East Packsaddle
Subterranean Fauna Baseline Survey

Report to BHP Western Australian Iron Ore

6 January 2025

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Executive Summary

BHP Western Australian Iron Ore (BHP WAIO) is currently investigating the East Packsaddle area (hereafter referred to as the Study Area), located immediately east of Mining Area C and approximately 70 km north-west of Newman in the central Pilbara region of Western Australia.

BHP WAIO commissioned Biologic Environmental Survey Pty Ltd (Biologic) to undertake a detailed, three-phase subterranean fauna baseline survey across the Study Area (~8,800 ha). The aim of the survey was to increase knowledge of the troglofauna and stygofauna values present within the Study Area, to inform and support future environmental approvals. During the current three-phase survey (Phase 1: May 11th 2022 to March 3rd 2023; Phase 2: June 14th to September 8th 2023; Phase 3: April 11th to June 18th 2024), a total of 595 troglofauna and 118 stygofauna samples were collected from 144 sites. Additionally, subterranean fauna records from previous studies within and surrounding the Study Area were considered and incorporated herein.

A total of 50 troglofauna species/OTUs were identified during this survey, comprising arachnids, isopods, myriapods, diplurans, and insects. Nineteen of these taxa were only recorded as singletons or from a single site within the Study Area, and a further 14 were found to be locally restricted (<20 km known linear range). The remaining 17 taxa were found to be more widespread (>20 km linear range). In total, 43 troglofauna taxa (32 from the current survey and 11 from previous surveys) are currently only known to occur within the Study Area.

Twenty-eight stygofauna species/OTUs were identified during this survey comprising worms, mites, amphipods, syncarids, isopods, copepods, and ostracods. Thirteen of these taxa were either singletons/found from single sites (five taxa) or locally restricted (eight taxa). The remaining 15 taxa were found to be more widespread. To date, 14 taxa (eight from the current survey and six from previous surveys) are only known from within the Study Area.

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Glossary

BC Act	Western Australian Biodiversity Conservation Act 2016
BHP WAIO	BHP Western Australian Iron Ore
BIF	Banded Iron Formation
BoM	Bureau of Meteorology
cf	In taxonomy, cf refers to a species that closely matches the species following the designation, but differs morphologically in some minor ways
DBCA	Department Biodiversity, Conservation and Attractions
DO	Dissolved oxygen
EC	Electrical conductivity
EIA	Environmental Impact Assessment
EPA	Western Australian Environmental Protection Authority
EPBC	Environment Protection and Biodiversity Conservation
LTA	Long-term average
mbgl	Metres below ground level
nr	In taxonomy, nr refers to a potentially undescribed species nearest to the species following the designation
ORP	Oxidation reduction potential
OTU	Operational taxonomic unit – species-equivalent taxonomic unit based on COI or 12S cluster similarity
PEC	Priority Ecological Communities
SRE	Short-range Endemic
TEC	Threatened Ecological Communities
WAM	Western Australian Museum

1 Introduction

1.1 Background

BHP Western Australian Iron Ore (BHP WAIO) is currently in the process of investigating the East Packsaddle area (hereafter referred to as the Study Area), located immediately east of Mining Area C and approximately 70 km north-west of Newman in the central Pilbara region of Western Australia (Figure 1.1).

BHP WAIO commissioned Biologic Environmental Survey Pty Ltd (Biologic) to undertake a detailed, three-phase subterranean fauna baseline survey across the Study Area (~8,800 ha). The aim of the survey was to increase knowledge of the troglofauna and stygofauna values present within and surrounding the Study Area to inform and support future environmental approvals.

1.2 Scope and Objectives

This report aims to provide:

- Description of the environment within the Study Area relevant for subterranean fauna;
- Desktop review of subterranean fauna in the Study Area and wider local/ subregional area;
- Background information relevant to the survey design and implementation, and rationalisation of any departures from the relevant guidance documentation;
- A characterisation of troglofauna and stygofauna habitats in the Study Area;
- Results of detailed subterranean fauna surveys within the Study Area to date;
- Results of morphological and genetic comparisons of species collected from the Study Area during the current survey; and
- A description of the distribution of all stygofauna and troglofauna species recorded from the Study Area and surrounds during the current survey.

1.3 Compliance

This assessment was carried out in acknowledgement of the following guidelines and recommendations developed by the relevant state and federal regulatory bodies:

- EPA (2021b) T*echnical Guidance - Subterranean Fauna Surveys for Environmental Impact Assessment*;
- EPA (2016a) *Environmental Factor Guideline Subterranean Fauna*; and
- EPA (2021a) *Statement of environmental principles, factors, objectives and aims of Environmental Impact Assessment*.

1.4 Subterranean fauna

Subterranean fauna are animals that spend most or all of their lives in underground habitats such as caves, vugs, and aquifers. The subterranean fauna communities of WA are globally significant due to their high levels of biodiversity and endemism (EPA, 2016a). Previous estimates of subterranean species richness in WA ranged from 3,000 in the Pilbara alone (Halse, 2018) to over 4,000 in the western half of Australia (Guzik *et al.*, 2010) but the results of more recent sampling and genetic sequencing point to far higher numbers. Additionally, many areas of WA are undersampled, with sampling coverage biased towards areas that are of interest to mining. Surveys in unsampled areas, as well as molecular analyses of new and existing specimens, frequently unearth new putative species (e.g. Abrams *et al.*, 2019).

With the exceptions of three species of fish and one species of blind snake, all the recorded species of subterranean fauna in WA are invertebrates (Alpin, 1998; EPA, 2016a; Larson *et al.*, 2013; Moore, 2019). They are typically categorised as either troglofauna (air-breathing species that live above the water table, including beetles, arachnids and myriapods) or stygofauna (aquatic species that inhabit aquifers, including crustaceans, beetles, annelid worms, and gastropods), although this distinction is ecological rather than systematic. For example, within the order Coleoptera (beetles) there are species of both troglofauna and stygofauna. Species can be further categorised based on their ecological dependence on subterranean habitats: troglobites and stygobites are obligate inhabitants of subterranean habitats; troglophiles and stygophiles use surface habitats at least occasionally; and trogloxenes and stygoxenes use subterranean habitats opportunistically. However, the reliability of this type of classification is limited by ecological information, and assumptions about the ecology of a species are usually based on morphology and collection data (Howarth & Moldovan, 2018). Populations within species can also be partitioned between epigean and subterranean habitats (Harms, 2018).

Obligate subterranean fauna species usually have small geographic ranges due to the limited extent and connectivity of suitable habitat within the wider landscape. For example, individual calcrete aquifers within arid zones act as 'subterranean islands' that support rich and highly endemic assemblages of subterranean fauna (Cooper *et al.*, 2002; Humphreys, 2001). This can also be the case with other isolated geological features such as elevated ranges (DEC, 2007).

Species with restricted ranges are more susceptible to disturbance-induced conservation impacts than those that are widespread (Ponder & Colgan, 2002). Many (and potentially most) species of subterranean fauna in WA can be classified as short-range endemics (SRE; Harvey, 2002), primarily due to having geographic ranges of less than 10,000 km^2 and poor dispersal capabilities. This renders subterranean species highly vulnerable to the effects of habitat removal. Nevertheless, estimates of species ranges can be constrained by the coverage, intensity and success of sampling (Eberhard *et al.*, 2009) and are often based on few records, limited ecological data, and limited understandings of habitat.

704000 712000 720000 728000 736000

7468500

7462000

7455500

IBRA Region
Pilbara

IBRA Subregion
Chichester
Fortescue
Hamersley
Roebourne

Port Hedland
Karratha
Newman

Yandicoogina Creek
Weeli Wolli Creek
MAC C East
HD1 Flat Top
West Angelas Rd
Weeli Wolli Creek

LEGEND
Study Area
Live Mining Tenement
Operating Mine
Local Road
Rail
Weeli Wolli PEC
Major Surface Hydrology

Biologic
Scale 1:92,000
0 1 2 3 4 Km
Coordinate System: GDA2020 MGA Zone 50
Projection: Transverse Mercator
Datum: GDA2020 Created 18/11/2024

Port Hedland
Karratha
Exmouth
Newman

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Figure 1.1: Study Area and regional context

2 Existing Environment

2.1 Biogeography

The Study Area is located in the Pilbara bioregion, as defined by the Interim Biogeographic Regionalisation of Australia (IBRA; Thackway & Cresswell, 1995). The Pilbara bioregion is characterised by vast coastal plains and inland mountain ranges with cliffs and deep gorges (Thackway & Cresswell, 1995). Within the Pilbara bioregion, the Study Area is located within the Hamersley (PIL 3) subregion (Figure 1.1). The significant and dominant feature of this subregion is the Hamersley Range, a mountainous plateau of some 450 km in length, which receives considerably higher rainfall than the surrounding subregion. The plateau is dissected by deeply incised gorges, containing extensive permanent spring-fed streams and pools (Kendrick, 2003). Drainage is into the Fortescue River to the north, the Ashburton River to the south, or the Robe River to the west (Kendrick, 2003). Mulga low woodland over bunch grasses on fine-textured soils dominates in valley floors, while snappy gum (*Eucalyptus leucophloia*) over *Triodia brizoides* predominates on the skeletal soils of the ranges (Kendrick, 2003).

2.2 Climate

The Pilbara bioregion has a semi-desert to tropical climate characterised by low and variable rainfall (occurring mostly during summer), high daily temperatures, high diurnal temperature variability and high evaporation rates (Thackway & Cresswell, 1995). Maximum daily temperatures can exceed 35° C during summer (October to April), decreasing to approximately 22° C to 30° C during winter (June to August) (BoM, 2024). Average total annual rainfall ranges from 200 mm to 350 mm, mostly during summer. Rainfall is sporadic and there are significant fluctuations between years (Leighton, 2004; McKenzie *et al.*, 2009).

2.3 Topography

The topography of the area is highly mountainous. The Study Area occurs primarily within the eastern section of the Packsaddle Range, a tall and narrow mountain range formed in Brockman Iron Formation (Figure 2.1). Packsaddle Range strikes from east to west and terminates at Weeli Wolli Creek in the east of the Study Area (Figure 2.1). The range is heavily dissected by gorges, gullies, and drainage lines, which primarily drain south into a wide valley occurring approximately 300 m below (Figure 2.1). This valley, which is bound by the Jirrpalpur Range to the south, features vast undulating stony plains and low hills.

The Packsaddle Range connects with other mountainous habitats north of the range (Figure 2.1). Immediately to the east of Packsaddle Range lies Weeli Wolli Creek. The creek is surrounded by hills of outcropping Banded Iron Formation and flows north via a narrow channel past the confluence with Marillana Creek. Weeli Wolli Creek flows into the Fortescue River Valley, approximately 70 km north of the Study Area.

700000
712000
724000
736000
7472000
7464000
7456000

Packsaddle Range
Jirrpalpur Range
Weeli Wolli Spring
Weeli Wolli Creek
Pebble Mouse Creek

LEGEND

Study Area
Weeli Wolli PEC

Surface Hydrology
Major
Minor
Direction

Elevation (mAHD)
450 - 500
550 - 650
700 - 800
850 - 950
1000 - 1200

Biologic

Scale 1:125,000
0 1 2 3 4 5 Km

Coordinate System: GDA2020 MGA Zone 50
Projection: Transverse Mercator
Datum: GDA2020 Created 14/11/2024

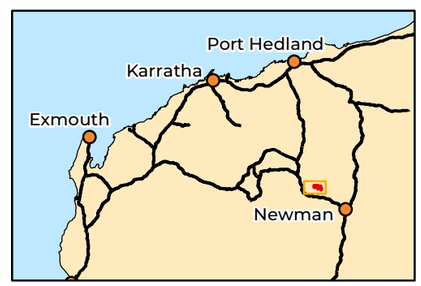

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Figure 2.1: Topography (50 m intervals)

2.1 Surface hydrology and catchments

The Study Area is located within the Weeli Wolli Creek catchment (Figure 2.2). The catchment covers an area of approximately 4,100 km^2 and is divided into three sub catchments comprising the Upper Weeli Wolli Creek subcatchment, the Marillana Creek subcatchment, and the Lower Weeli Wolli Creek subcatchment. The Study Area lies within the Upper Weeli Wolli Creek subcatchment.

Drainage within the Study Area is eastwards towards Weeli Wolli Creek, and then follows Weeli Wolli Creek to the north. Weeli Wolli Creek is approximately 70 km long and drains into Fortescue Marsh, although these systems are only directly connected during flood events.

Immediately east of the Study Area, groundwater flow is constrained by a geological barrier where high permeability rock units meet low permeability bedrock, forcing groundwater to the surface and creating Weeli Wolli Spring (EPA, 2018). Weeli Wolli Spring feeds numerous pools, with subsurface flow varying from a trickle to significant flows (van Leeuwen, 2009). A shallow groundwater system with extensive areas of calcrete is present upgradient of the spring.

Prior to mining in the area, much of Weeli Wolli Creek, aside from a 2-3 km section downstream of the spring, was ephemeral and flowed only in response to significant rainfall events, with some years of no flow. The spring and creek are now affected by drawdown and discharge from mining operations in the area, altering this historic groundwater flow into the spring system. The spring is currently maintained by dewatering discharge from Rio Tinto's nearby Hope Downs 1 mine, which has led to an increase in perennial surface water flows from 2-3 km pre-mining, to around 20 km, depending on wet season rainfall, flooding, and discharge volumes.

Numerous tributaries are associated with Weeli Wolli Creek. In the vicinity of the Study Area, the major tributary is Marillana Creek, which flows into Weeli Wolli Creek approximately 18 km downstream of the spring. The Marillana Creek catchment covers an area of approximately 2,050 km^2. Its headwaters arise from the Hamersley Range, and the creek flows in an east and north-easterly direction through the Munjina Claypan.

700000 712000 724000 736000

7472000

7464000

7456000

Packsaddle Range

Weeli Wolli Spring

Weeli Wolli Creek

Jirrpalpur Range

Pebble Mouse Creek

LEGEND

Study Area

Weeli Wolli PEC

Surface Hydrology

Major

Minor

Direction

Drainage Subcatchment

Lower Weeli Wolli Creek

Upper Weeli Wolli Creek

Marillana Creek

Unnamed

Biologic

Scale 1:125,000

0 1 2 3 4 5 Km

Coordinate System: GDA2020 MGA Zone 50
Projection: Transverse Mercator
Datum: GDA2020 Created 18/11/2024

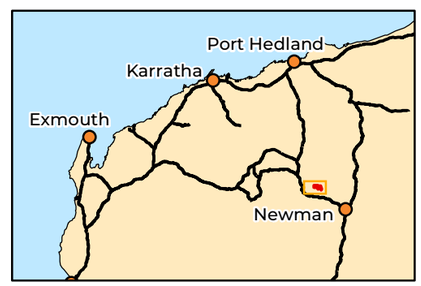

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Figure 2.2: Surface drainage of the Study Area

2.2 Geology

The east-west striking Packsaddle Range formed in Brockman Iron Formation dominates the local stratigraphy of the Study Area. The Brockman Iron Formation is composed of a sequence of interbedded Banded Iron Formation (BIF), shales, siltstones, and cherts. A conceptual cross section of the Brockman Iron Formation associated with the Packsaddle Range deposits is shown in Figure 2.3 and Figure 2.4.

East Packsaddle comprises the most easterly 13 km of the 50 km long Packsaddle Range. At the location of the Study Area, the four members of the Banded Iron formation comprise:

- **Yandicoogina Shale Member** – A 60 m thick sequence of interbedded chert and shale with dolerite sills, located at the top of the formation.
- **Joffre Member** – This member is approximately 360 m thick and is dominated by BIF with minor shale bands.
- **Whaleback Shale** – This member consists of 50 m of shale interbedded with chert and BIF.
- **Dales Gorge Member** – This member, which is approximately 150 m thick, hosts most of the mineralisation of the Packsaddle Range deposits. The Dales Gorge Member is the basal member of the Brockman Iron Formation and comprises an interlayered sequence of BIF and shale macrobands.

All four members have the potential to provide highly suitable habitat for subterranean fauna where sufficiently weathered/fractured, potentially forming a relatively continuous network of suitable subterranean fauna habitat along the Packsaddle Range.

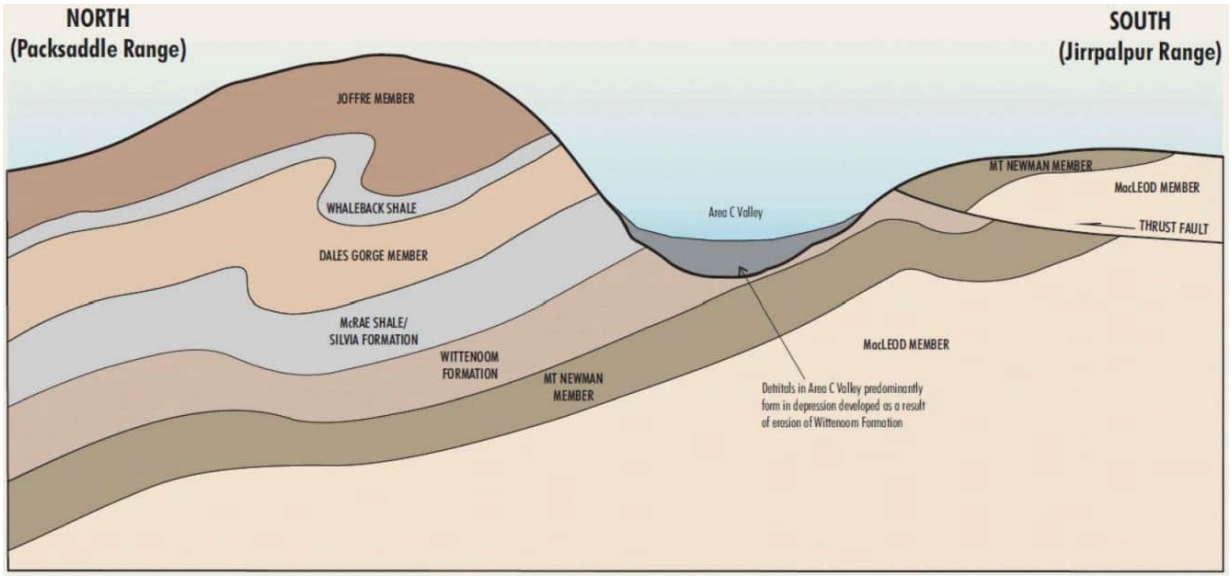

Figure 2.3: Conceptual cross section of Packsaddle Range and the valley below (from BHP, 2016b)

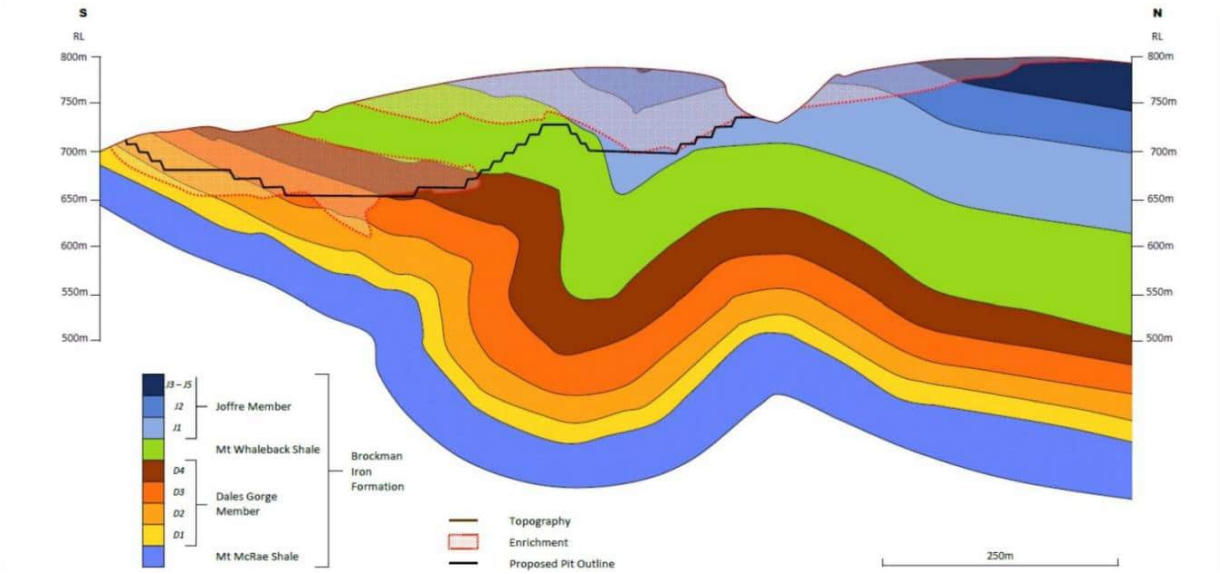

Figure 2.4: Geological cross section of a Packsaddle Range deposit located west of the Study Area (from BHP, 2016b)

Immediately south of Packsaddle Range lies a wide valley colloquially known as Area C Valley, which was formed by preferential weathering and erosion of the relatively soft Wittenoom Formation (comprising repeated sequenced of dolomite, shale, and BIF) (Figure 2.3). The Wittenoom Formation is overlain by Tertiary detritals comprised of alluvium, colluvium, sands, silts, and clays, which have been deposited in the valley over time (Figure 2.5).

The Area C valley leads into Weeli Wolli Creek immediately east of the Study Area. Weeli Wolli Creek has been formed in much the same way, via preferential weathering of the soft Wittenoom Formation. The eroded Wittenoom Formation at Weeli Wolli Creek has also since been overlain by Tertiary Detritals, which have been deposited from the surrounding outcrops over time. The Tertiary sediments are up to 75 m thick upstream of Weeli Wolli Spring, and approximately 20 m thick at the location of the spring.

Upstream of Weeli Wolli Spring, an extensive calcrete deposit has been formed within the detritals (Figure 2.5). The calcrete deposit extends from the surface to more than 30 m below the water table. It is highly permeable and vuggy and provides highly prospective habitats for subterranean fauna. The calcrete deposit is underlain by layers of alluvium, clay, sand, and gravel of variable permeability.

710000

720000

730000

7464000

7456000

Packsaddle Range

Weeli Wolli Spring

792 m

937 m

945 m

917 m

Surface Geology (GSWA 1:20,000)

- Jeerinah Formation (pelite, shale, chert, BIF, dolerite sills)
- Wittenoom Formation (dolomite, chert, shale, BIF)
- Marra Mamba Formation (chert, BIF, pelite)
- Mt McRae Shale & Mt Sylvia Formation
- Channel iron deposits (CID) & Ferricrete (laterite)
- Alluvium (consolidated)
- Silcrete
- Colluvium & alluvium
- Calcrete
- Oakover lacustrine limestone
- Ferruginous pisolites
- Martite goethitic supergene ore
- Brockman Iron Formation (BIF, chert, shale)
- Weeli Wolli Formation (BIF, shale, dolerite sills)
- Dolerite dykes
- Alluvium (drainage channels)

LEGEND

- Study Area

Biologic

Scale 1:78,000

0 1 2 3 Km

Coordinate System: GDA2020 MGA Zone 50
Projection: Transverse Mercator
Datum: GDA2020 Created 07/01/2025

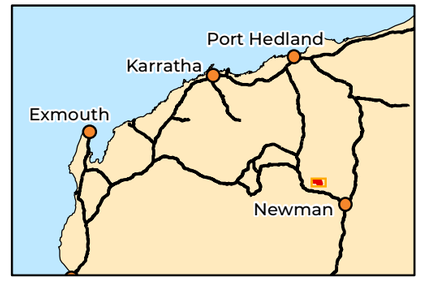

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Figure 2.5: Surface geology of the Study Area (GSWA 1:20,000)

2.3 Hydrogeology

Two main aquifers are present within the Study Area, the Fortescue Valley detrital aquifer and the deeper Wittenoom aquifer occurring below. The two aquifers are conceptually interrelated and connected, notwithstanding localised influences from dykes and low-permeability strata.

The Weeli Wolli Spring area has shallow groundwater (less than 5 metres below ground level [mbgl]) in the immediate area of the Spring, resulting in interaction and connectivity between the groundwater and terrestrial environment (through both surface water connection and vegetation). The key ecological features have evolved and adapted to this shallow groundwater regime. Stygofauna are hosted in shallow aquifers (notably calcrete) and their habitat is maintained by saturation of these aquifers. The vegetation community comprises both obligate and facultative (opportunistic) phreatophytes that utilise this shallow groundwater.

The bedrock under Weeli Wolli Spring and the calcrete aquifer immediately upstream of it comprises (from RPS, 2015):

- Wittenoom Formation. The Paraburdoo member farthest from the spring has a high permeability whereas the Bee Gorge member, stratigraphically higher than the Paraburdoo member and closer to the spring, is of low permeability. The Wittenoom formation occurs at depths of between 40-70 mbgl and gets shallower closer to the spring as the more weathering resistant Bee Gorge member subcrops.
- Mount Sylvia Formation (low permeability).
- Mount McRae Shale (low permeability).
- Brockman Iron Formation (unmineralised and of low permeability).

Along the northern extent of the catchment the Brockman Iron Formation and Mt McRae Shale, which are particularly resistant to erosion, form a prominent ridge (Wildflower Range). Weeli Wolli Creek flows through this ridge (across the regional geological strike) in a narrow fault-controlled valley. Under the creek, the Brockman Iron and Mt McRae Formations rise to shallow subcrop.

The Tertiary sediments contain an extensive calcrete deposit that has a saturated thickness of around 5 m and is vuggy and permeable. Based on the morphology of Australian groundwater calcrete and because the base of the calcrete sits just below the water table, Weeli Wolli Spring is likely to be an area of active calcrete formation. The calcrete is incised by the creek channel which is in-filled with Quaternary alluvium. The calcrete is underlain by poorly sorted alluvium of clay, sands, and gravels that overlie the bedrock.

The prospective habitats for stygofauna in the Weeli Wolli Creek Catchment comprise the palaeochannel aquifers (Tertiary detritals and calcrete formation), and the underlying weathered dolomite of the Wittenoom Formation, all of which occur extensively throughout

the catchment (Biota, 2010). The BIF flanking the palaeochannels is considered to be less prospective. Channel iron deposits in the Marillana Creek sub-catchment and the Lower Weeli Wolli Creek sub-catchment are recognised as good stygofauna habitat.

Groundwater exchange between aquifers in the Weeli Wolli Creek Catchment is considered to be high (Biota, 2010). The ranges of most stygofauna taxa are therefore expected to extend across the catchment, although fauna densities and occurrence are likely to be variable in different geologies and depend on localised water chemistry conditions. Given this interpretation of habitat, it is considered unlikely that any of the aquifers in the Study Area represent small scale disconnected habitats, and stygofauna in this area have generally been shown to have wide ranges across the catchment (Biota, 2010; Eberhard *et al.*, 2009; Eberhard & Humphreys, 1999).

3 Desktop Assessment

3.1 Desktop assessment methods

3.1.1 Collation of fauna and sampling data

Available records of subterranean taxa within a 40 km radius surrounding the Study Area were compiled from the following sources:

- Collection databases of the Western Australian Museum (WAM) for crustaceans, arachnids and myriapods, insects and molluscs (searched September 2023).
- EPBC (Environment Protection and Biodiversity Conservation) Protected Matters search tool (searched March 2024 within 40 km radius around Project centroid).
- Dandjoo (searched October 2024 within 40 km radius around Project centroid).
- BHP subterranean fauna database (provided May 2022).
- Previous reports and data from stygofauna surveys in the Study Area.

Data were filtered by collection method, habitat, taxonomy, and other relevant data fields to exclude terrestrial or non-stygofauna records. WAM registration numbers were cross referenced between data sources to avoid duplication. Higher order identifications were not considered to represent distinct taxa if they were potentially represented elsewhere in the search results by lower order records.

Reports from subterranean fauna surveys within and surrounding the Study Area were reviewed for local and regional context. Reports from relevant surveys are listed below:

- Yandi Junction South-East (JSE) Expansion: Baseline Stygofauna Assessment (Biota, 2005).
- Area C North Mining Area - Ministers North (Subterranean Ecology, 2010).
- Jinaryi Troglofauna Assessment (Bennelongia, 2010).
- Jinayri Mining Lease Stygofauna Surveys (Ecowise Environmental, 2010).
- Yandicoogina Subterranean Fauna Assessment. Phases 1-5 (Biota, 2010).
- Weeli Wolli Creek Catchment: 2011 Stygofauna Sampling (Bennelongia, 2013).
- Packsaddle East Subterranean Fauna: Baseline Report (Bennelongia, 2015c).
- Mining Area C, Life of Project: Stygofauna Assessment (Bennelongia, 2015a).
- Mining Area C, Life of Project: Troglofauna Assessment (Bennelongia, 2015b).
- Ministers North Subterranean Fauna Survey (Bennelongia, 2018).

3.1.2 Threatened and Priority Ecological Communities

Threatened Ecological Communities (TECs) are biological assemblages occurring in a particular habitat which have been endorsed by the Minister of Environment to be under threat of modification or destruction from various processes. Priority Ecological Communities (PECs)

are ecological communities that are recognised to be of significance, but do not meet the formal criteria for a TEC.

Occurrences of PECs and TECs in the vicinity of the Study Area relevant to subterranean fauna were identified using the most recent lists published by the DBCA.

3.2 Desktop assessment results

3.2.1 Database search results

The WAM and BHP subterranean fauna database searches within 40 km of the Study Area revealed 405 troglofauna taxa (including potential troglofauna) from 22 higher taxonomic groups (Appendix B, Figure 3.1) and 169 stygofauna taxa (including potential stygofauna) from 12 higher taxonomic groups (Appendix C, Figure 3.2). A further 109 troglofauna and 44 stygofauna taxa were not considered further due to indeterminate taxonomy (see Appendix A for complete list of taxa, including collection locations). Due to potential synonymies, unresolved taxonomy, and outdated/obsolete identifications, the WAM and BHP database searches are an unreliable estimate of the species diversity within the search area. Appendix A provides a detailed list of all database search records, including collection locations.

The troglofauna species that have been recorded in the search area include spiders, harvestmen, palpigrades, pseudoscorpions, mites, schizomids, centipedes, millipedes, pauropods, symphylans, cockroaches, beetles and weevils, diplurans, isopods, flies, hemipterans, and silverfish (Appendix A).

The stygofauna species that have been recorded in the search area include amphipods, bathynellids, cyclopoid and harpacticoid copepods, isopods, and ostracods (Appendix A).

