



Biologic

ENVIRONMENTAL
SURVEY

**MAC Phase 4
Aquatic Monitoring
Dry 2022 and Wet
2023**

Molecular
Systematics
Analysis

Report to BHP WAIO

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Glossary

| | |
|------------------------|--|
| Bootstrap | Value between 0 and 100 that indicates the robustness of the node in a phylogenetic tree. |
| COI | Cytochrome Oxidase subunit 1, a mitochondrial gene commonly used in phylogenetic studies and used as a DNA barcode to identify species. |
| GenBank | Annotated open access sequence database of all publicly available nucleotide sequences and their protein translations. |
| Monophyletic | A grouping of specimens that all share a common ancestor, inferred by sequence data. The sequences within the monophyletic group will all be more closely related to each other, relative to sequences outside of the monophyletic group. This grouping is often referred to as a lineage or clade and is graphically represented in phylogenies/trees by sharing a single node with a high bootstrap value. |
| OTU | Operational taxonomic unit – species-equivalent taxonomic unit based on COI or 12S cluster similarity. |
| Study Area | Survey Area sites, plus Reference sites (MACREF1, MACREF2, Weeli Wolli Spring, Bens Oasis, Skull Springs, and Running Waters). |
| Study sequences | Sequences derived from the specimens collected by Biologic for analysis in this report. Sequences not included in the Study sequences are referred to as non-Study sequences |
| Study specimens | Specimens collected by Biologic for analysis in this report. |
| Survey Area | Stretch of Marillana Creek that was the focus of the aquatic survey |

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1 Introduction

1.1 Background

BHP WAIO commissioned Biologic Environmental Survey Pty Ltd (Biologic) to undertake a molecular systematics analysis (DNA barcoding) of 37 specimens collected from Marillana Creek (the Survey Area) and associated Reference sites.

The Survey Area comprises sites from Marillana Creek. Reference sites were from MACREF1, MACREF2, Weeli Wolli Spring, Bens Oasis, Skull Springs, and Running Waters. Collectively, the Survey Area plus the Reference sites are referred to as the Study Area. Specimens were collected in September 2022. And March – May 2023.

Newly sampled specimens from the Study Area are collectively referred to as the Study specimens. Sequences derived from the Study specimens are collectively referred to as the Study sequences. Sequences not included in the Study sequences are referred to as non-Study sequences.

The aims and objectives of the molecular systematics analysis were to:

- Undertake DNA sequencing of 37 aquatic fauna specimens to obtain barcoding sequences of the mitochondrial gene Cytochrome Oxidase subunit 1 (COI; Hebert *et al.*, 2003b),
- Investigate the interspecific and intraspecific relationships among sequences of each higher taxonomic group (i.e. use the results of the DNA analysis to indicate how many different OTU/species are likely to occur within each genus or relevant higher taxon); and,
- Investigate the relationships among sequences from the Study Area and relevant previous sequences from the wider region, using available DNA databases (i.e. compare the results of the current analysis with accessible DNA databases to assess whether any of the species/ OTUs from the Study Area have been collected previously or more widely beyond the Study Area).

This document reports the methods and results of the molecular systematics analysis. All sequence data will be uploaded to GenBank (<https://www.ncbi.nlm.nih.gov/genbank/>) as per Biologic Molecular Systematics standard procedure.

2 Methods

2.1 Sub-sample Preparation

A total of 37 specimens collected from the Study Area by Biologic were selected for molecular systematics analysis (Table 2.1). The specimens were chosen based on their geographic spread across the Study Area to assist with understanding species distributions. Adequate redundancy in specimen selection was incorporated to account for any potential sequence generation failure. Specimens in good condition were chosen to increase their DNA extraction potential.

Where whole specimens were available, tissue preparation was undertaken by removing a leg or another body part less important for taxonomic identification, briefly drying off the ethanol, and placing the tissue in ATL buffer. In some instances, for very small and/or juvenile specimens, the entire animal was utilised. Again, these were briefly dried and placed in ATL buffer. Greatest care was taken to decontaminate all tools and equipment between samples, using bleach and repeated rinsing in deionised water. Table 2.1 provides details of the taxonomic orders chosen for molecular analysis. Further taxonomic clarification for each specimen included in the analysis can be found in Appendix A.

Table 2.1: Taxonomic groups from the Study Area included in the analysis, with a summary of PCR and sequencing success

| Class | Fail | Pass | Total |
|--------------|----------|-----------|-----------|
| Arachnida | 1 | 8 | 9 |
| Malacostraca | | 5 | 5 |
| Maxillipoda | 1 | 2 | 3 |
| Maxillopoda | | 3 | 3 |
| Ostracoda | 4 | 10 | 14 |
| Symphyla | | 3 | 3 |
| Total | 6 | 31 | 37 |

2.2 DNA Extraction, Amplification and Sequencing

DNA extraction and sequencing methods were in line with standard methods (e.g. Edgecombe *et al.*, 2019; Framenau *et al.*, 2018; Huey *et al.*, 2019; Perina *et al.*, 2018), as follows:

Subsampled tissue/specimen was placed directly into ATL buffer for extraction using the QIAGEN DNeasy Blood and Tissue extraction kit, and DNA extraction followed the manufacturer's protocols. DNA extractions were amplified by Polymerase Chain Reaction (PCR) using Folmer PCR primers (LCO1490, HCO2198; Folmer *et al.*, 1994) to assess the variability of COI. For some specimens that did not amplify using the Folmer primers, alternative primers amplifying the same part of COI were used, such as C1-J2329 and C1-J1718 (Perina *et al.*, 2018; Simon *et al.*, 1994).

The resulting PCR product was cleaned up and sequenced by the Australian Genomic Research Facility (AGRF) Perth node. Molecular laboratory workflows were managed using GENEIOUS Prime (Kearse *et al.*, 2012) with the Biocode plugin (<http://www.mooreabiocode.org>). Raw sequence data were edited and assembled in GENEIOUS, and final consensus sequences were then available for downstream analysis.

2.3 Specimen Selection for Comparative Analysis

DNA comparisons were typically conducted at the order level (Table 2.1). Comparative sequences were from GenBank (a publicly available DNA sequence database) and Biologic's unpublished DNA sequence libraries, using two separate methods.

- BLAST (Basic Local Alignment Search Tool): a method for rapidly searching a DNA sequence library to identify similar sequences. Sequences were searched using the "blastn" function, which returns similar matches.
- Taxonomic Curation: BLAST occasionally fails to identify sequences that could be considered useful for comparison, such as species that might be genetically distant, but are required to be included in the analysis for comparison. Taxonomically relevant specimens were identified using the available taxonomic classifications and identifications in those databases.

The final phylogenies and distance matrices in this report were pruned back to those sequences that can be provided to the Client, with any matches to sequences that cannot be provided to the Client discussed in the relevant sections.

2.4 Analysis and Interpretation of Alignments and Phylogenies

For each taxonomic group, the selected sequences were aligned using the MAFFT (Multiple Alignment using Fast Fourier Transform) algorithm (Kato *et al.*, 2002). Trees were

constructed on resulting alignments using the RaxML (Stamatakis, 2014) plugin in GENEIOUS Prime, using 1,000 bootstrap replicates and the GTR+G substitution model.

To delimit taxonomic units using molecular data, we integrated multiple lines of evidence, including:

- Genetic distance threshold method (~8% pairwise distances at COI, see below);
- Morphological identifications, where available;
- Geographic information; and
- Interpretation of phylogenetic topology.

Fauna-specific genetic distance thresholds for delimiting species and OTUs were used wherever possible, based on published literature and available previous reports. Where these thresholds were not available, the assessment used average divergence thresholds for related groups or higher taxa developed by broad-level studies (e.g. Hebert *et al.*, 2003a). In general, $\leq 8\%$ COI divergence is seen as appropriate to determine OTUs (Hebert *et al.*, 2003a), however, higher or lower divergences are sometimes justified depending on the organism studied. Unless otherwise stated, we considered sequences that exhibited COI divergences $\leq 8\%$ to belong to the same OTU.

The branching pattern and statistical robustness of the nodes (measured using bootstrap support) is also used to inform OTU delimitation. OTUs form monophyletic groups (or lineages), and so if an unknown sequence falls within a lineage comprised of other sequences that have already been identified as a single OTU or species, then that unknown sequence likely shares the same OTU/species as those sequences it is nested within (e.g. see Figure 2.1). Additionally, distinct OTUs typically have large internode distances separating OTUs, with short internode distances within the OTU/species.

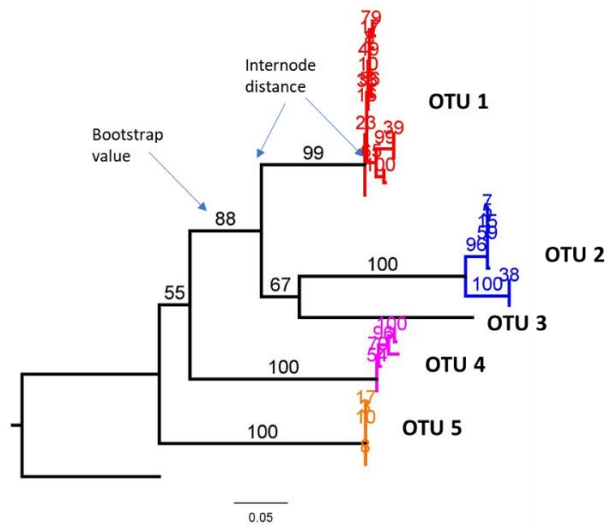


Figure 2.1: Example phylogeny showing delimited OTUs with internode distances and bootstrap values indicated

2.5 Constraints and Limitations

The analysis was constrained by the breadth of data available to undertake comparisons, the accessibility of pre-existing regional sequences, and the success rate of genetic sequencing, which can be affected by specimen collection, preservation, storage methods and contamination. Best practises were followed during specimen collection, preservation, and storage, prior to specimens arriving at Biologic’s laboratories. All care was taken to ensure that the risks of laboratory contamination, data handling issues, and specimen management issues were minimised within Biologic’s laboratories throughout the subsampling, processing and genetic analysis.

The databases used for regional comparisons included GenBank and Biologic’s sequence libraries. While these sequence databases, in combination, comprise a large portion of the subterranean fauna genetic work undertaken in the Pilbara region, it is acknowledged that there may be many other relevant sequences from third party project areas nearby or elsewhere in the region that were not available for comparison at the time of the study. GenBank is dynamic database, and the addition of new sequences and altered taxonomic classifications could not be included into this report if they occurred after 20th August 2023.

DNA barcoding using the mitochondrial gene COI, while useful for explaining genetic differences between closely related or moderately related species, is limited in its ability to resolve deeper phylogenetic relationships among taxa at higher taxonomic levels (e.g. genus, family, order). In the current study, phylogenetic relationships among species/OTUs >25% COI divergence are treated with caution. If further resolution of deeper phylogeny is important for project goals, this could be investigated using a multiple gene approach.

3 Results and Discussion

A total of 37 specimens were processed for sequencing by Biologic (Table 2.1). Sequences were successfully derived for 35 of these specimens (94.6% of specimens). Of these 35 sequences, four did not produce a high-quality sequence (less than 80% of untrimmed bases in the sequence were of high quality) or were high quality sequences of an organism that was not the target organism (likely contamination). This left 31 high quality sequences for analysis (88.6% of sequences). The orders of the sequences are tabulated in Table 3.1.

In total, 22 OTUs have been designated to specimens from the Study Area, five of these being specific to this study (Table 3.1). The results of each taxonomic group's analysis are described in the subsequent sections.

Table 3.1: Summary of species and OTUs recovered from samples successfully sequenced in this study, organised by taxon

| Taxa | Number of Study specimens | Matches non-Study sequences | Survey Area sites | Reference sites | Linear range / Distribution |
|---|---------------------------|-----------------------------|-------------------|-----------------|-----------------------------|
| Arachnida | | | | | |
| Trombidiformes | | | | | |
| Anisitsiellidae | | | | | |
| <i>Rutacarus</i> `sp. Biologic-ACAR005` | 1 | yes | ✘ | ✓ | 2.0 km |
| <i>Rutacarus</i> `sp. Biologic-ACAR007` | 1 | yes | ✓ | ✘ | 42.5 km |
| <i>Rutacarus</i> `sp. Biologic-ACAR022` | 1 | no | ✓ | ✘ | singleton |
| Hydryphantidae | | | | | |
| <i>Wandesia</i> `sp. Biologic-ACAR008` | 1 | yes | ✓ | ✘ | 168.3 km |
| <i>Wandesia</i> `sp. Biologic-ACAR009` | 2 | yes | ✓ | ✘ | 98.9 km |
| Mideopsidae | | | | | |
| <i>Guineaxonopsis</i> `sp. Biologic-ACAR011` | 1 | yes | ✓ | ✘ | 275.2 km |
| Piersigiidae | | | | | |
| <i>Stygalimnochaes</i> `sp. Biologic-ACAR026` | 1 | no | ✘ | ✓ | singleton |
| Malacostraca | | | | | |
| Amphipoda | | | | | |
| Paramelitidae | | | | | |
| <i>Chydaekata</i> `sp. E TLF-2008` | 1 | yes | ✘ | ✓ | 49.0 km |
| Paramelitidae `sp. Biologic-AMPH045` | 1 | yes | ✘ | ✓ | 27.0 km |
| Bathynellacea | | | | | |
| Parabathynellidae | | | | | |

| Taxa | Number of Study specimens | Matches non-Study sequences | Survey Area sites | Reference sites | Linear range / Distribution |
|--|---------------------------|-----------------------------|-------------------|-----------------|-----------------------------|
| <i>Atopobathynella` sp. Biologic-PBAT019`</i> | 3 | yes | ✓ | ✓ | 79.6 km |
| Maxillopoda | | | | | |
| Harpactiocioda | | | | | |
| Canthocamptidae | | | | | |
| <i>Canthocamptidae` sp. Biologic-HARP059`</i> | 3 | no | ✓ | ✗ | 1.0 km |
| Parastenocarididae | | | | | |
| <i>Parastenocaris` sp. Biologic-HARP022`</i> | 1 | yes | ✗ | ✓ | 325.4 km |
| Phyllognathopodidae | | | | | |
| <i>nr Phyllognathopus` sp. Biologic-HARP058`</i> | 1 | no | ✓ | ✗ | singleton |
| Ostracoda | | | | | |
| Podocopida | | | | | |
| Candonidae | | | | | |
| <i>Candonopsis` sp. Biologic-OSTR009`</i> | 1 | yes | ✗ | ✓ | 506.6 km |
| <i>Candonopsis` sp. Biologic-OSTR044`</i> | 1 | yes | ✓ | ✗ | 171.5 km |
| <i>Notacandona modesta</i> | 1 | yes | ✗ | ✓ | 2.7 km |
| Cyprididae | | | | | |
| <i>Cypretta` sp. Biologic-OSTR029`</i> | 3 | yes | ✗ | ✓ | 506.6 km |
| <i>Cypridopsis` sp. Biologic-OSTR011`</i> | 2 | yes | ✗ | ✓ | Global |
| <i>Ilyodromus` sp. Biologic-OSTR014`</i> | 1 | yes | ✗ | ✓ | 504.7 km |
| <i>Ilyodromus` sp. Biologic-OSTR036`</i> | 1 | yes | ✓ | ✗ | 314.7 km |
| Symphyla | | | | | |
| Cephalostigmata | | | | | |
| Scutigereididae | | | | | |
| <i>Hanseniella` sp. Biologic-SYMP055`</i> | 1 | yes | ✓ | ✗ | single site |
| <i>Hanseniella` sp. Biologic-SYMP069`</i> | 2 | no | ✓ | ✓ | 3.7 km |

3.1 Trombidiformes (mites)

Eight mite sequences were delimited to form seven OTUs from four families: Anisitsiellidae, Hydryphantidae, Mideopsidae, and Piersigiidae (Figure 3.1). All OTUs were more than 8.7% divergent from all other sequences in the analysis and had intraspecific divergences of less than 1.7% (Table 3.2). *Rutacarus` sp. Biologic-ACAR022`* and *Stygolimnochaes` sp. Biologic-ACAR026`* were singletons and newly sequenced OTUs, while all other sequences matched previously sequenced OTUs. These OTUs had linear ranges between 2.0 km (*Rutacarus` sp. Biologic-ACAR005`*) and 275.2 km (*Guineaxonopsis` sp. Biologic-ACAR011`*) (Table 3.1).

