SRE04-T2-WPp	20°50`38.10"S	116°23`54.10"E	PES: 31000
WAM C62646	Malacostraca	Isopoda	Armadillidae	*Acanthodillo*	sp. indet.	WA: Port Hedland, 26 km S	20°33`12.1"S	118°33`41.4"E	
WAM C62873	Malacostraca	Isopoda	Armadillidae	*Acanthodillo*	sp. indet.	WA: Central Pilbara	20°48`41.076"S	117°03`27.252"E	
WAM C62942	Malacostraca	Isopoda	Armadillidae	*Acanthodillo*	sp. indet.	WA: Karratha to Millstream-Chichester N. P.	20°59`07.08"S	116°52`51.978"E	
WAM C63174	Malacostraca	Isopoda	Armadillidae	*Acanthodillo*	sp. indet.	WA: Karratha, 30 km NE	20°39`30.15838"S	117°06`38.24699"E	
WAM C66488	Malacostraca	Isopoda	Armadillidae	*Acanthodillo*	sp. indet.	WA: ca. 30 km, SW from Pannawonica	21°47`07.841"S	116°05`57.618"E	
WAM C76215	Malacostraca	Isopoda	Armadillidae	*Acanthodillo*	`sp. indet. A (eramurra)`	WA: Eramurra, ca. 58.5km SW of Karratha	20°53`47.40"S	116°17`56.74"E	
WAM C76217	Malacostraca	Isopoda	Armadillidae	*Acanthodillo*	`sp. indet. A (eramurra)`	WA: Eramurra, ca. 43km SW of Karratha	20°50`35.84"S	116°25`57.87"E	
WAM C76218	Malacostraca	Isopoda	Armadillidae	*Acanthodillo*	`sp. indet. B (eramurra)`	WA: Eramurra, ca. 46.5km SW of Karratha	20°50`38.10"S	116°23`54.10"E	
WAM C76219	Malacostraca	Isopoda	Armadillidae	*Acanthodillo*	`sp. indet. B (eramurra)`	WA: Eramurra, ca. 47km SW of Karratha	20°50`48.04"S	116°23`27.63"E	
WAM C85948	Malacostraca	Isopoda	Armadillidae	*Acanthodillo*	`sp. indet. A (eramurra)`	WA: Eramurra, ca. 57km SW of Karratha	20°53`35.97"S	116°18`29.31"E	
WAM C85949	Malacostraca	Isopoda	Armadillidae	*Acanthodillo*	sp. indet.	WA: Cleaverville, 3.5 km S	20°40`37.34"S	117°02`14.431"E	
WAM C85950	Malacostraca	Isopoda	Armadillidae	*Acanthodillo*	`sp. indet. A (eramurra)`	WA: Eramurra, ca. 53km SW of Karratha	20°52`13.30"S	116°20`28.11"E	
WAM C85951	Malacostraca	Isopoda	Armadillidae	*Acanthodillo*	`sp. indet. A (eramurra)`	WA: Eramurra, ca. 47km SW of Karratha	20°50`48.04"S	116°23`27.63"E	
WAM C85952	Malacostraca	Isopoda	Armadillidae	*Acanthodillo*	`sp. indet. A (eramurra)`	WA: Eramurra, ca. 58.5km SW of Karratha	20°53`47.40"S	116°17`56.74"E	
WAM C85953	Malacostraca	Isopoda	Armadillidae	*Acanthodillo*	`sp. indet. A (eramurra)`	WA: Eramurra, ca. 46.5km SW of Karratha	20°50`38.10"S	116°23`54.10"E	
WAM T150888	Arachnida	Araneae	Halonoproctidae	*Conothele*	`MYG726`	WA; Erramurra, 53.5 km SW. of Karratha	20°53'55.87"S	116°21'36.93"E	