The Protected Matters search tool did not return any subterranean fauna records within the Search Area. The Dandjoo search yielded approximately 200 invertebrate taxa (mostly higher order identifications; Appendix A) that could represent subterranean fauna. However, as the same taxonomic groups were already represented in the more detailed fauna databases, these records are not considered further herein.

Of the 405 troglofauna taxa recorded from the search area, 27 were recorded from within the Study Area (Figure 3.1, Table 3.1). Of these, 11 taxa were found exclusively from within the Study Area. Of the 169 stygofauna taxa recorded from the search area, 33 were recorded from within the Study Area (Figure 3.2, Table 3.1). Of these, six taxa were only collected from within the Study Area.

Table 3.1: Historical records of taxa found from within the Study Area and their distributions (taxa found only from within the Study Area are highlighted in gold)

Lowest identification	Distribution*	Also found outside Study Area	N° of sites	N° of specimens/ records
Troglofauna				
Arachnida				
Dampetrus `sp. B01 (nr isolatus)`	25.8 km	Yes	7	7
Draculoides `SCH022` (B2 gp)	34 km	Yes	16	26
Draculoides `SCH024`	Single site	No	1	3
Draculoides `SCH025`	Singleton	No	1	1
Draculoides `SCH067`	36.1 km	Yes	15	27
Indohya `PSE186`	Single site	No	1	2
Indohya sp. B06	Single site	No	1	2
Opiliones sp. B02	26.6 km	Yes	2	2
Palpigradi `sp. B01`	21.3 km	Yes	2	6
Palpigradi `sp. B19`	Singleton	No	1	1
Tyrannochthonius `sp. B37`	Singleton	No	1	1
Diplopoda				
Lophoturus madecassus	50+ km	Yes	154	990
Insecta				
Brentidae sp. B02	Singleton	No	1	1
Cryptorhynchinae sp. B19	Singleton	No	1	1
Dodecastyla sp. B02	50+ km	Yes	23	50
Meenoplidae `sp. B04`	30.1 km	Yes	1	2
Nicoletiidae `sp. B02`	22.1 km	Yes	2	3
Nocticola `sp. BLA001`	50+ km	Yes	1	4
Nocticola cockingi s.l.	50+ km	Yes	88	248
Phaconeura sp. B02 s.l.	43 km	Yes	16	217
Phaconeura sp. B04	50+ km	Yes	25	163
Ptinella `sp. Helix-CPT003`	Widespread	Yes	1	1
Ptinella sp. B01 (=MC)	42.7 km	Yes	4	150
Malacostraca				
Armadillidae `sp. B11`	Singleton	No	1	1
Troglarmadillo sp. B59	Singleton	No	1	1
Pauropoda				
Pauropodidae sp. B01 s.l.	26.5 km	Yes	8	13
Symphyla				
Hanseniella sp. B09	Singleton	No	1	1

Lowest identification	Distribution*	Also found outside Study Area	N° of sites	N° of specimens/ records
Stygofauna				
Arachnida				
Halacaridae sp. B01	0.5 km	No	2	2
Recifella sp. P1 (nr *umala*) (PSW)	Widespread	Yes	1	1
Oligochaeta				
Ainudrilus sp. WA26 (PSS)	Single site	No	1	11
Enchytraeus sp. AP PSS1 s.l.	50+ km	Yes	10	233
Enchytraeus sp. AP PSS2 s.l.	44.5 km	Yes	5	26
Phreodrilidae sp. AP DVC s.l.	50+ km	Yes	20	121
Pristina longiseta	Widespread	Yes	1	5
Malacostraca				
Bathynella sp. 1 (Weeli Wolli)	Singleton	No	1	1
Chydaekata `sp. E`	36.3 km	Yes	23	105
Maarrka weeliwollii	50+ km	Yes	22	42
Paramelitidae `sp. B02`	47.8 km	Yes	16	152
Paramelitidae `sp. B03`	50+ km	Yes	2	3
Paramelitidae Genus 2 sp. B02	50+ km	Yes	54	579
Paramelitidae Genus 2 sp. B03	11.6 km	Yes	2	9
Pygolabis weeliwolli	28.3 km	Yes	13	114
Maxillopoda				
Australoeucyclops karaytugi	16.4 km	Yes	3	8
Diacyclops cockingi	50+ km	Yes	27	529
Diacyclops humphreysi	50+ km	Yes	22	614
Diacyclops humphreysi s.l.	50+ km	Yes	54	2337
Diacyclops sobeprolatus	50+ km	Yes	24	822
Gordanitocrella trajani	31.5 km	Yes	17	230
Mesocyclops brooksi	50+ km	Yes	5	11
Mesocyclops holynskae	Singleton	No	1	3
Microcyclops varicans	50+ km	Yes	9	575
Schizopera sp. B02	0.5 km	No	3	5
Ostracoda				
Cypretta seurati	Widespread	Yes	1	15
Deminutiocandona mica	Single site	No	1	8
Gomphodella yandii	20.4 km	Yes	11	120
Meridiescandona facies	50+ km	Yes	17	225
Meridiescandona lucerna	39.9 km	Yes	10	78
Meridiescandona marillanae	33.7 km	Yes	11	113
Notacandona boultoni	38.9 km	Yes	10	68
Notacandona modesta	12.1 km	Yes	5	31

* 'Widespread' denotes taxa found to have distributions >50 km, often extending beyond the search area.

645000 680000 715000 750000 785000

7500000 7470000 7440000

Marillana Creek

Turee Creek

Western 4

Hairpin

Yandicoogina Creek

South Flank

HDI Flat Top

Coondiner Creek

Fortescue River

Angelo River

Fortescue River

Historical Troglofauna Records (Orders)

- Araneae
- Blattodea
- Cephalostigmata
- Coleoptera
- Diplura
- Diptera
- Geophilomorpha
- Hemiptera
- Isopoda
- Opiliones
- Palpigradi
- Polydesmida
- Polyxenida
- Pseudoscorpiones
- Schizomida
- Scolopendromorpha
- Spirobolida
- Tetramerocerata
- Zygentoma

LEGEND

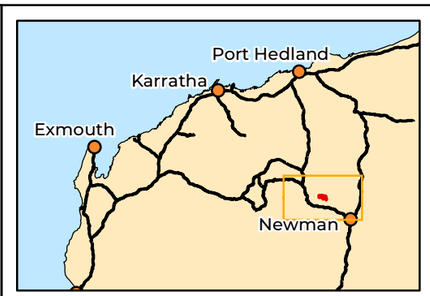
- Desktop Search Area
- Study Area
- Operating Mine
- Major Surface Hydrology
- ◇ Troglofauna sampling site

Biologic

Scale 1:400,000

0 5 10 15 Km

Coordinate System: GDA2020 MGA Zone 50
Projection: Transverse Mercator
Datum: GDA2020 Created 04/12/2024



BHP WAIO

East Packsaddle: Subterranean Fauna Baseline Survey

Figure 3.1: Historical troglofauna records within 40 km of the Study Area

645000 680000 715000 750000 785000

7500000 7470000 7440000

Marillana Creek
Turee Creek
Western 4
Harpin
Yandicoogina Creek
MAC East
South Flank
HDI Flat Top
Goondine Creek
Fortescue River
Angelo River
Fortescue River

Historical Stygofauna Records (Orders)

Amphipoda	Haplotaxida
Bathynellacea	Harpacticoida
Calanoida	Isopoda
Cyclopoida	Podocopida
Enchytraeida	Trombidiformes

LEGEND

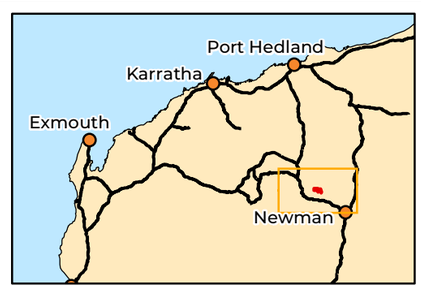
- Desktop Search Area
- Study Area
- Operating Mine
- Major Surface Hydrology
- ◇ Stygofauna sampling site

Biologic

Scale 1:400,000

0 5 10 15 Km

Coordinate System: GDA2020 MGA Zone 50
Projection: Transverse Mercator
Datum: GDA2020 Created 04/12/2024



BHP WAIO
East Packsaddle: Subterranean Fauna Baseline Survey

Figure 3.2: Historical stygofauna records within 40 km of the Study Area

3.2.2 Previous surveys within and nearby the Study Area

3.2.2.1 Subterranean fauna surveys at Mining Area C, East Packsaddle, and South Flank

Nearly 800 stygofauna samples were collected at Mining Area C and surrounds (Bennelongia, 2015a, 2015c), located approximately 15 km west of the Study Area. Stygofauna samples were collected between 2007 and 2015, and sampling locations included bores closer to the Study Area, such as locations on Packsaddle Range as well as within the upper Weeli Wolli Creek catchments (Bennelongia, 2015a, 2015c). A total of 51 stygofauna species from 10 higher level groups were identified, comprising flatworms (1 species), nematodes (treated as 1 species, but potentially more), rotifers (4 species), oligochaetes (7 species), mites (3 species), ostracods (8 species), copepods (13 species), syncarids (5 species), amphipods (8 species), and isopods (1 species) (Bennelongia, 2015a).

Over 4000 troglofauna samples were collected at Mining Area C and surrounds (including East Packsaddle and West Packsaddle, South Flank, and Jinidi) between 2007 and 2015 (Bennelongia, 2015b, 2015c). At least 92 species of troglofauna belonging to 17 orders have been identified, comprising five orders of arachnid (Pseudoscorpiones, Palpigradi, Schizomida, Araneae, Opiliones), one order of crustaceans (Isopoda), five orders of myriapods (Scolopendrida, Polyxenida, Pauropoda, and Cephalostigmata), and six orders of hexapod (Diplura, Zygentoma, Blattodea, Hemiptera, Coleoptera, and Diptera) (Bennelongia, 2015b).

3.2.2.2 Subterranean fauna surveys at Jinidi

Bennelongia conducted a troglofauna assessment at Jinidi, immediately south-east of the Study Area, between 2008 and 2009 (Bennelongia, 2010). Five iron ore bodies were investigated during the survey, namely OB13, OB14, OB15, OB16 and OB41, collecting a total of 382 scrape samples and 415 trap samples. From a total of 240 troglofauna specimens at least 24 species from 14 orders were found, comprising Schizomida, Pseudoscorpiones, Palpigradi, Opiliones, Araneae, Scolopendromorpha, Polyxenida Cephalostigmata, Diplura, Zygentoma, Blattodea, Hemiptera, Coleoptera, and Diptera. The troglofauna community was noted to be moderately rich compared to other areas of the Pilbara. Four species (Opilionida sp. B3, Pselaphinae sp. B5, Carabidae sp. B1 and Symphyla sp. B5) were found to be restricted to the Jinidi study site.

Ecowise Environmental conducted a stygofauna survey at Jinidi between 2008 and 2009 (Ecowise Environmental, 2010), sampling 151 bores and collecting 79 stygofauna specimens. Six taxa were collected during the survey, comprising worms, copepods, and bathynellids, of which five were of indeterminate taxonomy.

3.2.2.3 Subterranean fauna surveys at Ministers North

Subterranean Ecology (2009-2010; Subterranean Ecology, 2010) and Bennelongia (2017-2018; Bennelongia, 2018) conducted baseline subterranean fauna surveys at Ministers North, located ~6 km north of the Study Area. A total of 56 stygofauna and 234 troglofauna samples were

collected. In total, 47 stygofaunal animals belonging to seven species and 386 troglofaunal animals belonging to 39 species were collected from Ministers North and its immediate surrounds. The stygofauna community consisted of a nematode, oligochaetes, a copepod and an amphipod. The troglofaunal community was diverse, with 13 higher level groups represented. Thirty-one taxa were considered to restricted to the tenement and its immediate vicinity.

3.2.2.4 Subterranean fauna surveys at Yandicoogina

Biota Environmental Consultants (Biota) sampled a total of 68 bores at Yandicoogina, located approximately 15 km north-east of the Study Area, over five phases between 2003 and 2009 (Biota, 2010). A high abundance and diversity of stygofauna was identified, comprising 46 stygofauna taxa from nine orders (Amphipoda, Bathynellacea, Isopoda, Cyclopoida, Harpacticoida, Ostracoda, Hydracarina, Oligochaeta, and flat worms). The considerable taxonomic richness of the stygofauna collected was attributed to the presence and extent of alluvial and calcrete aquifer habitats associated with the major drainages at Yandicoogina and surrounds (Biota, 2010). Troglofauna from four higher level groups were identified, comprising Schizomida, Aranea, Pseudoscorpiones, and Polyxenida (Biota, 2010).

3.2.2.5 Subterranean fauna surveys at Weeli Wolli Creek Catchment

Bennelongia sampled 64 bores from the Upper and Lower Weeli Wolli and Rhodes Ridge, collecting 111 samples (Bennelongia, 2013). The samples yielded a total of 985 stygofauna specimens, comprising 26 species belonging to seven higher order groups. This report also incorporated the results of previous sampling in the Upper and Lower Weeli Wolli Creek Catchments, increasing the total number of stygofauna species to 51 (comprising 11 higher order groups including flatworms, nematodes rotifers, aphanoneurans, oligochaetes, mites, ostracods, copepods, syncarids, amphipods, and isopods). These catchments therefore host a rich stygofauna community, with most of them (47 species) reported as being relatively widespread.

3.2.2.6 Stygofauna surveys at Yandi Junction South East (JSE)

Biota (2005) sampled a total of 23 bores between Marillana and Weeli Wolli Creeks (the Yandi JSE Expansion). The survey collected flatworms (unidentified but potentially unique to the study area), oligochaetes (unidentified), water mites (3 taxa), ostracods (3 taxa), copepods (2 taxa), amphipods (4 taxa), and isopods (2 taxa). The abundance and diversity of stygofauna collected from the area was attributed to the extent of alluvial and calcrete aquifer habitats associated with the major drainages in the area.

3.2.3 Priority and Threatened Ecological Communities

One PEC relevant to subterranean fauna occurs within the Study Area, the Priority 1 Weeli Wolli Spring community (Figure 1.1).

According to the DBCA PEC listing "the spring and creekline are also noted for their relatively high diversity of stygofauna, and this is probably attributed to the large-scale calcrete and alluvial aquifer system associated with the creek" (DBCA, 2023). An analysis of the WAM and BHP subterranean fauna databases revealed 33 distinct stygofauna taxa (plus ten indeterminate taxa) occurring within and nearby (<5 km) the Weeli Wolli PEC. Of these, six are currently only known from within the PEC (these are the same taxa identified as being restricted to the Study Area in the database search results above; Table 3.1), whilst the remaining 27 occur beyond the PEC and the Study Area. It is likely that there are some taxonomic limitations with the historic data, particularly limited genetic sequencing that may constrain the ability to resolve species-level identifications and conduct wider regional comparisons. Nevertheless, the diversity of stygofauna is notable, and is part of the reason Weeli Wolli Spring is considered a Priority 1 ecological community. In 2014, a series of groundwater dependent pools upstream of Weeli Wolli Spring were added to the Priority listing by the former Department of Parks and Wildlife as a second occurrence of the Weeli Wolli Spring PEC (BHP, 2016a). These pools are colloquially known as Ben's Oasis. Ben's Oasis is located approximately 20 km upstream, and to the south, of Weeli Wolli Spring. In this area, groundwater dependent vegetation including mature *Eucalyptus camaldulensis* and *Melaleuca argentea* are concentrated along a relatively narrow creek channel adjacent to groundwater fed water pools.

The permanent water and saturated sediment at Weeli Wolli Spring provide habitat for a unique assemblage of herbs and sedges, comprising *Stylidium weeli wolli*, *Lobelia arnhemiaca*, *Cladium procerum*, and *Fimbristylis sieberiana* (van Leeuwen, 2009). The area also provides important habitat for birds and other fauna including bats. The high ecological value of Weeli Wolli Spring led to its listing as a Priority 1 PEC.

4 Methods

4.1 Survey design

4.1.1 Survey timing and personnel

The current survey was undertaken over three phases and seven trips between November 2022 and June 2024 (Table 4.1). Sampling was conducted under DBCA Regulation 27 licences BA27000769 and BA27000987 (Appendix D). Shae Callan and Michael Curran led the survey planning, with Fabian Rudin and Anton Mittra leading fieldwork. Hayley Hampton, Chao Lyu, Nick Stevens, Ruby McKenna, and Siobhan Paget also conducted field sampling.

Table 4.1: Summary of field survey details

Survey Phase	Trip	Season	Mobilisation dates	Sampling type	Personnel
Phase 1	Trip 1	Wet season	May 11th to 17th 2022	Net-hauling	Michael Curran, Siobhan Paget & Ruby McKenna
	Trip 2	Dry season	November 13th to 25th 2022	Trap deployment Net-scraping Net-hauling	Michael Curran & Fabian Rudin
	Trip 3	Wet season	February 27th to March 3rd 2023	Trap pick-up	Michael Curran & Hayley Hampton
Phase 2	Trip 4	Wet season	June 14th to 16th 2023 June 24th to July 1st 2023	Trap deployment Net-scraping Net-hauling	Fabian Rudin & Chao Lyu
	Trip 5	Dry season	September 4th to 8th 2023	Trap pick-up Net-scraping Net-hauling	Fabian Rudin & Nick Stevens
Phase 3	Trip 6	Wet season	April 11th to 18th 2024	Trap deployment Net-scraping Net-hauling	Anton Mittra & Hayley Hampton
	Trip 7	Wet season	June 14th to 18th 2024	Trap pick-up Net-scraping Net-hauling	Anton Mittra & Hayley Hampton

4.1.2 Weather

Long-term and survey-specific climate data (rainfall from 1971 – 2024, temperature data from 1996 – 2024) were obtained from the Bureau of Meteorological (BOM) weather station at Newman Airport (station number 7176), approximately 70 km south-east of the Study Area.

Minimum and maximum temperatures were mostly on par with the long-term average (LTA) in the months prior to all trips, being slightly below LTA prior to Trip 2 and slightly above LTA prior to Trip 6 (Figure 4.1).

There were significant, above-LTA rain events within 3 months prior to trips 1, 2, 4, and 6, while there was below average rainfall prior to Trips 3, 5, and 7 (Figure 4.1).

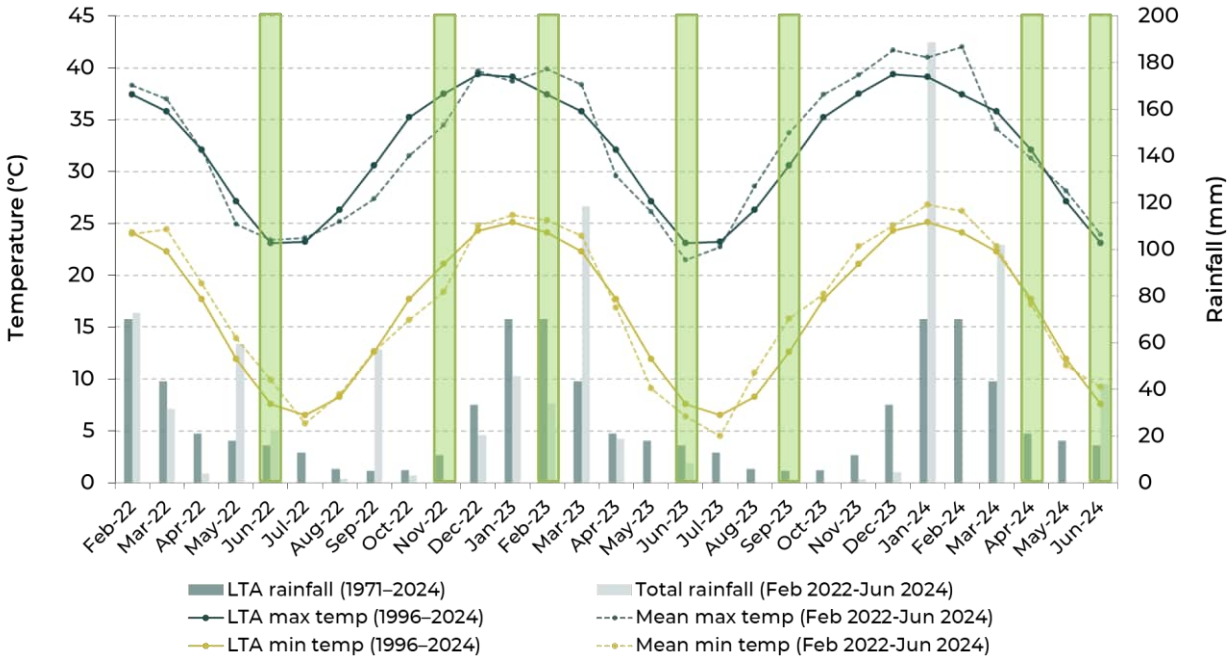


Figure 4.1: Long-term average and current (2022-2024) climatic data at Newman Aero, Station 7176 (BOM 2024)
Note: Data includes total monthly rainfall (mm) and average monthly maximum and minimum temperatures (°C). Approximate survey timing is indicated by the green boxes.

The prevailing climatic conditions prior to and during the current survey were unlikely to have constrained sampling efficacy in relation to subterranean fauna. Indeed, the above-average rainfall received in the months prior to Trips 1, 2, 4, and 6 (during which 93.5% of the scrape and haul samples were taken) would have been expected to increase subterranean fauna activity.

4.1.3 Site selection and sample effort

Subterranean fauna sampling sites were selected based on a variety of factors including spatial spread and coverage of prospective habitat units. Site specific factors of groundwater bores and drill holes were also considered, these included: slotted interval depth with regards to prospective aquifer targets, construction details, time since drilling, and accessibility for sampling. Sampling for stygofauna was undertaken by net-hauling cased bores (production or monitoring bores) and uncased exploration drill holes. Sampling for troglofauna was undertaken by net-scraping and trapping uncased exploration drill holes. Uncased bores intercepting groundwater were sampled for both troglofauna and stygofauna (scrape-hauling).

In total, 595 troglofauna samples (scrapes, scrape-hauls, and traps) were collected from 130 drill holes across the Study Area (Figure 4.2, Table 4.2). A total of 118 stygofauna samples (hauls and scrape-hauls) were collected from 50 bores and drillholes across the Study Area (Figure 4.3). Details of bores and drill holes sampled are provided in Appendix E.

Table 4.2: Subterranean fauna sampling effort during the current survey

Phase	N° sites sampled	N° of scrape samples	N° of scrape-haul samples	N° of haul samples	N° trap samples collected	Total
Phase 1	138	81	35	14	97	228
Phase 2	107	75	35	4	89	203
Phase 3	107	64	26	4	93	187
Total Troglofauna	130	220	96		279	**595**
Total Stygofauna	50		96	22		**118**

712000
716500
721000
725500
730000

7466600
7462900
7459200

Weeli Wolli Spring
Weeli Wolli Creek
West Angelas Rd

LEGEND

- Study Area
- Local Road
- Rail
- Weeli Wolli PEC
- Major Surface Hydrology

Troglofauna Sampling

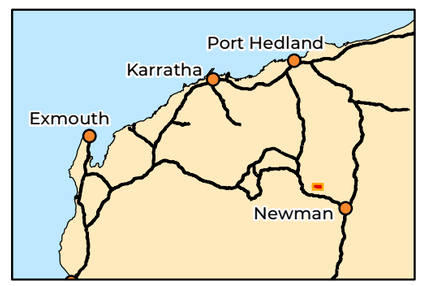
- Scrape
- Trap

Biologic

Scale 1:55,000

0 0.5 1 1.5 2 Km

Coordinate System: GDA2020 MGA Zone 50
Projection: Transverse Mercator
Datum: GDA2020 Created 14/11/2024



BHP WAIO

East Packsaddle: Subterranean Fauna Baseline Survey

Figure 4.2: Troglofauna sample effort during current survey

712000
716500
721000
725500
730000

7466600
7462900
7459200

Weeli Wolli Spring
Weeli Wolli Creek
West Angelas Rd

LEGEND

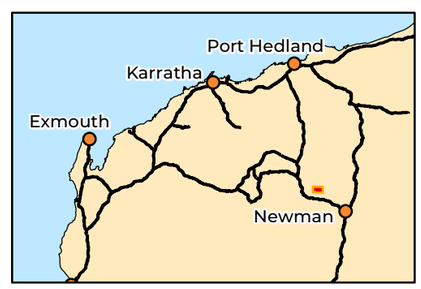
Study Area
Local Road
Rail
Weeli Wolli PEC
Major Surface Hydrology

Stygofauna Sampling
Haul

Biologic

Scale 1:55,000
0 0.5 1 1.5 2 Km

Coordinate System: GDA2020 MGA Zone 50
Projection: Transverse Mercator
Datum: GDA2020 Created 14/11/2024



BHP WAIO
East Packsaddle: Subterranean Fauna Baseline Survey

Figure 4.3: Stygofauna sample effort during current survey

4.1.4 Sampling methods

4.1.4.1 Stygofauna net-hauling

Stygofauna were sampled by net-hauling using weighted plankton nets in accordance with published technical guidance (EPA, 2016b, 2021b). Sampling net diameter was selected subject to the diameter of each hole and to reduce equipment damage/loss via snagging. For example, 100–150 mm holes were sampled using nets with diameters of 90 mm, while 50 mm piezometer bores were sampled with 40 mm diameter nets. As per EPA guidance, each sampling site was hauled (net lowered to the end of the hole and retrieved) a maximum of eight times during a single visit (up to four hauls using a 150 µm mesh net and up to four using a 53 µm mesh net). Each 'haul sample' therefore comprises all hauls undertaken during a site visit. Instances when less than the recommended number net-scrapes were undertaken were due to site specific limitations, such as thick sediment or drillers lubricant blocking net, or net snagging on blockages. The base of each net was fitted with a sample receptacle with a 50 µm mesh base to allow filtration. The net was agitated at the base of each haul to maximise the collection of benthic animals, before being retrieved at a moderate pace. The contents of the net and receptacle were flushed into a bucket following each haul. The resultant composite sample was elutriated to remove coarse sediments, filtered through a 53 µm mesh net to reduce water content, and transferred to a 120 mL polycarbonate vial. Samples were preserved in 100% ethanol and stored on ice and/or refrigerated to promote DNA fixation. Troglofauna net-scraping

Troglofauna were sampled in uncased drill holes by scraping each hole using a haul net with 150 µm mesh sidewalls. A custom-built scraping attachment was attached above the net to dislodge and collect fauna from the bore walls. As per EPA guidance, each sampling site was scraped (net lowered to the end of the hole and retrieved) four times (but up to eight in a few cases during this survey) during a single visit (each 'scrape sample' therefore comprises all scrapes undertaken during a site visit). Instances when less than the recommended number net-scrapes were undertaken were due to site specific limitations, such as thick sediment or drillers lubricant blocking net, or net snagging on blockages. The contents of the net were flushed into a bucket, elutriated, and preserved as per stygofauna net-hauling.

Where the water table was intercepted, a combined troglofauna scrape/stygofauna net-haul sample (scrape-haul) was collected comprising up to eight hauls along the full length of the hole including both above and below the water table.

4.1.4.2 Trapping

Custom-made cylindrical PVC traps (approximately 50 mm × 300 mm) used to sample troglofauna in uncased drill holes. Each trap was baited with leaf litter (spinifex or Acacia sourced from the Pilbara region) and/or pea straw that had been sterilised using a microwave.

Traps were lowered on a nylon cord to a suitable depth and left in situ for six to eight weeks before being retrieved and transported back to the Biologic laboratory. The contents of each trap were then processed in Tullgren funnels for approximately three days.

4.1.5 Water physicochemistry

Prior to stygofauna sampling, a basic suite of physicochemical water quality parameters (electrical conductivity [EC], pH, Redox oxidation reduction potential [ORP], and dissolved oxygen [DO]) was measured with a multiparameter water quality meter from a groundwater sample collected from the top of the water table using a plastic bailer.

4.2 Specimen identification

4.2.1 Morphological identification

Sorting of subterranean fauna from the preserved samples was done with forceps and pipettes under dissecting microscopes in the Biologic laboratory. Subsequent parataxonomy and taxonomic identification was completed under dissecting microscopes and compound microscopes, as necessary. Preliminary identification of subterranean fauna involved identification of specimens to morphotype classifications utilising published literature and available taxonomic keys for each group. Morphotypes from each sample were preserved in 100% ethanol to allow for further morphological and molecular analyses. Unique specimen tracking codes were assigned to each individual specimen. Species comparisons and alignments were performed using specimens collected beyond the Study Area across the wider sub-regional area. Dr Juliana Pille Arnold, Dr Giulia Perina, and Alex Riemer completed specialist taxonomic identifications and regional comparisons of stygofauna. Morgan Lythe and Christopher Taylor undertook troglofauna taxonomic identifications.

4.2.2 Molecular analysis and identification

Taxonomic limitations associated with subterranean fauna sampling are well known (Biota, 2013; Finston *et al.*, 2011; Halse *et al.*, 2014). Identifications can often be inconclusive due to morphological conservatism, where subterranean faunal groups lack diagnostic characters required for identification (Finston *et al.*, 2011). Shared morphologies can then lead to morphotype groupings that underrepresent the true taxonomic diversity of a community, whilst morphological plasticity can falsely inflate taxonomic diversity. DNA barcoding has been developed as a reliable tool for the designation of taxonomic identity and distinguishing between cryptic species. Molecular analysis was undertaken to confirm species level identifications, enable comparison with specimens recorded locally and regionally, and enable ongoing assessment of the significance and species composition of the stygo- and troglofauna communities present at East Packsaddle.

Biologic completed genetic analyses (DNA barcoding using mitochondrial COI) on a subset of specimens from taxa at each site to validate morphological identifications. Regional genetic alignments were undertaken for each genetically determined operational taxonomic unit (OTU), using available public genetic databases (GenBank), BHP's subterranean fauna databases as well as Biologic's own sequence library (comprising almost 4000 quality assured DNA sequences). Dr Joel Huey, Stephanie Floeckner, and Liesel Morgan completed the genetic analyses and regional comparisons. Appendix F provides further details regarding the methods of DNA extraction, sequencing, and analysis.

Overall sequencing success was very high (95% sequencing success), with 220 viable sequences obtained from 231 specimens selected for molecular analysis (Table 4.3).