Rutacarus `sp. Biologic-ACAR005` and *Stygolimnochaes* `sp. Biologic-ACAR026` were only found in Reference sites, while all other mite OTUs were restricted to Survey Area sites.

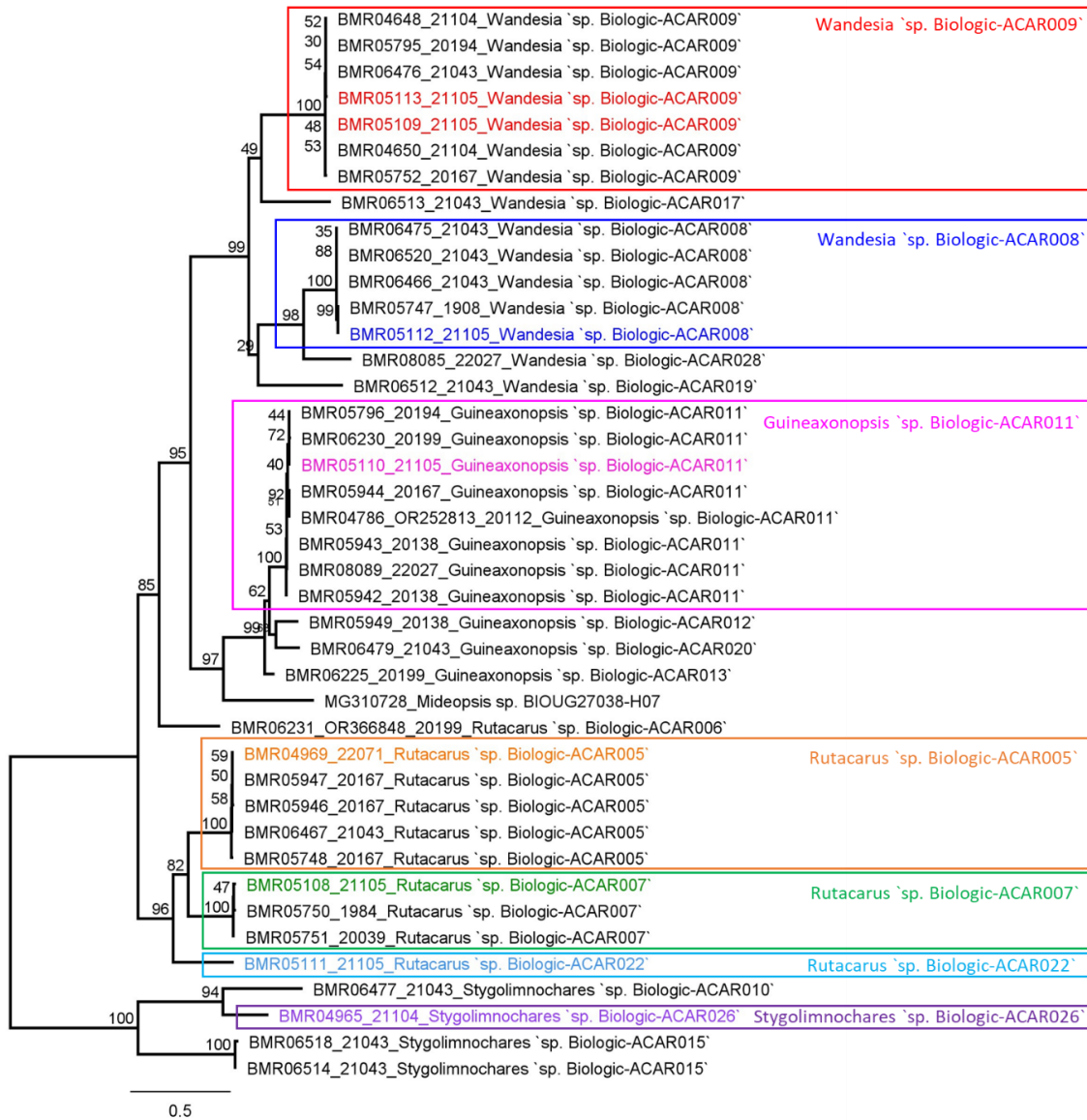


Figure 3.1: Phylogeny for the Trombidiformes dataset, with bootstrap values

Table 3.2: Pairwise distances (%) for the mite dataset

| COI Pairwise Distances (%) | BMR04648 | BMR05795 | BMR04650 | BMR05109 | BMR05113 | BMR06476 | BMR05752 | BMR06513 | BMR05747 | BMR05112 | BMR06466 | BMR06475 | BMR06520 | BMR08085 | BMR06512 | BMR04786 | BMR05944 | BMR05942 | BMR08089 | BMR05943 | BMR05796 | BMR06230 | BMR05110 | BMR06225 | BMR06479 | BMR05949 | MG310728 | BMR05748 | BMR05946 | BMR04969 | BMR05947 | BMR06467 | BMR05750 | BMR05751 | BMR05108 | BMR05111 | BMR06231 | BMR06477 | BMR04965 | BMR06514 | BMR06518 |
|---|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|
| BMR04648_21104_Wandesia 'sp. Biologic-ACAR009' | 0.0 | 0.2 | 0.2 | 0.2 | 0.0 | 0.4 | 16.6 | 17.8 | 17.8 | 17.7 | 17.7 | 17.7 | 19.3 | 19.7 | 21.1 | 20.9 | 21.1 | 20.8 | 20.3 | 20.8 | 20.9 | 20.9 | 20.1 | 21.5 | 22.1 | 20.0 | 21.5 | 21.5 | 21.6 | 21.7 | 21.9 | 21.6 | 22.1 | 22.2 | 21.3 | 21.9 | 29.8 | 30.1 | 27.7 | 27.7 | |
| BMR05795_20194_Wandesia 'sp. Biologic-ACAR009' | 0.0 | 0.2 | 0.2 | 0.2 | 0.0 | 0.4 | 16.6 | 17.8 | 17.8 | 17.7 | 17.7 | 17.7 | 19.3 | 19.7 | 21.1 | 20.9 | 21.1 | 20.8 | 20.3 | 20.8 | 20.9 | 20.9 | 20.1 | 21.5 | 22.1 | 20.0 | 21.5 | 21.5 | 21.6 | 21.7 | 21.9 | 21.6 | 22.1 | 22.2 | 21.3 | 21.9 | 29.8 | 30.1 | 27.7 | 27.7 | |
| BMR04650_21104_Wandesia 'sp. Biologic-ACAR009' | 0.2 | 0.2 | 0.0 | 0.3 | 0.2 | 0.2 | 16.7 | 18.0 | 18.0 | 17.8 | 17.8 | 17.8 | 19.2 | 19.5 | 20.9 | 20.7 | 20.8 | 20.6 | 20.1 | 20.6 | 20.7 | 20.7 | 19.9 | 21.3 | 21.9 | 19.9 | 21.7 | 21.6 | 21.8 | 21.8 | 22.0 | 21.9 | 22.3 | 22.4 | 21.5 | 22.1 | 30.0 | 30.3 | 27.6 | 27.6 | |
| BMR05109_21105_Wandesia 'sp. Biologic-ACAR009' | 0.2 | 0.2 | 0.0 | 0.3 | 0.2 | 0.2 | 16.7 | 18.0 | 18.1 | 17.8 | 17.8 | 17.8 | 19.2 | 19.5 | 20.9 | 20.7 | 20.8 | 20.6 | 20.0 | 20.6 | 20.7 | 20.7 | 19.9 | 21.3 | 21.9 | 19.9 | 21.7 | 21.6 | 21.7 | 21.8 | 22.0 | 21.7 | 22.2 | 22.3 | 22.4 | 21.6 | 22.1 | 29.9 | 30.2 | 27.5 | 27.5 |
| BMR05113_21105_Wandesia 'sp. Biologic-ACAR009' | 0.2 | 0.2 | 0.3 | 0.3 | 0.2 | 0.5 | 16.6 | 18.0 | 18.1 | 17.8 | 17.8 | 17.8 | 19.5 | 19.5 | 21.4 | 21.0 | 21.2 | 21.0 | 20.5 | 20.9 | 21.0 | 21.0 | 20.2 | 21.7 | 22.0 | 19.8 | 21.4 | 21.3 | 21.4 | 21.5 | 21.7 | 21.8 | 22.3 | 22.4 | 21.3 | 21.6 | 29.6 | 29.9 | 27.5 | 27.5 | |
| BMR06476_21043_Wandesia 'sp. Biologic-ACAR009' | 0.0 | 0.0 | 0.2 | 0.2 | 0.2 | 0.5 | 15.9 | 17.4 | 17.6 | 17.0 | 17.0 | 17.0 | 19.4 | 20.0 | 21.1 | 20.7 | 21.0 | 20.8 | 20.2 | 20.8 | 20.9 | 20.9 | 21.6 | 22.7 | 23.1 | 21.2 | 22.6 | 22.3 | 22.5 | 22.6 | 22.9 | 21.6 | 22.0 | 22.1 | 21.8 | 21.9 | 31.3 | 32.4 | 30.4 | 30.0 | |
| BMR05752_20167_Wandesia 'sp. Biologic-ACAR009' | 0.4 | 0.4 | 0.2 | 0.2 | 0.5 | 0.5 | 16.7 | 18.2 | 18.2 | 18.0 | 18.0 | 18.0 | 19.4 | 19.8 | 20.8 | 20.6 | 20.7 | 20.5 | 20.2 | 20.9 | 20.9 | 20.9 | 20.2 | 21.5 | 21.8 | 20.1 | 21.5 | 21.5 | 21.7 | 21.7 | 22.0 | 21.7 | 22.2 | 22.3 | 21.4 | 22.4 | 30.2 | 30.5 | 27.5 | 27.5 | |
| BMR06513_21043_Wandesia 'sp. Biologic-ACAR017' | 16.6 | 16.6 | 16.7 | 16.7 | 16.6 | 15.9 | 16.7 | 18.9 | 18.9 | 18.9 | 18.9 | 18.9 | 18.4 | 19.5 | 21.6 | 21.2 | 20.8 | 20.6 | 20.8 | 21.3 | 21.5 | 21.5 | 21.9 | 22.7 | 22.0 | 23.5 | 21.8 | 22.1 | 21.9 | 22.0 | 22.0 | 22.3 | 22.7 | 22.6 | 22.8 | 22.1 | 26.9 | 30.3 | 28.5 | 28.8 | |
| BMR05747_1908_Wandesia 'sp. Biologic-ACAR008' | 17.8 | 17.8 | 18.0 | 18.0 | 18.0 | 17.4 | 18.2 | 18.9 | 0.0 | 0.8 | 0.8 | 0.8 | 13.4 | 18.8 | 20.7 | 20.4 | 20.6 | 20.8 | 20.3 | 20.8 | 20.9 | 20.7 | 19.3 | 20.1 | 20.3 | 21.2 | 23.4 | 23.0 | 23.1 | 23.2 | 23.4 | 23.4 | 24.0 | 21.6 | 20.8 | 26.8 | 30.9 | 28.9 | 29.1 | | |
| BMR05112_21105_Wandesia 'sp. Biologic-ACAR008' | 17.8 | 17.8 | 18.0 | 18.1 | 18.1 | 17.6 | 18.2 | 18.9 | 0.0 | 0.8 | 0.8 | 0.8 | 13.4 | 18.9 | 20.7 | 20.5 | 20.8 | 21.0 | 20.5 | 20.9 | 21.0 | 20.8 | 19.5 | 20.1 | 20.3 | 21.4 | 23.5 | 23.1 | 23.3 | 23.3 | 23.5 | 23.6 | 23.6 | 24.1 | 21.6 | 20.8 | 26.9 | 31.0 | 29.0 | 29.2 | |
| BMR06466_21043_Wandesia 'sp. Biologic-ACAR008' | 17.7 | 17.7 | 17.8 | 17.8 | 17.8 | 17.0 | 18.0 | 18.9 | 0.8 | 0.8 | 0.0 | 0.0 | 12.8 | 18.5 | 20.7 | 20.1 | 20.6 | 20.8 | 20.3 | 20.5 | 20.6 | 20.4 | 19.3 | 19.8 | 19.7 | 21.4 | 23.1 | 22.7 | 22.8 | 22.9 | 23.1 | 23.6 | 23.6 | 24.2 | 21.3 | 21.0 | 26.6 | 30.3 | 28.6 | 28.8 | |
| BMR06475_21043_Wandesia 'sp. Biologic-ACAR008' | 17.7 | 17.7 | 17.8 | 17.8 | 17.8 | 17.0 | 18.0 | 18.9 | 0.8 | 0.8 | 0.0 | 0.0 | 12.8 | 18.5 | 20.7 | 20.1 | 20.6 | 20.8 | 20.3 | 20.5 | 20.6 | 20.4 | 19.3 | 19.8 | 19.7 | 21.4 | 23.1 | 22.7 | 22.8 | 22.9 | 23.1 | 23.6 | 23.6 | 24.2 | 21.3 | 21.0 | 26.6 | 30.3 | 28.6 | 28.8 | |
| BMR06520_21043_Wandesia 'sp. Biologic-ACAR008' | 17.7 | 17.7 | 17.8 | 17.8 | 17.8 | 17.0 | 18.0 | 18.9 | 0.8 | 0.8 | 0.0 | 0.0 | 12.8 | 18.5 | 20.7 | 20.1 | 20.6 | 20.8 | 20.3 | 20.5 | 20.6 | 20.4 | 19.3 | 19.8 | 19.7 | 21.4 | 23.1 | 22.7 | 22.8 | 22.9 | 23.1 | 23.6 | 23.6 | 24.2 | 21.3 | 21.0 | 26.6 | 30.3 | 28.6 | 28.8 | |
| BMR08085_22027_Wandesia 'sp. Biologic-ACAR028' | 19.3 | 19.3 | 19.2 | 19.2 | 19.5 | 19.4 | 19.4 | 18.4 | 13.4 | 13.4 | 12.8 | 12.8 | 12.8 | 18.5 | 21.8 | 21.3 | 21.3 | 21.5 | 21.2 | 21.4 | 21.5 | 21.3 | 21.2 | 21.2 | 20.3 | 22.2 | 24.6 | 24.5 | 24.4 | 24.4 | 24.5 | 23.2 | 22.7 | 23.3 | 23.3 | 24.7 | 30.4 | 30.6 | 30.8 | 31.1 | |
| BMR06512_21043_Wandesia 'sp. Biologic-ACAR019' | 19.7 | 19.7 | 19.5 | 19.5 | 19.5 | 20.0 | 19.8 | 19.5 | 18.8 | 18.9 | 18.5 | 18.5 | 18.5 | 22.9 | 22.4 | 22.6 | 22.8 | 22.7 | 21.7 | 21.7 | 21.7 | 21.7 | 21.8 | 21.8 | 21.7 | 21.4 | 21.7 | 24.2 | 24.6 | 24.4 | 24.5 | 24.4 | 24.2 | 23.8 | 24.3 | 25.2 | 21.2 | 31.0 | 31.6 | 29.3 | 30.0 |
| BMR04786_OR252813_20112_Guineaxonopsis 'sp. Biologic-ACAR011' | 21.1 | 21.1 | 20.9 | 20.9 | 21.4 | 21.1 | 20.8 | 21.6 | 20.7 | 20.7 | 20.7 | 20.7 | 21.8 | 22.9 | 0.0 | 0.9 | 0.7 | 1.0 | 0.8 | 1.1 | 0.9 | 9.7 | 11.9 | 10.7 | 20.0 | 21.9 | 22.0 | 21.8 | 21.9 | 21.5 | 22.8 | 22.7 | 22.8 | 20.5 | 19.6 | 28.1 | 30.6 | 30.1 | 29.2 | | |
| BMR05944_20167_Guineaxonopsis 'sp. Biologic-ACAR011' | 20.9 | 20.9 | 20.7 | 20.7 | 21.0 | 20.7 | 20.6 | 21.2 | 20.4 | 20.5 | 20.1 | 20.1 | 20.1 | 21.3 | 22.4 | 0.0 | 0.9 | 0.7 | 1.0 | 1.3 | 1.5 | 1.4 | 9.4 | 11.3 | 10.3 | 18.4 | 21.5 | 21.6 | 21.4 | 21.5 | 21.2 | 22.6 | 22.5 | 22.6 | 21.1 | 19.4 | 26.8 | 28.7 | 29.3 | 29.0 | |
| BMR05942_20138_Guineaxonopsis 'sp. Biologic-ACAR011' | 21.1 | 21.1 | 20.8 | 20.8 | 21.2 | 21.0 | 20.7 | 20.8 | 20.6 | 20.8 | 20.6 | 20.6 | 20.6 | 21.3 | 22.6 | 0.9 | 0.9 | 0.2 | 1.0 | 1.2 | 1.6 | 1.3 | 8.8 | 11.3 | 11.0 | 19.3 | 21.1 | 21.2 | 21.0 | 21.1 | 20.7 | 21.4 | 21.2 | 21.4 | 19.9 | 19.3 | 27.2 | 29.0 | 30.3 | 29.4 | |
| BMR08089_22027_Guineaxonopsis 'sp. Biologic-ACAR011' | 20.8 | 20.8 | 20.6 | 20.6 | 21.0 | 20.8 | 20.5 | 20.6 | 20.8 | 21.0 | 20.8 | 20.8 | 20.8 | 21.5 | 22.8 | 0.7 | 0.7 | 0.2 | 0.8 | 1.0 | 1.3 | 1.1 | 9.1 | 11.5 | 11.2 | 19.3 | 21.4 | 21.5 | 21.2 | 21.4 | 21.0 | 21.6 | 21.5 | 21.6 | 20.1 | 19.5 | 27.4 | 29.2 | 30.5 | 29.7 | |
| BMR05943_20138_Guineaxonopsis 'sp. Biologic-ACAR011' | 20.3 | 20.3 | 20.1 | 20.0 | 20.5 | 20.2 | 20.2 | 20.8 | 20.3 | 20.5 | 20.3 | 20.3 | 20.3 | 21.2 | 22.7 | 1.0 | 1.0 | 1.0 | 0.8 | 1.0 | 1.2 | 1.0 | 9.4 | 11.6 | 11.3 | 19.1 | 21.5 | 21.6 | 21.4 | 21.5 | 21.1 | 21.6 | 21.5 | 21.6 | 20.2 | 19.3 | 27.0 | 29.3 | 30.3 | 29.4 | |
| BMR05796_20194_Guineaxonopsis 'sp. Biologic-ACAR011' | 20.8 | 20.8 | 20.6 | 20.6 | 20.9 | 20.8 | 20.9 | 21.3 | 20.8 | 20.9 | 20.5 | 20.5 | 20.5 | 21.4 | 21.7 | 0.8 | 1.3 | 1.2 | 1.0 | 1.0 | 0.4 | 0.4 | 9.3 | 10.6 | 10.2 | 17.4 | 21.3 | 21.4 | 21.2 | 21.3 | 21.0 | 22.6 | 22.5 | 22.6 | 21.5 | 19.7 | 27.0 | 28.7 | 29.4 | 29.1 | |
| BMR06230_20199_Guineaxonopsis 'sp. Biologic-ACAR011' | 20.9 | 20.9 | 20.7 | 20.7 | 21.0 | 20.9 | 20.9 | 21.5 | 20.9 | 21.0 | 20.6 | 20.6 | 20.6 | 21.5 | 21.7 | 1.1 | 1.5 | 1.6 | 1.3 | 1.2 | 0.4 | 0.5 | 9.4 | 10.6 | 10.3 | 17.5 | 21.4 | 21.4 | 21.3 | 21.4 | 21.1 | 22.8 | 22.7 | 22.8 | 21.6 | 19.9 | 27.1 | 28.9 | 29.5 | 29.2 | |
| BMR05110_21105_Guineaxonopsis 'sp. Biologic-ACAR011' | 20.9 | 20.9 | 20.7 | 20.7 | 21.0 | 20.9 | 20.9 | 21.5 | 20.7 | 20.8 | 20.4 | 20.4 | 20.4 | 21.3 | 21.8 | 0.9 | 1.4 | 1.3 | 1.1 | 1.0 | 0.4 | 0.5 | 9.6 | 10.8 | 10.4 | 17.2 | 21.5 | 21.6 | 21.4 | 21.5 | 21.2 | 22.4 | 22.3 | 22.4 | 21.6 | 19.9 | 26.9 | 28.7 | 29.5 | 29.2 | |
| BMR06225_20199_Guineaxonopsis 'sp. Biologic-ACAR013' | 20.1 | 20.1 | 19.9 | 19.9 | 20.2 | 21.6 | 20.2 | 21.9 | 19.3 | 19.5 | 19.3 | 19.3 | 19.3 | 21.2 | 21.8 | 9.7 | 9.4 | 8.8 | 9.1 | 9.4 | 9.3 | 9.4 | 9.6 | 9.4 | 11.2 | 18.4 | 22.4 | 22.3 | 22.2 | 22.3 | 22.5 | 22.4 | 22.3 | 22.8 | 20.2 | 19.9 | 27.5 | 27.2 | 29.5 | 29.5 | |
| BMR06479_21043_Guineaxonopsis 'sp. Biologic-ACAR020' | 21.5 | 21.5 | 21.3 | 21.4 | 21.7 | 22.7 | 21.5 | 22.7 | 20.1 | 20.1 | 19.8 | 19.8 | 19.8 | 21.2 | 21.7 | 11.9 | 11.3 | 11.3 | 11.5 | 11.6 | 10.6 | 10.6 | 10.8 | 9.4 | 11.0 | 18.7 | 20.9 | 20.8 | 20.7 | 20.9 | 22.4 | 22.3 | 22.8 | 20.8 | 20.5 | 28.3 | 27.4 | 29.8 | 29.8 | | |
| BMR05949_20138_Guineaxonopsis 'sp. Biologic-ACAR012' | 22.1 | 22.1 | 21.9 | 22.0 | 22.0 | 23.1 | 21.8 | 22.0 | 20.3 | 20.3 | 19.7 | 19.7 | 19.7 | 20.3 | 21.4 | 10.7 | 10.3 | 11.0 | 11.2 | 11.3 | 10.2 | 10.3 | 10.4 | 11.2 | 11.0 | 18.5 | 20.7 | 20.9 | 20.7 | 20.8 | 20.7 | 24.2 | 23.7 | 24.2 | 20.7 | 20.0 | 27.1 | 27.6 | 27.4 | 27.4 | |
| MG310728_Mideopsis sp. BIOUG27038-H07 | 20.0 | 20.0 | 19.9 | 19.8 | 19.8 | 21.2 | 20.1 | 23.5 | 21.2 | 21.4 | 21.4 | 21.4 | 21.4 | 22.2 | 21.7 | 20.0 | 18.4 | 19.3 | 19.3 | 19.1 | 17.4 | 17.5 | 17.2 | 18.4 | 18.7 | 18.5 | 21.7 | 21.4 | 21.5 | 21.6 | 21.8 | 23.2 | 23.1 | 23.2 | 22.2 | 21.2</ | | | | | |