Table 4.3: Taxonomic groups included in the DNA analysis and summary of sequencing success

Class	Order	Family	Number of specimens	Sequences derived	Success (%)
Arachnida	Araneae	Indeterminate family	12	12	100
		Oonopidae	1	1	100
		Orsolobidae	2	2	100
	Palpigradi	Indeterminate family	9	8	89
	Pseudoscorpiones	Chthoniidae	26	25	96
		Hyidae	7	5	71
	Schizomida	Hubbardiidae	33	33	100
	Trombidiformes	Pezidae	3	2	67
Chilopoda	Scolopendromorpha	Cryptopidae	1	1	100
		Scolopendridae	2	2	100
Clitellata	Enchytraeida	Enchytraeidae	3	3	100
	Haplotaxida	Naididae	6	6	100
		Phreodrilidae	6	4	67
Entognatha	Diplura	Japygidae	4	4	100
		Parajapygidae	2	2	100
		Projapygidae	2	1	50
Insecta	Blattodea	Nocticolidae	7	7	100
	Coleoptera	Indeterminate family	1	0	0
		Carabidae	2	2	100
		Curculionidae	4	4	100
		Latridiidae	1	1	100
		Ptiliidae	2	2	100
		Staphylinidae	2	2	100
	Hemiptera	Meenoplidae	5	5	100
	Zygentoma	Nicoletiidae	7	7	100
Malacostraca	Amphipoda	Paramelitidae	22	22	100
	Bathynellacea	Parabathynellidae	3	3	100
	Isopoda	Indeterminate family	7	7	100
		Armadillidae	2	2	100
		Tainisopidae	2	2	100
Maxillopoda	Cyclopoida	Cyclopidae	10	10	100
	Harpacticoida	Ameiridae	4	4	100
		Miraciidae	1	1	100
		Parastenocarididae	1	1	100

Class	Order	Family	Number of specimens	Sequences derived	Success (%)
Ostracoda	Podocopida	Candonidae	14	12	86
		Limnocytheridae	1	1	100
Pauropoda		Indeterminate family	8	8	100
	Tetramerocerata	Pauropodidae	3	3	100
Symphyla	Cephalostigmata	Scolopendrellidae	1	1	100
		Scutigerellidae	2	2	100
Grand Total			**231**	**220**	**95**

4.3 Rationalisation of morphological and molecular identifications

Final taxonomic affiliations for specimens were determined, with combined consideration of morphological and molecular analyses, according to the following protocol:

1. Specimens belonging to groups with comprehensive taxonomic treatments (*i.e.*, formally described), which were not sequenced, were assigned their morphological determinations as final identification.
2. For specimens that were morphologically identified but sequencing failed, the morphological species was retained as the final identification.
3. Where the same specimens were sequenced and morphologically identified, and the two data sets arrived at a matching and consistent taxon (*i.e.*, morphological species 'X' always equated to lineage 'X'), then the final identification was assigned as the lowest taxonomic rank, with the lineage name used as the species epithet.
4. Where the same specimens were sequenced and morphologically identified, and the two data sets did not align (*i.e.*, morphological species 'X' equated to multiple lineages), then the final identifications were split into species-level taxa based on the sequencing results and assigned the relevant lineage name as the species epithet.
5. Where specimens had not been, or could not be, morphologically identified (denoted by the indeterminate 'sp.'), and were sequenced, then the lineage name was used for the final identification.

4.4 Determining species ranges

An assessment of species potential ranges was made in the context of the Study Area, the extent of sampling, and the occurrence of local habitat units. The assessment was based on the collection data available, historical/regional sampling records, and the habitat/ecological information available. The assessment aimed to determine which species were more likely to be limited to particular habitats within the Study Area (in comparison to species known to occur more widely beyond the Study Area), based on:

- Collection data: a 'known linear range' was calculated for each species known from two or more sites by measuring the linear distance between the two furthest collection sites. This is not presented as an accurate estimate of the actual species' range, or a precise

measure of the species' potential distribution throughout its range. Uncertainties related to sampling constraints and factors influencing the actual distributions need to be accounted for. Nevertheless, the 'known linear range' provides an initial indication of the minimum known range where the species is newly recorded. It also provides an early basis for comparison of widely distributed *vs* narrowly distributed species, and an opportunity to assess against the nominal range criterion for SRE species;

- Habitat information: the habitat units (aquifers, BIF) from which a species has been collected and the extent and inferred connectivity (or isolation) of that habitat, including the presence of dispersal barriers, such as dykes. Collection records within particular habitat settings sometimes facilitate a degree of inference about potential wider distributions *e.g.,* hyporheic fauna collected from major drainage lines;
- Biological/ecological information: multiple factors where information is available, including but not limited to life history traits, dispersal abilities, degree of troglo- or stygomorphy (such as eye reduction, depigmentation, elongation of sensory appendages), ecological category of the taxon group (stygobitic vs stygoxenic/ stygophilic; troglobitic vs trogloxenic/troglophilic), known distributions and species assemblage turnover patterns of other species within the group; and
- The WAM's current categorisation framework for short-range endemic (SRE) invertebrates (Table 4.4). This system assigns one of three categories (Confirmed SRE, Potential SRE, and Widespread) to each species based on its likely range relative to the criterion proposed for short-range endemism by Harvey (2002) of having a total range of less than 10,000 km^2.

Table 4.4: SRE categorisation of the WAM

	Taxonomic Certainty	Taxonomic Uncertainty
Distribution <10 000km^2	**Confirmed SRE** • A known distribution of < 10,000km^2. • The taxonomy is well known. • The group is well represented in collections and/ or *via* comprehensive sampling.	**Potential SRE** • Patchy sampling has resulted in incomplete knowledge of geographic distribution. • Incomplete taxonomic knowledge. • The group is not well represented in collections. • Category applies where there are significant knowledge gaps. **SRE Sub-categories may apply:** A) Data Deficient B) Habitat Indicators C) Morphology Indicators D) Molecular Evidence
Distribution >10 000km^2	**Widespread** (not an SRE) • A known distribution of > 10,000km^2. • The taxonomy is well known. • The group is well represented in collections and/ or *via* comprehensive sampling.	

4.5 Constraints and limitations

Limitations to the taxonomic and ecological understanding of subterranean fauna provide challenges when interpreting survey results, particularly when combining current and historical datasets. Subterranean fauna occupy habitats that are difficult to access and are mainly sampled via bores and drill holes. Yields of animals are typically low, which may either reflect naturally low densities of animals or be the result of sampling limitations. Some sampling artefacts are unavoidable, and large sampling efforts are required to achieve survey completeness, due to relatively low detection rates and high proportions of infrequently detected species. As some species are difficult to detect reliably throughout their range, confident assessment of species distributions is challenging, despite high repeated sampling effort.

Within these general constraints, the survey findings are based upon the best available information despite some inherent residual uncertainties. Specific limitations relating to the current and previous survey data are listed below.

- Spatial/geographical spread of sampling – sampling was limited by the distribution, accessibility, and suitability of bores within the Study Area. Bore availability varied throughout the Study Area, partly due to some areas having been rehabilitated prior to the survey. The sampling plan for each survey was refined to enhance spatial coverage where possible to fill key knowledge gaps in the understanding of species distributions and habitats. Given the distribution of samples across the Study Area, with some gaps remaining (Figure 4.2 and Figure 4.3), this is considered a moderate limitation.
- Depth of drilling – the depth of drilling in some areas, particularly in the western half of the Study Area, limited the number of drill holes intercepting groundwater habitats (*i.e.* suitable for stygofauna sampling). Best efforts were made to maximise stygofauna sample effort by repeated bore/drillhole sampling where groundwater was intercepted. Given the distribution of stygofauna samples (Figure 4.3), with some gaps remaining, this is considered a moderate limitation.
- Groundwater physicochemical measurements from bailer sampling – some bores/ holes were obstructed or too deep (>60 m) to sample successfully by bailer. Due care was taken to exclude obviously erroneous results, but bailer samples can sometimes alter physicochemical measurements (*e.g.* DO, temperature). The conditions sampled by bailer sampling in bores may not reflect the conditions within the wider aquifer and were thus interpreted cautiously. This is considered a minor limitation.
- Taxonomy and genetics – specimens were identified using a combination of morphological and genetic analyses wherever possible. Best practices were followed in the field and laboratory to enhance success rates of genetic sampling. However, a small proportion of sequence failure and contamination is unavoidable. Extra care was taken

to omit any erroneous, low confidence, or contaminated DNA sequences. The genetics report (Appendix F) contains full details and specific constraints and limitations of the genetic analyses undertaken for the survey. Given the sequencing success rate achieved (Table 4.3), this is considered a minor limitation.

- Sub-sampling for genetic analysis – the high number of specimens collected necessitated sub-sampling to complete genetic analysis. Detailed parataxonomic work was undertaken on each group to provide a basis for genetic sub-sampling of the putative species per site. The level of parataxonomic resolution prior to genetic analysis differed between groups and was limited by existing taxonomic frameworks. Sampling, parataxonomy, morphological identifications, and genetic analyses were undertaken in a cyclical, iterative approach to fill knowledge gaps in the understanding of species distributions within the Study Area. Not all specimens were able to be sequenced, and it is possible that some taxa may remain undetected within the material. Nevertheless, confirmation of the same OTUs being repeatedly detected in the same bores/habitats between multiple subsequent surveys provided a high degree of confidence in the overall distribution patterns of most subterranean fauna species. Despite this, sub-sampling will inherently result in only a subset of all specimens being identified with a high degree of certainty, and this is therefore considered to be a moderate limitation.

5 Results

5.1 Troglofauna

Of the 595 troglofauna samples collected during the current survey, 258 samples yielded 1,346 specimens from eight subterranean fauna groups. Using a combination of morphological identifications and molecular analyses, 50 distinct troglofauna species/OTUs were determined (Table 5.1, Figure 5.1 – Figure 5.5), comprising arachnids, isopods, diplurans, insects, centipedes, pauropods, and symphylans.

A further 31 indeterminate higher-level taxa represented leftover material from subsampling for molecular identifications, and specimens unable to be identified to species level (Table 5.2). All leftover specimen material was stored appropriately such that it may be subsampled again during future rounds of molecular analysis, if needed for EIA of any particular taxon group or species.

Based on current linear ranges (Table 5.1, the 50 troglofauna taxa recorded from the Study Area during this survey can be broken into four groups according to their known distributions:

- Regionally widespread throughout the Pilbara (100 – 1000 km linear range) – 6 taxa;
- Locally widespread within/beyond the Study Area (20 – 100 km linear range) – 11 taxa;
- Locally restricted within/nearby the Study Area (linear range <20 km) – 14 taxa; and
- Known from a single site within the Study Area – 19 taxa.

Table 5.1: Troglofauna taxa recorded from the Study Area (current survey)

Taxonomy	N° specimens	N° sites	Sample type	Distribution and known linear range	Found outside Study Area	Ecological/SRE status
CHELICERATA						
Arachnida						
Araneae						
Araneae `sp. Biologic-ARAN092`	2	1	Scrape	Single site	No	Troglobite, Potential SRE
Araneae `sp. Biologic-ARAN093`	3	3	Scrape	Locally restricted (3.3 km)	No	Troglobite, Potential SRE
Araneae `sp. Biologic-ARAN094`	7	6	Scrape	Locally restricted (4.0 km)	No	Troglobite, Potential SRE
Orsolobidae `sp. Biologic-ARAN091`	2	2	Scrape	Locally restricted (3.8 km)	No	Troglobite, Potential SRE
Prethopalpus `sp. Biologic-ARAN115`	1	1	Trap	Singleton	No	Troglobite, Potential SRE
Palpigradi						
Palpigradi `sp. Biologic-PALP075`	1	1	Scrape	Singleton	No	Troglobite, Potential SRE
Palpigradi `sp. Biologic-PALP077`	6	6	Scrape	Locally restricted (3.6 km)	No	Troglobite, Potential SRE
Palpigradi `sp. Biologic-PALP086`	1	1	Scrape	Singleton	No	Troglobite, Potential SRE
Pseudoscorpiones						
Chthoniidae `sp. Biologic-PSEU186`	1	1	Scrape	Singleton	No	Troglobite, Potential SRE
Chthoniidae `sp. Biologic-PSEU188`	10	10	Trap & Scrape	Locally restricted (3.2 km)	No	Troglobite, Potential SRE
Chthoniidae `sp. Biologic-PSEU191`	4	3	Trap & Scrape	Locally restricted (1.5 km)	No	Troglobite, Potential SRE
Chthoniidae `sp. Biologic-PSEU192`	2	2	Scrape	Locally restricted (1.3 km)	No	Troglobite, Potential SRE
Chthoniidae `sp. Biologic-PSEU193`	5	5	Trap & Scrape	Locally restricted (2.5 km)	No	Troglobite, Potential SRE
Chthoniidae `sp. Biologic-PSEU195`	3	3	Scrape	Locally restricted (1.1 km)	No	Troglobite, Potential SRE
Indohya `sp. Biologic-PSEU183`	4	3	Trap & Scrape	Locally restricted (2.2 km)	No	Troglobite, Potential SRE
Indohya `sp. Biologic-PSEU184`	1	1	Scrape	Singleton	No	Troglobite, Potential SRE
Schizomida						
Draculoides `sp. Biologic-SCHI023`	4	4	Trap & Scrape	Locally restricted (1.6 km)	No	Troglobite, Potential SRE
Draculoides `sp. WAM-SCH067`	29	29	Trap & Scrape	Locally widespread (39.3 km)	Yes	Troglobite, Potential SRE

Taxonomy	N° specimens	N° sites	Sample type	Distribution and known linear range	Found outside Study Area	Ecological/SRE status
CRUSTACEA						
Malacostraca						
Isopoda						
Oniscidea `sp. Biologic-ISOP152`	6	6	Trap & Scrape	Locally restricted (3.4 km)	No	Troglofauna, Potential SRE
Troglarmadillo `sp. Biologic-ISOP151`	2	1	Trap & Scrape	Single site	No	Troglobite, Potential SRE
HEXAPODA						
Entognatha						
Diplura						
Japygidae `sp. B34`	3	3	Scrape	Locally widespread (33.9 km)	Yes	Troglofauna, Potential SRE
Japygidae `sp. DPL005`	1	1	Scrape	Locally widespread (25.2 km)	Yes	Troglofauna, Potential SRE
Parajapygidae `sp. Biologic-DIPL090`	1	1	Scrape	Singleton	No	Troglofauna, Potential SRE
Parajapygidae `sp. Biologic-DIPL092`	1	1	Scrape	Singleton	No	Troglofauna, Potential SRE
Projapygidae `sp. Biologic-DIPL108`	1	1	Scrape	Singleton	No	Troglofauna, Potential SRE
Insecta						
Blattodea						
Nocticola cockingi	7	6	Scrape	Locally widespread (77.3 km)	Yes	Troglophile/xene, Potential SRE
Nocticola quartermainei	1	1	Scrape	Regionally widespread (100+ km)	Yes	Troglophile/xene, Widespread
Coleoptera						
Cryptorhynchinae `sp. B10`	1	1	Scrape	Locally restricted (16.3 km)	Yes, also found from Ministers North (Bennelongia, 2018)	Troglofauna, Potential SRE
Curculionidae `sp. B02`	3	3	Scrape	Locally widespread (39.9 km)	Yes	Troglofauna, Potential SRE
Latridiidae `sp. Biologic-COLE052`	1	1	Trap	Regionally widespread (381.5 km)	Yes	Troglophile/xene, Widespread
Pselaphinae `sp. Biologic-COLE008`	2	2	Trap	Locally widespread (87 km)	Yes	Troglophile/xene, Potential SRE
Ptinella `sp. Helix-CPT003`	2	2	Trap	Regionally widespread (456 km)	Yes	Troglophile/xene, Widespread
Typhlozuphium humicolum	2	2	Scrape	Locally widespread (29 km)	Yes	Troglobite, Potential SRE

Taxonomy	N° specimens	N° sites	Sample type	Distribution and known linear range	Found outside Study Area	Ecological/SRE status
Hemiptera						
Phaconeura `sp. Biologic-HEMI003`	3	3	Scrape	Locally widespread (83.3 km)	Yes	Troglophile/xene, Potential SRE
Phaconeura `sp. WAM-PHAC001`	2	2	Scrape	Regionally widespread (707.2 km)	Yes	Troglophile/xene, Widespread
Zygentoma						
Atelurinae `sp. Biologic-ZYGE071`	5	5	Trap & Scrape	Locally restricted (6 km)	No	Troglofauna, Potential SRE
Trinemura `sp. Biologic-ZYGE038`	2	2	Scrape	Locally widespread (47.2 km)	Yes	Troglofauna, Potential SRE
MYRIAPODA						
Chilopoda						
Scolopendromorpha						
Cormocephalus pyropygus	2	2	Scrape	Regionally widespread (185.1 km)	Yes	Troglophile/xene, Widespread
Cryptops `sp. Biologic-CHIL048`	1	1	Scrape	Locally widespread (58 km)	Yes	Troglofauna, Potential SRE
Pauropoda						
Pauropoda `sp. Biologic-PAUR072`	1	1	Scrape	Singleton	No	Troglofauna, Potential SRE

Taxonomy	N° specimens	N° sites	Sample type	Distribution and known linear range	Found outside Study Area	Ecological/SRE status
Pauropoda `sp. Biologic-PAUR073`	1	1	Scrape	Singleton	No	Troglofauna, Potential SRE
Pauropoda `sp. Biologic-PAUR074`	2	2	Scrape	Locally widespread (33.6 km)	Yes	Troglofauna, Potential SRE
Pauropoda `sp. Biologic-PAUR075`	1	1	Scrape	Singleton	No	Troglofauna, Potential SRE
Pauropoda `sp. Biologic-PAUR085`	1	1	Scrape	Singleton	No	Troglofauna, Potential SRE
Pauropoda `sp. Biologic-PAUR086`	1	1	Trap	Singleton	No	Troglofauna, Potential SRE
Pauropoda `sp. Biologic-PAUR087`	1	1	Scrape	Singleton	No	Troglofauna, Potential SRE
Tetramerocerata						
Decapauropus `sp. WAM-PAUD002`	3	3	Scrape	Regionally widespread (228.5 km)	Yes	Troglophile/xene, Widespread
Symphyla						
Cephalostigmata						
Hanseniella `sp. Biologic-SYMP077`	1	1	Scrape	Singleton	No	Troglofauna, Potential SRE
Hanseniella `sp. Biologic-SYMP088`	1	1	Scrape	Singleton	No	Troglofauna, Potential SRE
Scolopendrellidae `sp. Biologic-SYMP089`	1	1	Scrape	Singleton	No	Troglofauna, Potential SRE

Table 5.2: Troglofauna higher order taxa recorded from Study Area (current survey)

Taxonomy	N° of specimens	N° of sites	Ecological/SRE status	Taxonomic comments
CHELICERATA				
Arachnida				
Araneae `sp. indet.`	3	1	Troglofauna, Uncertain	Indeterminate higher-level taxon (order). DNA not tested. May represent other Araneae sp. collected from the Study Area.
Palpigradi `sp. indet.`	6	2	Potential troglobite, Uncertain	Indeterminate higher-level taxon (order). DNA not tested. May represent other Palpigradi sp. collected from the Study Area.
Chthoniidae `sp. indet.`	12	9	Troglobite, Uncertain	Indeterminate higher-level taxon (family). DNA not tested. May represent other Chthoniidae sp. collected from the Study Area.
Indohya `sp. indet.`	3	3	Troglobite, Uncertain	Indeterminate higher-level taxon (genus). DNA not tested. May represent other *Indohya* sp. collected from the Study Area.
Draculoides `sp. indet.`	63	31	Troglobite, Uncertain	Indeterminate higher-level taxon (genus). DNA not tested. May represent other *Draculoides* sp. collected from the Study Area.
CRUSTACEA				
Malacostraca				
Philosciidae `sp. indet.`	31	7	Troglofauna, Uncertain	Indeterminate higher-level taxon (family). DNA not tested.
HEXAPODA				
Entognatha				
Diplura `sp. indet.`	3	3	Troglofauna, Uncertain	Indeterminate higher-level taxon (order). DNA not tested. May represent other Diplura sp. collected from the Study Area.
Japygidae `sp. indet.`	1	1	Potential troglobite, Uncertain	Indeterminate higher-level taxon (family). DNA not tested. May represent Japygidae `sp. B34` collected from the same site.
Projapygidae `sp. indet.`	1	1	Troglofauna, Uncertain	Indeterminate higher-level taxon (family). DNA failed.
Insecta				
Insecta `sp. indet.`	3	2	Troglofauna, Uncertain	Indeterminate higher-level taxon (class). DNA not tested. May represent other Insecta sp. collected from the Study Area.
Blattodea `sp. indet.`	5	5	Troglophile/xene, Uncertain	Indeterminate higher-level taxon (order). DNA not tested. May represent other Blattodea sp. collected from the Study Area.
Nocticola `sp. indet.`	319	51	Troglofauna, Uncertain	Indeterminate higher-level taxon (genus). DNA not tested. May represent other *Nocticola* sp. collected from the Study Area.

Taxonomy	N° of specimens	N° of sites	Ecological/SRE status	Taxonomic comments
Coleoptera `sp. indet.`	18	9	Troglofauna, Uncertain	Indeterminate higher-level taxon (order). DNA not tested (1 specimen); DNA not tested (17 specimens). May represent other Coleoptera sp. collected from the Study Area.
Cryptorhynchinae `sp. indet.`	2	1	Troglofauna, Uncertain	Indeterminate higher-level taxon (subfamily). DNA not tested.
Curculionidae `sp. indet.`	94	14	Troglofauna, Uncertain	Indeterminate higher-level taxon (family). DNA not tested. May represent other Curculionidae sp. collected from the Study Area.
Pselaphinae `sp. indet.`	3	1	Troglofauna, Uncertain	Indeterminate higher-level taxon (subfamily). DNA not tested.
Staphylinidae `sp. indet.`	67	2	Troglofauna, Uncertain	Indeterminate higher-level taxon (family). DNA not tested.
Diptera `sp. indet.`	5	1	Troglophile/xene, Uncertain	Indeterminate higher-level taxon (order). DNA not tested.
Sciaridae `sp. indet.`	159	14	Troglofauna, Uncertain	Indeterminate higher-level taxon (family). DNA not tested.
Meenoplidae `sp. indet.`	51	17	Troglophile/xene, Uncertain	Indeterminate higher-level taxon (family). DNA not tested. May represent other Meenoplidae sp. collected from the Study Area.
Phaconeura `sp. indet.`	22	12	Troglophile/xene, Uncertain	Indeterminate higher-level taxon (genus). DNA not tested. May represent other *Phaconeura* sp. collected from the Study Area.
Formicidae `sp. indet.`	1	1	Troglophile/xene, Uncertain	Indeterminate higher-level taxon (family). DNA not tested.
Atelurinae `sp. indet.`	7	5	Troglophile/xene, Uncertain	Indeterminate higher-level taxon (subfamily). DNA not tested. May represent other Atelurinae sp. collected from the Study Area.
Trinemura `sp. indet.`	1	1	Troglofauna, Uncertain	Indeterminate higher-level taxon (genus). DNA not tested.
Zygentoma `sp. indet.`	2	2	Troglofauna, Uncertain	Indeterminate higher-level taxon (order). DNA not tested. May represent other Zygentoma sp. collected from the Study Area.
MYRIAPODA				
Myriapoda `sp. indet.`	3	2	Troglofauna, Uncertain	Indeterminate higher-level taxon (subphylum). DNA not tested. May represent other Myriapoda sp. collected from the Study Area.
Chilopoda				
Scolopendromorpha `sp. indet.`	3	1	Troglofauna, Uncertain	Indeterminate higher-level taxon (order). DNA not tested. May represent other Scolopendromorpha sp. collected from the Study Area.
Diplopoda				
Lophoproctidae `sp. indet.`	200	22	Troglophile/xene, Uncertain	Indeterminate higher-level taxon (family). DNA not tested.
Polyxenida `sp. indet.`	41	4	Troglofauna, Uncertain	Indeterminate higher-level taxon (order). DNA not tested.

Taxonomy	N° of specimens	N° of sites	Ecological/SRE status	Taxonomic comments
Pauropoda				
Pauropoda `sp. indet.`	67	3	Troglophile/xene, Uncertain	Indeterminate higher-level taxon (class). DNA not tested. May represent other Pauropoda sp. collected from the Study Area.
Symphyla				
Symphyla `sp. indet.`	1	1	Troglofauna, Uncertain	Indeterminate higher-level taxon (class). DNA not tested. May represent other Symphyla sp. collected from the Study Area.

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Weeli Wolli Creek

Weeli Wolli Spring

Araneae
- Araneae `sp. Biologic-ARAN092`
- Araneae `sp. Biologic-ARAN093`
- Araneae `sp. Biologic-ARAN094`
- Orsolobidae `sp. Biologic-ARAN091`
- *Prethopalpus* `sp. Biologic-ARAN115`

Palpigradi
- Palpigradi `sp. Biologic-PALP075`
- Palpigradi `sp. Biologic-PALP077`
- Palpigradi `sp. Biologic-PALP086`

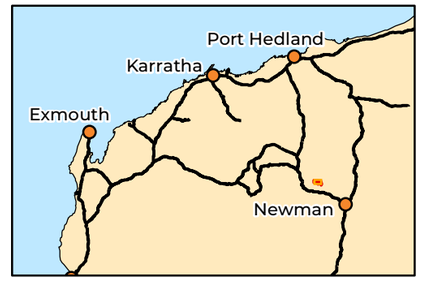
LEGEND
- Study Area
- Rail
- Weeli Wolli PEC
- Major Surface Hydrology
- Troglofauna Sampling Site

Biologic

Scale 1:40,000

0 0.5 1 1.5 Km

Coordinate System: GDA2020 MGA Zone 50
Projection: Transverse Mercator
Datum: GDA2020 Created 05/12/2024



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East Packsaddle: Subterranean Fauna Baseline Survey

Figure 5.1: Troglofauna recorded from the Study Area: Araneae and Palpigradi

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Weeli Wolli Creek

Weeli Wolli Spring

Pseudoscorpiones

- Chthoniidae `sp. Biologic-PSEU186`
- Chthoniidae `sp. Biologic-PSEU188`
- Chthoniidae `sp. Biologic-PSEU191`
- Chthoniidae `sp. Biologic-PSEU192`
- Chthoniidae `sp. Biologic-PSEU193`
- Chthoniidae `sp. Biologic-PSEU195`
- *Indohya* `sp. Biologic-PSEU183`
- *Indohya* `sp. Biologic-PSEU184`

Schizomida

- *Draculoides* `sp. Biologic-SCHI023`
- *Draculoides* `sp. WAM-SCH067`

LEGEND

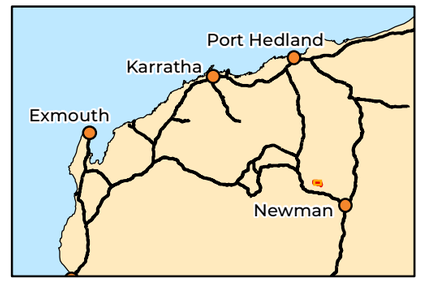
- Study Area
- Rail
- Weeli Wolli PEC
- Major Surface Hydrology
- Troglofauna Sampling Site

Biologic

Scale 1:40,000

0 0.5 1 1.5 Km

Coordinate System: GDA2020 MGA Zone 50
Projection: Transverse Mercator
Datum: GDA2020 Created 20/11/2024



BHP WAIO

East Packsaddle: Subterranean Fauna Baseline Survey

Figure 5.2: Troglofauna recorded from the Study Area: Schizomida and Pseudoscorpiones

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Weeli Wolli Creek

Weeli Wolli Spring

Blattodea
- *Nocticola cockingi*
- *Nocticola quartermainei*

Diplura
- Japygidae `sp. B34`
- Japygidae `sp. DPL005`
- Parajapygidae `sp. Biologic-DIPL090`
- Parajapygidae `sp. Biologic-DIPL092`
- Projapygidae `sp. Biologic-DIPL108`

Isopoda
- Oniscidea `sp. Biologic-ISOP152`
- *Troglarmadillo* `sp. Biologic-ISOP151`

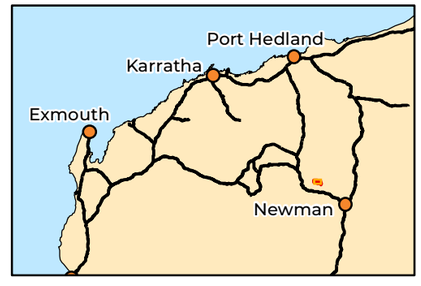
LEGEND
- Study Area
- Rail
- Weeli Wolli PEC
- Major Surface Hydrology
- Troglofauna Sampling Site

Biologic

Scale 1:40,000

0 0.5 1 1.5 Km

Coordinate System: GDA2020 MGA Zone 50
Projection: Transverse Mercator
Datum: GDA2020 Created 20/11/2024



BHP WAIO

East Packsaddle: Subterranean Fauna Baseline Survey

Figure 5.3: Troglofauna recorded from the Study Area: Blattodea, Diplura and Isopoda

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Weeli Wolli Creek

Weeli Wolli Spring

Coleoptera

- Coleoptera, Cryptorhynchinae `sp. B10`
- Coleoptera, Curculionidae `sp. B02`
- Coleoptera, Latridiidae `sp. Biologic-COLE052`
- Pselaphinae `sp. Biologic-COLE008`
- *Ptinella* `sp. Helix-CPT003`
- *Typhlozuphium humicolum*

Hemiptera

- *Phaconeura* `sp. Biologic-HEMI003`
- *Phaconeura* `sp. WAM-PHAC001`

Zygentoma

- Atelurinae `sp. Biologic-ZYGE071`
- *Trinemura* `sp. Biologic-ZYGE038`

LEGEND

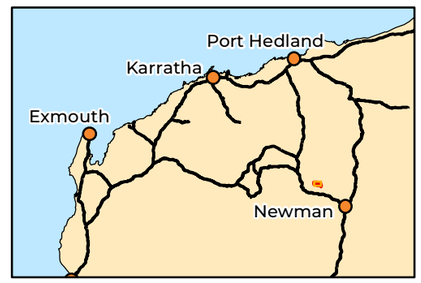
- Study Area
- Rail
- Weeli Wolli PEC
- Major Surface Hydrology
- Troglofauna Sampling Site

Biologic

Scale 1:40,000

0 0.5 1 1.5 Km

Coordinate System: GDA2020 MGA Zone 50
Projection: Transverse Mercator
Datum: GDA2020 Created 20/11/2024



BHP WAIO

East Packsaddle: Subterranean Fauna Baseline Survey

Figure 5.4: Troglofauna recorded from the Study Area: Coleoptera, Hemiptera and Zygentoma

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Chilopoda

Cormocephalus pyropygus

Cryptops `sp. Biologic-CHIL048`

Pauropoda

Decapauropus `sp. WAM-PAUD002`

Pauropoda `sp. Biologic-PAUR072`

Pauropoda `sp. Biologic-PAUR073`

Pauropoda `sp. Biologic-PAUR074`

Pauropoda `sp. Biologic-PAUR075`

Pauropoda `sp. Biologic-PAUR085`

Pauropoda `sp. Biologic-PAUR086`

Pauropoda `sp. Biologic-PAUR087`

Symphyla

Hanseniella `sp. Biologic-SYMP088`

Hanseniella `sp. Biologic-SYMP077`

Scolopendrellidae `sp. Biologic-SYMP089`

Weeli Wolli Spring

Weeli Wolli Creek

LEGEND

Study Area

Weeli Wolli PEC

Major Surface Hydrology

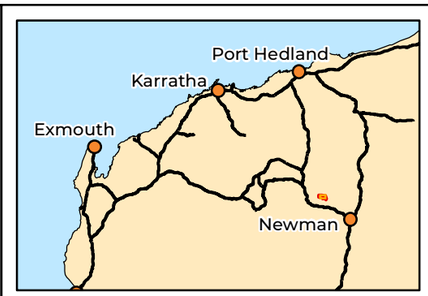
Troglofauna Sampling Site

Biologic

Scale 1:30,000

0 0.5 1 Km

Coordinate System: GDA2020 MGA Zone 50
Projection: Transverse Mercator
Datum: GDA2020 Created 20/11/2024



BHP WAIO

East Packsaddle: Subterranean Fauna Baseline Survey

Figure 5.5: Troglofauna recorded from the Study Area: Chilopoda, Pauropoda and Symphyla

5.2 Stygofauna

Of the 118 stygofauna samples collected during the current survey, 48 samples yielded 1,703 specimens from eight subterranean fauna groups. Using a combination of morphological identifications and molecular analyses, 28 distinct stygofauna species/OTUs were determined (Table 5.3, Figure 5.6 – Figure 5.9), comprising worms, water mites, amphipods, bathynellids, isopods, copepods, and ostracods.