3.2 Amphipoda

Two amphipod sequences matched two previously sequenced paramelitid OTUs: *Chydaekata`sp. E TLF-2008`* and *Paramelitidae`sp. Biologic-AMPH045`* (Figure 3.2). These OTUs were both restricted to the Reference sites in the Study sequences.

Chydaekata`sp. E TLF-2008` was first sequenced by Finston *et al.* (2007), and is commonly found in Weeli Wollie and Marilana Creeks. It is more than 13.9% divergent from all other sequences in the analysis and has an intraspecific divergence of less than 4.5% (Table 3.3).

Paramelitidae`sp. Biologic-AMPH045` was closely related to *Paramelitidae`sp. Biologic-AMPH019`* and *Paramelitidae`sp. Biologic-AMPH020`* (7.9%-10.6%) with an intraspecific genetic distance of less than 1.8% (Table 3.3). This OTU has a linear distance of 27.0 km (Table 3.1).

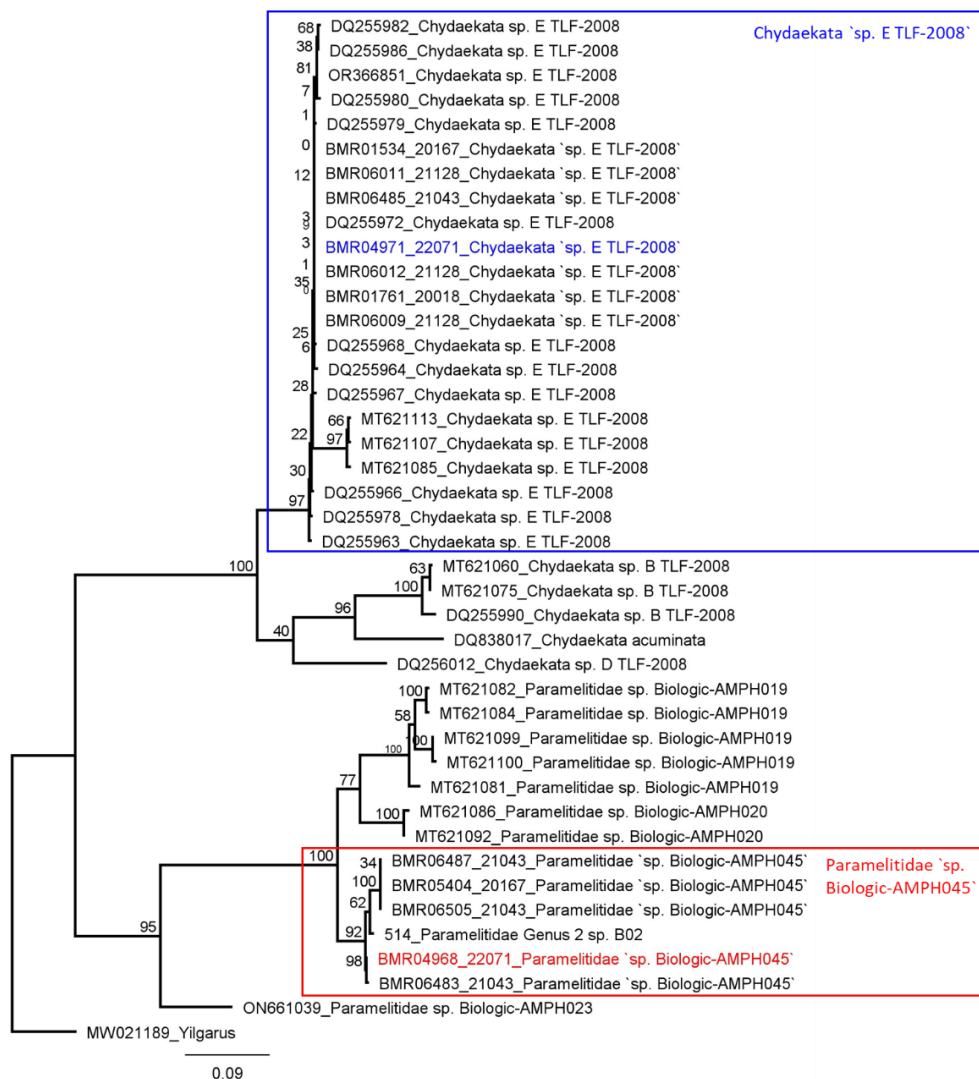


Figure 3.2: Phylogeny for the Amphipoda dataset, with bootstrap values

Table 3.3: Pairwise distances (%) for the Amphipoda dataset

| COI Pairwise Distances (%) | 514 | BMR06483 | BMR04968 | BMR05404 | BMR06487 | BMR06505 | MT621086 | MT621092 | MT621081 | MT621082 | MT621084 | MT621099 | MT621100 | ON661039 | MW021189 | BMR01534 | BMR01761 | BMR06009 | BMR06011 | BMR06012 | BMR06485 | DQ255972 | BMR04971 | DQ255968 | DQ255979 | DQ255964 | DQ255982 | DQ255986 | OR366851 | DQ255980 | DQ255967 | DQ255963 | DQ255978 | DQ255966 | MT621085 | MT621107 | MT621113 | DQ256012 | DQ255990 | MT621060 | MT621075 | DQ838017 | | | | |
|---|------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|------|------|------|------|
| 514_Paramelitidae Genus 2 sp. B02 | 0.9 | 0.8 | 1.2 | 1.2 | 1.2 | 8.5 | 8.5 | 9.3 | 8.8 | 8.8 | 9.9 | 10.2 | 17.2 | 19.2 | 23.6 | 23.6 | 23.6 | 23.6 | 23.6 | 23.6 | 23.6 | 23.6 | 23.4 | 23.4 | 23.6 | 23.3 | 23.1 | 23.3 | 23.3 | 23.4 | 23.4 | 23.6 | 23.4 | 24.0 | 24.0 | 23.9 | 21.3 | 23.6 | 24.1 | 23.9 | 24.8 | | | | | |
| BMR06483_21043_Paramelitidae 'sp. Biologic-AMPH045' | 0.9 | 0.2 | 1.7 | 1.7 | 1.7 | 8.4 | 8.1 | 8.8 | 8.7 | 8.7 | 9.7 | 10.0 | 17.4 | 19.3 | 23.9 | 23.9 | 23.9 | 23.9 | 23.9 | 23.9 | 23.9 | 23.7 | 23.7 | 23.9 | 23.6 | 23.4 | 23.6 | 23.6 | 23.7 | 23.7 | 23.9 | 23.7 | 24.3 | 24.3 | 24.2 | 21.5 | 24.2 | 24.7 | 24.5 | 25.3 | | | | | | |
| BMR04968_22071_Paramelitidae 'sp. Biologic-AMPH045' | 0.8 | 0.2 | 1.5 | 1.5 | 1.5 | 8.2 | 7.9 | 9.0 | 8.5 | 8.5 | 9.6 | 9.9 | 17.2 | 19.2 | 23.8 | 23.7 | 23.7 | 23.7 | 23.7 | 23.7 | 23.7 | 23.6 | 23.6 | 23.6 | 23.4 | 23.6 | 23.3 | 23.1 | 23.3 | 23.3 | 23.4 | 23.4 | 23.6 | 23.6 | 24.0 | 24.0 | 23.9 | 21.2 | 23.6 | 24.1 | 23.9 | 25.0 | | | | |
| BMR05404_20167_Paramelitidae 'sp. Biologic-AMPH045' | 1.2 | 1.7 | 1.5 | 0.0 | 0.0 | 9.0 | 9.0 | 9.7 | 9.3 | 9.3 | 10.3 | 10.6 | 17.7 | 19.8 | 23.6 | 23.6 | 23.6 | 23.6 | 23.6 | 23.6 | 23.6 | 23.6 | 23.6 | 23.4 | 23.4 | 23.6 | 23.3 | 23.1 | 23.3 | 23.3 | 23.4 | 23.4 | 23.6 | 23.4 | 24.0 | 24.0 | 23.9 | 21.2 | 23.6 | 24.1 | 23.9 | 25.0 | | | | |
| BMR06487_21043_Paramelitidae 'sp. Biologic-AMPH045' | 1.2 | 1.7 | 1.5 | 0.0 | 0.0 | 9.0 | 9.0 | 9.7 | 9.3 | 9.3 | 10.3 | 10.6 | 17.7 | 19.8 | 23.6 | 23.6 | 23.6 | 23.6 | 23.6 | 23.6 | 23.6 | 23.6 | 23.4 | 23.4 | 23.6 | 23.3 | 23.1 | 23.3 | 23.3 | 23.4 | 23.4 | 23.6 | 23.4 | 24.0 | 24.0 | 23.9 | 21.2 | 23.6 | 24.1 | 23.9 | 25.0 | | | | | |
| BMR06505_21043_Paramelitidae 'sp. Biologic-AMPH045' | 1.2 | 1.7 | 1.5 | 0.0 | 0.0 | 9.0 | 9.0 | 9.7 | 9.3 | 9.3 | 10.3 | 10.6 | 17.7 | 19.8 | 23.6 | 23.6 | 23.6 | 23.6 | 23.6 | 23.6 | 23.6 | 23.6 | 23.4 | 23.4 | 23.6 | 23.3 | 23.1 | 23.3 | 23.3 | 23.4 | 23.4 | 23.6 | 23.4 | 24.0 | 24.0 | 23.9 | 21.2 | 23.6 | 24.1 | 23.9 | 25.0 | | | | | |
| MT621086_Paramelitidae sp. Biologic-AMPH020 | 8.5 | 8.4 | 8.2 | 9.0 | 9.0 | 9.0 | 0.5 | 8.5 | 8.5 | 8.5 | 9.0 | 9.3 | 18.3 | 18.7 | 24.9 | 24.8 | 24.8 | 24.8 | 24.8 | 24.8 | 24.8 | 24.8 | 24.8 | 24.8 | 24.5 | 24.3 | 24.5 | 24.5 | 24.6 | 24.8 | 24.9 | 24.6 | 24.2 | 24.3 | 24.5 | 22.6 | 25.1 | 25.6 | 25.7 | 25.3 | | | | | | |
| MT621092_Paramelitidae sp. Biologic-AMPH020 | 8.5 | 8.1 | 7.9 | 9.0 | 9.0 | 9.0 | 0.5 | 8.4 | 8.2 | 8.8 | 9.1 | 18.4 | 18.7 | 25.2 | 25.1 | 25.1 | 25.1 | 25.1 | 25.1 | 25.1 | 25.1 | 25.1 | 25.1 | 25.2 | 25.1 | 25.1 | 24.8 | 24.6 | 24.8 | 24.8 | 24.9 | 25.1 | 25.2 | 24.9 | 24.5 | 24.6 | 24.8 | 22.9 | 25.4 | 25.7 | 25.9 | 25.4 | | | | |
| MT621081_Paramelitidae sp. Biologic-AMPH019 | 9.3 | 8.8 | 9.0 | 9.7 | 9.7 | 9.7 | 8.5 | 8.4 | 2.9 | 2.9 | 3.2 | 3.5 | 18.9 | 20.9 | 25.6 | 25.7 | 25.7 | 25.7 | 25.7 | 25.7 | 25.7 | 25.7 | 25.7 | 25.7 | 25.8 | 25.5 | 25.7 | 25.4 | 25.2 | 25.4 | 25.2 | 25.5 | 25.5 | 25.7 | 25.5 | 25.7 | 25.5 | 25.7 | 24.1 | 26.2 | 26.2 | 26.3 | 26.0 | | | |
| MT621082_Paramelitidae sp. Biologic-AMPH019 | 8.8 | 8.7 | 8.5 | 9.3 | 9.3 | 9.3 | 8.5 | 8.2 | 2.9 | 2.9 | 3.0 | 3.3 | 18.4 | 20.4 | 25.5 | 25.5 | 25.5 | 25.5 | 25.5 | 25.5 | 25.5 | 25.5 | 25.5 | 25.5 | 25.5 | 25.5 | 25.5 | 25.2 | 25.1 | 25.2 | 25.1 | 25.4 | 25.4 | 25.5 | 25.4 | 25.2 | 25.4 | 25.2 | 23.9 | 26.2 | 26.3 | 26.5 | 26.0 | | | |
| MT621084_Paramelitidae sp. Biologic-AMPH019 | 8.8 | 8.7 | 8.5 | 9.3 | 9.3 | 9.3 | 8.5 | 8.2 | 2.9 | 2.9 | 3.0 | 3.3 | 18.4 | 20.1 | 25.5 | 25.5 | 25.5 | 25.5 | 25.5 | 25.5 | 25.5 | 25.5 | 25.5 | 25.5 | 25.5 | 25.5 | 25.7 | 25.4 | 25.5 | 25.2 | 25.1 | 25.2 | 25.1 | 25.4 | 25.4 | 25.5 | 25.4 | 25.2 | 25.4 | 25.2 | 23.9 | 26.2 | 26.3 | 26.0 | | |
| MT621099_Paramelitidae sp. Biologic-AMPH019 | 9.9 | 9.7 | 9.6 | 10.3 | 10.3 | 10.3 | 9.0 | 8.8 | 3.2 | 3.0 | 3.0 | 0.3 | 18.4 | 21.0 | 25.8 | 25.8 | 25.8 | 25.8 | 25.8 | 25.8 | 25.8 | 25.8 | 25.8 | 25.8 | 25.8 | 25.8 | 26.0 | 25.7 | 25.8 | 25.5 | 25.4 | 25.5 | 25.4 | 25.8 | 26.1 | 26.3 | 26.1 | 25.7 | 25.5 | 25.7 | 23.5 | 26.0 | 26.5 | 26.3 | 26.0 | |