A further 25 indeterminate higher-level taxa represented leftover material from subsampling for molecular identifications, and specimens unable to be identified to species level (Table 5.4). All leftover specimen material was stored appropriately such that it may be subsampled again during future rounds of molecular analysis, if needed for EIA of any particular taxon group or species.

Based on current linear ranges (Table 5.3), the 28 stygofauna taxa recorded from the Study Area can be broken into four groups according to their known distributions:

- Regionally widespread throughout the Pilbara (100 – 1000 km linear range) – 6 taxa;
- Locally widespread within/beyond the Study Area (20 – 100 km linear range) – 9 taxa;
- Locally restricted within/nearby the Study Area (linear range <20 km) – 8 taxa; and
- Known from a single site within the Study Area – 5 taxa.

Table 5.3: Stygofauna taxa recorded from the Study Area (current survey)

Taxonomy	N° specimens	N° sites	Distribution and known linear range	Found outside Study Area	Ecological/SRE status
ANNELIDA					
Clitellata					
Enchytraeida					
Enchytraeidae `sp. Biologic-OLIG159`	1	1	Singleton	No	Stygophile/xene, Potential SRE
Enchytraeidae `sp. E6 LB-2015`	2	2	Regionally widespread (477.4 km)	Yes	Stygophile/xene, Widespread
Haplotaxida					
Naididae `sp. N1 LB-2015`	5	4	Locally restricted (13.1 km)	Yes, also found from Yandicoogina (Brown *et al.*, 2015)	Stygophile/xene, Potential SRE
Nais `sp. Biologic-OLIG117`	1	1	Singleton	No	Stygophile/xene, Potential SRE
*Nais variabilis**	24	1	Regionally widespread (100+ km)	Yes	Stygophile/xene, Widespread
Phreodrilidae `sp. P11 LB-2015`	4	4	Regionally widespread (434.6 km)	Yes	Stygophile/xene, Widespread
Pristina jenkinae	67	3	Regionally widespread (100+ km)	Yes	Stygophile/xene, Widespread
CHELICERATA					
Arachnida					
Trombidiformes					
Pezidae `sp. Biologic-ACAR003`	2	1	Locally restricted (11.3 km)	Yes, also found from Ministers North (Biologic, unpublished data)	Stygofauna, potential SRE
CRUSTACEA					
Malacostraca					
Amphipoda					
Chydaekata `sp. E TLF-2008`	7	4	Locally widespread (50.3 km)	Yes	Stygobite, Potential SRE
Maarrka weeliwollii	5	3	Locally widespread (84.1 km)	Yes	Stygobite, Potential SRE
Paramelitidae `sp. Biologic-AMPH024`	2	2	Locally widespread (22.3 km)	Yes	Stygobite, Potential SRE
Paramelitidae `sp. Biologic-AMPH070`	9	5	Locally restricted (14.8 km)	Yes, also found from Marillana Creek (Biologic, 2023a)	Stygobite, Potential SRE
Bathynellacea					
Atopobathynella `sp. Biologic-PBAT019`	3	1	Locally widespread (81.4 km)	Yes	Stygobite, Potential SRE

Taxonomy	N° specimens	N° sites	Distribution and known linear range	Found outside Study Area	Ecological/SRE status
Isopoda					
Isopoda `sp. Biologic-ISOP153`	1	1	Singleton	No	Stygofauna, potential SRE
Pygolabis weeliwolli	3	1	Locally widespread (28.3 km)	Yes	Stygobite, Potential SRE
Maxillopoda (Copepoda)					
Cyclopoida					
Diacyclops `sp. Biologic-CYCL037`	10	6	Locally widespread (29.3 km)	Yes	Stygofauna, potential SRE
Diacyclops cockingi	3	1	Regionally widespread (100+ km)	Yes	Stygophile/xene, Widespread
Harpacticoida					
Gordanitocrella `sp. Biologic-HARP030`	4	3	Locally restricted (2.8 km)	No	Stygobite, Potential SRE
Gordanitocrella trajani	22	3	Locally widespread (31.5 km)	Yes	Stygobite, Potential SRE
Parastenocaris `sp. Biologic-HARP032`	1	1	Singleton	No	Stygobite, Potential SRE
Schizopera `sp. Biologic-HARP031`	1	1	Locally restricted (2.9 km)	No	Stygobite, Potential SRE
Ostracoda					
Podocopida					
Gomphodella `sp. Biologic-OSTR078`	1	1	Locally restricted (1.5 km)	No	Stygofauna, Potential SRE
Gomphodella yandii	20	1	Regionally widespread (100+ km)	Yes	Stygophile/xene, Widespread
Meridiescandona `sp. Biologic-OSTR057`	8	3	Locally restricted (18.4 km)	Yes, also collected from an adjacent survey area (Biologic, unpublished data)	Stygobite, Potential SRE
*Meridiescandona marillanae**	551	2	Locally widespread (33.7 km)	Yes	Stygobite, Potential SRE
*Notacandona boultoni**	61	2	Locally widespread (38.9 km)	Yes	Stygobite, Potential SRE
Notacandona modesta	11	2	Locally restricted (12.1 km)	Yes, also found from Pebble Mouse Creek (BHP database)	Stygobite, Potential SRE
Vestalenula `sp. indet.`**	1	1	Singleton	No	Stygofauna, Potential SRE

* There is uncertainty around these morphological identifications, as each has been found to represent multiple distinct genetic lineages.

** This indeterminate taxon is treated as being potentially unique to the local groundwater habitat because it is the only representative of its genus from this survey (including desktop assessment). However, this specimen likely represents either *Vestalenula marmonieri* or *Vestalenula matildae,* as all 22 *Vestalenula* specimens sequenced by Biologic to date have represented these two species; both are widespread throughout the Pilbara. One of these specimens (*Vestalenula matildae*) was collected from Weeli Wolli Creek within the Study Area (Biologic, 2023b), five specimens (*V. matildae* and *V. marmonieri*) were collected from Yandi Creek and Marillana Creek (~5-10 km north of Study Area), and the remaining specimens were collected >40 km from the Study Area. Genetic analysis of the specimen collected during the current survey was not possible due to the absence of soft tissue material (empty valve), limiting external comparisons.

Table 5.4: Stygofauna higher order taxa recorded from Study Area (current survey)

Taxonomy	N° of specimens	N° of sites	Ecological/SRE status	Taxonomic comments
NEMATODA				
Nematoda `spp.`	10	3	Uncertain stygofauna, not assessed in EIA	Indeterminate higher-level taxon (phylum). DNA not tested.
ANNELIDA				
Clitellata				
Enchytraeidae `sp. indet.`	20	3	Stygophile/xene, Uncertain	Indeterminate higher-level taxon (family). DNA not tested. May represent other Enchytraeidae sp. collected from the Study Area.
Naididae `sp. indet.`	11	1	Stygofauna, Uncertain	Indeterminate higher-level taxon (family). DNA not tested. May represent other Naididae sp. collected from the Study Area.
Naidinae `sp. indet.`	9	2	Stygofauna, Uncertain	Indeterminate higher-level taxon (family). DNA not tested. May represent other Naididae sp. collected from the Study Area.
Phreodrilidae `sp. indet.`	81	4	Stygofauna, Uncertain	Indeterminate higher-level taxon (family). DNA failed (2 specimens); DNA not tested (79 specimens). May represent Phreodrilidae `sp. P11 LB-2015` collected from the same sites.
CHELICERATA				
Arachnida				
Acari `sp. indet.`	2	2	Stygofauna, Uncertain	Indeterminate higher-level taxon (subclass). DNA not tested. May represent other Acari sp. collected from the Study Area.
Cunaxidae `sp. indet.`	1	1	Stygofauna, Uncertain	Indeterminate higher-level taxon (family). DNA not tested.
Halacaridae `sp. indet.`	1	1	Stygofauna, Uncertain	Indeterminate higher-level taxon (family). DNA not tested.
Pezidae `sp. indet.`	8	1	Stygofauna, Uncertain	Indeterminate higher-level taxon (family). DNA failed (1 specimen); DNA not tested (7 specimens). May represent Pezidae `sp. Biologic-ACAR003` collected from the same site.
CRUSTACEA				
Malacostraca				
Amphipoda `sp. indet.`	1	1	Stygofauna, Uncertain	Indeterminate higher-level taxon (order). DNA not tested. May represent other Amphipoda sp. collected from the Study Area.
Chydaekata `sp. indet.`	4	1	Stygobite, Uncertain	Indeterminate higher-level taxon (genus). DNA not tested. Likely represents *Chydaekata* `sp. E TLF-2008` collected from the same site.
Paramelitidae `sp. indet.`	199	9	Stygobite, Uncertain	Indeterminate higher-level taxon (family). DNA not tested. May represent other Paramelitidae sp. collected from the Study Area.

Taxonomy	N° of specimens	N° of sites	Ecological/SRE status	Taxonomic comments
Atopobathynella `sp. indet.`	45	1	Stygobite, Uncertain	Indeterminate higher-level taxon (genus). DNA not tested. May represent *Atopobathynella* `sp. Biologic-PBAT019` collected from the same site.
Pygolabis `sp. indet.`	4	1	Stygobite, Uncertain	Indeterminate higher-level taxon (genus). DNA not tested. Likely represent *Pygolabis weeliwolli* collected from the same site.
Maxillopoda (Copepoda)				
Cyclopoida `sp. indet.`	100	3	Stygofauna, Uncertain	Indeterminate higher-level taxon (order). DNA not tested. May represent other Cyclopoida sp. collected from the Study Area.
Diacyclops cf. *cockingi*	23	2	Stygofauna, Uncertain	Indeterminate higher-level taxon (genus). DNA not tested. May represent *Diacyclops cockingi*.
Diacyclops cf. *humphreysi*	49	3	Stygofauna, Uncertain	Indeterminate higher-level taxon (genus). DNA not tested. May represent *Diacyclops humphreysi*.
Diacyclops nr *humphreysi*	30	2	Stygofauna, Uncertain	Indeterminate higher-level taxon (genus). DNA not tested. May represent *Diacyclops humphreysi*.
Harpacticoida `sp. indet.`	19	1	Stygofauna, Uncertain	Indeterminate higher-level taxon (order). DNA not tested. May represent other Harpacticoida sp. collected from the Study Area.
Parastenocaris `sp. indet.`	6	1	Stygobite, Uncertain	Indeterminate higher-level taxon (genus). DNA not tested. May represent *Parastenocaris* `sp. Biologic-HARP032` collected from the same site.
Ostracoda				
Ostracoda `sp. indet.`	86	2	Stygofauna, Uncertain	Indeterminate higher-level taxon (class). DNA not tested. May represent other Ostracoda sp. collected from the Study Area.
Candonidae `sp. indet.`	6	2	Stygobite, Uncertain	Indeterminate higher-level taxon (family). DNA not tested. May represent other Candonidae sp. collected from the Study Area.
Gomphodella `sp. indet.`	6	1	Stygofauna, Uncertain	Indeterminate higher-level taxon (genus). DNA not tested. May represent other *Gomphodella* sp. collected from the Study Area.
Meridiescandona `sp. indet.`	150	1	Stygobite, Uncertain	Indeterminate higher-level taxon (genus). DNA not tested. May represent other *Meridiescandona* sp. collected from the Study Area.
Notacandona `sp. indet.`	2	2	Stygobite, Uncertain	Indeterminate higher-level taxon (genus). DNA not tested. May represent other *Notacandona* sp. collected from the Study Area.

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7465000 7460000

Weeli Wolli Creek

Weeli Wolli Spring

Bathynellacea

Atopobathynella `sp. Biologic-PBAT019`

Enchytraeida

Enchytraeidae `sp. Biologic-OLIG159`

Enchytraeidae `sp. E6 LB-2015`

Haplotaxida

Naididae `sp. N1 LB-2015`

Nais `sp. Biologic-OLIG117`

Nais variabilis

Phreodrilidae `sp. P11 LB-2015`

Pristina jenkinae

Trombidiformes

Pezidae `sp. Biologic-ACAR003`

LEGEND

Study Area

Local Road

Rail

Weeli Wolli PEC

Major Surface Hydrology

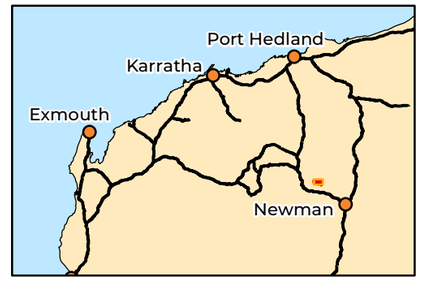
Stygofauna Sampling Site

Biologic

Scale 1:50,000

0 0.5 1 1.5 2 Km

Coordinate System: GDA2020 MGA Zone 50
Projection: Transverse Mercator
Datum: GDA2020 Created 05/12/2024



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East Packsaddle: Subterranean Fauna Baseline Survey

Figure 5.6: Stygofauna recorded from the Study Area: Bathynellacea, Enchytraeida, Haplotaxida and Trombidiformes

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7466600 7462900

Weeli Wolli Creek

Weeli Wolli Spring

Weeli Wolli Creek

Amphipoda

- *Chydaekata* `sp. E TLF-2008`
- *Maarrka weeliwollii*
- Paramelitidae `sp. Biologic-AMPH024`
- Paramelitidae `sp. Biologic-AMPH070`

Isopoda

- Isopoda `sp. Biologic-ISOP153`
- *Pygolabis weeliwolli*

LEGEND

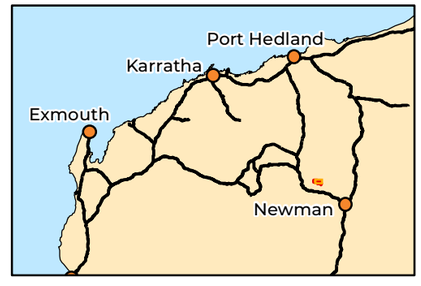
- Study Area
- Rail
- Weeli Wolli PEC
- Major Surface Hydrology
- Stygofauna Sampling Site

Biologic

Scale 1:40,000

0 0.5 1 1.5 Km

Coordinate System: GDA2020 MGA Zone 50
Projection: Transverse Mercator
Datum: GDA2020 Created 20/11/2024



BHP WAIO

East Packsaddle: Subterranean Fauna Baseline Survey

Figure 5.7: Stygofauna recorded from the Study Area: Amphipoda and Isopoda

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7465000

7460000

Weeli Wolli Spring

Weeli Wolli Creek

Cyclopoida

Diacyclops `sp. Biologic-CYCL037`

Diacyclops cockingi

Harpacticoida

Gordanitocrella `sp. Biologic-HARP030`

Gordanitocrella trajani

Parastenocaris `sp. Biologic-HARP032`

Schizopera `sp. Biologic-HARP031`

LEGEND

Study Area

Weeli Wolli PEC

Stygofauna Sampling Site

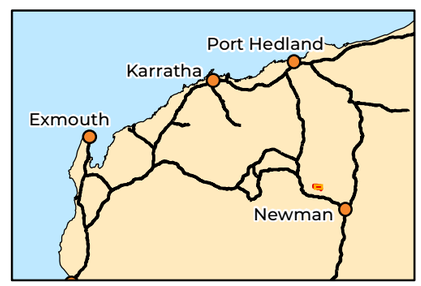
Major Surface Hydrology

Biologic

Scale 1:40,000

0 0.5 1 1.5 Km

Coordinate System: GDA2020 MGA Zone 50
Projection: Transverse Mercator
Datum: GDA2020 Created 20/11/2024



BHP WAIO

East Packsaddle: Subterranean Fauna Baseline Survey

Figure 5.8: Stygofauna recorded from the Study Area: Cyclopoida and Harpacticoida

715000 720000 725000 730000

7465000 7460000

Weeli Wolli Creek

Weeli Wolli Spring

Podocopida

- *Gomphodella* `sp. Biologic-OSTR078`
- *Gomphodella yandii*
- *Meridiescandona* `sp. Biologic-OSTR057`
- *Meridiescandona marillanae*
- *Notacandona boultoni*
- *Notacandona modesta*
- *Vestalenula* `sp. indet.`

LEGEND

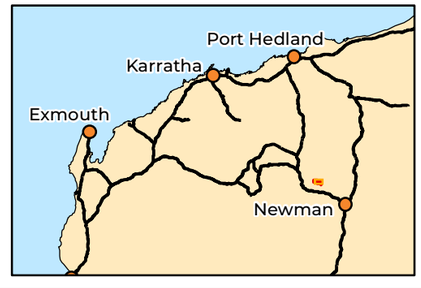
- Study Area
- Rail
- Weeli Wolli PEC
- Major Surface Hydrology
- Stygofauna Sampling Site

Biologic

Scale 1:45,000

0 0.5 1 1.5 Km

Coordinate System: GDA2020 MGA Zone 50
Projection: Transverse Mercator
Datum: GDA2020 Created 20/11/2024



BHP WAIO
East Packsaddle: Subterranean Fauna Baseline Survey

Figure 5.9: Stygofauna recorded from the Study Area: Podocopida

5.3 Water physicochemistry

Groundwater physicochemistry was recorded from 31 bores throughout the Study Area, with measurements taken during multiple visits for some of them. This is summarised in Table 5.5 and discussed briefly below.

The pH of the groundwater ranged from 6.57 to 7.91 across all sites, however the mean pH was 7.21 indicating generally neutral conditions suitable for stygofauna (Humphreys, 2008). The EC measurements showed that the average salinity of the groundwater ranged from fresh to slightly brackish (EC <3,500 µS/cm). These levels are well within the range suitable for stygofauna and can support rich stygofauna assemblages (Halse *et al.*, 2014). Average groundwater temperatures ranged from 28.0 to 31.3 °C.

Redox ORP measurements are typically variable between sites due to individual bore conditions (*i.e.* newly created bore, contaminated bore) rather than representative of overall aquifer conditions. The redox potential of groundwater is a non-specific measure of the system's capacity to oxidise or reduce materials through chemical reactions and has important implications for metal mobility, bio-availability, and toxicity (Schuring *et al.*, 1999). The groundwater in sampling areas showed positive or near positive average ORPs (ranging from -77.8 to +89.2) indicating an oxidizing environment suitable for stygofauna occurrence.

The groundwater of the Study Area was typical of central Pilbara groundwater (circumneutral pH, fresh to brackish salinity, and positive/near-positive ORP). Overall, the groundwater chemistry measured throughout the Study Area was found to be suitable for stygofauna.

Table 5.5: Groundwater physicochemical measurements recorded within the Study Area

Groundwater Quality Parameter	Max	Min	Mean	SErr
Temperature (℃)	31.3	28.0	29.5	0.14
pH (log)	7.91	6.57	7.21	0.05
ORP (mV)	89.2	-77.8	18.8	8.7
EC (µS/cm)	1488	379	972	54

5.4 Sampling adequacy

Overall, the total sampling effort undertaken during the current survey (as described in Section 4.1.3) meets or exceeds current EPA guidance (2021b) for subterranean fauna. Subterranean fauna were sampled over a minimum of three phases to account for seasonal changes, appropriate sampling methodology was used, and the number of sites sampled was appropriate for the size of the Study Area. The EPA recommends that at least as many samples are taken in reference areas as within impact areas. As the impact areas are not yet known, this assessment of sampling adequacy will need to be re-assessed once impact areas are

determined. Nevertheless, the current survey sampled more than 100 sites per phase for troglofauna (Table 4.2), resulting in a total of 595 troglofauna samples taken (198.3 per phase). The EPA recommends sampling at least 30 impact sites and 30 reference sites for troglofauna per phase and given the considerable sampling effort undertaken during this survey, it is relatively likely that this has been achieved. Similarly, sampling a minimum of 10 impact sites and 10 reference sites per phase is recommended for stygofauna by the EPA, with the current survey sampling considerably more (between 30 and 49 sites per phase, Table 4.2), resulting in 118 samples (39.3 per phase).

As outlined in Section 4.5, bore availability varied throughout the area, resulting in most samples taken from the eastern two-thirds of the Study Area (Figure 4.2 and Figure 4.3). Nevertheless, within these constraints, adequate spatial coverage across habitat types was achieved for both troglofauna and stygofauna. Most of the sampling sites were located within geologies known to support subterranean fauna, such as martite-goethite, banded iron formations, and colluvials/alluvials (Figure 2.5). This is reflected in the fact that of the 130 sites sampled for troglofauna, 97 yielded troglofauna taxa (74.6%). Of the 50 sites sampled for stygofauna, 21 yielded stygofauna taxa (42%). These fauna strike rates are comparable or higher than those from similar surveys in the Pilbara (*e.g.* Biologic, 2019, 2022).

Overall, sampling in the Study Area to date has been able to meet or exceed EPA guidance. However, whether more sampling is required for a formal EPA assessment will depend on the location and extent of impacts in the Study Area.

6 Discussion

6.1 Troglofauna

A total of 50 troglofauna species/OTUs were identified during this survey, comprising arachnids, isopods, diplurans, insects, and myriapods. Nineteen of these taxa were only recorded as singletons or from a single site within the Study Area, and a further 14 were found to be locally restricted (<20 km known linear range). The remaining 17 taxa were found to be more widespread (>20 km linear range). In total, 43 troglofauna taxa (32 from the current survey and 11 from previous surveys) are currently only known to occur within the Study Area (Table 6.1). Each troglofauna group is discussed in more detail below.

Table 6.1: Troglofauna taxa currently only known from within the Study Area

Lowest identification	Distribution	N° of sites	N° of specimens/ records
Current survey			
Arachnida			
Araneae `sp. Biologic-ARAN092`	Single site	2	1
Araneae `sp. Biologic-ARAN093`	Locally restricted (3.3 km)	3	3
Araneae `sp. Biologic-ARAN094`	Locally restricted (4.0 km)	6	7
Orsolobidae `sp. Biologic-ARAN091`	Locally restricted (3.8 km)	2	2
Prethopalpus `sp. Biologic-ARAN115`	Singleton	1	1
Palpigradi `sp. Biologic-PALP075`	Singleton	1	1
Palpigradi `sp. Biologic-PALP077`	Locally restricted (3.6 km)	6	6
Palpigradi `sp. Biologic-PALP086`	Singleton	1	1
Chthoniidae `sp. Biologic-PSEU186`	Singleton	1	1
Chthoniidae `sp. Biologic-PSEU188`	Locally restricted (3.2 km)	10	10
Chthoniidae `sp. Biologic-PSEU191`	Locally restricted (1.5 km)	4	3
Chthoniidae `sp. Biologic-PSEU192`	Locally restricted (1.3 km)	2	2
Chthoniidae `sp. Biologic-PSEU193`	Locally restricted (2.5 km)	5	5
Chthoniidae `sp. Biologic-PSEU195`	Locally restricted (1.1 km)	3	3
Indohya `sp. Biologic-PSEU183`	Locally restricted (2.2 km)	4	3
Indohya `sp. Biologic-PSEU184`	Singleton	1	1
Draculoides `sp. Biologic-SCHI023`	Locally restricted (1.6 km)	4	4
Malacostraca			
Oniscidea `sp. Biologic-ISOP152`	Locally restricted (3.4 km)	6	6
Troglarmadillo `sp. Biologic-ISOP151`	Single site	2	1
Entognatha			
Parajapygidae `sp. Biologic-DIPL090`	Singleton	1	1
Parajapygidae `sp. Biologic-DIPL092`	Singleton	1	1
Projapygidae `sp. Biologic-DIPL108`	Singleton	1	1

Lowest identification	Distribution	N° of sites	N° of specimens/ records
Insecta			
Atelurinae `sp. Biologic-ZYGE071`	Locally restricted (6 km)	5	5
Pauropoda			
Pauropoda `sp. Biologic-PAUR072`	Singleton	1	1
Pauropoda `sp. Biologic-PAUR073`	Singleton	1	1
Pauropoda `sp. Biologic-PAUR075`	Singleton	1	1
Pauropoda `sp. Biologic-PAUR085`	Singleton	1	1
Pauropoda `sp. Biologic-PAUR086`	Singleton	1	1
Pauropoda `sp. Biologic-PAUR087`	Singleton	1	1
Symphyla			
Hanseniella `sp. Biologic-SYMP077`	Singleton	1	1
Hanseniella `sp. Biologic-SYMP088`	Singleton	1	1
Scolopendrellidae `sp. Biologic-SYMP089`	Singleton	1	1
Previous surveys			
Arachnida			
Draculoides `SCH024`	Single site	1	3
Draculoides `SCH025`	Singleton	1	1
Indohya `PSE186`	Single site	1	2
Indohya sp. B06	Single site	1	2
Palpigradi `sp. B19`	Singleton	1	1
Tyrannochthonius `sp. B37`	Singleton	1	1
Insecta			
Brentidae sp. B02	Singleton	1	1
Cryptorhynchinae sp. B19	Singleton	1	1
Malacostraca			
Armadillidae `sp. B11`	Singleton	1	1
Troglarmadillo sp. B59	Singleton	1	1
Symphyla			
Hanseniella sp. B09	Singleton	1	1

6.1.1 Arachnida (Araneae, Palpigradi, Pseudoscorpiones, Schizomida)

Troglobitic arachnids are known to be highly range-restricted and there is a high likelihood of SRE taxa occurring in this group. Of the 29 arachnid taxa (18 from the current survey and 11 from previous surveys) collected from the Study Area, only five (comprising *Draculoides* `sp. WAM-SCH067` from this survey and previous surveys [Plate 6-1], and *Dampetrus* `sp. B01`, *Draculoides* `SCH022`, Opiliones sp. B02, and Palpigradi `sp. B01` from previous surveys) have been recorded from outside the Study Area to date.

Plate 6-1: *Draculoides* `sp. WAM-SCH067` collected from the current survey

Troglobitic spiders, palpigrades, pseudoscorpions (example Plate 6-2), and schizomids tend to have very limited dispersal capabilities (*e.g.* Mammola & Isaia, 2017; Ribera *et al.*, 2018) and are commonly recorded as singletons or found to have small linear ranges. Therefore, there is a low likelihood that the arachnid taxa found within the Study Area are regionally widespread.

Plate 6-2: *Indohya* `sp. Biologic-PSEU183` collected from the current survey

6.1.2 Malacostraca (Isopoda)

Of the four (two from the current survey and two from a previous survey) isopod taxa collected from the Study Area (Figure 5.3), none have been found more widely to date. *Troglarmadillo* `sp. Biologic-ISOP151` from this survey (Plate 6-3), and *Troglarmadillo* sp. B59 and Armadillidae sp. B11 from a previous survey (Bennelongia, 2015c), belong to groups that are known to include highly restricted troglobitic species throughout the Pilbara region, including many dispersal-limited subterranean species (S. Judd pers. comm. 2019) and are therefore

considered unlikely to be regionally widespread. The remaining taxon (Oniscidea `sp. Biologic-ISOP152`) was determined to be a troglophile/xene due to the presence of reduced eyes/some pigmentation and therefore reasonably likely to be found outside Study Area.

Plate 6-3: *Troglarmadillo* `sp. Biologic-ISOP151` collected from the current survey

6.1.3 Entognatha (Diplura)

Of the five dipluran taxa collected within the Study Area (Figure 5.3), three were detected as singletons (Parajapygidae `sp. Biologic-DIPL090`, Parajapygidae `sp. Biologic-DIPL092`, and Projapygidae `sp. Biologic-DIPL108`) and two were found within and outside of the Study Area (Japygidae `sp. B34` and Japygidae `sp. DPL005`) . Diplurans are small invertebrates that are found in deep leaf litter, soils, and subterranean habitats where they predate on small arthropods, nematodes, and enchytraeids. Specimens are always elongated, wingless, eyeless, and pale, which makes it difficult to distinguish troglomorphy. As a precaution, most diplurans collected during troglofauna surveys are considered to be potential troglofauna. Relatively little is known about species distributions and patterns of endemicity. The limited available data suggests that members of this group tend to be relatively range restricted. As such, from a total of 30 Japygidae OTUs in Biologic's genetic databases at the time of writing, approximately two thirds of the OTUs (n=20) were singletons. Of those with linear ranges, the average linear range was approximately 11.3 km (min 0.3 km – max 34 km) (Biologic, unpublished data).

6.1.4 Insecta (Blattodea, Coleoptera, Hemiptera, Zygentoma)

Many subterranean insect taxa are more highly vagile than other troglofauna and have relatively wide distributions, although may still be within the nominal limits for SRE species (following Harvey, 2002). Of the 11 insect taxa found within the Study Area from the current

survey (Figure 5.3 and Figure 5.4), only one (Atelurinae `sp. Biologic-ZYGE071`) was found exclusively from within the Study Area. Most silverfish (Zygentoma) in the subfamily Atelurinae are regarded as soil fauna or trogloxenic due to habitation of termite and ant nests, but are commonly collected from drill holes (Smith & McRae, 2014). It is therefore considered unlikely that Atelurinae `sp. Biologic-ZYGE071` is restricted to the Study Area. One beetle, Cryptorhynchinae `sp. B10`, found from the Study Area had previously been recorded from Ministers North, ~16 km north of the Study Area (Bennelongia, 2018). The remaining ten insect taxa from the current survey, including five beetles (example Plate 6-4), two cockroaches, one silverfish, and two hemipterans, all had distributions >29 km.