| MT621100_Paramelitidae sp. Biologic-AMPH019 | 10.2 | 10.0 | 9.9 | 10.6 | 10.6 | 10.6 | 9.3 | 9.1 | 3.5 | 3.3 | 3.3 | 0.3 | 18.6 | 21.2 | 25.8 | 25.8 | 25.8 | 25.8 | 25.8 | 25.8 | 25.8 | 25.8 | 25.8 | 25.8 | 26.0 | 25.7 | 25.8 | 25.5 | 25.4 | 25.5 | 25.4 | 25.8 | 26.1 | 26.3 | 26.1 | 26.0 | 25.8 | 26.0 | 23.8 | 26.3 | 26.8 | 26.6 | 26.3 | | | |
| ON661039_Paramelitidae sp. Biologic-AMPH023 | 17.2 | 17.4 | 17.2 | 17.7 | 17.7 | 17.7 | 18.3 | 18.4 | 18.9 | 18.4 | 18.4 | 18.4 | 18.6 | 17.1 | 21.7 | 21.7 | 21.7 | 21.7 | 21.7 | 21.7 | 21.7 | 21.7 | 21.7 | 21.7 | 21.5 | 21.5 | 21.4 | 21.7 | 21.5 | 21.7 | 21.8 | 21.5 | 21.4 | 21.5 | 21.7 | 22.0 | 22.3 | 22.4 | 18.8 | 24.3 | 24.0 | 24.1 | 21.5 | | | |
| MW021189_Vilgarus | 19.2 | 19.3 | 19.2 | 19.8 | 19.8 | 19.8 | 18.7 | 18.7 | 20.9 | 20.4 | 20.1 | 21.0 | 21.2 | 17.1 | 19.9 | 19.8 | 19.8 | 19.8 | 19.8 | 19.8 | 19.8 | 19.8 | 19.8 | 19.9 | 19.6 | 19.6 | 19.6 | 19.5 | 19.6 | 19.8 | 19.8 | 19.8 | 19.8 | 19.8 | 19.5 | 19.8 | 19.5 | 19.8 | 19.9 | 20.1 | 20.7 | 20.6 | 20.7 | 21.5 | | |
| BMR01534_20167_Chydaekata 'sp. E TLF-2008' | 23.6 | 23.9 | 23.8 | 23.6 | 23.6 | 23.6 | 24.9 | 25.2 | 25.6 | 25.5 | 25.5 | 25.8 | 25.8 | 21.7 | 19.9 | 0.1 | 0.1 | 0.1 | 0.1 | 0.1 | 0.1 | 0.1 | 0.1 | 0.2 | 0.2 | 0.4 | 0.7 | 0.4 | 0.8 | 0.7 | 0.5 | 3.9 | 3.7 | 3.9 | 14.3 | 15.5 | 15.0 | 15.1 | 16.5 | | | | | | | |
| BMR01761_20018_Chydaekata 'sp. E TLF-2008' | 23.6 | 23.9 | 23.7 | 23.6 | 23.6 | 23.6 | 24.8 | 25.1 | 25.7 | 25.5 | 25.5 | 25.8 | 25.8 | 21.7 | 19.8 | 0.1 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.2 | 0.2 | 0.3 | 0.6 | 0.5 | 0.3 | 0.6 | 0.3 | 0.8 | 0.6 | 0.5 | 4.0 | 3.8 | 4.0 | 14.3 | 15.4 | 14.9 | 15.1 | 16.6 | | | | |
| BMR06009_21128_Chydaekata 'sp. E TLF-2008' | 23.6 | 23.9 | 23.7 | 23.6 | 23.6 | 23.6 | 24.8 | 25.1 | 25.7 | 25.5 | 25.5 | 25.8 | 25.8 | 21.7 | 19.8 | 0.1 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.2 | 0.2 | 0.3 | 0.6 | 0.5 | 0.3 | 0.6 | 0.3 | 0.8 | 0.6 | 0.5 | 4.0 | 3.8 | 4.0 | 14.3 | 15.4 | 14.9 | 15.1 | 16.6 | | | | |
| BMR06011_21128_Chydaekata 'sp. E TLF-2008' | 23.6 | 23.9 | 23.7 | 23.6 | 23.6 | 23.6 | 24.8 | 25.1 | 25.7 | 25.5 | 25.5 | 25.8 | 25.8 | 21.7 | 19.8 | 0.1 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.2 | 0.2 | 0.3 | 0.6 | 0.5 | 0.3 | 0.6 | 0.3 | 0.8 | 0.6 | 0.5 | 4.0 | 3.8 | 4.0 | 14.3 | 15.4 | 14.9 | 15.1 | 16.6 | | | | |
| BMR06012_21128_Chydaekata 'sp. E TLF-2008' | 23.6 | 23.9 | 23.7 | 23.6 | 23.6 | 23.6 | 24.8 | 25.1 | 25.7 | 25.5 | 25.5 | 25.8 | 25.8 | 21.7 | 19.8 | 0.1 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.2 | 0.2 | 0.3 | 0.6 | 0.5 | 0.3 | 0.6 | 0.3 | 0.8 | 0.6 | 0.5 | 4.0 | 3.8 | 4.0 | 14.3 | 15.4 | 14.9 | 15.1 | 16.6 | | | | |
| BMR06485_21043_Chydaekata 'sp. E TLF-2008' | 23.6 | 23.9 | 23.7 | 23.6 | 23.6 | 23.6 | 24.8 | 25.1 | 25.7 | 25.5 | 25.5 | 25.8 | 25.8 | 21.7 | 19.8 | 0.1 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.2 | 0.2 | 0.3 | 0.6 | 0.5 | 0.3 | 0.6 | 0.3 | 0.8 | 0.6 | 0.5 | 4.0 | 3.8 | 4.0 | 14.3 | 15.4 | 14.9 | 15.1 | 16.6 | | | | |
| DQ255972_Chydaekata sp. E TLF-2008 | 23.6 | 23.9 | 23.7 | 23.6 | 23.6 | 23.6 | 24.8 | 25.1 | 25.7 | 25.5 | 25.5 | 25.8 | 25.8 | 21.7 | 19.8 | 0.1 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.2 | 0.2 | 0.3 | 0.6 | 0.5 | 0.3 | 0.6 | 0.3 | 0.8 | 0.6 | 0.5 | 4.0 | 3.8 | 4.0 | 14.3 | 15.4 | 14.9 | 15.1 | 16.6 | | | | |
| BMR04971_22071_Chydaekata 'sp. E TLF-2008' | 23.6 | 23.9 | 23.7 | 23.6 | 23.6 | 23.6 | 24.8 | 25.1 | 25.7 | 25.5 | 25.5 | 25.8 | 25.8 | 21.7 | 19.8 | 0.1 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.2 | 0.2 | 0.3 | 0.6 | 0.5 | 0.3 | 0.6 | 0.3 | 0.8 | 0.6 | 0.5 | 4.0 | 3.8 | 4.0 | 14.3 | 15.4 | 14.9 | 15.1 | 16.6 | | | | |
| DQ255968_Chydaekata sp. E TLF-2008 | 23.4 | 23.7 | 23.6 | 23.4 | 23.4 | 23.4 | 24.9 | 25.2 | 25.8 | 25.7 | 26.0 | 26.0 | 21.5 | 19.9 | 0.2 | 0.2 | 0.2 | 0.2 | 0.2 | 0.2 | 0.2 | 0.2 | 0.2 | 0.2 | 0.3 | 0.5 | 0.8 | 0.8 | 0.9 | 0.8 | 0.5 | 0.9 | 0.8 | 1.1 | 1.1 | 0.9 | 4.1 | 4.0 | 4.1 | 14.2 | 15.5 | 15.2 | 16.7 | | | |
| DQ255979_Chydaekata sp. E TLF-2008 | 23.4 | 23.7 | 23.6 | 23.4 | 23.4 | 23.4 | 24.8 | 25.1 | 25.5 | 25.4 | 25.4 | 25.7 | 25.7 | 21.5 | 19.6 | 0.2 | 0.2 | 0.2 | 0.2 | 0.2 | 0.2 | 0.2 | 0.2 | 0.3 | 0.5 | 0.8 | 0.6 | 0.5 | 0.8 | 0.5 | 0.8 | 0.5 | 0.8 | 0.6 | 0.4 | 4.1 | 4.0 | 4.1 | 14.2 | 15.2 | 14.8 | 14.9 | 16.4 | | | |
| DQ255964_Chydaekata sp. E TLF-2008 | 23.6 | 23.9 | 23.7 | 23.6 | 23.6 | 23.6 | 24.8 | 25.1 | 25.7 | 25.5 | 25.5 | 25.8 | 25.8 | 21.4 | 19.6 | 0.4 | 0.3 | 0.3 | 0.3 | 0.3 | 0.3 | 0.3 | 0.3 | 0.3 | 0.3 | 0.3 | 0.5 | 0.5 | 0.6 | 0.6 | 0.8 | 0.2 | 0.2 | 0.5 | 0.8 | 0.9 | 1.1 | 0.9 | 4.1 | 4.0 | 4.1 | 14.2 | 15.5 | 15.1 | 15.2 | 16.4 |
| DQ255982_Chydaekata sp. E TLF-2008 | 23.3 | 23.6 | 23.4 | 23.3 | 23.3 | 23.3 | 24.5 | 24.8 | 25.4 | 25.2 | 25.2 | 25.5 | 25.5 | 21.7 | 19.6 | 0.4 | 0.3 | 0.3 | 0.3 | 0.3 | 0.3 | 0.3 | 0.3 | 0.3 | 0.3 | 0.5 | 0.5 | 0.6 | 0.6 | 0.8 | 0.2 | 0.2 | 0.5 | 0.8 | 0.9 | 1.1 | 0.9 | 4.1 | 4.0 | 4.1 | 14.2 | 15.5 | 15.1 | 15.2 | 16.3 | |
| OR366851_Chydaekata sp. E TLF-2008 | 23.3 | 23.6 | 23.4 | 23.3 | 23.3 | 23.3 | 24.5 | 24.8 | 25.4 | 25.2 | 25.2 | 25.5 | 25.5 | 21.7 | 19.6 | 0.4 | 0.3 | 0.3 | 0.3 | 0.3 | 0.3 | 0.3 | 0.3 | 0.3 | 0.3 | 0.5 | 0.5 | 0.6 | 0.6 | 0.8 | 0.2 | 0.2 | 0.5 | 0.8 | 0.9 | 1.1 | 0.9 | 4.1 | 4.0 | 4.1 | 14.2 | 15.5 | 15.1 | 15.2 | 16.4 | |
| DQ255980_Chydaekata sp. E TLF-2008 | 23.3 | 23.6 | 23.4 | 23.3 | 23.3 | 23.3 | 24.5 | 24.8 | 25.4 | 25.2 | 25.2 | 25.5 | 25.5 | 21.7 | 19.6 | 0.4 | 0.3 | 0.3 | 0.3 | 0.3 | 0.3 | 0.3 | 0.3 | 0.3 | 0.3 | 0.5 | 0.5 | 0.6 | 0.6 | 0.8 | 0.2 | 0.2 | 0.5 | 0.8 | 0.9 | 1.1 | 0.9 | 4.1 | 4.0</ | | | | | | | |