There were two beetles found only from the Study Area during previous surveys, namely Brentidae sp. B02 and Cryptorhynchinae sp. B19 (Bennelongia, 2015c). For both taxa, conducting wider regional comparisons is constrained by the absence of genetic sequence data and the fact that troglofaunal representatives from the Brentidae family and Cryptorhynchinae subfamily are rarely collected. Bennelongia noted that troglofaunal members of the Curculionidae family (to which the subfamily Cryptorhynchinae belongs) often exhibit distributions in the order of tens of kilometres and that Cryptorhynchinae sp. B19 may therefore occur beyond the Study Area (Bennelongia, 2015c). The same applies to Cryptorhynchinae `sp. B10` from the current survey.

Plate 6-4: *Typhlozuphium humicolum* collected from the current survey

6.1.5 Myriapoda (Chilopoda, Pauropoda, Symphyla)

Of the 13 myriapod taxa (pauropods, millipedes, centipedes, and symphylans) collected within the Study Area (Figure 5.5), nine were recorded as singletons from the current survey, comprising six pauropods (Pauropoda `sp. Biologic-PAUR072`, Pauropoda `sp. Biologic-PAUR073`, Pauropoda `sp. Biologic-PAUR075`, Pauropoda `sp. Biologic-PAUR085`, Pauropoda `sp. Biologic-PAUR086`, and Pauropoda `sp. Biologic-PAUR087`) and three

symphylans (*Hanseniella* `sp. Biologic-SYMP077`, *Hanseniella* `sp. Biologic-SYMP088`, and Scolopendrellidae `sp. Biologic-SYMP089`). An additional myriapod, the symphylan *Hanseniella* sp. B09, was recorded as a singleton from a previous survey (Bennelongia, 2015c). The remaining three myriapods have been detected both inside and outside of the Study Area, comprising three pauropods (Pauropoda `sp. Biologic-PAUR074`, *Decapauropus* `sp. WAM-PAUD002`, and Pauropodidae sp. B01 s.l.).

Pauropods are tiny myriapods that are found in soils and subterranean habitats. Specimens are always delicate, eyeless, and pale, which makes it difficult to distinguish troglomorphy. The taxonomy of the WA fauna is poorly known, and there is typically very little information to assess whether pauropods that are detected during troglofauna sampling originate in underground cavities or from soils. As a precaution, most pauropods are considered to be potential troglofauna, but species distributions and patterns of endemicity are poorly known. From a total of 85 pauropod OTUs in Biologic's genetic databases at the time of writing, the vast majority were singletons (66 OTUs, equalling 79% of the OTUs in the database). Of those with linear ranges, the average linear range was approximately 60 km (min 0.1 km – max 406 km) (Biologic, unpublished data).

Symphyla are small detritivores that are found in deep leaf litter, soils, and subterranean habitats. Specimens are always elongated, eyeless, and pale, which makes it difficult to distinguish troglomorphy. As a precaution, most Symphyla collected during troglofauna surveys are considered to be potential troglofauna. The taxonomy of the group is well documented to family and genus, but little is known about species distributions and patterns of endemicity. From a total of 84 Symphyla OTUs in Biologic's genetic databases at the time of writing, more than half of the OTUs were singletons (53 singleton OTUs). Of those with linear ranges, the average linear range was approximately 10 km (min 0.8 km – max 34 km) (Biologic, unpublished data).

Chilopoda represents a class of predatory centipedes. Specimens belonging to this class are frequently elongated, eyeless and pale, making it difficult to distinguish troglomorphy. As such, centipedes of the genus *Cryptops* are always eyeless and pale, which makes it difficult to determine whether the apparent troglomorphy is due to an ecological adaptation to subterranean habitats or not. Recent genetic research has revealed a number of highly divergent *Cryptops* lineages from the Pilbara and Yilgarn regions (Edgecombe *et al.*, 2019), and unpublished information suggests that even terrestrial and soil dwelling *Cryptops* can be SRE. From the 22 *Cryptops* OTUs in the Biologic sequence library at the time of writing, the majority of OTUs were singletons, although a few widely occurring OTUs were recorded with ranges up to 44 km (Biologic, unpublished data).

Previous studies throughout the Pilbara region have shown that highly restricted troglobitic species are known to occur within Symphyla and Pauropoda. Recent genetic research has revealed a number of highly divergent lineages from the Pilbara and Yilgarn regions (Edgecombe *et al.*, 2019). It is therefore possible that the ten singleton myriapods from the Study Area (nine from the current survey and one from previous surveys) have small distribution ranges.

6.2 Stygofauna

Twenty-eight stygofauna species/OTUs were identified during the current survey, comprising worms, mites, amphipods, syncarids, isopods, copepods, and ostracods. Thirteen of these taxa were either singletons/found from single sites (five taxa) or locally restricted (eight taxa). The remaining 15 taxa were found to be more widespread. To date, 14 taxa (eight from the current survey and six from previous surveys) are only known from within the Study Area. Each of the groups is discussed in more detail below. All taxa restricted to the Study Area (Table 6.2) occur within or nearby (<5 km) the Weeli Wolli Spring PEC. Although the ecological significance of the PEC is in part due to a diverse stygofauna assemblage, many of the taxa found within and nearby the PEC have been found further downstream and elsewhere outside of the Study Area. The groundwater system in the PEC comprises an unconfined aquifer sequence including calcrete and detritals (BHP, 2015), potentially resulting in good stygofauna habitat connectivity along the creek (Bennelongia, 2015a). It is therefore possible that taxa currently only known from within the Study Area occur more widely.

Table 6.2: Stygofauna taxa currently only known from within the Study Area

Lowest identification	Distribution	N° of sites	N° of specimens/ records
Current survey			
Clitellata			
Enchytraeidae `sp. Biologic-OLIG159`	Singleton	1	1
Nais `sp. Biologic-OLIG117`	Singleton	1	1
Malacostraca			
Isopoda `sp. Biologic-ISOP153`	Singleton	1	1
Maxillopoda			
Gordanitocrella `sp. Biologic-HARP030`	Locally restricted (2.8 km)	4	3
Parastenocaris `sp. Biologic-HARP032`	Singleton	1	1
Schizopera `sp. Biologic-HARP031`	Locally restricted (2.9 km)	1	1
Ostracoda			
Gomphodella `sp. Biologic-OSTR078`	Locally restricted (1.5 km)	1	1
Vestalenula `sp. indet.`	Singleton	1	1
Previous surveys			

Lowest identification	Distribution	N° of sites	N° of specimens/ records
Arachnida			
Halacaridae sp. B01	Locally restricted (0.5 km)	2	2
Clitellata			
Ainudrilus sp. WA26 (PSS)	Single site	1	11
Malacostraca			
Bathynella sp. 1 (Weeli Wolli)	Singleton	1	1
Maxillopoda			
Mesocyclops holynskae	Singleton	1	3
Schizopera sp. B02	Locally restricted (0.5 km)	3	5
Ostracoda			
Deminutiocandona mica	Single site	1	8

6.2.1 Oligochaeta (Enchytraeida, Haplotaxida)

Three families of aquatic oligochaetes are represented in this study, comprising Enchytraeidae, Phreodrilidae, and Naididae (see Figure 5.6)

Enchytraeid worms are ubiquitous throughout the Yilgarn and Pilbara regions, occurring in terrestrial waters, soils, and subterranean ecosystems above and below the water table. Enchytraeids are amphibious, due to their ability to live in water films in soils and subterranean cavities above groundwater. Specimens are always thin, eyeless, and pale, which makes it difficult to distinguish stygomorphy. In the Pilbara region, most Enchytraeid OTUs are typically widely occurring throughout catchments and in many cases, region wide (Brown et al., 2015). As these worms are not limited to groundwater habitats and are usually widespread, it is reasonable to assume wider potential habitat suitability (for any new singleton taxa) than for most other stygofauna groups. From a total of 71 enchytraid OTU's from the Yilgarn and Pilbara regions in Biologic's genetic databases at the time of writing, approximately half of the OTUs (33 OTUs) were singletons. Of those with linear ranges, the average linear range was approximately 183 km (min 0.5 km – max 695 km) (Biologic, unpublished data).

Oligochaete worms in the families Phreodrillidae and Naididae are regularly collected in groundwater throughout the Pilbara and Yilgarn regions. Phreodrillidae are often found to occur widely throughout regional catchments, while Naididae worms are regularly collected from surface waters and many multi-regional and cosmopolitan species are known. The morphological and genetic taxonomy of these groups is reasonably well documented, and specimens are always eyeless and pale, which means that it is difficult to distinguish any relative degree of stygomorphy. Biologic's genetic databases have 76 phreodrilid OTU's from

the Yilgarn and Pilbara regions. Of these, more than half of the OTUs (50 OTUs) were singletons. Of those with linear ranges, the average linear range was approximately 59 km (min 0.5 km – max 709 km) (Biologic, unpublished data). Similarly, the majority of the naidid OTUs from the Yilgarn and Pilbara within Biologic's database are currently singletons (19 out of 27 OTUs). Of those with linear ranges, the average linear range was approximately 145 km (min 1 km – max 451 km) (Biologic, unpublished data).

It is therefore considered likely that the oligochaete taxa recorded as singletons – *Nais* `sp. Niologic-OLIG117`[1] and Enchytraeidae `sp. Biologic-OLIG159` from the current survey and *Ainudrilus* sp. WA26 (Bennelongia, 2015a) from a previous survey – occur within the wider local area or catchment. The same is to be expected for Naididae `sp. N1 LB-2015`, the only other oligochaete with a short known linear range of 13.1 km (recorded from within and outside the Study Area). Naididae `sp. N1 LB-2015`had previously also been recorded from Yandicoogina (Brown *et al.*, 2015), ~ 13 km northeast of the Study Area.

6.2.2 Arachnida (Acari)

Although subterranean water mites have their highest biodiversity within the riverine, hyporheic zones and are classed as members of the 'permanent hyporheos' or the community that occurs within the deep sand and gravel beds associated with areas of groundwater discharge (Gilbert *et al.*, 1994). They typically characterise the transition zone between the temporary or shallow hyporheic ecozone and the groundwater hypogean environment (Boulton & Hancock, 2006; Humphreys, 2006) and most stygofaunal mites have been found to be widespread. Pezidae `sp. Biologic-ACAR003` from the current survey (Figure 5.6) has also been found ~ 11 km north of the Study Area at Ministers North (Biologic, unpublished data) and is expected to have a much wider distribution than currently known. Similarly, Halacaridae sp. B01 from a previous survey (Bennelongia, 2015a) is expected to be found beyond the Study Area given habitat connectivity along Weeli Wolli Creek (Bennelongia, 2016). Taxonomic limitations (particularly the absence of genetic sequence data) constrain species-level identification and therefore regional distribution analysis of this taxon.

6.2.3 Malacostraca (Amphipoda, Bathynellacea, Isopoda)

Stygofaunal amphipods and isopods are known to have varying distribution ranges across the Pilbara, comprising both locally and regionally widespread species as well as more restricted

[1] This specimen was genetically compared to available *Nais variabilis* sequences on GenBank and found to be 16-20% divergent. The *Nais variabilis* specimens found from the same site as *Nais* `sp. Niologic-OLIG117` were morphologically identified, and it should be noted that there is some uncertainty about the morphological identification of *Nais variabilis*, as the GenBank sequences form two lineages, ~10% divergent from each other.

species. This is reflected in this study, with all but one taxon (the singleton Isopoda `sp. Biologic-ISOP153`) found both inside and outside the Study Area (Figure 5.6 and Figure 5.7), with linear ranges between 14.8 and 84.1 km (examples Plate 6-5). The only amphipod with <20 km distribution range (14.8 km), Paramelitidae `sp. Biologic-AMPH070`, was found at Marillana Creek, north of the Study Area (Biologic, 2023a).

Bathynellids are exclusively stygobitic, and many range-restricted species and morphospecies known to occur in the region (Perina *et al.*, 2018, 2019a; Perina *et al.*, 2019b). They are known to have limited dispersal abilities due to their habit of crawling over the sub-strata as opposed to free-swimming within water-filled subterranean cavities (Coineau & Camacho, 2013; Schminke, 1974). However, some bathynellids have been found to have wider distributions, as observed for *Atopobathynella* `sp. Biologic-PBAT019` (linear range 81.4 km) from this survey. The singleton Bathynella sp. 1, collected during a previous survey from Weeli Wolli Creek (Bennelongia, 2015a), is currently only known from within the Study Area. However, taxonomic limitations (particularly the absence of genetic sequence data), constrains species-level identification and therefore regional distribution analysis of this taxon. It has been considered unlikely that Bathynella sp. 1 is restricted to its currently known location, given habitat connectivity downstream (Bennelongia, 2016).

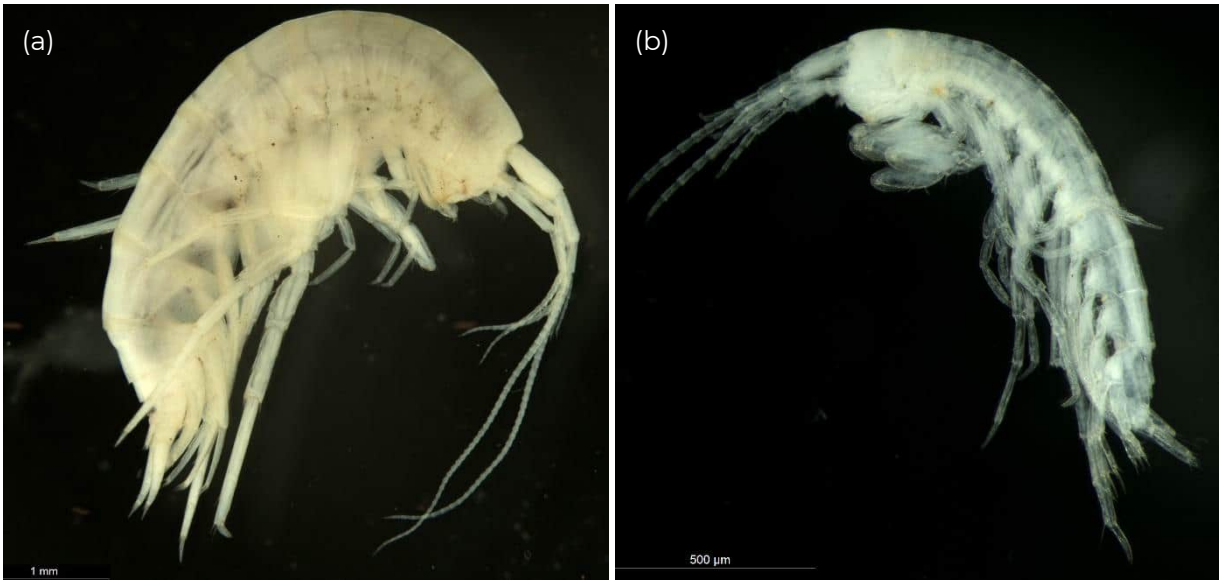


Plate 6-5: *Chydaekata* `sp. E TLF-2008` (a) & *Maarrka weeliwollii* (b) collected from the current survey

6.2.4 Copepoda (Cyclopoida, Harpacticoida)

Cyclopoid copepods are among the most highly vagile stygofauna taxa regionally and throughout Australia, and many of the species in the Pilbara are considered locally or even regionally widespread (*e.g. Diacyclops cockingi* from the current survey; Plate 6-6). Nevertheless, the existing taxonomic framework is almost exclusively built on morphological identification, and very little DNA analysis has been undertaken to confirm species boundaries.

Recent surveys which utilised a larger proportion of molecular analysis for species identifications have shown that molecular analysis of morphologically described, named species of cyclopoid often reveals several distinct OTUs which are genetically distinct from each other (despite morphological similarities). A better regional genetic framework is needed to assess the potential for locally restricted taxa within these otherwise widely occurring named species (or species groups). From a total of 94 cyclopoid OTUs from the Pilbara and Yilgarn regions in Biologic's genetic databases at the time of writing, approximately half of the OTUs (45 OTUs) were singletons. Of those with linear ranges, the average linear range was approximately 114 km (min 0.9 km – max 685 km) (Biologic, unpublished data). The cyclopoid *Mesocyclops holynskae*, found from a single site during a previous survey (Karanovic, 2006), is currently the only cyclopoid known exclusively from the Study Area. The absence of genetic sequencing of this taxon constrains the ability to conduct wider regional comparisons. Nevertheless, based on the inferred extent and connectivity of habitat within the Study Area and the known agility of the members within this group, it is reasonable to assume that *Mesocyclops holynskae* is likely to occur more widely than currently recorded.

Stygal harpacticoids are regularly collected in groundwater throughout the Pilbara. Unlike the highly-vagile free-swimming cyclopoids, many harpacticoids are 'crawling' taxa and thus may be more limited in their dispersal patterns. Accordingly, DNA studies in the Yilgarn have uncovered significant radiations of unique and highly restricted stygal harpacticoids in response to discontinuous habitats (*i.e.* Karanovic & Cooper, 2012; Karanovic et al., 2014). The genetic sequence data from Biologic's database confirms these patterns, with the vast majority of the 88 OTUs in the database currently representing singletons (62 singleton sequences out of 88 OTUs). The average linear range of the remaining OTUs was approximately 48 km (min 0.2 km – max 328 km). In this context, some harpacticoid taxa may have greater potential to disperse throughout catchments, while others appear to be much more range restricted. Of the four harpacticoid taxa from this survey (Figure 5.8), all but one (*Gordanitocrella trajani*) are known exclusively from inside the Study Area to date (*Gordanitocrella* `sp. Biologic-HARP030`, *Schizopera* `sp. Biologic-HARP031`, and *Parastenocaris* `sp. Biologic-HARP032`; Plate 6-6). The only harpacticoid restricted to the Study Area from previous surveys was *Schizopera* sp. B02 (Bennelongia, 2015a). The absence of genetic sequences from this taxon constrains the ability to conduct wider regional comparisons. It is likely that the taxa currently restricted to the Study Area occur further downstream based on the inferred extent and connectivity of habitat.

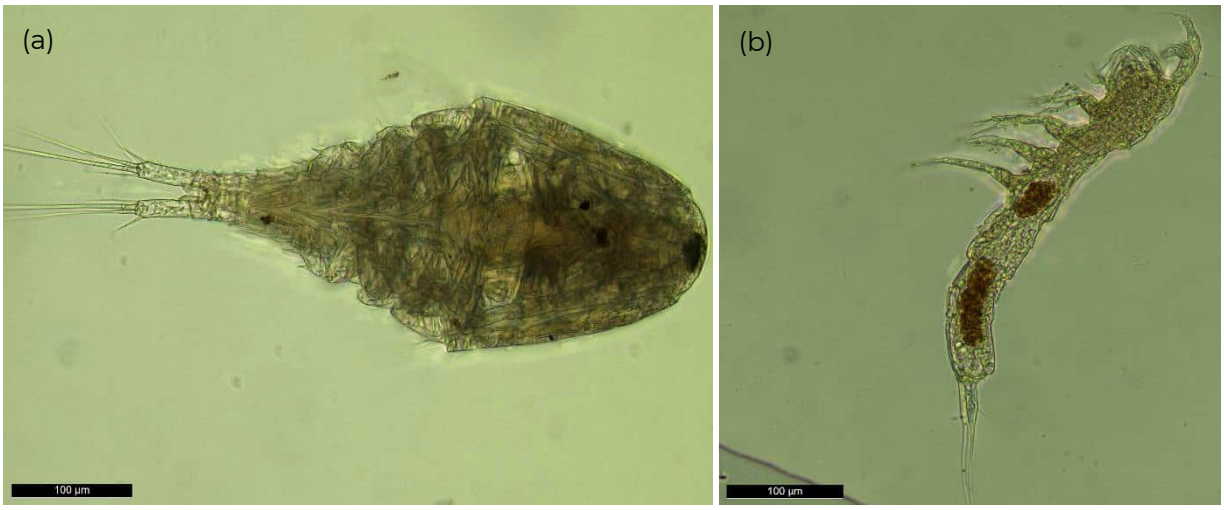


Plate 6-6: *Diacyclops cockingi* (a) & *Parastenocaris* `sp. Biologic-HARP032` (b) collected from the current survey

6.2.5 Ostracoda

The distributions of stygofaunal ostracods in the Pilbara range from widespread to highly range-restricted (Reeves *et al.*, 2007). Three of the seven ostracod taxa from this survey were found to have wide (>33 km) distributions (*e.g. Meridiescandona marillanae* Plate 6-7; Figure 5.9). Of the remaining four taxa recorded from this survey, two (*Gomphodella* `sp. Biologic-OSTR078` and *Vestalenula* `sp. indet.`) are only known from within the Study Area to date but are expected to occur outside the Study Area based on inferred extent and connectivity of habitat. *Vestalenula* `sp. indet.` is considered potentially unique to the local groundwater habitat as it is the only representative of its genus from this survey and the desktop assessment. However, this specimen likely represents either *Vestalenula marmonieri* or *Vestalenula matildae*, as all *Vestalenula* sequenced by Biologic to date (22 specimens) have represented these two species; both are widespread throughout the Pilbara (Biologic, unpublished data). Genetic analysis of this specimen was not possible due to the absence of soft tissue material (only an empty valve was found), limiting regional comparisons. The two other locally restricted taxa have also been recorded from outside the Study Area are *Meridiescandona* `sp. Biologic-OSTR057` was recorded from an adjacent project, ~18 km from the Study Area (Biologic, unpublished data) and *Notacandona modesta*, recorded from Pebble Mouse Creek, ~12 km south of the Study Area (Bennelongia, unpublished data). The only ostracod taxon restricted to the Study Area from previous surveys, *Deminutiocandona mica* (Karanovic, 2005), is currently only know from Weeli Wolli Spring. The lack of genetic sequencing of this taxon constrains the ability to conduct wider regional comparisons. Nevertheless, it is likely that this taxon occurs further downstream from its currently known locations due the extent and connectivity of habitat.

Plate 6-7: *Meridiescandona marillanae* collected from the current survey

7 Key findings

Subterranean fauna habitat

- The main geological formations relevant for subterranean fauna habitat within the Study Area comprise:
    - Weathered/fractured banded iron formation of the Brockman Iron Formation;
    - Weathered dolomite of the Wittenoom Formation;
    - The palaeochannel aquifers and alluvial/colluvial valleys;
    - Calcrete deposits.
- The groundwater chemistry throughout the Study Area was found to be suitable for stygofauna.

Sampling adequacy

- The current survey (3 phases, including dry and wet season sampling) collected 595 troglofauna samples from 130 sites and 118 stygofauna samples from 50 sites, meeting/exceeding EPA recommendations.
- Sites were located across a variety of geologies that are known to support subterranean fauna (*e.g.* BIF or colluvials/alluvials).
- Of the 130 sites sampled for troglofauna, 97 yielded troglofauna taxa (74.6%); of the 50 sites sampled for stygofauna, 21 yielded stygofauna taxa (42%).

Troglofauna

- 50 troglofauna taxa were recorded from the East Packsaddle Study Area during the current survey, and a further 27 from previous studies.
- 43 taxa (32 from the current survey and a further 11 from previous studies) are only known from within the Study Area to date. These include 24 arachnids, four isopods, three diplurans, three insects, and nine myriapods taxa (from the current and previous surveys).
- Some of the taxa found exclusively from within the Study Area may occur more widely throughout the immediate local extent of their habitat beyond the currently known sampling locations.
- 30 taxa were only recorded as singletons or from a single site. This may indicate the rarity of the taxa or a result of sampling limitations.
- 14 potentially range (locally) restricted troglofauna taxa were found exclusively within the Study Area, comprising spiders, pseudoscorpions, schizomids, isopods, and silverfish.

Stygofauna

- 28 stygofauna taxa were recorded from the East Packsaddle Study Area during the current survey, and a further 33 from previous studies.
- 14 taxa (eight from the current survey and six from previous studies) are only known from within the Study Area to date. These include one mite, one isopod, three worms, five copepods, one syncarid, and three ostracods.
- Nine of the 14 taxa restricted to the Study Area were only recorded as singletons or from a single site (current and previous survey). This may indicate the rarity of the taxa or a result of sampling limitations. The remaining five taxa restricted to the Study Area had distributions of 0.5 to 2.9 km (Table 6.2).
- Some of the taxa found exclusively from within the Study Area may occur more widely throughout the immediate local extent of their habitat beyond the currently known sampling locations.
- All taxa restricted to the Study Area occur within or nearby (<5 km) the Weeli Wolli Spring PEC.

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9 Appendices

Appendix A: Database search data

This appendix was provided in a separate spreadsheet (21128_EastPack_SF_database_search_data.xlsx)

Appendix B: Troglofauna species recorded within 40 km of Study Area

Order	Family	Lowest identification	N° of records	Source
Arachnida				
Araneae		Araneae `sp. S5`	3	WAM
		Araneae `sp. S7`	1	WAM
	Gnaphosidae	Gnaphosidae `sp. S3`	2	WAM
		Gnaphosidae `sp. wonmunna`	2	WAM
		Gnaphosidae sp. B01	1	BHP
		nr *Encoptarthria* sp. B01	12	BHP & WAM
	Linyphiidae	Linyphiidae `sp. OP`	1	WAM
		Linyphiidae sp. B03 (=Araneae sp. S05)	17	BHP
		Linyphiidae sp. OP	2	BHP
	Oonopidae	Oonopidae `sp. MC`	1	WAM
		Oonopidae `sp. MJ`	2	WAM
		Oonopidae sp. B19-DNA	1	BHP
		Oonopidae sp. MJ	2	BHP
		Pelicinus sp. B02	8	BHP & WAM
		Pelicinus sp. B05	1	BHP
		Prethopalpus `BAR116`	1	BHP
		Prethopalpus `DNA01`	4	WAM
		Prethopalpus `marillana`	2	WAM
		Prethopalpus `sp. B27`	1	WAM
		Prethopalpus `sp. MA`	1	WAM
		Prethopalpus boltoni	2	WAM
		Prethopalpus julianneae	1	BHP & WAM
		Prethopalpus maini	6	BHP & WAM
		Prethopalpus pearsoni	1	BHP & WAM
		Prethopalpus sp. (Araneae sp. S07)	1	BHP
		Prethopalpus sp. B18 (=?Araneae sp. S05)	4	BHP
		Prethopalpus sp. B32	1	BHP & WAM
	Symphytognathidae	*Anapistula* sp. B02	1	BHP
		Symphytognathidae `sp. S1`	1	WAM
Opiliones		Opiliones sp. B02	2	BHP & WAM
		Opiliones sp. B03	1	BHP & WAM

Order	Family	Lowest identification	N° of records	Source
	Assamiidae	*Dampetrus* `*isolatus*?`	1	WAM
		Dampetrus `sp. B01 (nr *isolatus*)`	7	BHP & WAM
		Dampetrus sp. B05 (nr *isolatus*)	1	BHP
Palpigradi		Palpigradi `sp. B01`	2	WAM
		Palpigradi `sp. B19`	1	WAM
		Palpigradi `sp. OP`	1	WAM
		Palpigradi sp. B01	18	BHP
		Palpigradi sp. B23	1	BHP
		Palpigradi sp. MC	1	BHP
		Palpigradi sp. OP	4	BHP
		Palpigradi sp. UM	1	BHP
	Eukoeneniidae	*Eukoenenia* sp. S01	2	BHP
Pseudoscorpiones	**Chthoniidae**	Chthoniidae `PSE204`	3	WAM
		Chthoniidae `sp. HLX PC056`	1	WAM
		Chthoniidae `sp. HLX PC057`	1	WAM
		Chthoniidae sp. MJ	1	BHP
		Lagynochthonius `PSE039`	41	BHP & WAM
		Lagynochthonius `PSE043`	1	WAM
		Lagynochthonius `PSE045`	3	BHP & WAM
		Lagynochthonius `PSE096`	1	WAM
		Lagynochthonius `PSE097`	1	WAM
		Lagynochthonius `PSE165`	6	WAM
		Lagynochthonius `sp. 2`	2	WAM
		Lagynochthonius `sp. Packsaddle`	3	WAM
		Lagynochthonius `*yandi*`	1	WAM
		Lagynochthonius sp. B19	1	BHP
		Lagynochthonius sp. B20 (= sp. S04)	3	BHP
		Lagynochthonius sp. S03	4	BHP
		Tyrannochthonius ` sp. MA`	1	WAM
		Tyrannochthonius ` sp. S4`	5	WAM
		Tyrannochthonius ` sp. S5`	1	WAM
		Tyrannochthonius `DNA05`	1	WAM

Order	Family	Lowest identification	N° of records	Source
		Tyrannochthonius `PSE046`	6	BHP & WAM
		Tyrannochthonius `PSE050`	8	BHP & WAM
		Tyrannochthonius `PSE055`	9	BHP & WAM
		Tyrannochthonius `PSE066`	8	BHP
		Tyrannochthonius `sp. B37`	1	WAM
		Tyrannochthonius `sp. OP`	1	WAM
		Tyrannochthonius aridus	1	BHP & WAM
		Tyrannochthonius sp. OP	1	BHP
		Tyrannochthonius sp. S05	1	BHP
	Hyidae	*Indohya* `PSE005`	7	BHP & WAM
		Indohya `PSE150`	1	WAM
		Indohya `PSE179`	5	WAM
		Indohya `PSE186`	2	WAM
		Indohya sp. B06	1	BHP
	Lechytiidae	*Lechytia* `PSE201`	16	WAM
	Olpiidae	*Beierolpium* `DNA01`	1	WAM
		Linnaeolpium `w1`	1	WAM
		Olpiidae `Helix sp. H-PO016`	1	WAM
		Olpiidae `sp. MA`	1	WAM
		Olpiidae `sp. MC`	1	WAM
		Olpiidae `sp. MJ1`	2	WAM
		Olpiidae `sp. MJ2`	1	WAM
		Olpiidae `sp. MJ3`	1	WAM
		Olpiidae sp. MC	2	BHP
		Olpiidae sp. MJ1	2	BHP
		Olpiidae sp. MJ2	1	BHP
		Olpiidae sp. MJ3	1	BHP
Schizomida	**Hubbardiidae**	*Draculoides* `BSC007` (B2 gp)	2	BHP
		Draculoides `BSC021` (B2 gp)	1	BHP
		Draculoides `BSC022` (B2 gp)	4	BHP
		Draculoides `BSC024`	1	BHP
		Draculoides `BSC027`	5	BHP