3.3 Bathynellacea

Three parabathynellid sequences formed a single OTU, matching the previously sequenced *Atopobathynella* sp. Biologic-PBAT019` (Figure 3.3). Not all representative sequences of this OTU are included in Figure 3.3 and Table 3.4 as they are not publicly available. However, all subsequent discussion of this OTU includes sequences Biologic currently identifies as *Atopobathynella* sp. Biologic-PBAT019`.

This OTU comprised sequences from an unusually large geographic distribution for *Atopobathynella* (Table 3.1). The OTU inhabits Turee Ck East subcatchment (flowing south west into the Ashburton), the Weeli Wolli subcatchment, and the Fortescue River catchment. These sequences have an intraspecific genetic distance of up to 7.8% (data not shown).

There is some residual uncertainty about OTU designations within the 'PBAT019' lineage, with two main hypotheses based on data available at the time of writing:

- These sequences could represent a single OTU with a potential geographic range across three subcatchments (linear range 79.6 km).
- There could be four distinct OTUs within the PBAT019 lineage.
 - Note: These OTUs would have intraspecific genetic distances of less than 4.7%, and interspecific distances of more than 6%. In this scenario one OTU would also still exhibit an unusual distribution across two regional subcatchments at Turee Creek/Weeli Wolli Creek.

At this point we are cautiously grouping these sequences into a single OTU based on intraspecific genetic distances and the phylogenetic branching pattern with a grade of short internode distances and poor bootstrap support. Further analysis, including morphology, is ongoing to resolve this OTU. This OTU was found in Survey Area and Reference sites.

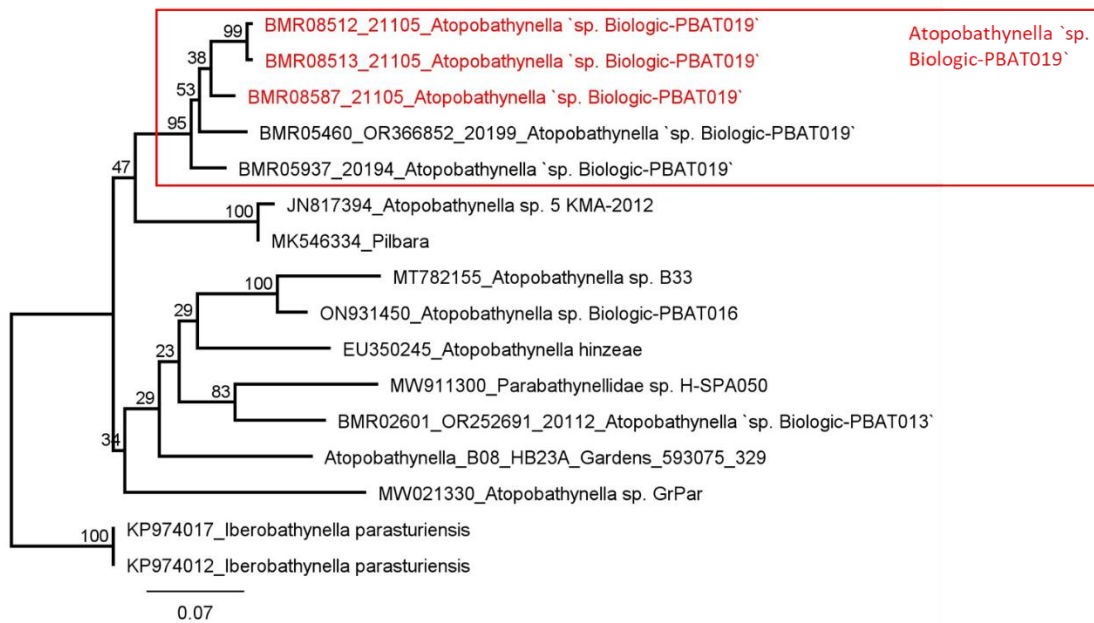


Figure 3.3. Phylogeny for the Bathynellacea dataset, with bootstrap values

Table 3.4: Pairwise distances (%) for the Bathynellacea dataset

| COI Pairwise Distances (%) | 593075 | MK546334 | JN817394 | BMR05460 | BMR08512 | BMR08513 | BMR08587 | BMR05937 | MW911300 | BMR02601 | EU350245 | MT782155 | ON931450 | MW021330 | KP974012 | KP974017 |
|--|--------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|
| Atopobathynella_B08_HB23A_Gardens_593075_329 | 13.9 | 14.7 | 16.1 | 13.9 | 14.3 | 14.8 | 16.5 | 15.0 | 15.4 | 15.2 | 14.5 | 13.6 | 14.9 | 17.0 | 17.0 | 17.0 |
| MK546334_Pilbara | 13.9 | 1.2 | 11.9 | 10.6 | 11.3 | 10.6 | 11.0 | 13.7 | 14.1 | 15.9 | 16.3 | 13.3 | 16.8 | 15.7 | 15.7 | 15.7 |
| JN817394_Atopobathynella sp. 5 KMA-2012 | 14.7 | 1.2 | 13.1 | 11.9 | 12.4 | 11.7 | 12.1 | 14.7 | 14.5 | 17.0 | 16.8 | 14.2 | 16.3 | 16.6 | 16.6 | 16.6 |
| BMR05460_OR366852_20199_Atopobathynella `sp. Biologic-PBAT019` | 16.1 | 11.9 | 13.1 | 6.2 | 6.2 | 4.8 | 5.7 | 18.1 | 14.5 | 13.4 | 17.6 | 14.9 | 17.0 | 15.0 | 15.0 | 15.0 |
| BMR08512_21105_Atopobathynella `sp. Biologic-PBAT019` | 13.9 | 10.6 | 11.9 | 6.2 | 0.6 | 4.4 | 6.0 | 15.3 | 15.2 | 14.5 | 15.4 | 14.4 | 15.5 | 14.5 | 14.5 | 14.5 |
| BMR08513_21105_Atopobathynella `sp. Biologic-PBAT019` | 14.3 | 11.3 | 12.4 | 6.2 | 0.6 | 4.4 | 6.0 | 15.3 | 15.2 | 14.5 | 15.5 | 14.7 | 16.1 | 14.8 | 14.8 | 14.8 |
| BMR08587_21105_Atopobathynella `sp. Biologic-PBAT019` | 14.8 | 10.6 | 11.7 | 4.8 | 4.4 | 4.4 | 4.6 | 16.7 | 13.2 | 14.8 | 16.7 | 14.2 | 15.9 | 14.8 | 14.8 | 14.8 |
| BMR05937_20194_Atopobathynella `sp. Biologic-PBAT019` | 16.5 | 11.0 | 12.1 | 5.7 | 6.0 | 6.0 | 4.6 | 16.5 | 13.4 | 14.1 | 17.0 | 14.4 | 15.6 | 14.3 | 14.3 | 14.3 |
| MW911300_Parabathynellidae sp. H-SPA050 | 15.0 | 13.7 | 14.7 | 18.1 | 15.3 | 15.3 | 16.7 | 16.5 | 12.1 | 16.5 | 16.8 | 15.3 | 16.9 | 17.8 | 17.8 | 17.8 |
| BMR02601_OR252691_20112_Atopobathynella `sp. Biologic-PBAT013` | 15.4 | 14.1 | 14.5 | 14.5 | 15.2 | 15.2 | 13.2 | 13.4 | 12.1 | 13.4 | 17.0 | 13.1 | 16.3 | 17.0 | 17.0 | 17.0 |
| EU350245_Atopobathynella hinzeae | 15.2 | 15.9 | 17.0 | 13.4 | 14.5 | 14.5 | 14.8 | 14.1 | 16.5 | 13.4 | 15.2 | 12.7 | 16.7 | 15.2 | 15.2 | 15.2 |
| MT782155_Atopobathynella sp. B33 | 14.5 | 16.3 | 16.8 | 17.6 | 15.4 | 15.5 | 16.7 | 17.0 | 16.8 | 17.0 | 15.2 | 8.0 | 18.4 | 17.0 | 17.0 | 17.0 |
| ON931450_Atopobathynella sp. Biologic-PBAT016 | 13.6 | 13.3 | 14.2 | 14.9 | 14.4 | 14.7 | 14.2 | 14.4 | 15.3 | 13.1 | 12.7 | 8.0 | 16.9 | 16.9 | 16.9 | 16.9 |
| MW021330_Atopobathynella sp. GrPar | 14.9 | 16.8 | 16.3 | 17.0 | 15.5 | 16.1 | 15.9 | 15.6 | 16.9 | 16.3 | 16.7 | 18.4 | 16.9 | 18.5 | 18.5 | 18.5 |
| KP974012_lberobathynella parasturiensis | 17.0 | 15.7 | 16.6 | 15.0 | 14.5 | 14.8 | 14.8 | 14.3 | 17.8 | 17.0 | 15.2 | 17.0 | 16.9 | 18.5 | 0.0 | 0.0 |
| KP974017_lberobathynella parasturiensis | 17.0 | 15.7 | 16.6 | 15.0 | 14.5 | 14.8 | 14.8 | 14.3 | 17.8 | 17.0 | 15.2 | 17.0 | 16.9 | 18.5 | 0.0 | 0.0 |

3.4 Maxillopoda (Copepoda)

Five copepod OTUs formed three OTUs, from three families: Canthocamptidae, Parastenocarididae, and Phyllognathopodidae (Figure 3.4). These OTUs had interspecific genetic distances of more than 16.5% and intraspecific genetic distances of less than 4.5% (Table 3.5).

Canthocamptidae `sp. Biologic-HARP059` comprised three sequences, all from the Survey Area. These sequences were all morphologically identified as canthocamptids, but from two different genera, *Elaphoidella* and *Australocamptus*. Canthocamptidae `sp. Biologic-HARP059` was nested among canthocamptids, but with weak support, so we are retaining the family name until more information is available.

Parastenocaris `sp. Biologic-HARP022` was sampled in the Reference sites but had been previously sampled across a wide distribution (linear distance of 325 km; Table 3.1).

nr *Phyllognathopus* `sp. Biologic-HARP058` was originally morphologically identified as Harpacticoida sp. and it failed to match other sequences, forming its own OTU. However, the phylogenetic analysis recovered it as nested among GenBank sequences of the genus *Phyllognathopus*. A reassessment of the morphology did not contradict this identification and so we have assigned nr *Phyllognathopus*. This OTU was restricted to the Survey Area sites.

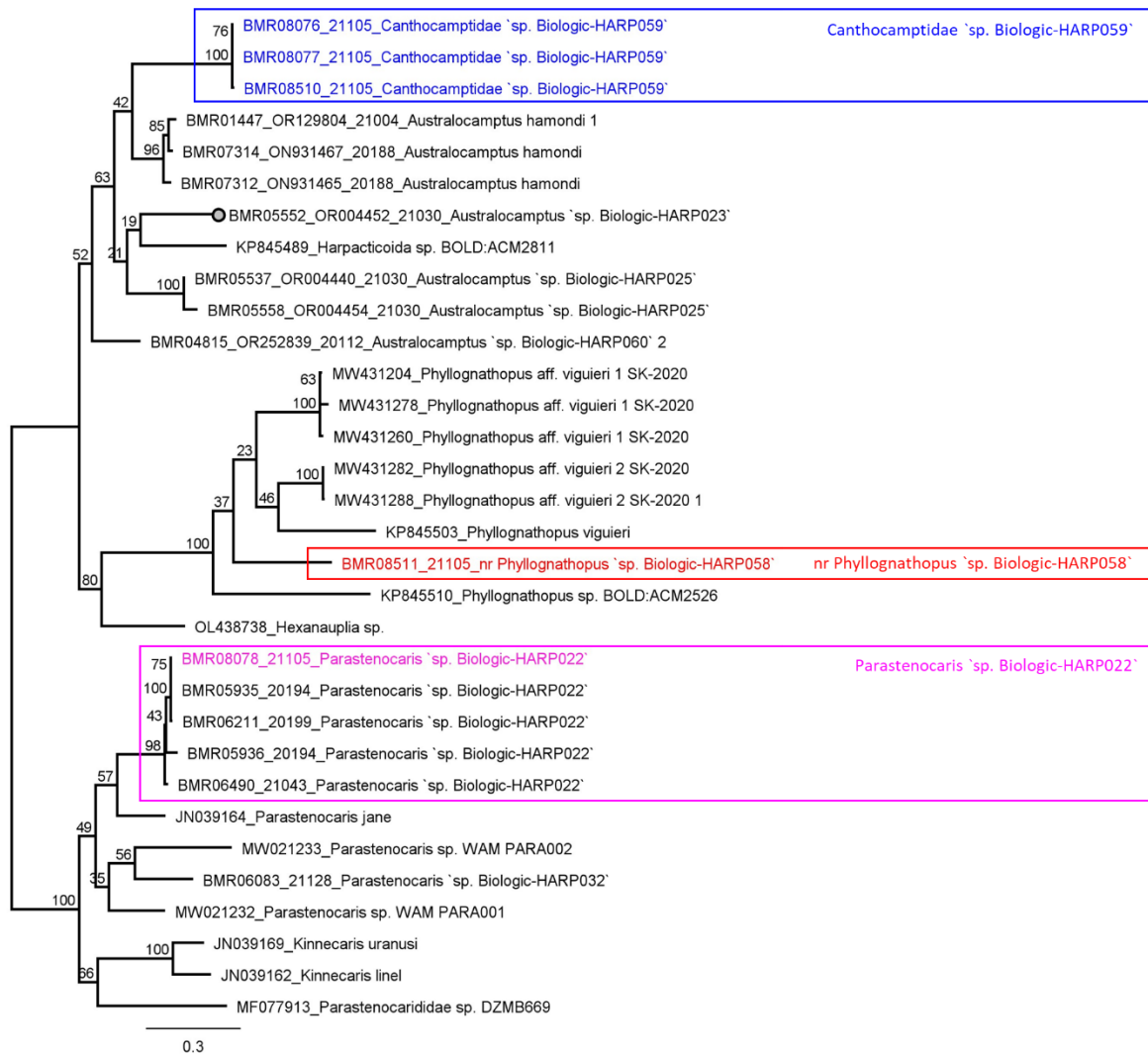


Figure 3.4. Phylogeny for the Copepoda dataset, with bootstrap values

Table 3.5: Pairwise distances (%) for the copepod dataset

| COI Pairwise Distances (%) | BMR01447 | BMR07314 | BMR07312 | BMR05537 | BMR05558 | BMR04815 | BMR05552 | BMR08076 | BMR08077 | BMR08510 | KP845489 | OL438738 | BMR05935 | BMR08078 | BMR06211 | BMR06490 | BMR05936 | JN039164 | NW021232 | BMR06083 | NW021233 | JN039162 | JN039169 | MF077913 | KP845503 | MW431204 | NW431260 | NW431278 | NW431282 | NW431288 | BMR08511 | KP845510 |
|--|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|
| BMR01447_OR129804_21004_Australocamptus hamondi 1 | | 2.4 | 4.6 | 15.8 | 15.8 | 15.1 | 18.7 | 18.1 | 18.1 | 17.2 | 17.5 | 18.3 | 26.4 | 26.4 | 26.7 | 25.8 | 26.2 | 24.3 | 25.2 | 23.1 | 25.5 | 27.0 | 23.3 | 29.9 | 23.1 | 23.1 | 23.1 | 24.7 | 26.5 | 26.6 | 23.9 | 26.3 |
| BMR07314_ON931467_20188_Australocamptus hamondi | 2.4 | | 3.6 | 16.0 | 16.6 | 16.0 | 18.7 | 17.6 | 17.6 | 17.1 | 17.4 | 18.6 | 27.1 | 27.1 | 27.3 | 26.4 | 26.9 | 24.8 | 25.4 | 23.8 | 25.7 | 27.3 | 24.5 | 29.9 | 23.4 | 23.0 | 23.0 | 24.2 | 26.8 | 26.9 | 25.0 | 26.6 |
| BMR07312_ON931465_20188_Australocamptus hamondi | 4.6 | 3.6 | | 15.4 | 16.2 | 14.4 | 18.5 | 17.7 | 17.7 | 17.2 | 17.2 | 18.3 | 27.0 | 27.0 | 27.3 | 26.3 | 26.8 | 24.3 | 24.1 | 23.8 | 25.1 | 25.9 | 25.2 | 29.1 | 23.2 | 24.0 | 24.0 | 25.0 | 26.3 | 26.2 | 25.0 | 27.1 |
| BMR05537_OR004440_21030_Australocamptus `sp. Biologic-HARP025` | 15.8 | 16.0 | 15.4 | | 3.2 | 16.3 | 17.1 | 20.9 | 20.9 | 19.2 | 17.4 | 20.4 | 27.3 | 27.3 | 27.5 | 27.1 | 27.1 | 26.4 | 26.5 | 26.2 | 25.9 | 26.1 | 26.1 | 28.0 | 24.6 | 23.1 | 23.5 | 25.0 | 25.9 | 25.8 | 25.9 | 27.6 |
| BMR05558_OR004454_21030_Australocamptus `sp. Biologic-HARP025` | 15.8 | 16.6 | 16.2 | 3.2 | | 16.7 | 18.1 | 21.4 | 21.4 | 19.9 | 17.4 | 20.7 | 27.8 | 27.8 | 28.0 | 27.5 | 27.5 | 27.1 | 27.6 | 27.3 | 26.4 | 26.1 | 26.1 | 28.0 | 24.6 | 22.5 | 22.5 | 24.3 | 25.2 | 25.0 | 24.7 | 27.1 |
| BMR04815_OR252839_20112_Australocamptus `sp. Biologic-HARP060` 2 | 15.1 | 16.0 | 14.4 | 16.3 | 16.7 | | 17.8 | 19.4 | 19.4 | 19.0 | 16.9 | 17.4 | 25.8 | 25.8 | 26.0 | 25.8 | 26.0 | 23.8 | 24.3 | 22.9 | 26.6 | 25.9 | 25.2 | 29.2 | 21.9 | 22.8 | 22.6 | 24.5 | 24.5 | 24.7 | 23.0 | 26.6 |
| BMR05552_OR004452_21030_Australocamptus `sp. Biologic-HARP023` | 18.7 | 18.7 | 18.5 | 17.1 | 18.1 | 17.8 | | 19.6 | 19.6 | 19.1 | 18.6 | 23.0 | 26.7 | 26.7 | 26.9 | 26.7 | 27.1 | 26.4 | 25.4 | 21.8 | 27.5 | 26.1 | 26.8 | 27.6 | 26.2 | 26.0 | 26.0 | 27.4 | 25.7 | 26.0 | 27.7 | 27.8 |
| BMR08076_21105_Canthocamptidae `sp. Biologic-HARP059` | 18.1 | 17.6 | 17.7 | 20.9 | 21.4 | 19.4 | 19.6 | | 0.0 | 0.2 | 20.3 | 21.2 | 26.4 | 26.4 | 26.7 | 26.4 | 26.2 | 26.9 | 25.8 | 25.1 | 27.9 | 27.5 | 28.0 | 28.7 | 27.9 | 28.9 | 28.4 | 29.5 | 29.6 | 29.6 | 29.3 | 29.1 |
| BMR08077_21105_Canthocamptidae `sp. Biologic-HARP059` | 18.1 | 17.6 | 17.7 | 20.9 | 21.4 | 19.4 | 19.6 | 0.0 | | 0.2 | 20.3 | 21.2 | 26.4 | 26.4 | 26.7 | 26.4 | 26.2 | 26.9 | 25.8 | 25.1 | 27.9 | 27.5 | 28.0 | 28.7 | 27.9 | 28.9 | 28.4 | 29.5 | 29.6 | 29.6 | 29.3 | 29.1 |
| BMR08510_21105_Canthocamptidae `sp. Biologic-HARP059` | 17.2 | 17.1 | 17.2 | 19.2 | 19.9 | 19.0 | 19.1 | 0.2 | 0.2 | | 19.6 | 19.8 | 26.7 | 26.7 | 26.9 | 26.7 | 26.4 | 27.1 | 26.1 | 25.3 | 28.2 | 27.7 | 28.2 | 28.9 | 27.5 | 27.4 | 27.0 | 28.6 | 28.2 | 28.5 | 28.1 | 29.3 |
| KP845489_Harpacticoida sp. BOLD:ACM2811 | 17.5 | 17.4 | 17.2 | 17.4 | 17.4 | 16.9 | 18.6 | 20.3 | 20.3 | 19.6 | | 23.0 | 26.7 | 26.7 | 26.9 | 26.7 | 27.5 | 26.4 | 26.5 | 23.8 | 26.8 | 27.5 | 26.6 | 30.3 | 23.3 | 25.3 | 25.3 | 27.0 | 25.8 | 26.0 | 25.6 | 29.5 |
| OL438738_Hexanauplia sp. | 18.3 | 18.6 | 18.3 | 20.4 | 20.7 | 17.4 | 23.0 | 21.2 | 21.2 | 19.8 | 23.0 | | 25.3 | 25.3 | 25.6 | 24.9 | 24.7 | 24.3 | 23.0 | 24.9 | 26.1 | 27.7 | 27.3 | 31.0 | 22.8 | 22.6 | 22.8 | 23.8 | 24.4 | 24.4 | 25.3 | 26.2 |
| BMR05935_20194_Parastenocaris `sp. Biologic-HARP022` | 26.4 | 27.1 | 27.0 | 27.3 | 27.8 | 25.8 | 26.7 | 26.4 | 26.4 | 26.7 | 26.7 | 25.3 | | 0.0 | 0.2 | 2.4 | 4.2 | 17.4 | 16.6 | 19.4 | 21.4 | 22.1 | 21.9 | 22.2 | 27.9 | 30.6 | 30.8 | 32.2 | 30.0 | 30.2 | 31.1 | 32.6 |
| BMR08078_21105_Parastenocaris `sp. Biologic-HARP022` | 26.4 | 27.1 | 27.0 | 27.3 | 27.8 | 25.8 | 26.7 | 26.4 | 26.4 | 26.7 | 26.7 | 25.3 | 0.0 | | 0.2 | 2.4 | 4.2 | 17.4 | 16.6 | 19.4 | 21.4 | 22.1 | 21.9 | 22.2 | 27.9 | 30.6 | 30.8 | 32.2 | 30.0 | 30.2 | 31.1 | 32.6 |
| BMR06211_20199_Parastenocaris `sp. Biologic-HARP022` | 26.7 | 27.3 | 27.3 | 27.5 | 28.0 | 26.0 | 26.9 | 26.7 | 26.7 | 26.9 | 25.6 | 0.2 | 0.2 | | 2.6 | 4.4 | 17.6 | 16.8 | 19.6 | 21.6 | 22.4 | 22.1 | 22.5 | 27.9 | 30.6 | 30.8 | 32.2 | 30.0 | 30.2 | 31.1 | 32.6 | |
| BMR06490_21043_Parastenocaris `sp. Biologic-HARP022` | 25.8 | 26.4 | 26.3 | 27.1 | 27.5 | 25.8 | 26.7 | 26.4 | 26.4 | 26.7 | 24.9 | 2.4 | 2.4 | 2.6 | | 4.0 | 17.1 | 16.6 | 18.9 | 21.2 | 21.9 | 21.5 | 21.5 | 28.1 | 30.6 | 30.8 | 32.2 | 30.2 | 30.5 | 30.8 | 32.4 | |
| BMR05936_20194_Parastenocaris `sp. Biologic-HARP022` | 26.2 | 26.9 | 26.8 | 27.1 | 27.5 | 26.0 | 27.1 | 26.2 | 26.2 | 26.4 | 27.5 | 24.7 | 4.2 | 4.2 | 4.4 | 4.0 | | 17.4 | 17.0 | 19.4 | 21.4 | 22.6 | 21.7 | 21.8 | 28.6 | 30.8 | 31.5 | 32.4 | 30.5 | 30.7 | 31.1 | 32.6 |
| JN039164_Parastenocaris jane | 24.3 | 24.8 | 24.3 | 26.4 | 27.1 | 23.8 | 26.4 | 26.9 | 26.9 | 27.1 | 26.4 | 24.3 | 17.4 | 17.4 | 17.6 | 17.1 | 17.4 | | 19.0 | 19.7 | 19.9 | 20.3 | 19.8 | 25.3 | 27.3 | 30.1 | 30.3 | 31.0 | 30.8 | 31.0 | 31.9 | 32.4 |
| MW021232_Parastenocaris sp. WAM PARA001 | 25.2 | 25.4 | 24.1 | 26.5 | 27.6 | 24.3 | 25.4 | 25.8 | 25.8 | 26.1 | 26.5 | 23.0 | 16.6 | 16.6 | 16.8 | 16.6 | 17.0 | 19.0 | | 18.5 | 20.1 | 21.7 | 21.7 | 24.8 | 28.0 | 29.8 | 30.0 | 30.0 | 28.8 | 29.0 | 28.3 | 31.6 |
| BMR06083_21128_Parastenocaris `sp. Biologic-HARP032` | 23.1 | 23.8 | 23.8 | 26.2 | 27.3 | 22.9 | 21.8 | 25.1 | 25.1 | 25.3 | 23.8 | 24.9 | 19.4 | 19.4 | 19.6 | 18.9 | 19.4 | 18.5 | | 20.1 | 21.0 | 22.6 | 23.8 | 25.7 | 28.2 | 28.2 | 28.9 | 29.6 | 29.8 | 31.5 | 29.7 | |
| MW021233_Parastenocaris sp. WAM PARA002 | 25.5 | 25.7 | 25.1 | 25.9 | 26.4 | 26.6 | 27.5 | 27.9 | 27.9 | 28.2 | 26.8 | 26.1 | 21.4 | 21.4 | 21.6 | 21.2 | 21.4 | 19.9 | 20.1 | | 20.1 | 21.8 | 22.9 | 22.5 | 26.7 | 31.3 | 31.5 | 31.8 | 30.0 | 30.3 | 34.0 | 31.5 |
| JN039162_Kinneccaris linel | 27.0 | 27.3 | 25.9 | 26.1 | 26.1 | 25.9 | 26.1 | 27.5 | 27.5 | 27.7 | 27.5 | 27.7 | 22.1 | 22.1 | 22.4 | 21.9 | 22.6 | 20.3 | 21.7 | 21.0 | 21.8 | | 12.8 | 23.6 | 28.6 | 30.3 | 30.5 | 31.2 | 29.8 | 30.1 | 30.8 | 31.2 |
| JN039169_Kinneccaris uranusii | 23.3 | 24.5 | 25.2 | 26.1 | 26.1 | 25.2 | 26.8 | 28.0 | 28.0 | 28.2 | 26.6 | 27.3 | 21.9 | 21.9 | 22.1 | 21.5 | 21.7 | 19.8 | 21.7 | 22.6 | 22.9 | 12.8 | | 24.5 | 29.3 | 29.4 | 29.4 | 31.0 | 30.3 | 30.5 | 30.5 | 29.8 |
| MF077913_Parastenocarididae sp. DZMB669 | 29.9 | 29.9 | 29.1 | 28.0 | 28.0 | 29.2 | 27.6 | 28.7 | 28.7 | 28.9 | 30.3 | 31.0 | 22.2 | 22.2 | 22.5 | 21.5 | 21.8 | 25.3 | 24.8 | 23.8 | 22.5 | 23.6 | 24.5 | | 32.1 | 31.9 | 32.4 | 31.9 | 31.0 | 31.3 | 35.2 | 32.2 |
| KP845503_Phylognathopus viguieri | 23.1 | 23.4 | 23.2 | 24.6 | 24.6 | 21.9 | 26.2 | 27.9 | 27.9 | 27.5 | 23.3 | 22.8 | 27.9 | 27.9 | 27.9 | 28.1 | 28.6 | 27.3 | 28.0 | 25.7 | 26.7 | 28.6 | 29.3 | 32.1 | | 19.9 | 20.1 | 21.1 | 17.8 | 17.9 | 22.3 | 23.1 |
| MW431204_Phylognathopus aff. viguieri 1 SK-2020 | 23.1 | 23.0 | 24.0 | 23.1 | 22.5 | 22.8 | 26.0 | 28.9 | 28.9 | 27.4 | 25.3 | 22.6 | 30.6 | 30.6 | 30.6 | 30.6 | 30.8 | 30.1 | 29.8 | 28.2 | 31.3 | 30.3 | 29.4 | 31.9 | 19.9 | | 1.0 | 2.3 | 17.4 | 17.6 | 19.3 | 24.8 |
| MW431260_Phylognathopus aff. viguieri 1 SK-2020 | 23.1 | 23.0 | 24.0 | 23.5 | 22.5 | 22.6 | 26.0 | 28.4 | 28.4 | 27.0 | 25.3 | 22.8 | 30.8 | 30.8 | 30.8 | 30.8 | 31.5 | 30.3 | 30.0 | 28.2 | 31.5 | 30.5 | 29.4 | 32.4 | 20.1 | 1.0 | | 2.9 | 17.4 | 17.6 | 18.9 | 24.7 |
| MW431278_Phylognathopus aff. viguieri 1 SK-2020 | 24.7 | 24.2 | 25.0 | 25.0 | 24.3 | 24.5 | 27.4 | 29.5 | 29.5 | 28.6 | 27.0 | 23.8 | 32.2 | 32.2 | 32.2 | 32.2 | 32.4 | 31.0 | 30.0 | 28.9 | 31.8 | 31.2 | 31.0 | 31.9 | 21.1 | 2.3 | 2.9 | | 18.8 | 19.0 | 21.0 | 25.3 |
| MW431282_Phylognathopus aff. viguieri 2 SK-2020 | 26.5 | 26.8 | 26.3 | 25.9 | 25.2 | 24.5 | 25.7 | 29.6 | 29.6 | 28.2 | 25.8 | 24.4 | 30.0 | 30.0 | 30.0 | 30.2 | 30.5 | 30.8 | 28.8 | 29.6 | 30.0 | 29.8 | 30.3 | 31.0 | 17.8 | 17.4 | 17.4 | 18.8 | | 0.2 | 20.6 | 23.6 |
| MW431288_Phylognathopus aff. viguieri 2 SK-2020 1 | 26.6 | 26.9 | 26.2 | 25.8 | 25.0 | 24.7 | 26.0 | 29.6 | 29.6 | 28.5 | 26.0 | 24.4 | 30.2 | 30.2 | 30.2 | 30.5 | 30.7 | 31.0 | 29.0 | 29.8 | 30.3 | 30.1 | 30.5 | 31.3 | 17.9 | 17.6 | 17.6 | 19.0 | 0.2 | 20.3 | 23.6 | |
| BMR08511_21105_Harpacticoida `sp. Biologic-HARP058` | 23.9 | 25.0 | 25.0 | 25.9 | 24.7 | 23.0 | 27.7 | 29.3 | 29.3 | 28.1 | 25.6 | 25.3 | 31.1 | 31.1 | 31.1 | 30.8 | 31.1 | 31.9 | 28.3 | 31.5 | 34.0 | 30.8 | 30.5 | 35.2 | 22.3 | 19.3 | 18.9 | 21.0 | 20.6 | 20.3 | 23.6 | |
| KP845510_Phylognathopus sp. BOLD:ACM2526 | 26.3 | 26.6 | 27.1 | 27.6 | 27.1 | 26.6 | 27.8 | 29.1 | 29.1 | 29.3 | 29.5 | 26.2 | 32.6 | 32.6 | 32.6 | 32.4 | 32.6 | 32.4 | 31.6 | 29.7 | 31.5 | 31.2 | 29.8 | 32.2 | 23.1 | 24.8 | 24.7 | 25.3 | 23.6 | 23.6 | 23.6 | |