Order	Family	Lowest identification	N° of records	Source
		Draculoides `BSC034-DNA` (B2 gp)	1	BHP
		Draculoides `BSC036` (SCH030 complex)	2	BHP
		Draculoides `BSC037`	11	BHP
		Draculoides `BSC039`	2	BHP
		Draculoides `BSC042-DNA`	4	BHP
		Draculoides `Helix sp. H-SCH046`	1	WAM
		Draculoides `Helix sp. H-SCH051`	1	WAM
		Draculoides `Helix sp. H-SCH057`	1	WAM
		Draculoides `Helix sp. H-SCH059`	3	WAM
		Draculoides `Helix sp. H-SCH060`	7	WAM
		Draculoides `Helix sp. H-SCH061`	10	WAM
		Draculoides `MJ`	20	BHP
		Draculoides `SCH002`	4	WAM
		Draculoides `SCH012?`	2	WAM
		Draculoides `SCH012`	44	BHP & WAM
		Draculoides `SCH013`	17	BHP & WAM
		Draculoides `SCH018`	2	WAM
		Draculoides `SCH018` (B2 gp)	1	BHP
		Draculoides `SCH020`	6	BHP & WAM
		Draculoides `SCH021`	6	BHP
		Draculoides `SCH022` (B2 gp)	18	BHP
		Draculoides `SCH023?`	1	WAM
		Draculoides `SCH023`	15	WAM
		Draculoides `SCH023` (B2 gp)	8	BHP
		Draculoides `SCH024`	3	WAM
		Draculoides `SCH025`	1	WAM
		Draculoides `SCH034`	1	WAM
		Draculoides `SCH037`	19	WAM
		Draculoides `SCH054`	29	WAM
		Draculoides `SCH055`	4	WAM
		Draculoides `SCH063`	1	WAM
		Draculoides `SCH064`	1	WAM

Order	Family	Lowest identification	N° of records	Source
		Draculoides `SCH065`	1	WAM
		Draculoides `SCH067`	23	WAM
		Draculoides `SCH068`	10	WAM
		Draculoides `SCH069`	12	WAM
		Draculoides `SCH071`	13	WAM
		Draculoides `SCH072`	5	WAM
		Draculoides `SCH075`	8	WAM
		Draculoides `SCH076`	5	WAM
		Draculoides `SCH079`	7	WAM
		Draculoides `SCH081`	45	WAM
		Draculoides `SCH092`	14	WAM
		Draculoides `SCH097`	26	WAM
		Draculoides `SCH105`	5	WAM
		Draculoides `SCH106`	2	WAM
		Draculoides `SCH107`	2	WAM
		Draculoides `SCH109`	1	WAM
		Draculoides `sp. 01`	1	WAM
		Draculoides `sp. 03`	3	WAM
		Draculoides `sp. B16`	5	WAM
		Draculoides `sp. B20`	4	WAM
		Draculoides `sp. B46`	1	WAM
		Draculoides `sp. B47`	6	WAM
		Draculoides `sp. B55`	1	WAM
		Draculoides `sp. B58`	2	WAM
		Draculoides `sp. B59-DNA`	1	WAM
		Draculoides `sp. Koodaideri/Yandi`	3	WAM
		Draculoides `sp. MJ`	1	WAM
		Draculoides `sp. SPB2`	1	WAM
Geophilomorpha	**Geophilidae**	Chilenophilinae sp. B02	2	BHP
		Chilenophilinae sp. B07	1	BHP
		Ribautia `sp. B02`	1	WAM
	Schendylidae	*Australoschendyla* sp. B06	2	BHP

Order	Family	Lowest identification	N° of records	Source
Scolopendromorpha	**Cryptopidae**	*Cryptops* `BSCOL059-DNA`	1	BHP
		Cryptops `sp. DNA17`	1	WAM
		Cryptops `sp. MJ`	1	WAM
		Cryptops `sp. PS1`	1	WAM
		Cryptops sp. B07 (=Scolopendrida sp. S02)	8	BHP & WAM
		Cryptops sp. B10 (=Scolopendrida sp. S05)	1	BHP
		Cryptops sp. B15	3	BHP
		Cryptops sp. B39	1	BHP
	Scolopendridae	*Cormocephalus* `CHI003`	1	BHP
		Cormocephalus `sp. B02`	1	WAM
		Cormocephalus pyropygus	1	WAM
		Cormocephalus sagmus	1	WAM
		Scolopendra laeta	1	WAM
		Scolopendridae sp. B01	1	BHP
		Scolopendridae sp. S05	1	BHP & WAM
Diplopoda				
Polydesmida		Polydesmida sp. B11	2	BHP
Polyxenida	**Lophoproctidae**	*Lophoturus madecassus*	190	BHP & WAM
	Polyxenidae	Polyxenidae `sp. DNA01`	2	WAM
		Polyxenidae `sp. DNA02`	1	WAM
Spirobolida	**Trigoniulidae**	Trigoniulidae sp. B06	1	BHP
Entognatha				
Diplura	**Japygidae**	Japygidae `BDP155` (DPL002)	1	BHP
		Japygidae `BDP159`	4	BHP
		Japygidae `BDP164`	1	BHP
		Japygidae `DPL002` s.l.	22	BHP
		Japygidae `DPL005`	2	BHP
		Japygidae `DPL007`	1	BHP
		Japygidae `DPL017`	1	BHP
		Japygidae `sp. B04`	2	WAM
		Japygidae `sp. B34`	1	WAM
		Japygidae `sp. DPL002`	1	WAM

Order	Family	Lowest identification	N° of records	Source
		Japygidae `sp. DPL007`	1	WAM
		Japygidae `sp. DPL011`	3	WAM
		Japygidae `sp. DPL017`	2	WAM
		Japygidae `sp. Won1`	2	WAM
		Japygidae sp. S01	2	BHP
		Japygidae sp. S02_MJ	2	BHP
	Parajapygidae	Parajapygidae `DPL020`	4	BHP
		Parajapygidae `DPL023`	1	BHP
		Parajapygidae `sp. DPL020`	1	WAM
		Parajapygidae `sp. DPL023`	1	WAM
		Parajapygidae `sp. DPL024`	1	WAM
		Parajapygidae sp. B25	1	BHP
		Parajapygidae sp. B27	1	BHP
		Parajapygidae sp. MJ1	1	BHP
		Parajapygidae sp. MJ2	1	BHP
		Parajapygidae sp. S03	1	BHP
	Projapygidae	Projapygidae `MJ` (DPR001)	2	BHP
		Projapygidae `OP` (DPR003)	1	BHP
		Projapygidae `sp. B09`	1	WAM
		Projapygidae `sp. Won1`	1	WAM
		Projapygidae `sp. Won2`	1	WAM
		Projapygidae `sp. Won3`	1	WAM
		Projapygidae `UM` (DPR002)	1	BHP
		Projapygidae sp. B02	1	BHP
		Projapygidae sp. B05	1	BHP
		Projapygidae sp. B10	1	BHP
Insecta				
Blattodea		Blattodea `sp. B02`	2	WAM
	Blattidae	Blattidae `sp. B06`	1	WAM
		Blattidae `sp. S2`	28	WAM
		Blattidae sp. B06 (= sp. S02)	77	BHP
		Blattidae sp. OP	1	BHP

Order	Family	Lowest identification	N° of records	Source
	Nocticolidae	*Nocticola* `BBL038` (*cockingi* s.l.)	4	BHP
		Nocticola `sp. B07`	1	WAM
		Nocticola `sp. B29 (nr sp. B10)`	1	WAM
		Nocticola `sp. B31`	1	WAM
		Nocticola `sp. BLA001`	4	WAM
		Nocticola `sp. BLA003`	2	WAM
		Nocticola `sp. BLA004`	1	WAM
		Nocticola `sp. S1`	31	WAM
		Nocticola `sp. Won1`	6	WAM
		Nocticola cockingi	8	BHP
		Nocticola cockingi s.l.	97	BHP
		Nocticola quartermainei	2	BHP
		Nocticola quartermainei s.l.	49	BHP
		Nocticola sp. B36 (*cockingi* s.l.)	46	BHP
		Nocticola 'sp. BIOLOGIC-BLAT002'	3	WAM
		Nocticola 'sp. BIOLOGIC-BLAT003'	6	WAM
		Nocticola 'sp. BIOLOGIC-BLAT004'	1	WAM
		Nocticolidae `sp. MA`	2	WAM
		Nocticolidae `sp. S3`	6	WAM
Coleoptera		Coleoptera `sp. B06`	1	WAM
		Coleoptera gen 1 sp. B06	2	BHP
		Coleoptera sp. B09	1	BHP
	Brentidae	Brentidae sp. B02	1	BHP
	Carabidae	Anillini sp. OP	2	BHP
		Anillini sp. S08	1	BHP
		Bembidiinae sp. B01	1	BHP
		Bembidiinae sp. B08	1	BHP
		Carabidae `sp. Won1`	1	WAM
		Carabidae sp. B01	1	BHP
		Gracilanillus sp. B09	1	BHP
		Typhlozuphium humicolum	4	BHP & WAM
		Typhlozuphium longipenne	1	BHP & WAM

Order	Family	Lowest identification	N° of records	Source
		Typhlozuphium sp. B02	2	BHP
		Typhlozuphium sp. B03	1	BHP
		Typhlozuphium sp. B04	1	BHP
		Zuphiini sp. B04	1	BHP
		Zuphiini sp. UM	1	BHP
	Curculionidae	Cryptorhynchinae `sp. MA`	1	WAM
		Cryptorhynchinae sp. B10	2	BHP
		Cryptorhynchinae sp. B19	1	BHP
		Cryptorhynchinae sp. B20 (=sp. MA)	1	BHP
		Cryptorhynchinae sp. MJ	2	BHP
		Cryptorhynchinae sp. S03	1	BHP
		Curculionidae `sp. B10`	3	WAM
		Curculionidae Genus 1 `sp. B02 (= sp. S02)`	27	WAM
		Curculionidae Genus 1 `sp. B14`	3	WAM
		Curculionidae Genus 1 `sp. B15 (B02=S02 clade)`	2	WAM
		Curculionidae Genus 1 sp. B02 (=Curculionidae sp. S02)	60	BHP
		Curculionidae Genus 1 sp. B14	2	BHP
		Curculionidae Genus 1 sp. B15 (B02=S02 clade)	4	BHP
		Curculionidae sp. UM	1	BHP
		Cyclominae `sp. MA`	2	WAM
	Ptiliidae	*Ptinella* `sp. Helix-CPT003`	1	WAM
		Ptinella sp. B01 (=MC)	4	BHP
		Rodwayia sp. B02	1	BHP
	Staphylinidae	nr *Claviger* sp. B01	1	BHP
		Pselaphinae sp. B01	8	BHP
		Pselaphinae sp. B02	1	BHP
		Pselaphinae sp. B12	1	BHP
		Pselaphinae sp. S04	2	BHP
		Pselaphinae sp. UM	2	BHP
		Staphylinidae `sp. B02`	1	WAM
Diptera	**Sciaridae**	Sciaridae `sp. B01`	4	WAM
		Sciaridae sp. B01	104	BHP

Order	Family	Lowest identification	N° of records	Source
		Sciaridae sp. B03	2	BHP
		Sciaridae sp. B05	1	BHP
Hemiptera	**Cixiidae**	Cixiidae sp. B02	48	BHP
	Meenoplidae	Meenoplidae `sp. B02`	2	WAM
		Meenoplidae `sp. B04`	2	WAM
		Meenoplidae `sp. B08`	1	WAM
		Meenoplidae `sp. MA`	1	WAM
		Meenoplidae `sp. Won1`	1	WAM
		Meenoplidae `sp. Won2`	2	WAM
		Meenoplidae `sp. Won3`	1	WAM
		Nisia 'sp. BIOLOGIC-HEMI001'	1	WAM
		Phaconeura `BHE030`	1	BHP
		Phaconeura `BHE032`	5	BHP
		Phaconeura sp. B02 (B form)	3	BHP
		Phaconeura sp. B02 (D form)	3	BHP
		Phaconeura sp. B02 s.l. (=Meenoplidae sp. S01)	20	BHP
		Phaconeura sp. B03 (winged, remnant eyes)	4	BHP
		Phaconeura sp. B04	41	BHP
		Phaconeura sp. B06	8	BHP
		Phaconeura sp. B13	11	BHP
		Phaconeura sp. B19	6	BHP
Zygentoma	**Nicoletiidae**	Atelurinae `sp. MJ_UM_MA`	7	BHP & WAM
		Atelurinae `Won1`	1	WAM
		Atelurinae `Won2`	1	WAM
		Atelurinae sp. B04	1	BHP
		Dodecastyla `BZY084` (nr *crypta*)	1	BHP
		Dodecastyla crypta	59	BHP & WAM
		Dodecastyla sp. B02 (=Atelurodes sp. S02)	29	BHP
		Nicoletiidae `sp. B02`	3	WAM
		Trinemura `sp. B25`	1	WAM
		Trinemura sp. ?UM	1	BHP
		Trinemura sp. B02 (nr *watsoni*)	9	BHP

Order	Family	Lowest identification	N° of records	Source
		Trinemura sp. B09	6	BHP
		Trinemura sp. B32	1	BHP
		Trinemura sp. UM	1	BHP
Malacostraca				
Isopoda	**Armadillidae**	*Acanthodillo* `sp. won1`	1	WAM
		Armadillidae `sp. B03`	7	WAM
		Armadillidae `sp. B06`	3	WAM
		Armadillidae `sp. B11`	1	WAM
		Armadillidae `sp. B13`	2	WAM
		Armadillidae `sp. B14`	3	WAM
		Armadillidae `sp. B4`	1	WAM
		Armadillidae `sp. B6`	1	WAM
		Armadillidae `sp. ISO001`	1	WAM
		Armadillidae sp. B07	2	BHP
		Buddelundia `sp. 19`	1	WAM
		Troglarmadillo `BIS345`	1	BHP
		Troglarmadillo `sp. A`	1	WAM
		Troglarmadillo `sp. B44`	1	WAM
		Troglarmadillo `sp. DNA03`	1	WAM
		Troglarmadillo `sp. S14`	1	WAM
		Troglarmadillo B03	3	BHP
		Troglarmadillo sp. B11	5	BHP
		Troglarmadillo sp. B13	3	BHP
		Troglarmadillo sp. B14	1	BHP
		Troglarmadillo sp. B36	1	BHP
		Troglarmadillo sp. B37	3	BHP
		Troglarmadillo sp. B57	1	BHP
		Troglarmadillo sp. B58	1	BHP
		Troglarmadillo sp. B59	1	BHP
		Troglarmadillo sp. B62	2	BHP
		Troglarmadillo sp. B64 (= sp. S14)	6	BHP
		Troglarmadillo sp. B65	1	BHP

Order	Family	Lowest identification	N° of records	Source
		Troglarmadillo sp. OP	2	BHP
		Troglarmadillo sp. S10	1	BHP
	Philosciidae	Philosciidae `sp. B03`	2	WAM
		Philosciidae `sp. B04`	1	WAM
		Philosciidae `sp. B10`	1	WAM
		Philosciidae `sp. B15`	1	WAM
		Philosciidae `sp. B16`	1	WAM
		Philosciidae sp. B03	1	BHP
		Philosciidae sp. MA	1	BHP
	Stenoniscidae	Stenoniscidae `sp. DNA01`	2	WAM
Pauropoda				
		Pauropoda sp. MA	1	BHP
		Pauropoda sp. MJ	1	BHP
		Pauropoda sp. OP	1	BHP
		Pauropoda sp. S04	2	BHP
		Pauropoda sp. UM	1	BHP
Tetramerocerata	**Pauropodidae**	*Allopauropus* `sp. B11`	2	WAM
		Decapauropus sp. B01	1	BHP
		Decapauropus sp. B02	1	BHP
		Decapauropus tenuis	1	WAM
		Pauropodidae `BPU076`	1	BHP
		Pauropodidae `BPU078`	1	BHP
		Pauropodidae `sp. B01`	3	WAM
		Pauropodidae `sp. B04`	4	WAM
		Pauropodidae `sp. B06`	2	WAM
		Pauropodidae `sp. B07`	1	WAM
		Pauropodidae `sp. B14`	2	WAM
		Pauropodidae `sp. B15`	1	WAM
		Pauropodidae sp. B01 s.l.	8	BHP
		Pauropodidae sp. B12	1	BHP
		Pauropodidae sp. B13	1	BHP
		Pauropodidae sp. B14	3	BHP

Order	Family	Lowest identification	N° of records	Source
		Pauropodidae sp. B16	1	BHP
		Polypauropus `sp. B01`	1	WAM
Symphyla				
		Symphyla sp. B04 (BHP)	1	BHP
		Symphyla sp. MJ	1	BHP
		Symphyla sp. OP1	5	BHP
		Symphyla sp. OP2	3	BHP
		Symphyla sp. UM	1	BHP
Cephalostigmata		Cephalostigmata `sp. DNA06`	3	WAM
		Cephalostigmata `sp. DNA07`	1	WAM
		Cephalostigmata `sp. DNA08`	1	WAM
		Cephalostigmata `sp. Yandi`	1	WAM
	Scolopendrellidae	*Symphylella* sp. B03	1	BHP
		Symphylella sp. B13	1	BHP
	Scutigerellidae	*Hanseniella* `sp. B21`	1	WAM
		Hanseniella `sp. MA`	1	WAM
		Hanseniella sp. B07	5	BHP
		Hanseniella sp. B08	4	BHP
		Hanseniella sp. B09	1	BHP
		Hanseniella sp. B14	5	BHP
		Hanseniella sp. B34	1	BHP
		Hanseniella sp. B35	1	BHP
		Hanseniella sp. B36-DNA	1	BHP
		Hanseniella sp. B37-DNA	1	BHP
		Hanseniella sp. B42-DNA	1	BHP
		Hanseniella sp. B43-DNA	1	BHP
		Hanseniella sp. MA	3	BHP
		Scutigerella sp. B03	4	BHP
Total number of troglofauna records			**2145**	
Number of unique taxonomic units (species, morphospecies, OTUs)			**405**	

Appendix C: Stygofauna species recorded within 40 km of Study Area

Order	Family	Lowest identification	N° of records	Source
Aphanoneura				
	Aeolosomatidae	*Aeolosoma* sp. 1 (PSS)	3	BHP
Arachnida				
Trombidiformes	**Halacaridae**	Halacaridae sp. B01	2	BHP
	Unionicolidae	*Recifella* sp. P1 (nr *umala*) (PSW)	1	BHP
Bdelloidea				
		Bdelloidea sp. 2:2	4	BHP
		Bdelloidea sp. 2:3	2	BHP
		Bdelloidea sp. 5:4	1	BHP
Clitellata				
Enchytraeida	**Enchytraeidae**	Enchytraeidae `3 bundle` s.l. (short sclero)	3	BHP
		Enchytraeidae `PST1` s.l. (E06)	11	BHP
		Enchytraeidae sp. E06-08	1	BHP
		Enchytraeidae sp. E06-09	1	BHP
		Enchytraeidae sp. E06-B02	1	BHP
		Enchytraeidae sp. E06-B03	1	BHP
		Enchytraeidae sp. E07	9	BHP
		Enchytraeidae sp. E08	1	BHP
		Enchytraeidae sp. E09	1	BHP
		Enchytraeidae sp. E11 (2 bundle short sclero)	3	BHP
		Enchytraeidae sp. E12	1	BHP
		Enchytraeidae sp. E12-01	1	BHP
		Enchytraeidae sp. OP	5	BHP
		Enchytraeus sp. AP PSS1 s.l.	11	BHP
		Enchytraeus sp. AP PSS2 s.l.	6	BHP & WAM
Haplotaxida	**Haplotaxidae**	Haplotaxidae sp. S01	1	BHP
	Naididae	*Dero* (*Dero*) *nivea*	1	BHP
		Naididae sp. S03	2	BHP
		Pristina longiseta	1	BHP
	Phreodrilidae	*Insulodrilus lacustris* s.l. Pilbara type 2/3 (PSS)	2	BHP
		Phreodrilidae `BOL038` (AP SVC)	1	BHP
		Phreodrilidae sp. AP DVC s.l.	23	BHP
		Phreodrilidae sp. AP SVC s.l.	10	BHP
		Phreodrilidae sp. P02	2	BHP
		Phreodrilidae sp. P04	5	BHP
		Phreodrilidae sp. P11	1	BHP
		Phreodrilidae sp. P12	11	BHP

Order	Family	Lowest identification	N° of records	Source
	Tubificidae	*Ainudrilus* sp. WA26 (PSS)	1	BHP
		Tubificidae `stygo type 5`	2	BHP
		Tubificidae sp. B09	1	BHP
Malacostraca				
Amphipoda	**Neoniphargidae**	Neoniphargidae sp. B03	7	BHP
	Paramelitidae	*Chydaekata* `sp. E`	34	BHP & WAM
		Chydaekata `sp. B01`	1	WAM
		Chydaekata `sp. MJ1-UM1`	7	WAM
		Chydaekata `sp. OB1`	2	WAM
		Chydaekata `sp. S2`	1	WAM
		Chydaekata acuminata	18	BHP & WAM
		Chydaekata sp. B01	4	BHP
		Chydaekata sp. MJ1-UM1	171	BHP
		Chydaekata sp. S01	2	BHP
		Maarrka `sp. MA`	1	WAM
		Maarrka `sp. MJ1-UM1`	23	WAM
		Maarrka etheli	2	WAM
		Maarrka sp. MA	2	BHP
		Maarrka sp. MJ1-UM1	25	BHP
		Maarrka weeliwollii	34	BHP & WAM
		Paramelitidae `sp. 2 (DEC)`	35	WAM
		Paramelitidae `sp. 2 (DEC/PSS)`	22	WAM
		Paramelitidae `sp. 3`	1	WAM
		Paramelitidae `sp. B01`	1	WAM
		Paramelitidae `sp. B02`	17	WAM
		Paramelitidae `sp. B03`	2	WAM
		Paramelitidae `sp. B16`	3	WAM
		Paramelitidae `sp. B2`	1	WAM
		Paramelitidae `sp. B25`	1	WAM
		Paramelitidae `sp. B26`	1	WAM
		Paramelitidae `sp. Coondiner`	7	WAM
		Paramelitidae `sp. MA-Mindy`	40	WAM
		Paramelitidae `sp. MJ1-UM1`	23	WAM
		Paramelitidae `sp. MJ2-UM2-S5`	15	WAM
		Paramelitidae `sp. nr. 2 (DEC)`	18	WAM
		Paramelitidae `sp. OB1`	2	WAM
		Paramelitidae `sp. OB3`	3	WAM

Order	Family	Lowest identification	N° of records	Source
		Paramelitidae `sp. OP1`	3	WAM
		Paramelitidae `sp. OP2`	2	WAM
		Paramelitidae `sp. S4`	2	WAM
		Paramelitidae `sp. S5/S6`	2	WAM
		Paramelitidae `sp. S5`	1	WAM
		Paramelitidae Genus 2 `BAM151`	1	BHP
		Paramelitidae Genus 2 sp. B02	91	BHP
		Paramelitidae Genus 2 sp. B03	2	BHP
		Paramelitidae Genus 2 sp. B21 (=S06)	5	BHP
		Paramelitidae sp. B03	23	BHP
		Paramelitidae sp. B16	2	BHP
		Paramelitidae sp. B26 (Helix-AMP018)	38	BHP
		Paramelitidae sp. Coondiner	5	BHP
		Paramelitidae sp. MJ1-UM1	113	BHP
		Paramelitidae sp. OP1	2	BHP
		Paramelitidae sp. OP2	1	BHP
		Paramelitidae sp. S04 (BR South)	18	BHP
		Paramelitidae sp. S05	5	BHP
		Pilbarus `sp. Biologic-AMPH001`	2	WAM
Bathynellacea		Bathynellacea sp. 1 (Weeli Wolli)	1	BHP
		Bathynellacea sp. 2 (South Flank)	1	BHP
	Bathynellidae	*Pilbaranella* `sp. A`	4	WAM
		Pilbaranella `sp. B`	2	WAM
		Pilbaranella ethelensis	15	WAM
	Parabathynellidae	*Atopobathynella* `sp. A Kood`	1	WAM
		Atopobathynella `sp. B Kood`	1	WAM
		Atopobathynella `sp. B04`	2	WAM
		Atopobathynella `sp. B07`	1	WAM
		Atopobathynella `sp. MJ`	4	BHP & WAM
		Atopobathynella sp. B04	1	BHP
		Atopobathynella sp. S02	4	BHP
		Billibathynella `BSY187-DNA`	3	BHP
		Billibathynella `sp. S1`	8	WAM
		Billibathynella cassidis	3	WAM
		nr *Billibathynella* sp. B01	1	BHP
		nr *Billibathynella* sp. B02 (=Parabathynellidae sp. S03)	25	BHP
		nr *Notobathynella* sp. S01	5	BHP

Order	Family	Lowest identification	N° of records	Source
		nr. *Billibathynella* `sp. B01`	1	WAM
		nr. *Billibathynella* `sp. B02`	2	WAM
		Parabathynellidae `sp. B08`	1	WAM
		Parabathynellidae `sp. MJ`	1	WAM
		Parabathynellidae `sp. won1`	2	WAM
		Parabathynellidae sp. MC	3	BHP
		Parabathynellidae sp. MJ	6	BHP
		Parabathynellidae sp. OP	1	BHP
		Parabathynellidae sp. S02	2	BHP
Isopoda	**Microcerberidae**	*Coxicerberus* `sp. OB2`	1	WAM
	Tainisopidae	*Pygolabis* `sp. 6`	2	WAM
		Pygolabis `sp. B06 (=BIOTA yandi sp. 1)`	2	WAM
		Pygolabis `sp. MJ-UM`	55	BHP & WAM
		Pygolabis humphreysi	36	BHP & WAM
		Pygolabis weeliwolli	34	BHP & WAM
Maxillopoda				
Calanoida	**Ridgewayiidae**	*Stygoridgewayia trispinosa*	2	BHP
Cyclopoida	**Cyclopidae**	*Anzcyclops* `sp. OB`	1	WAM
		Australoeucyclops karaytugi	5	WAM
		Diacyclops `BCY059` (*humphreysi* s.l.)	16	BHP
		Diacyclops cockingi	36	BHP & WAM
		Diacyclops humphreysi	40	WAM
		Diacyclops humphreysi s.l.	89	BHP
		Diacyclops scanloni	4	BHP & WAM
		Diacyclops sobeprolatus	25	BHP & WAM
		Dussartcyclops sp. B10	2	BHP & WAM
		Mesocyclops brooksi	5	BHP & WAM
		Mesocyclops darwini	1	WAM
		Mesocyclops holynskae	3	WAM
		Mesocyclops notius	1	WAM
		Metacyclops nr. *pilbaricus*	1	WAM
		Microcyclops varicans	12	BHP & WAM
		Orbuscyclops westaustraliensis	1	BHP & WAM
		Pescecyclops sp. B01 (nr *pilbaricus*)	1	BHP
		Pilbaracyclops sp. B03 (nr *frustratio*)	2	BHP
		Thermocyclops aberrans	2	WAM
		Thermocyclops decipiens	2	BHP & WAM

Order	Family	Lowest identification	N° of records	Source
Harpacticoida	**Ameiridae**	*Gordanitocrella trajani*	29	BHP & WAM
		Nitocrella karanovici	2	WAM
	Canthocamptidae	*Australocamptus* `sp. B06`	1	WAM
		Elaphoidella sp. S02	1	BHP
		nr *Epactophanes* sp. B01	1	BHP
	Miraciidae	*Schizopera* sp. B02	5	BHP
	Parastenocarididae	*Parastenocaris* `COP001`	1	BHP
		Parastenocaris `sp. B25`	1	WAM
		Parastenocaris jane	11	BHP & WAM
Ostracoda				
Podocopida	**Candonidae**	Candonidae `BOS1183`	1	BHP
		Candonidae `sp. MJ-UM1`	31	BHP & WAM
		Candonidae `sp. OP1`	2	BHP & WAM
		Deminutiocandona mica	4	WAM
		Deminutiocandona murrayi	10	BHP
		Meridiescandona `sp. BOS 171`	1	WAM
		Meridiescandona facies	33	BHP & WAM
		Meridiescandona lucerna	12	BHP & WAM
		Meridiescandona marillanae	16	BHP & WAM
		Notacandona ?boultoni	1	BHP
		Notacandona boultoni	20	BHP & WAM
		Notacandona modesta	9	BHP & WAM
		Notacandona quasiboultoni	1	BHP
		Origocandona grommike	3	BHP
	Cyprididae	*Cypretta seurati*	1	BHP & WAM
		Sarscypridopsis ochracea	1	BHP
	Limnocytheridae	*Gomphodella alexanderi*	6	WAM
		Gomphodella yandii	18	BHP & WAM
Total number of stygofauna records			**1681**	
Number of unique taxonomic units (species, morphospecies, OTUs)			**169**	

Appendix D: Fauna collection licences

Department of **Biodiversity, Conservation and Attractions**

FAUNA TAKING (BIOLOGICAL ASSESSMENT) LICENCE

Regulation 27, Biodiversity Conservation Regulations 2018

Licence Number: BA27000987

Licence Holder: Syngeon Rodman
Biologic Environmental Survey
24 – 26 Wickham Street
EAST PERTH WA 6004

Date of Issue: 22/01/2024

Date Valid From: 22/01/2024
Date of Expiry: 21/01/2025

LICENSED ACTIVITIES

Subject to the terms and conditions on this licence, the licence holder may –

1. Undertake a three-phase detailed subterranean fauna survey of the Weeli Wolli and East Packsaddle areas for BHP Western Australia Iron Ore, to inform future environmental approvals. Sampling will be undertaken within proposed resource areas as well as regional reference areas in order to investigate the subterranean fauna assemblage of the area.

   Take fauna using troglofauna Scraping: scraping for troglofauna comprises four net-hauls of the above water table length of each hole, using a specially designed scraping attachment installed above the net (using a reinforced 150 µm weighted stygofauna net). Net-hauling for stygofauna comprises six hauls; three of which are undertaken a 50 micrometer [µm] net, and another three using a 150 µm net. The base of the net is fitted with a lead weight and a sample receptacle with a base mesh of 50 µm and Stygofauna occurring within near-surface groundwater habitats below stream beds (i.e. hyporheic habitats) can be sampled by Karaman sampling when the water table is elevated at or near the surface. Specimens to be lodged with the WA Museum upon completion of the project.