3.5 Ostracoda

Ten ostracod sequences formed seven OTUs from two families: Candonidae and Cyprididae (Figure 3.5). These seven OTUs were more than 13.2% divergent from all other sequences in the analysis and had intraspecific genetic distances of less than 5.7% (Table 3.6). Six of the OTUs had linear distances over 170 km (Table 3.1). *Candonopsis* sp. Biologic-OSTR044 and *Ilyodromus* sp. Biologic-OSTR036 were restricted to the Survey Area, while all other OTUs were only found in the Reference sites (Table 3.1).

Notacandona modesta had a linear distance of 2.7km and was only found in Reference sites (Table 3.1). This species has previously been recorded from Weeli Wolli Springs (Karanovic & Marmonier, 2003).

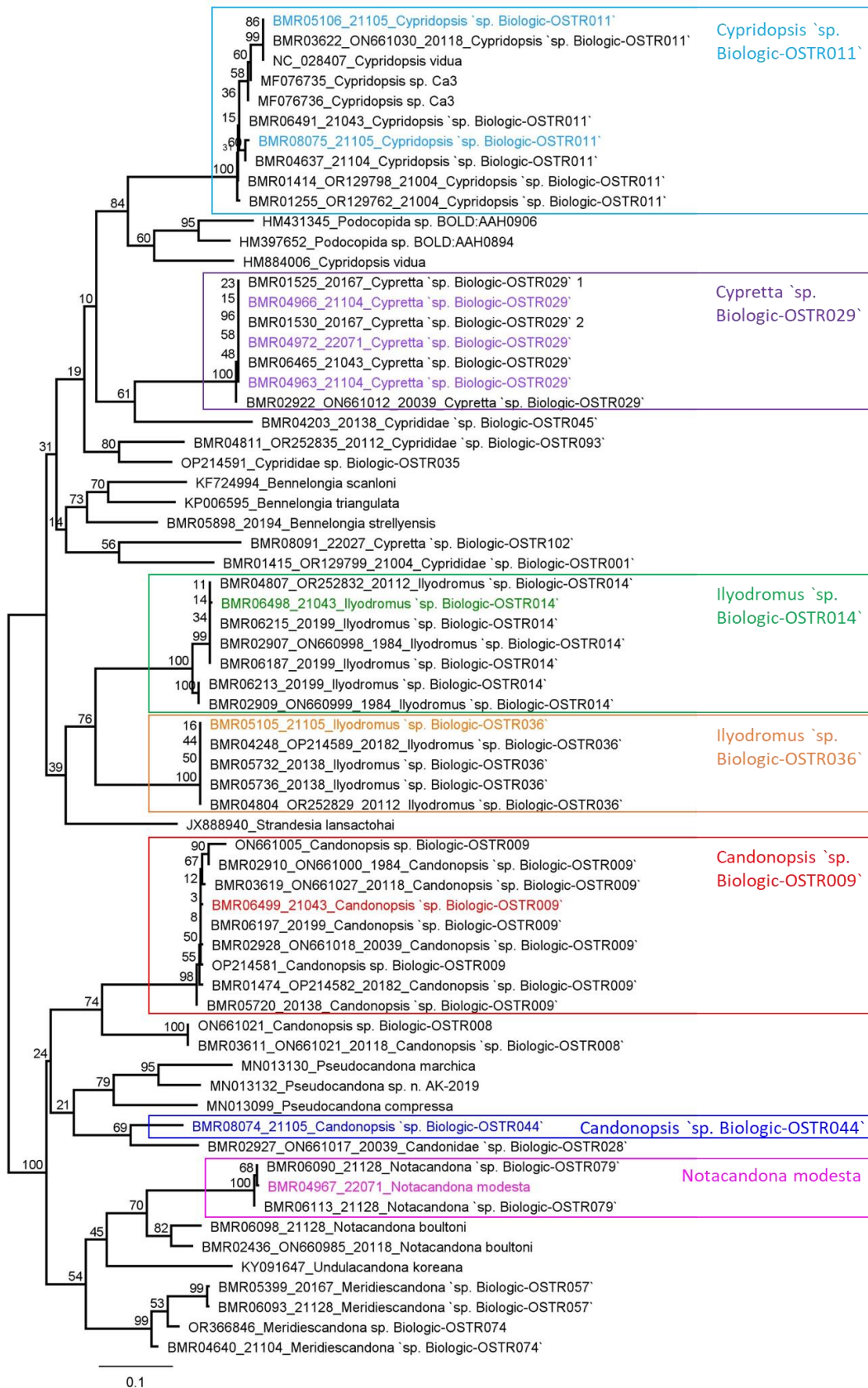


Figure 3.5. Phylogeny for the Ostracoda dataset, with bootstrap values

3.6 Symphyla

Three symphylian sequences formed two OTUs: *Hanseniella` sp. Biologic-SYMP055`* and *Hanseniella` sp. Biologic-SYMP069`* (Figure 3.6). These OTUs were more than 9.9% divergent from all other sequences in the analysis and had intraspecific genetic distances less than 2.5% (Table 3.7). *Hanseniella` sp. Biologic-SYMP055`* was again collected from the same site (MARC4) within the Survey Area. *Hanseniella` sp. Biologic-SYMP069`* was a new OTU and found in Survey Area and Reference sites.

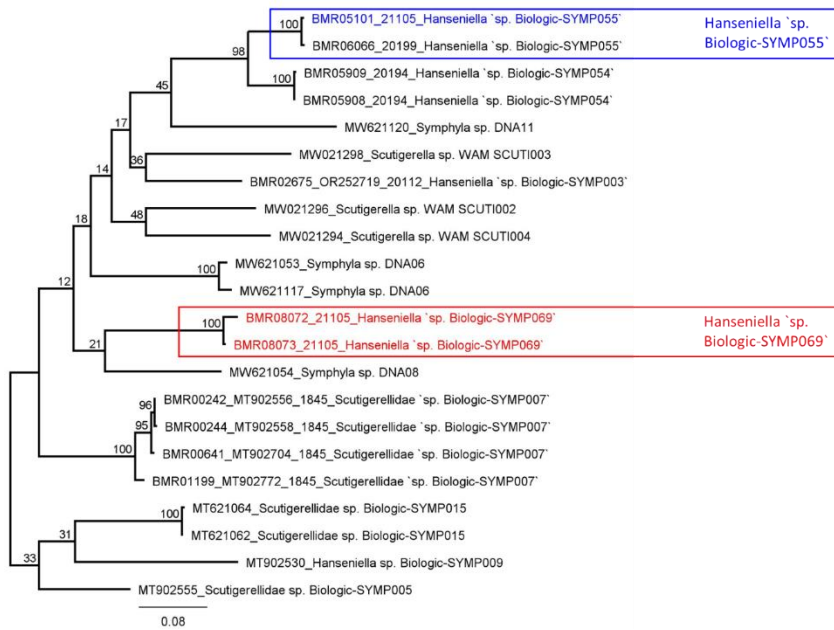


Figure 3.6. Phylogeny for the Symphyla dataset, with bootstrap values

Table 3.7: Pairwise distances (%) for the Symphyla dataset

| COI Pairwise Distances (%) | BMR00242 | BMR00244 | BMR00641 | BMR01199 | MT902555 | MT621062 | MT621064 | MMW021296 | BMR05908 | BMR05909 | BMR06066 | BMR05101 | MMW021053 | MMW021117 | MMW021294 | MMW021120 | BMR02675 | MMW021298 | MMW621054 | BMR08072 | BMR08073 | MT902530 |
|---|----------|----------|----------|----------|----------|----------|----------|-----------|----------|----------|----------|----------|-----------|-----------|-----------|-----------|----------|-----------|-----------|----------|----------|----------|
| BMR00242_MT902556_1845_Scutigerellidae` sp. Biologic-SYMP007` | | 0.2 | 0.8 | 3.3 | 15.7 | 19.0 | 18.6 | 16.7 | 19.3 | 19.2 | 17.5 | 17.5 | 18.1 | 18.6 | 18.8 | 21.6 | 17.3 | 19.0 | 17.7 | 19.5 | 18.4 | 19.9 |
| BMR00244_MT902558_1845_Scutigerellidae` sp. Biologic-SYMP007` | 0.2 | | 0.9 | 3.5 | 15.6 | 18.8 | 18.4 | 16.7 | 19.3 | 19.2 | 17.5 | 17.5 | 18.1 | 18.6 | 18.8 | 21.4 | 17.3 | 18.8 | 17.5 | 19.3 | 18.1 | 19.7 |
| BMR00641_MT902704_1845_Scutigerellidae` sp. Biologic-SYMP007` | 0.8 | 0.9 | | 3.2 | 15.6 | 19.5 | 18.9 | 17.1 | 19.4 | 19.3 | 17.8 | 17.8 | 18.0 | 18.4 | 18.6 | 21.4 | 17.5 | 19.3 | 17.9 | 20.2 | 19.2 | 19.9 |
| BMR01199_MT902772_1845_Scutigerellidae` sp. Biologic-SYMP007` | 3.3 | 3.5 | 3.2 | | 15.2 | 19.5 | 18.7 | 16.7 | 18.2 | 18.3 | 17.7 | 17.7 | 17.8 | 18.1 | 19.0 | 21.0 | 17.7 | 18.8 | 16.8 | 19.1 | 17.6 | 19.3 |
| MT902555_Scutigerellidae` sp. Biologic-SYMP005` | 15.7 | 15.6 | 15.6 | 15.2 | | 17.5 | 16.2 | 18.1 | 20.2 | 20.3 | 19.2 | 19.4 | 18.5 | 18.5 | 20.1 | 19.2 | 19.5 | 20.1 | 18.8 | 20.6 | 20.2 | 18.1 |
| MT621062_Scutigerellidae` sp. Biologic-SYMP015` | 19.0 | 18.8 | 19.5 | 19.5 | 17.5 | | 0.2 | 19.9 | 20.1 | 20.4 | 21.2 | 21.5 | 19.5 | 19.0 | 19.7 | 19.0 | 19.3 | 22.6 | 19.7 | 19.6 | 19.3 | 18.6 |
| MT621064_Scutigerellidae` sp. Biologic-SYMP015` | 18.6 | 18.4 | 18.9 | 18.7 | 16.2 | 0.2 | | 18.6 | 19.2 | 19.3 | 19.2 | 19.3 | 18.1 | 17.8 | 19.9 | 17.8 | 19.5 | 22.4 | 19.5 | 19.5 | 19.0 | 18.8 |
| MW021296_Scutigerella` sp. WAM SCUT1002` | 16.7 | 16.7 | 17.1 | 16.7 | 18.1 | 19.9 | 18.6 | | 17.4 | 17.4 | 19.0 | 18.9 | 17.8 | 18.0 | 17.5 | 19.2 | 16.4 | 17.9 | 19.7 | 17.8 | 18.8 | 21.7 |
| BMR05908_20194_Hanseniella` sp. Biologic-SYMP054` | 19.3 | 19.3 | 19.4 | 18.2 | 20.2 | 20.1 | 19.2 | 17.4 | | 0.2 | 10.1 | 10.0 | 16.0 | 15.7 | 18.0 | 18.3 | 17.8 | 18.3 | 19.3 | 19.2 | 18.6 | 20.6 |
| BMR05909_20194_Hanseniella` sp. Biologic-SYMP054` | 19.2 | 19.2 | 19.3 | 18.3 | 20.3 | 20.4 | 19.3 | 17.4 | 0.2 | | 10.2 | 10.0 | 16.0 | 15.7 | 17.7 | 18.3 | 17.9 | 18.4 | 19.7 | 19.3 | 18.9 | 20.6 |
| BMR06066_20199_Hanseniella` sp. Biologic-SYMP055` | 17.5 | 17.5 | 17.8 | 17.7 | 19.2 | 21.2 | 19.2 | 19.0 | 10.1 | 10.2 | | 0.5 | 18.4 | 18.2 | 19.0 | 17.5 | 18.1 | 18.8 | 19.2 | 20.4 | 20.0 | 21.2 |
| BMR05101_21105_Hanseniella` sp. Biologic-SYMP055` | 17.5 | 17.5 | 17.8 | 17.7 | 19.4 | 21.5 | 19.3 | 18.9 | 10.0 | 10.0 | 0.5 | | 18.1 | 17.9 | 19.0 | 17.7 | 18.1 | 18.8 | 18.8 | 20.4 | 20.0 | 21.2 |
| MW621053_Symphyla` sp. DNA06` | 18.1 | 18.1 | 18.0 | 17.8 | 18.5 | 19.5 | 18.1 | 17.8 | 16.0 | 16.0 | 18.4 | 18.1 | | 2.4 | 18.8 | 19.3 | 20.4 | 21.2 | 19.4 | 21.0 | 20.3 | 20.8 |
| MW621117_Symphyla` sp. DNA06` | 18.6 | 18.6 | 18.4 | 18.1 | 18.5 | 19.0 | 17.8 | 18.0 | 15.7 | 15.7 | 18.2 | 17.9 | 2.4 | | 17.9 | 19.5 | 20.6 | 21.7 | 19.0 | 19.9 | 18.9 | 20.8 |
| MW021294_Scutigerella` sp. WAM SCUT1004` | 18.8 | 18.8 | 18.6 | 19.0 | 20.1 | 19.7 | 19.9 | 17.5 | 18.0 | 17.7 | 19.0 | 19.0 | 18.8 | 17.9 | | 20.4 | 16.6 | 20.1 | 21.0 | 19.4 | 20.0 | 19.0 |
| MW621120_Symphyla` sp. DNA11` | 21.6 | 21.4 | 21.4 | 21.0 | 19.2 | 19.0 | 17.8 | 19.2 | 18.3 | 18.3 | 17.5 | 17.7 | 19.3 | 19.5 | 20.4 | | 19.0 | 21.7 | 21.0 | 22.0 | 20.7 | 22.6 |
| BMR02675_OR252719_20112_Hanseniella` sp. Biologic-SYMP003` | 17.3 | 17.3 | 17.5 | 17.7 | 19.5 | 19.3 | 19.5 | 16.4 | 17.8 | 17.9 | 18.1 | 18.1 | 20.4 | 20.6 | 16.6 | 19.0 | | 16.4 | 17.0 | 18.3 | 17.2 | 20.8 |
| MW021298_Scutigerella` sp. WAM SCUT1003` | 19.0 | 18.8 | 19.3 | 18.8 | 20.1 | 22.6 | 22.4 | 17.9 | 18.3 | 18.4 | 18.8 | 18.8 | 21.2 | 21.7 | 20.1 | 21.7 | 16.4 | | 19.7 | 19.8 | 20.0 | 19.0 |
| MW621054_Symphyla` sp. DNA08` | 17.7 | 17.5 | 17.9 | 16.8 | 18.8 | 19.7 | 19.5 | 19.7 | 19.3 | 19.7 | 19.2 | 18.8 | 19.4 | 19.0 | 21.0 | 21.0 | 17.0 | 19.7 | | 16.2 | 16.5 | 19.3 |
| BMR08072_21105_Hanseniella` sp. Biologic-SYMP069` | 19.5 | 19.3 | 20.2 | 19.1 | 20.6 | 19.6 | 19.5 | 17.8 | 19.2 | 19.3 | 20.4 | 20.4 | 21.0 | 19.9 | 19.4 | 22.0 | 18.3 | 19.8 | 16.2 | | 2.4 | 20.2 |
| BMR08073_21105_Hanseniella` sp. Biologic-SYMP069` | 18.4 | 18.1 | 19.2 | 17.6 | 20.2 | 19.3 | 19.0 | 18.8 | 18.6 | 18.9 | 20.0 | 20.0 | 20.3 | 18.9 | 20.0 | 20.7 | 17.2 | 20.0 | 16.5 | 2.4 | | 19.6 |
| MT902530_Hanseniella` sp. Biologic-SYMP009` | 19.9 | 19.7 | 19.9 | 19.3 | 18.1 | 18.6 | 18.8 | 21.7 | 20.6 | 20.6 | 21.2 | 21.2 | 20.8 | 20.8 | 19.0 | 22.6 | 20.8 | 19.0 | 19.3 | 20.2 | 19.6 | |