   Sampling to be undertaken in accordance to EPA Environmental Factor Guideline (2016), and Technical guidelines EAG 12 (EPA 2016b) and Subterranean Fauna Technical Guidance (EPA 2021).

LOCATIONS

1. BHP Western Australian Iron Ore (BHP WAIO) East Packsaddle, Weeli Wolli and Jinidi mine sites located 100 km northwest of the town of Newman.

AUTHORISED PERSONS

The following persons or persons of the specified class may assist in carrying out the licensed activities:

1. Syngeon Rodman
2. Phil Runham
3. Fabian Rudin
4. Anton Mittra
5. Juliana Pile Arnold

Department of Biodiversity, Conservation and Attractions

6. Morgan Lythe
7. Stephanie Floeckner
8. Siobhan Paget
9. Isabelle Johnansson
10. Courtney Wilkins
11. Mary van Wees
12. Chao Lyn
13. Aimee Carpenter
14. Liesel Morgan
15. Hayley Hampton
16. Jason Alexander

CONDITIONS

1. Fauna must not be taken on CALM land, (as defined in the Conservation and Land Management Regulations 2002), unless authorised by a written notice of a lawful authority issued under regulations 4 and 8 of the Conservation and Land Management Regulations 2002.
2. If persons, other than the licence holder, are authorised to carry out/assist in carrying out the activities under the licence, the licence holder must ensure those persons have read and understand the licence terms and conditions.
3. The written authorisation of the person in possession or occupation of the land accessed and upon which fauna is taken, as required under regulation 101(2) and referred to in "Additional information" below, must:
   a) state location details (including lot or location number, street/road, suburb and local government authority);
   b) state land owner or occupier name, and contact phone number;
   c) specify the time period that the authorisation is valid for;
   d) be signed and dated; and
   e) be attached to this licence at all times.
4. This licence, and any written authorisation or lawful authority which authorises the take of fauna on specified locations must be carried at all times while conducting licensed activities and be produced on demand by a wildlife officer.
5. If a species of fauna listed as a threatened species under Section 19 of the *Biodiversity Conservation Act 2016* is inadvertently captured, that species is to be released immediately at the point of capture. If the fauna is injured or deceased, the licence holder shall contact the DBCA Wildlife Licensing Section (wildlifelicensing@dbca.wa.gov.au) for advice on treatment or disposal. Details of any capture of threatened fauna must be included in the "Return of Fauna Taken."
6. The licence holder must not:
   a) release any fauna in any area where it does not naturally occur;
   b) transfer fauna to any other person or authority (other than the Western Australian Museum) unless approved in writing by the CEO; or
   c) dispose of the remains of fauna in any manner likely to interfere the natural or present day distribution of the species.
7. The licence holder must not take and remove more than ten specimens of any one protected species of fauna from any location less than 20km apart. Where exceptional circumstances make it necessary to take a larger number of specimens from a particular location in order to obtain adequate statistical data, the collector must proceed with circumspection and justify their actions to the Director General in advance.

Department of **Biodiversity, Conservation and Attractions**

8. All holotypes and syntypes and a half share of paratypes of species or subspecies permitted to be permanently taken under this licence must be donated to the Western Australian Museum. Duplicates (one pair in each case) of any species collected, which represents a significant extension of geographic range must be offered to the Western Australian Museum.
9. All specimens and material retained under the authority of this licence must be offered to the Western Australian Museum for loan, for inclusion in its collection, or on request be made available to other persons involved in relevant scientific studies.
10. The licence holder must create, compile and maintain records and information as required in a DBCA approved "Return of Fauna Taken" of all fauna taking activities as they occur.
11. A DBCA approved "Return of Fauna Taken" must be completed in full (including nil taking details) and submitted to DBCA Wildlife Licensing Section (wildlifelicensing@dbca.wa.gov.au) prior to the end of each annual period of the licence (from the valid from date) (refer to "Additional Information" section

Danny Stefoni
LICENSING OFFICER
WILDLIFE PROTECTION BRANCH

Delegate of CEO

ADDITIONAL INFORMATION

1. It is an offence to take any species of fauna listed as a threatened species under Section 19 of the *Biodiversity Conservation Act 2016* unless the person is authorised under Section 40. The penalty ranges between $300 000 and $500 000; Section 150 Biodiversity Conservation Act 2016.
2. Regulation 82 empowers the CEO to add, substitute or delete a term or condition of a licence or to correct errors. Such power may be exercised on application of a licence holder or by the CEO's own initiative. If an amendment to a licence term or condition is required, please contact the CEO or the Licensing Section on wildlifelicensing@dbca.wa.gov.au in the first instance. The licence holder, if adversely affected by a condition imposed in this licence, may apply to the State Administrative Tribunal for review of the decision of the CEO to impose that condition on a licence: regulation 89(2) Biodiversity Conservation Regulations 2018.
3. A person must not contravene a condition of a licence. The penalty for an offence involving the contravention of a condition of a licence is a fine of $10 000: regulation 84 of the Biodiversity Conservation Regulations 2018.
4. It is an offence for persons authorised by this licence to enter land that is not in their possession or under their control without first having the *prior* written authorisation of the current owner or occupier of the land to:

   a) enter the land; and

   b) carry out the activity authorised by this licence.

   The penalty for this offence is a fine of $5 000: regulation 101(2) of the Biodiversity Conservation Regulations 2018.

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5. The licence holder must be able to produce for inspection upon request any information or records required by regulation 85(2) of the Biodiversity Conservation Regulations 2018 Penalty $10 000. It is an offence to knowingly include false or misleading information or make statements in records: regulation 85(3) of the Biodiversity Conservation Regulations 2018 Penalty $10 000. It is an offence to include any information or make any statement in a return that the licence holder knows to be false or misleading in a material particular: regulation 86 (2) of the Biodiversity Conservation Regulations 2018 Penalty $10 000.
6. The approved DBCA "Return of Fauna Taken" data file can be downloaded from the DBCA webpage (https://www.dpaw.wa.gov.au/plants-and-animals/licences-and-authorities).
7. The issuing of a licence under the Biodiversity Conservation Regulations 2018 does not constitute an animal ethics approval or a licence to use animals for scientific purposes as required under the *Animal Welfare Act 2002*, Animal Welfare (Scientific Purposes) Regulations 2003. It is the responsibility of a licence applicant / licence holder to ensure that they comply with the requirements of all applicable legislation. Enquiries relating to the Animal Welfare Act licences and animal ethics approvals are to be directed to the Department of Primary Industries and Regional Development (https://www.agric.wa.gov.au/animalwelfare).
8. Threatened fauna can only be taken under a *Biodiversity Conservation Act 2016* Section 40 authorisation. Occurrences of threatened species must be reported to the CEO. For more information please see https://www.dpaw.wa.gov.au/plants-and-animals/threatened-species-and-communities/threatened-animals.
9. Any interaction involving Nationally Listed Threatened Fauna that may be invasive and/or harmful to the fauna may require approval from the Commonwealth Department of the Environment and Energy http://www.environment.gov.au/about-us/business-us/permits-assessments-licences. Interaction with such species is controlled by the Commonwealth *Environment Protection and Biodiversity Conservation Act 1999* and Environment Protection and Biodiversity Conservation Regulations 2000 as well as the *Biodiversity Conservation Act 2016* and Biodiversity Conservation Regulations 2018.

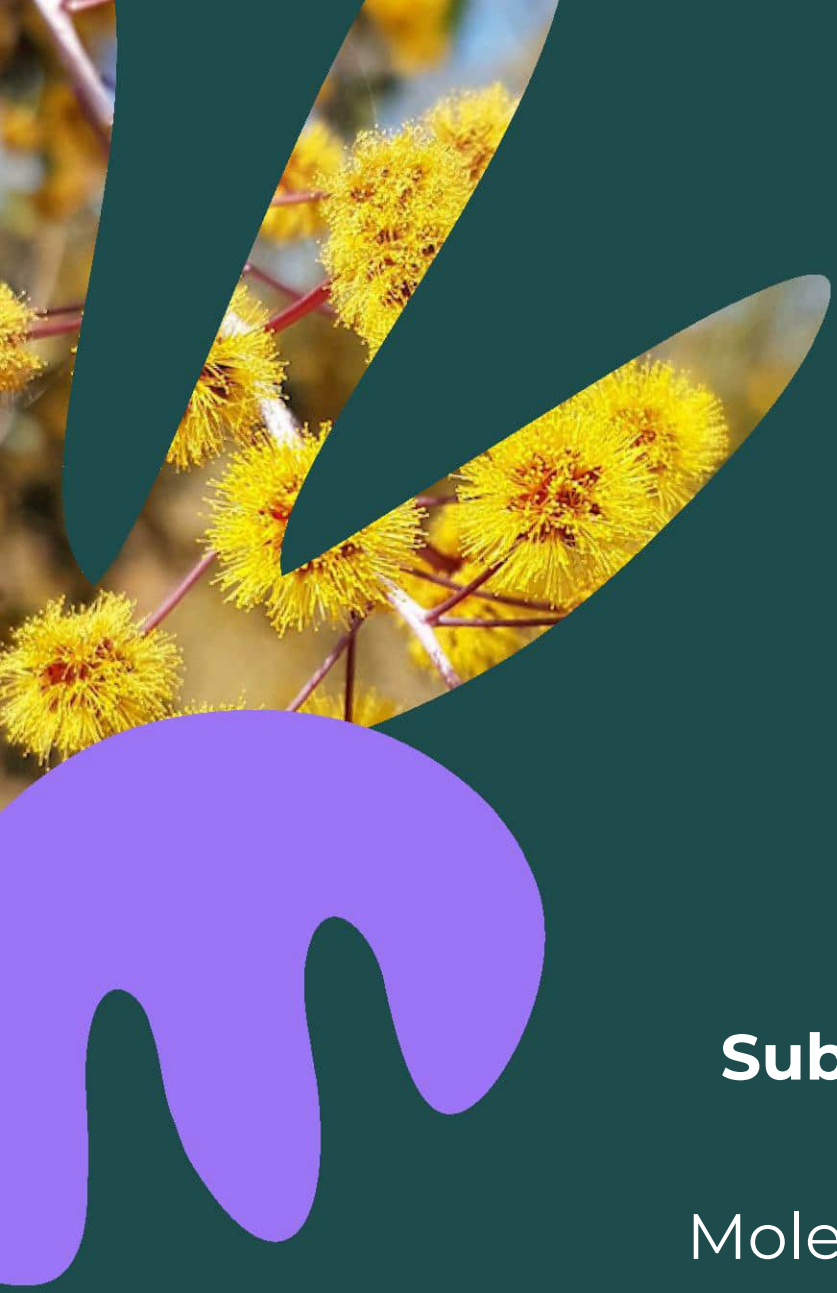
Appendix E: Bores and drill holes visited during the current survey

Site name	Latitude	Longitude	N° of trap samples collected	N° of scrape samples	N° of scrape-hauls	N° of haul samples
EEX0044	-22.91	119.1326	1			
EEX0046	-22.9148	119.1913	3	3		
EEX0047	-22.9138	119.1324	2	2		
EEX0049	-22.914	119.1706	1	3		
EEX0050	-22.9139	119.1632	2	3		
EEX0052	-22.9143	119.1788	3	2		
EEX0053	-22.9156	119.1855	2	3		
EEX0101	-22.9121	119.1323	1	1		
EEX0108	-22.9131	119.1916	1	2		
EEX0109	-22.9143	119.1845	3	3		
EEX0112	-22.9135	119.179	1			
EEX0685	-22.9136	119.2032	2	2		
EEX0711	-22.9203	119.1427	3	3		
EPS0148R	-22.9039	119.127	3	2		
EPS0186RG	-22.9135	119.161	3	3		
EPS0220R	-22.9107	119.152	3		3	
EPS0239R	-22.9074	119.1326		1		
EPS0240R	-22.9066	119.1325	2	3		
EPS0243R	-22.9071	119.1378	3	2		
EPS0244R	-22.907	119.1447	3	3		
EPS0246R	-22.9089	119.1448	2	3		
EPS0247R	-22.9079	119.1448	2	3		
EPS0257R	-22.9179	119.1447	1	1		
EPS0258R	-22.917	119.1449	3	3		
EPS0261R	-22.9141	119.1432	3	3		
EPS0271R	-22.9149	119.1756	2	1		
EPS0273R	-22.9132	119.1755	2		3	
EPS0305R	-22.9087	119.1664	3		3	
EPS0306R	-22.911	119.1935				1
EPS0421R	-22.9002	119.1007	3	3		
EPS0507R	-22.9048	119.1126	3	2		
EPS0548R	-22.9044	119.1258	3	2		
EPS0549R	-22.904	119.1255	1			
EPS0550R	-22.9044	119.1269	3	2		
EPS0569R	-22.9132	119.1287	1	1		
EPS0580R	-22.9043	119.1285	3	2		
EPS0588R	-22.9137	119.1302	3	3		
EPS0589R	-22.9133	119.1301	2	2		
EPS0590R	-22.9128	119.1301	3	3		
EPS0597R	-22.9173	119.1321	2			
EPS0602R	-22.914	119.1321	2	2		
EPS0603R	-22.9135	119.1322	3	1		
EPS0607R	-22.9177	119.1345	2	3		
EPS0622R	-22.9174	119.1373	2	2		
EPS0630R	-22.9084	119.1376	3	3		
EPS0632R	-22.9137	119.1397		1		
EPS0638R	-22.9097	119.1388	2	3		
EPS0639R	-22.9093	119.1385	2	3		
EPS0643R	-22.9203	119.1408	3	3		

Site name	Latitude	Longitude	N° of trap samples collected	N° of scrape samples	N° of scrape-hauls	N° of haul samples
EPS0653R	-22.9214	119.1418	2	2		
EPS0660R	-22.9179	119.1422	2	3		
EPS0717R	-22.9173	119.1321	3	3		
EPS0725R	-22.9119	119.1443	3	2		
EPS0730R	-22.9193	119.1462	1			
EPS0731R	-22.9193	119.1462	3	2		
EPS0745R	-22.9088	119.1476	2	3		
EPS0746R	-22.9133	119.1481	3	3		
EPS0747R	-22.9129	119.1481	2	3		
EPS0767R	-22.9151	119.1505	2	3		
EPS0768R	-22.9146	119.1505	3	3		
EPS0776R	-22.909	119.1505	3	1	2	
EPS0779R	-22.9187	119.1516	3	3		
EPS0787R	-22.9103	119.152	2	3		
EPS0793R	-22.9128	119.1531		1		
EPS0794R	-22.9124	119.1535	3	3		
EPS0813R	-22.9096	119.1553	3		4	
EPS0819R	-22.9204	119.1565	2	3		
EPS0824R	-22.9163	119.1562	2	3		
EPS0851R	-22.9206	119.1607	3	3		
EPS0852R	-22.9198	119.1614	3	3		
EPS0857R	-22.9101	119.1607	3		4	
EPS0864R	-22.9077	119.1634	3		4	
EPS0866R	-22.9236	119.1637	3	3		
EPS0867R	-22.9231	119.1637	2	3		
EPS0869R	-22.9223	119.1637	3	3		
EPS0879R	-22.9101	119.1637	3		4	
EPS0882R	-22.9264	119.1652	3	3		
EPS0883R	-22.926	119.1652	3	3		
EPS0887R	-22.9241	119.1651	2	3		
EPS0892R	-22.9219	119.1652	3	3		
EPS0894R	-22.921	119.1651	3	3		
EPS0899R	-22.9111	119.1651	3	3		
EPS0903R	-22.9256	119.1662	2	3		
EPS0908R	-22.9232	119.1665	3	3		
EPS0920R	-22.9212	119.168	3	2	1	
EPS0927R	-22.9106	119.1681	3		3	
EPS0928R	-22.9097	119.1681	2	3		
EPS0931R	-22.9278	119.1696		1		
EPS0938R	-22.921	119.1696	2	3		
EPS0940R	-22.9146	119.1696		1		
EPS0946R	-22.9278	119.171	2		3	
EPS0948R	-22.9269	119.171	3		4	
EPS0949R	-22.9263	119.171	3	3		
EPS0959R	-22.9122	119.1714			1	
EPS0960R	-22.9099	119.1713	3	3		
EPS0965R	-22.9273	119.1725			1	
EPS0969R	-22.9209	119.1725	3	3		
EPS0971R	-22.92	119.1725		1		

Site name	Latitude	Longitude	N° of trap samples collected	N° of scrape samples	N° of scrape-hauls	N° of haul samples
EPS0974R	-22.911	119.1724			1	
EPS0975R	-22.9258	119.1739			1	
EPS0977R	-22.9236	119.1741		1		
EPS0982R	-22.9148	119.1739	2	3		
EPS0984R	-22.9139	119.1741			1	
EPS0989R	-22.9221	119.1755			1	
EPS0990R	-22.9214	119.1754		1		
EPS0991R	-22.9204	119.1755	2	3		
EPS0996R	-22.9224	119.1769		1		
EPS0999R	-22.9191	119.1769			1	
EPS1009R	-22.9217	119.1784		1		
EPS1046R	-22.9138	119.1832	3		3	
EPS1054R	-22.9115	119.1842	3		3	
EPS1075R	-22.9113	119.1871	3		3	
EPS1078R	-22.9102	119.187	3		4	
EPS1096R	-22.9114	119.19	2		2	
EPS1097R	-22.9111	119.1901	2		3	
EPS1098R	-22.9106	119.19	3		4	
EPS1109R	-22.913	119.1914	3		4	
EPS1119R	-22.9137	119.1924	3		3	
EPS1121R	-22.9129	119.1927	3		3	
EPS1126R	-22.9136	119.1936	3		3	
EPS1130R	-22.9151	119.1944	3	3		
EPS1137R	-22.9119	119.1945	3	3		
EPS1142R	-22.9142	119.1959	3		4	
EPS1146R	-22.9125	119.1959	1	1		
EPS1147R	-22.9119	119.1959	3		3	
EPS1152R	-22.9151	119.1973	3		4	
EPS1158R	-22.9124	119.1973	3		3	
EPS1160R	-22.9157	119.1987			1	
EPS1172R	-22.9137	119.2046			1	
EPS1175R	-22.9114	119.2068				3
EXR0087	-22.9231	119.1588	3	2		
GBRS0143	-22.9177	119.0734	3	2		
GWB0016D	-22.9317	119.1848				1
GWB0016S	-22.9317	119.1848				1
GWB0017D	-22.9187	119.2006				1
GWB0017S	-22.9187	119.2006				1
GWB0018D	-22.9244	119.1969				1
GWB0018S	-22.9244	119.1969				1
GWB0019	-22.9499	119.2336				1
GWB0032D	-22.9173	119.2057				1
GWB0032S	-22.9173	119.2057				1
HEOP0478	-22.904	119.215				5
JNOB0023R	-22.9384	119.229				1
Old BHP Camp	-22.9145	119.2098				3
Total number of samples			**279**	**220**	**96**	**22**

Appendix F: Molecular systematics report



Biologic
ENVIRONMENTAL
SURVEY

East Packsaddle Subterranean Fauna Survey

Molecular Systematics Analysis

Report to BHP WAIO

6 January 2025

Document Status				
Revision No.	Author	Review / Approved for Issue	Approved for Issue to Name	Date
1	Liesel Morgan, Stephanie Floeckner, Joel Huey	Joel Huey	Tanya Carroll, Jennifer Carter	25/10/2024
2	Joel Huey, Fabian Rudin	Joel Huey	Jennifer Carter	10/12/2024

"IMPORTANT NOTE"

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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.
Incertae sedis	The term used for a taxonomic group where its broader relationships are unknown or undefined.
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	East Packsaddle area, located immediately east of Mining Area C in the central Pilbara region of Western Australia
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.

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1 Introduction

1.1 Background

BHP Western Australian Iron Ore (BHP WAIO) commissioned Biologic Environmental Survey Pty Ltd (Biologic) to undertake a molecular systematics analysis (DNA barcoding) of 231 specimens collected from East Packsaddle (the Study Area) between May 2022 and June 2024. The specimens collected from the subterranean fauna surveys during this time period 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 231 subterranean 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)
- 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 231 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/Order	Fail	Pass	Total
Arachnida			
Araneae	0	15	15
Palpigrades	1	8	9
Pseudoscorpiones	3	30	33
Schizomida	0	33	33
Trombidiformes	1	2	3
Chilopoda			
Scolopendromorpha	0	3	3
Malacostraca			
Amphipoda	0	22	22
Bathynellacea	0	3	3
Isopoda	0	11	11
Entognatha			
Diplura	1	7	8
Insecta			
Blattodea	0	7	7
Coleoptera	1	11	12

Class/Order	Fail	Pass	Total
Hemiptera	0	5	5
Zygentoma	0	7	7
Maxillopoda			
Cyclopoida	0	10	10
Harpacticoida	0	6	6
Oligochaeta			
Enchytraeida	0	3	3
Haplotaxida	0	4	4
Tubificida	2	6	8
Ostracoda			
Podocopida	2	13	15
Pauropoda			
Pauropoda	0	11	11
Symphyla			
Cephalostigmata	0	3	3
Total	**11**	**220**	**231**

2.2 DNA Extraction, Amplification and Sequencing

DNA extraction and sequencing methods followed 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).

For the cockroach (Blattodea) samples, we targeted a section of the COI gene that is non-overlapping with the region targeted by the aforementioned primers. This section is amplified using the primers L2020 and H2619 (Yamauchi *et al.*, 2004). This enabled comparison to the data published by Trotter *et al.* (2017), which described three species of *Nocticola* and provided a large comparative dataset.

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 (Katoh *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, ≤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 ≤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. Additionally, distinct OTUs typically have large internode distances separating OTUs, with short internode distances within the OTU/species.

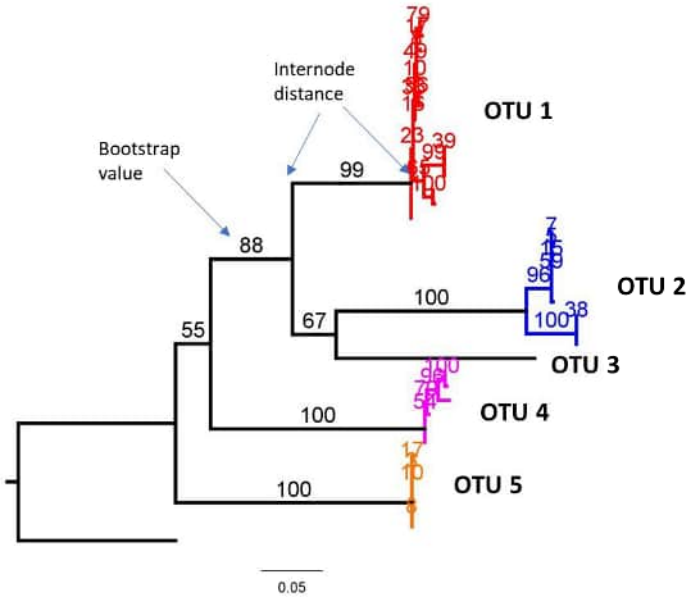

Figure 1. Example phylogeny showing delimited OTUs with internode distances and bootstrap values indicated

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 16th September 2024.

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 231 specimens were processed for sequencing by Biologic (Table 2.1). Sequences were successfully derived for 228 of these specimens (98.7% of specimens), with three failing to produce a PCR product. Of these 228 sequences, eight 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 220 high quality sequences for analysis (96.5% of sequences). The orders of the sequences are tabulated in Table 2.1.

In total, 70 OTUs have been designated to specimens from the Study Area, 38 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

OTU (genetic taxon)	Sequenced specimens	Matches to non-Study sequences	Linear Range
Araneae			
Araneae `sp. Biologic-ARAN092`	2	No	single site
Araneae `sp. Biologic-ARAN093`	3	No	3.3 km
Araneae `sp. Biologic-ARAN094`	7	No	4.0 km
Prethopalpus `sp. Biologic-ARAN115`	1	No	singleton
Orsolobidae `sp. Biologic-ARAN091`	2	No	3.8 km
Palpigrades			
Palpigradi `sp. Biologic-PALP075`	1	No	singleton
Palpigradi `sp. Biologic-PALP077`	6	No	3.6 km
Palpigradi `sp. Biologic-PALP086`	1	No	singleton
Pseudoscorpiones			
Chthoniidae `sp. Biologic-PSEU186`	1	No	singleton
Chthoniidae `sp. Biologic-PSEU188`	10	No	3.2 km
Chthoniidae `sp. Biologic-PSEU191`	4	No	1.5 km
Chthoniidae `sp. Biologic-PSEU192`	2	No	1.3 km
Chthoniidae `sp. Biologic-PSEU193`	5	No	2.5 km
Chthoniidae `sp. Biologic-PSEU195`	3	No	1.1 km
Indohya `sp. Biologic-PSEU183`	4	No	2.2 km
Indohya `sp. Biologic-PSEU184`	1	No	singleton
Schizomida			
Draculoides `sp. Biologic-SCHI023`	4	No	1.6 km

OTU (genetic taxon)	Sequenced specimens	Matches to non-Study sequences	Linear Range
Draculoides `sp. WAM-SCH067`	29	Yes	39.3 km
Trombidiformes			
Pezidae `sp. Biologic-ACAR003`	2	Yes	11.3 km
Chilopoda			
Cryptops `sp. Biologic-CHIL048`	1	Yes	56.1 km
Cormocephalus pyropygus	2	Yes	185.1 km
Malacostraca			
Chydaekata `sp. E TLF-2008`	7	Yes	50.3 km
Maarrka weeliwollii	4	Yes	84.1 km
Paramelitidae `sp. Biologic-AMPH024`	2	Yes	22.3 km
Paramelitidae `sp. Biologic-AMPH070`	9	Yes	14.8 km
Atopobathynella `sp. Biologic-PBAT019`	3	Yes	81.4 km
Troglarmadillo `sp. Biologic-ISOP151`	2	No	single site
Pygolabis weeliwolli	2	Yes	28.1 km
Isopoda `sp. Biologic-ISOP153`	1	No	singleton
Oniscidea `sp. Biologic-ISOP152`	6	No	3.4 km
Entognatha			
Japygidae `sp. B34`	3	Yes	33.9 km
Japygidae `sp. DPL005`	1	Yes	25.2 km
Parajapygidae `sp. Biologic-DIPL090`	1	No	singleton
Parajapygidae `sp. Biologic-DIPL092`	1	No	singleton
Projapygidae `sp. Biologic-DIPL108`	1	No	singleton
Insecta			
Nocticola cockingi	7	Yes	77.3 km
Latridiidae `sp. Biologic-COLE052`	1	Yes	381.5 km
*Typhlozuphium humicolum**	2	Yes	29.0 km
Cryptorhynchinae `sp. B10`	1	Yes	16.3 km
Curculionidae `sp. B02`	3	Yes	39.9 km
Pselaphinae `sp. Biologic-COLE008`	2	Yes	87.0 km
Ptinella `sp. Helix-CPT003`	2	Yes	456.0 km
Phaconeura `sp. Biologic-HEMI003`	3	Yes	83.3 km
Phaconeura `sp. WAM-PHAC001`	2	Yes	707.2 km
Atelurinae `sp. Biologic-ZYGE071`	5	No	6.0 km
Trinemura `sp. Biologic-ZYGE038`	2	Yes	47.2 km
Maxillopoda			
Diacyclops `sp. Biologic-CYCL037`	10	Yes	29.3 km
Gordanitocrella `sp. Biologic-HARP030`	4	No	2.8 km
Schizopera `sp. Biologic-HARP031`	1	No	2.9 km
Parastenocaris `sp. Biologic-HARP032`	1	No	singleton

OTU (genetic taxon)	Sequenced specimens	Matches to non-Study sequences	Linear Range
Oligochaeta			
Naididae `sp. N1 LB-2015`	5	Yes	13.1 km
Nais `sp. Biologic-OLIG117`	1	No	singleton
Enchytraeidae `sp. Biologic-OLIG159	1	Yes	398.0 km
Enchytraeidae `sp. E6 LB-2015`	2	Yes	477.4 km
Phreodrilidae `sp. P11 LB-2015`	4	Yes	434.6 km
Ostracoda			
Meridiescandona `sp. Biologic-OSTR057`	8	Yes	18.4 km
*Notacandona boultoni**	1	Yes	38.9 km
*Notacandona modesta**	2	Yes	12.1 km
Gomphodella `sp. Biologic-OSTR078`	1	Yes	1.5 km
Pauropoda			
Pauropoda `sp. Biologic-PAUR072`	1	No	singleton
Pauropoda `sp. Biologic-PAUR073`	1	No	singleton
Pauropoda `sp. Biologic-PAUR074`	2	Yes	33.6 km
Pauropoda `sp. Biologic-PAUR075`	1	No	singleton
Pauropoda `sp. Biologic-PAUR085`	1	No	singleton
Pauropoda `sp. Biologic-PAUR086`	1	No	singleton
Pauropoda `sp. Biologic-PAUR087`	1	No	singleton
Decapauropus `sp. WAM-PAUD002`	3	Yes	228.5 km
Symphyla			
Scolopendrellidae `sp. Biologic-SYMP089`	1	No	singleton
Hanseniella `sp. Biologic-SYMP077`	1	No	singleton
Hanseniella `sp. Biologic-SYMP088`	1	No	singleton

* Linear range based on matches including molecular matches and morphologically identified specimens in the desktop assessment

3.1 Arachnida

3.1.1 Araneae

Fifteen Araneae specimens were successfully sequenced and formed five OTUs, all restricted to the Study Area (Table 3.1, Figure 3.1). Araneae `sp. Biologic-ARAN092`, Araneae `sp. Biologic-ARAN093`and Araneae `sp. Biologic-ARAN094` did not group clearly in any Araneae families, with intraspecific divergences up to 8.7% and were more than 10.2% divergent from all other sequences in the analysis (Table 3.2). The linear ranges for these OTUs were 0-4.0 km (Table 3.1).

Orsolobidae `sp. Biologic-ARAN091`had intraspecific divergences less than 2.8% and was more than 17.8% divergent from all other sequences in the analysis, with a linear range of 3.8 km (Table 3.1, Table 3.2). The remaining OTU, *Prethopalpus* `sp. Biologic-ARAN115`, was a singleton that was more than 9.9% divergent from all other sequences in the analysis (Table 3.2).