4 Summary

Using well-established DNA extraction and sequencing methods, this molecular systematics analysis designated 22 distinct OTU/species to 31 high quality sequences from the Study Area. All OTUs, the areas in which they were found, and the specimen numbers per OTU are shown in Appendix A. The following are the key findings at the OTU/species level:

- Trombidiformes (COI): 7 OTUs, 2 restricted to the Study sequences, 5 matching non-survey sequences.
- Amphipoda (COI): 2 OTUs, all matching non-Study sequences.
- Bathynellacea (COI): 1 OTU, matching non-Study sequences.
- Maxillopoda (COI): 3 OTUs, one matching non-Study sequences, two unique to the Study sequences.
- Ostracoda (COI): 7 OTUs, all matching non-Study sequences.
- Symphyla (COI): 2 OTUs, one matching non-Study sequences, one unique to the Study sequences.

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Appendix A: Specimen Data

| BMR | Unique ID code | Site | Survey Area sites vs Reference sites | Dec_Lat | Dec_Long | Coll_Date | Coll_Method | Lowest_ID_Legacy | OTU_Name | Reaction_State |
|----------------------------------|----------------|-----------|--------------------------------------|-----------------|-------------|------------|-------------|----------------------------|---|----------------|
| Arachnida | | | | | | | | | | |
| Trombidiformes: Halacaridae | | | | | | | | | | |
| BMR04970 | 21718 | WWS/WWUD3 | ref | - 22.9178594 | 119.1998720 | 4/05/2023 | Hypo | ?Halacaridae sp. | | FAIL; bad seq |
| Trombidiformes: Anisitsiellidae | | | | | | | | | | |
| BMR04969 | 21831 | WWS/WWUD3 | ref | - 22.9178594 | 119.1998720 | 4/05/2023 | Hypo | <i>Rutacarus</i> sp. | <i>Rutacarus</i> `sp. Biologic-ACAR005` | PASS |
| BMR05108 | 19328 | MARC5 | survey | - 22.7198703 | 118.9616982 | 10/09/2022 | Hypo | <i>Rutacarus</i> sp. | <i>Rutacarus</i> `sp. Biologic-ACAR007` | PASS |
| BMR05111 | 19084 | MARC4 | survey | - 22.7200324 | 118.9506181 | 11/09/2022 | Hypo | <i>Rutacarus</i> sp. | <i>Rutacarus</i> `sp. Biologic-ACAR022` | PASS |
| Trombidiformes: Hydryphantidae | | | | | | | | | | |
| BMR05109 | 19351 | MARC5 | survey | - 22.7198703 | 118.9616982 | 10/09/2022 | Hypo | <i>Wandesia</i> sp. | <i>Wandesia</i> `sp. Biologic-ACAR009` | PASS |
| BMR05112 | 18962 | MARC3 | survey | - 22.7218479 | 118.9475145 | 11/09/2022 | Hypo | <i>Wandesia</i> sp. | <i>Wandesia</i> `sp. Biologic-ACAR008` | PASS |
| BMR05113 | 19329 | MARC2 | survey | - 22.7252598 | 118.9422899 | 10/09/2022 | Hypo | <i>Wandesia</i> sp. | <i>Wandesia</i> `sp. Biologic-ACAR009` | PASS |
| Trombidiformes: Mideopsidae | | | | | | | | | | |
| BMR05110 | 19051 | MARC4 | survey | - 22.7200324 | 118.9506181 | 11/09/2022 | Hypo | <i>Guineaxonopsis</i> sp. | <i>Guineaxonopsis</i> `sp. Biologic-ACAR011` | PASS |
| Trombidiformes: Piersigiidae | | | | | | | | | | |
| BMR04965 | 21833 | SS | ref | -21.8626821 | 121.0085309 | 21/03/2023 | Macro | <i>Stygolimnochaes</i> sp. | <i>Stygolimnochaes</i> `sp. Biologic-ACAR026` | PASS |
| Malacostraca | | | | | | | | | | |
| Amphipoda: Paramelitidae | | | | | | | | | | |
| BMR04968 | 21711 | WWS/WWUD3 | ref | - 22.9178594 | 119.1998720 | 4/05/2023 | Hypo | Paramelitidae sp. | Paramelitidae `sp. Biologic-AMPH045` | PASS |
| BMR04971 | 21773 | WWS/WWUD3 | ref | - 22.9178594 | 119.1998720 | 4/05/2023 | Macro | Paramelitidae sp. | <i>Chydaekata</i> `sp. E TLF-2008` | PASS |
| Bathynellacea: Parabathynellidae | | | | | | | | | | |
| BMR08512 | 19201 | MARC4 | survey | - 22.7200324 | 118.9506181 | 11/09/2022 | Hypo | <i>Atopobathynella</i> sp. | <i>Atopobathynella</i> `sp. Biologic-PBAT019` | PASS |

| BMR | Unique ID code | Site | Survey Area sites vs Reference sites | Dec_Lat | Dec_Long | Coll_Date | Coll_Method | Lowest_ID_Legacy | OTU_Name | Reaction_State |
|------------------------------------|----------------|-----------|--------------------------------------|-----------------|-------------|------------|-------------|----------------------------|--|--------------------|
| BMR08513 | 19244 | MARC4 | survey | - 22.7200324 | 118.9506181 | 11/09/2022 | Hypo | <i>Atopobathynella</i> sp. | <i>Atopobathynella</i> `sp. Biologic-PBAT019` | PASS |
| BMR08587 | 19803 | MACREF2 | ref | - 22.7234840 | 118.9362405 | 1/04/2023 | Hypo | <i>Atopobathynella</i> sp. | <i>Atopobathynella</i> `sp. Biologic-PBAT019` | PASS |
| Maxillopoda | | | | | | | | | | |
| Harpacticoida: Canthocamptidae | | | | | | | | | | |
| BMR08076 | 22910 | MARC4 | survey | - 22.7200324 | 118.9506181 | 1/04/2023 | Hypo | <i>Australocamptus</i> sp. | Canthocamptidae `sp. Biologic-HARP059` | PASS |
| BMR08077 | 22914 | MARC4 | survey | - 22.7200324 | 118.9506181 | 1/04/2023 | Hypo | <i>Australocamptus</i> sp. | Canthocamptidae `sp. Biologic-HARP059` | PASS |
| BMR08509 | 19003 | MARC4 | survey | - 22.7200324 | 118.9506181 | 11/09/2022 | Hypo | <i>Elaphoidella</i> sp. | | FAIL; bad sequence |
| BMR08510 | 19245 | MARC2 | survey | - 22.7252598 | 118.9422899 | 10/09/2022 | Hypo | <i>Elaphoidella</i> sp. | Canthocamptidae `sp. Biologic-HARP059` | PASS |
| Harpacticoida: Parastenocarididae | | | | | | | | | | |
| BMR08078 | 23004 | MACREF2 | ref | - 22.7234840 | 118.9362405 | 1/04/2023 | Hypo | <i>Parastenocaris</i> sp. | <i>Parastenocaris</i> `sp. Biologic-HARP022` | PASS |
| Harpacticoida: Phyllognathopodidae | | | | | | | | | | |
| BMR08511 | 19002 | MARC2 | survey | - 22.7252598 | 118.9422899 | 10/09/2022 | Hypo | Harpacticoida sp. | nr <i>Phyllognathopus</i> `sp. Biologic-HARP058` | PASS |
| Ostracoda | | | | | | | | | | |
| Podocopida: Candonidae | | | | | | | | | | |
| BMR04967 | 21771 | WWS/WWUD3 | ref | - 22.9178594 | 119.1998720 | 4/05/2023 | Hypo | <i>Notacandona modesta</i> | <i>Notacandona modesta</i> | PASS |
| BMR06499 | 18679 | RW | ref | -21.6861512 | 121.1250275 | 11/09/2022 | | <i>Candonopsis</i> sp. | <i>Candonopsis</i> `sp. Biologic-OSTR009` | PASS |
| BMR08074 | 22901 | MARC5 | survey | - 22.7198703 | 118.9616982 | 1/04/2023 | Macro | <i>Candonopsis</i> sp. | <i>Candonopsis</i> `sp. Biologic-OSTR044` | PASS |
| Podocopida: Cyprididae | | | | | | | | | | |
| BMR04963 | 6273 | SS | ref | -21.8626821 | 121.0085309 | 21/03/2023 | Macro | <i>Cyprretta</i> sp. | <i>Cyprretta</i> `sp. Biologic-OSTR029` | PASS |
| BMR04966 | 21595 | RW | ref | - 21.6859659 | 121.1252610 | 21/03/2023 | Macro | <i>Cyprretta</i> sp. | <i>Cyprretta</i> `sp. Biologic-OSTR029` | PASS |
| BMR04972 | 21717 | WWS/WWUD3 | ref | - 22.9178594 | 119.1998720 | 4/05/2023 | Macro | <i>Cyprretta</i> sp. | <i>Cyprretta</i> `sp. Biologic-OSTR029` | PASS |

| BMR | Unique ID code | Site | Survey Area sites vs Reference sites | Dec_Lat | Dec_Long | Coll_Date | Coll_Method | Lowest_ID_Legacy | OTU_Name | Reaction_State |
|---------------------------------|----------------|---------|--------------------------------------|-----------------|-------------|------------|-------------|---------------------------------|---|---------------------|
| BMR05103 | 19085 | MARC3 | survey | - 22.7218479 | 118.9475145 | 11/09/2022 | Macro | <i>Sarsypridopsis aculeata</i> | | FAIL; contamination |
| BMR05104 | 19345 | MARC3 | survey | - 22.7218479 | 118.9475145 | 11/09/2022 | Macro | <i>Cypridopsis</i> sp. | | FAIL; PCR |
| BMR05105 | 18932 | MARC6 | survey | - 22.7192288 | 118.9713275 | 9/09/2022 | Macro | <i>Ilyodromus</i> sp. | <i>Ilyodromus`</i> sp. Biologic-OSTR036` | PASS |
| BMR05106 | 19342 | MACREF1 | ref | - 22.8645516 | 119.1147254 | 11/09/2022 | Macro | <i>Cypridopsis</i> sp. | <i>Cypridopsis`</i> sp. Biologic-OSTR011` | PASS |
| BMR05107 | 18861 | MACREF1 | ref | - 22.8645516 | 119.1147254 | 11/09/2022 | Macro | <i>Cypretta</i> sp. | | FAIL; PCR |
| BMR06498 | 16927 | RW | ref | -21.6861512 | 121.1250275 | 11/09/2022 | | <i>Ilyodromus</i> sp. | <i>Ilyodromus`</i> sp. Biologic-OSTR014` | PASS |
| BMR08075 | 22793 | MACREF1 | ref | - 22.8645516 | 119.1147254 | 2/04/2023 | Rehydrate | <i>Cypridopsis</i> sp. | <i>Cypridopsis`</i> sp. Biologic-OSTR011` | PASS |
| Podocopida: Limnocytheridae | | | | | | | | | | |
| BMR05102 | 19215 | MARC3 | survey | - 22.7218479 | 118.9475145 | 11/09/2022 | Macro | <i>Limnocythere dorsosicula</i> | | FAIL; bad sequence |
| Symphyla | | | | | | | | | | |
| Cephalostigmata: Scutigrellidae | | | | | | | | | | |
| BMR05101 | 19156 | MARC4 | survey | - 22.7200324 | 118.9506181 | 11/09/2022 | Hypo | <i>Symphyla</i> sp. | <i>Hanseniella`</i> sp. Biologic-SYMP055` | PASS |
| BMR08072 | 22907 | MACREF2 | ref | - 22.7234840 | 118.9362405 | 1/04/2023 | Hypo | <i>Hanseniella</i> sp. | <i>Hanseniella`</i> sp. Biologic-SYMP069` | PASS |
| BMR08073 | 22700 | MARC6 | survey | -22.7191120 | 118.9715432 | 2/04/2023 | Hypo | <i>Hanseniella</i> sp. | <i>Hanseniella`</i> sp. Biologic-SYMP069` | PASS |