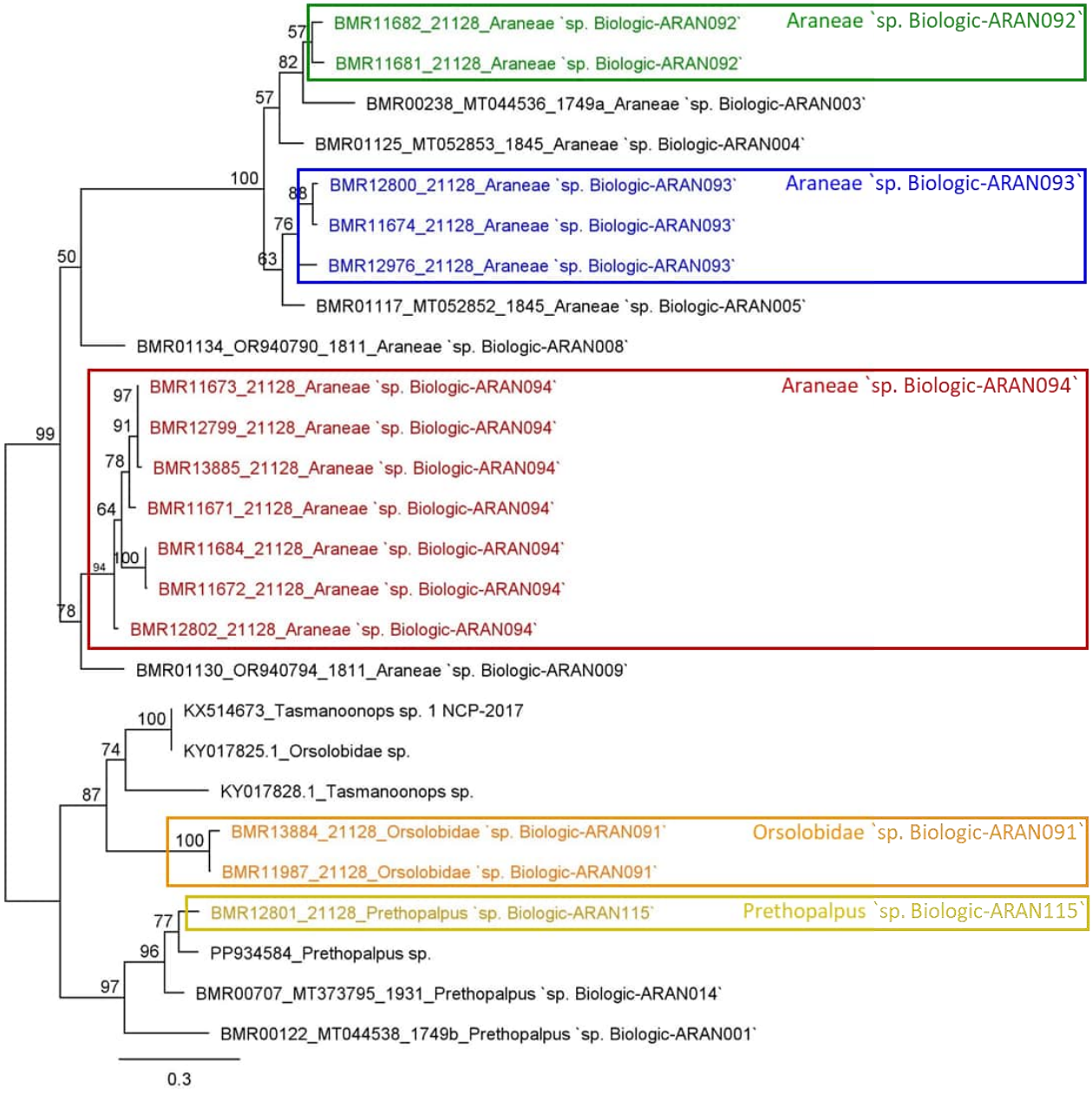

Figure 3.1. Phylogeny for the Araneae dataset, with bootstrap values

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

COI Pairwise Distances (%)	BMR00122	BMR00707	BMR12801	PP934584	BMR01130	BMR11671	BMR11673	BMR12799	BMR13885	BMR12802	BMR11672	BMR11684	BMR01134	BMR11987	BMR13884	KX514673	KY017825.1	KY017828.1	BMR00238	BMR11681	BMR11682	BMR01125	BMR01117	BMR12800	BMR12976	BMR11674
BMR00122_MT044538_1749b_Prethopalpus `sp. Biologic-ARAN001`		17.8	16.6	18.8	23.1	28.8	26.4	24.9	26.0	26.5	25.2	25.1	23.6	23.4	23.9	22.6	22.6	23.4	26.1	26.5	25.5	27.5	26.3	24.3	26.0	24.4
BMR00707_MT373795_1931_Prethopalpus `sp. Biologic-ARAN014`	17.8		10.0	12.6	23.3	24.5	21.6	21.0	20.7	22.8	22.9	22.7	23.6	23.6	24.5	21.3	21.3	20.9	25.5	24.9	24.2	25.8	24.9	23.9	24.9	22.2
BMR12801_21128_Prethopalpus `sp. Biologic-ARAN115`	16.6	10.0		10.2	23.3	27.7	25.6	22.6	25.3	25.2	24.3	24.1	24.0	22.3	22.5	21.7	21.7	21.2	26.3	26.1	25.0	26.9	26.6	24.0	26.0	22.5
PP934584_Prethopalpus sp.	18.8	12.6	10.2		25.1	28.3	24.9	24.8	24.9	25.2	26.7	26.7	26.4	25.8	26.0	22.3	22.5	21.4	26.9	28.4	27.3	27.4	27.9	25.7	28.4	22.9
BMR01130_OR940794_1811_Araneae `sp. Biologic-ARAN009`	23.1	23.3	23.3	25.1		14.0	13.0	13.4	13.7	11.1	13.7	13.3	16.0	22.2	22.2	22.2	22.2	24.0	22.8	24.1	23.6	23.3	22.5	22.0	22.9	22.2
BMR11671_21128_Araneae `sp. Biologic-ARAN094`	28.8	24.5	27.7	28.3	14.0		2.7	4.0	3.5	5.3	7.6	7.6	16.7	22.9	22.9	23.1	23.1	26.9	26.0	24.7	24.2	23.0	23.4	24.2	24.0	23.5
BMR11673_21128_Araneae `sp. Biologic-ARAN094`	26.4	21.6	25.6	24.9	13.0	2.7		0.0	0.9	5.6	7.7	7.7	16.3	20.9	20.9	20.9	20.9	24.4	24.0	23.9	24.1	21.6	21.6	23.1	22.7	22.5
BMR12799_21128_Araneae `sp. Biologic-ARAN094`	24.9	21.0	22.6	24.8	13.4	4.0	0.0		0.9	5.6	8.6	8.3	16.3	21.9	22.0	20.7	20.7	22.8	24.5	24.7	25.0	23.7	22.8	23.7	23.9	22.5
BMR13885_21128_Araneae `sp. Biologic-ARAN094`	26.0	20.7	25.3	24.9	13.7	3.5	0.9	0.9		6.5	7.3	7.3	15.9	20.5	20.5	20.9	20.9	24.0	24.4	23.7	23.9	21.1	21.6	23.1	22.9	22.9
BMR12802_21128_Araneae `sp. Biologic-ARAN094`	26.5	22.8	25.2	25.2	11.1	5.3	5.6	5.6	6.5		7.0	7.0	14.6	19.7	19.3	22.8	22.8	24.1	23.2	22.5	22.0	21.3	20.8	22.6	23.0	22.1
BMR11672_21128_Araneae `sp. Biologic-ARAN094`	25.2	22.9	24.3	26.7	13.7	7.6	7.7	8.6	7.3	7.0		0.3	15.4	21.6	20.8	21.4	21.4	24.6	25.4	23.8	23.5	24.8	24.3	22.5	22.5	22.3
BMR11684_21128_Araneae `sp. Biologic-ARAN094`	25.1	22.7	24.1	26.7	13.3	7.6	7.7	8.3	7.3	7.0	0.3		15.6	21.7	21.0	21.6	21.6	24.8	25.4	24.0	23.3	24.6	24.4	22.7	22.7	22.3
BMR01134_OR940790_1811_Araneae `sp. Biologic-ARAN008`	23.6	23.6	24.0	26.4	16.0	16.7	16.3	16.3	15.9	14.6	15.4	15.6		21.0	20.8	21.7	21.7	22.0	22.2	21.2	21.2	22.0	20.1	22.2	21.6	22.0
BMR11987_21128_Orsolobidae `sp. Biologic-ARAN091`	23.4	23.6	22.3	25.8	22.2	22.9	20.9	21.9	20.5	19.7	21.6	21.7	21.0		2.7	18.2	18.2	19.4	25.7	23.7	24.8	25.7	24.8	25.5	25.2	24.2
BMR13884_21128_Orsolobidae `sp. Biologic-ARAN091`	23.9	24.5	22.5	26.0	22.2	22.9	20.9	22.0	20.5	19.3	20.8	21.0	20.8	2.7		17.9	17.9	19.5	26.1	24.3	25.0	26.1	24.8	26.0	24.8	24.2
KX514673_Tasmanoonops sp. 1 NCP-2017	22.6	21.3	21.7	22.3	22.2	23.1	20.9	20.7	20.9	22.8	21.4	21.6	21.7	18.2	17.9		0.0	14.4	25.5	24.4	25.2	27.5	26.1	26.3	25.2	25.4
KY017825.1_Orsolobidae sp.	22.6	21.3	21.7	22.5	22.2	23.1	20.9	20.7	20.9	22.8	21.4	21.6	21.7	18.2	17.9	0.0		14.1	25.5	24.4	25.2	27.5	26.1	26.3	25.2	27.5
KY017828.1_Tasmanoonops sp.	23.4	20.9	21.2	21.4	24.0	26.9	24.4	22.8	24.0	24.1	24.6	24.8	22.0	19.4	19.5	14.4	14.1		27.7	26.2	28.1	27.2	27.2	28.0	28.8	26.5
BMR00238_MT044536_1749a_Araneae `sp. Biologic-ARAN003`	26.1	25.5	26.3	26.9	22.8	26.0	24.0	24.5	24.4	23.2	25.4	25.4	22.2	25.7	26.1	25.5	25.5	27.7		11.7	11.9	13.8	15.0	16.6	16.7	15.4
BMR11681_21128_Araneae `sp. Biologic-ARAN092`	26.5	24.9	26.1	28.4	24.1	24.7	23.9	24.7	23.7	22.5	23.8	24.0	21.2	23.7	24.3	24.4	24.4	26.2	11.7		5.3	12.1	14.0	15.5	13.9	12.1
BMR11682_21128_Araneae `sp. Biologic-ARAN092`	25.5	24.2	25.0	27.3	23.6	24.2	24.1	25.0	23.9	22.0	23.5	23.3	21.2	24.8	25.0	25.2	25.2	28.1	11.9	5.3		11.8	14.7	14.5	13.4	10.4
BMR01125_MT052853_1845_Araneae `sp. Biologic-ARAN004`	27.5	25.8	26.9	27.4	23.3	23.0	21.6	23.7	21.1	21.3	24.8	24.6	22.0	25.7	26.1	27.5	27.5	27.2	13.8	12.1	11.8		12.3	13.8	13.5	11.7
BMR01117_MT052852_1845_Araneae `sp. Biologic-ARAN005`	26.3	24.9	26.6	27.9	22.5	23.4	21.6	22.8	21.6	20.8	24.3	24.4	20.1	24.8	24.8	26.1	26.1	27.2	15.0	14.0	14.7	12.3		10.3	10.6	10.4
BMR12800_21128_Araneae `sp. Biologic-ARAN093`	24.3	23.9	24.0	25.7	22.0	24.2	23.1	23.7	23.1	22.6	22.5	22.7	22.2	25.5	26.0	26.3	26.3	28.0	16.6	15.5	14.5	13.8	10.3		7.9	2.0
BMR12976_21128_Araneae `sp. Biologic-ARAN093`	26.0	24.9	26.0	28.4	22.9	24.0	22.7	23.9	22.9	23.0	22.5	22.7	21.6	25.2	24.8	25.2	25.2	28.8	16.7	13.9	13.4	13.5	10.6	7.9		6.2
BMR11674_21128_Araneae `sp. Biologic-ARAN093`	24.4	22.2	22.5	22.9	22.2	23.5	22.5	22.5	22.9	22.1	22.3	22.3	22.0	24.2	24.2	25.4	27.5	26.5	15.4	12.1	10.4	11.7	10.4	2.0	6.2	

3.1.2 Palpigrades

Eight palpigrade specimens formed three OTUs that were unique to the Study Area (Table 3.1, Figure 3.2). Palpigradi `sp. Biologic-PALP075`and Palpigradi `sp. Biologic-PALP086`were both singletons with more than 14.4% and more than 18.5% divergence from all other sequences in the analysis, respectively (Table 3.3). Palpigradi `sp. Biologic-PALP077` comprised of six specimens with a linear range of 3.6 km, intraspecific divergences of less than 2.4% and was more than 13.6% divergent from all other sequences in the analysis (Table 3.1, Table 3.3).

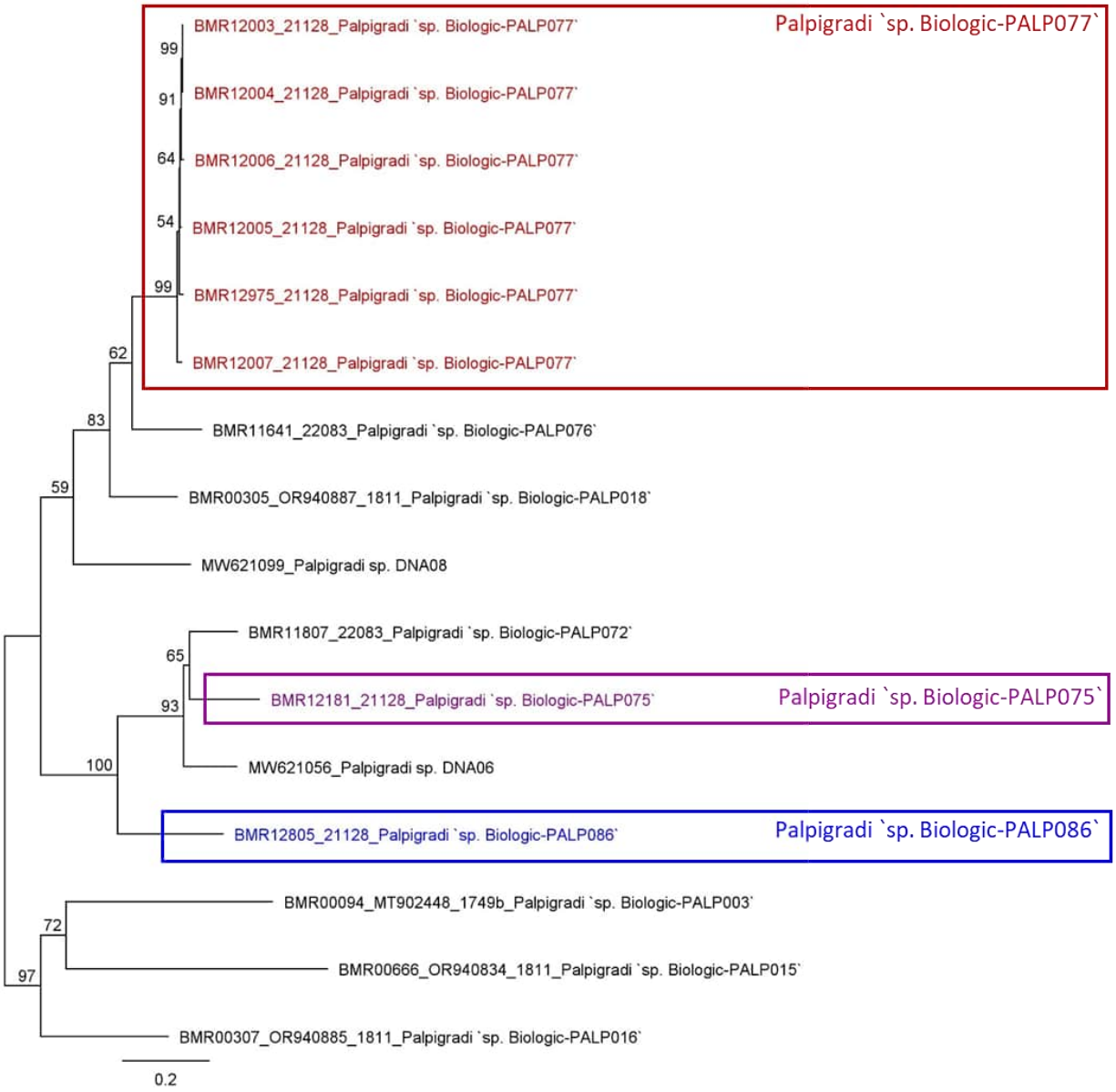

Figure 3.2. Phylogeny for the Palpigrades dataset, with bootstrap values

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

COI Pairwise Distances (%)	BMR00094	BMR00305	BMR11641	BMR12003	BMR12004	BMR12006	BMR12005	BMR12975	BMR12007	MW621099	BMR11807	MW621056	BMR12181	BMR12805	BMR00307	BMR00666
BMR00094_MT902448_1749b_Palpigradi `sp. Biologic-PALP003`		26.6	27.3	25.6	25.6	25.5	25.5	25.8	26.1	26.4	26.9	27.6	29.6	26.7	24.1	30.8
BMR00305_OR940887_1811_Palpigradi `sp. Biologic-PALP018`	26.6		15.3	16.0	16.0	16.3	15.4	15.6	15.6	18.8	22.3	21.8	22.0	22.6	23.1	29.8
BMR11641_22083_Palpigradi `sp. Biologic-PALP076`	27.3	15.3		13.7	13.7	14.0	13.9	14.2	14.5	19.2	23.5	23.7	21.8	20.9	23.5	28.9
BMR12003_21128_Palpigradi `sp. Biologic-PALP077`	25.6	16.0	13.7		0.0	0.8	0.9	1.5	2.1	19.8	21.7	21.5	21.5	21.8	22.1	30.2
BMR12004_21128_Palpigradi `sp. Biologic-PALP077`	25.6	16.0	13.7	0.0		0.8	0.9	1.5	2.1	19.8	21.7	21.5	21.5	21.8	22.1	30.2
BMR12006_21128_Palpigradi `sp. Biologic-PALP077`	25.5	16.3	14.0	0.8	0.8		1.1	1.7	2.3	19.4	21.8	21.7	21.5	22.0	22.1	29.5
BMR12005_21128_Palpigradi `sp. Biologic-PALP077`	25.5	15.4	13.9	0.9	0.9	1.1		1.2	1.8	19.2	22.0	22.0	22.0	21.7	22.0	29.6
BMR12975_21128_Palpigradi `sp. Biologic-PALP077`	25.8	15.6	14.2	1.5	1.5	1.7	1.2		2.3	19.8	22.1	22.1	21.2	21.8	22.0	30.1
BMR12007_21128_Palpigradi `sp. Biologic-PALP077`	26.1	15.6	14.5	2.1	2.1	2.3	1.8	2.3		19.7	21.1	21.8	21.1	22.0	22.0	29.8
MW621099_Palpigradi sp. DNA08	26.4	18.8	19.2	19.8	19.8	19.4	19.2	19.8	19.7		22.9	23.5	22.6	21.7	22.0	29.5
BMR11807_22083_Palpigradi `sp. Biologic-PALP072`	26.9	22.3	23.5	21.7	21.7	21.8	22.0	22.1	21.1	22.9		13.6	14.5	20.0	21.8	31.6
MW621056_Palpigradi sp. DNA06	27.6	21.8	23.7	21.5	21.5	21.7	22.0	22.1	21.8	23.5	13.6		15.4	18.8	24.9	32.2
BMR12181_21128_Palpigradi `sp. Biologic-PALP075`	29.6	22.0	21.8	21.5	21.5	21.5	22.0	21.2	21.1	22.6	14.5	15.4		20.0	23.5	32.8
BMR12805_21128_Palpigradi `sp. Biologic-PALP086`	26.7	22.6	20.9	21.8	21.8	22.0	21.7	21.8	22.0	21.7	20.0	18.8	20.0		24.6	30.7
BMR00307_OR940885_1811_Palpigradi `sp. Biologic-PALP016`	24.1	23.1	23.5	22.1	22.1	22.1	22.0	22.0	22.0	22.0	21.8	24.9	23.5	24.6		27.3
BMR00666_OR940834_1811_Palpigradi `sp. Biologic-PALP015`	30.8	29.8	28.9	30.2	30.2	29.5	29.6	30.1	29.8	29.5	31.6	32.2	32.8	30.7	27.3	

3.1.3 Pseudoscorpiones

Thirty pseudoscorpion specimens were successfully sequenced to form eight OTUs from two families, Chthoniidae and Hyidae. These OTUs were all unique to the Study Area (Table 3.1, Figure 3.3). Chthoniidae `sp. Biologic-PSEU186`was the only chthoniid singleton and was greater than 13% divergent from all other sequences in the analysis (Table 3.4). Chthoniidae `sp. Biologic-PSEU188` had intraspecific divergences less than 10.7%, was more than 14.8% divergent from all other sequences in the analysis and had a linear range of 3.2 km (Table 3.1, Table 3.4). Despite the high intraspecific genetic distance, this was considered a single OTU due to the topology of the tree where there were no clear internode gaps in the branches, and the lack of a clear barcode gap (Figure 3.3, Table 3.4). The remaining Chthoniidae OTUs had intraspecific divergences of less than 7.9%, were greater than 13.3% divergent from all other sequences in the analysis and had linear ranges between 1.1-2.5 km (Table 3.1, Table 3.4).

Indohya `sp. Biologic-PSEU184`was a singleton that was more than 8.3% divergent from other sequences in the analysis (Table 3.4). Four specimens comprise *Indohya* `sp. Biologic-PSEU183`, which had intraspecific divergences of less than 6%, was more than 8.3% divergent from all other sequences in the analysis, and had a linear range of 2.2 km (Table 3.1, Table 3.4).

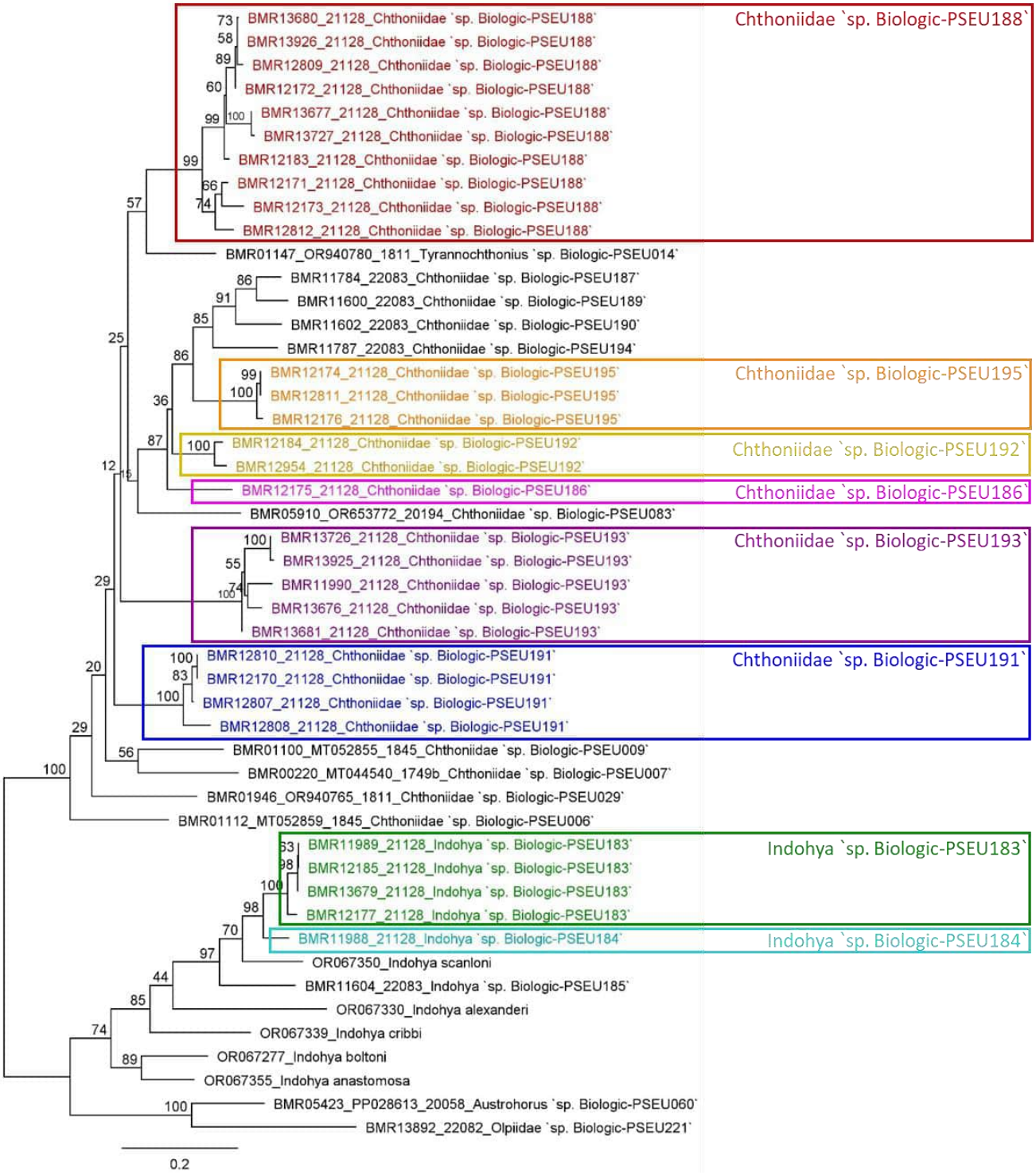

Figure 3.3. Phylogeny for the Pseudoscorpiones dataset, with bootstrap values

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

COI Pairwise Distances (%)	OR067277	OR067355	OR067339	OR067350	BMR11988	BMR11989	BMR12185	BMR13679	BMR12177	BMR11604	OR067330	BMR05423	BMR13892	BMR01147	BMR12171	BMR12173	BMR12812	BMR12172	BMR13680	BMR13926	BMR12809	BMR12183	BMR13677	BMR13727	BMR12175	BMR12954	BMR11600	BMR11784	BMR11602	BMR11787	BMR12170	BMR12810	BMR12807	BMR12808	BMR05910	BMR01100	BMR01946	BMR11990	BMR13676	BMR13681	BMR13726	BMR13925	BMR00220	BMR01112	BMR12811	BMR12174	BMR12176	BMR12184
OR067277_Indohya boltoni		13.3	20.5	20.9	21.1	23.1	21.8	21.5	22.2	22.1	22.6	21.4	24.4	26.6	22.2	21.4	23.7	23.6	25.5	25.5	25.6	23.6	25.1	24.9	25.1	25.2	24.2	25.1	23.1	24.5	23.6	23.6	23.7	24.3	23.3	24.6	26.1	26.9	26.9	26.6	28.1	28.3	25.4	24.8	23.4	21.4	21.6	23.3
OR067355_Indohya anastomosa	13.3		19.5	20.9	20.6	22.3	19.8	20.5	21.2	19.8	20.3	21.4	24.6	26.7	22.7	21.8	23.9	21.8	24.2	24.1	24.2	22.2	25.2	25.1	23.4	25.5	22.9	23.4	24.0	25.4	24.0	24.0	24.2	25.2	24.2	25.4	25.8	27.4	26.7	26.3	28.0	28.0	25.7	24.9	23.1	23.6	23.8	25.1
OR067339_Indohya cribbi	20.5	19.5		19.2	20.5	21.2	19.6	19.5	21.3	18.8	21.4	24.4	27.3	26.6	26.9	27.1	27.4	26.9	27.7	27.6	27.6	26.0	27.7	27.7	26.4	24.9	26.7	26.9	26.4	26.4	26.3	26.3	26.6	26.3	26.3	26.1	27.1	29.0	28.6	28.4	29.8	29.8	26.6	25.4	25.5	25.1	25.6	24.2
OR067350_Indohya scanloni	20.9	20.9	19.2		14.7	15.6	13.0	13.4	13.6	15.7	21.8	23.8	24.9	24.8	24.7	25.1	25.1	26.7	26.7	26.7	26.2	25.3	26.7	26.7	25.8	25.2	26.0	26.9	28.3	26.4	26.6	26.6	26.1	26.9	26.6	27.4	29.5	27.9	27.8	28.1	29.6	29.5	28.3	26.0	25.8	24.9	24.9	25.3
BMR11988_21128_Indohya `sp. Biologic-PSEU184`	21.1	20.6	20.5	14.7		8.6	8.4	10.4	10.5	16.8	22.7	24.1	25.8	25.2	21.4	20.5	25.8	22.9	26.4	26.4	26.4	22.2	27.2	27.1	25.5	26.3	26.8	27.8	28.1	28.4	27.2	27.2	27.1	27.2	27.1	28.0	28.0	27.1	29.0	29.0	30.7	30.5	29.3	26.7	26.7	22.7	22.7	23.3
BMR11989_21128_Indohya `sp. Biologic-PSEU183`	23.1	22.3	21.2	15.6	8.6		0.0	2.4	5.9	17.6	22.7	25.8	26.6	27.4	24.7	23.6	27.5	26.2	29.5	29.4	29.4	25.1	28.9	29.0	27.5	27.5	28.2	27.4	30.2	30.1	28.7	28.7	28.0	28.1	29.8	28.9	28.9	28.3	30.5	29.9	31.8	31.9	30.2	28.7	27.8	24.2	24.2	25.8
BMR12185_21128_Indohya `sp. Biologic-PSEU183`	21.8	19.8	19.6	13.0	8.4	0.0		0.0	3.2	15.9	20.5	25.1	25.6	24.9	24.7	23.6	25.8	26.2	26.4	26.6	26.5	25.1	26.4	26.7	26.0	25.6	25.3	24.4	27.1	27.8	26.0	26.0	25.3	25.1	27.5	25.3	25.6	26.9	27.1	26.7	29.1	29.5	27.3	25.3	24.2	24.2	24.2	25.8
BMR13679_21128_Indohya `sp. Biologic-PSEU183`	21.5	20.5	19.5	13.4	10.4	2.4	0.0		3.3	15.7	20.9	24.0	24.6	25.5	24.7	23.6	25.5	26.2	27.4	27.3	27.3	25.1	26.7	26.9	25.8	25.5	26.2	25.5	28.4	28.3	26.7	26.7	26.0	26.3	28.1	27.1	27.5	28.3	28.7	28.4	30.4	30.5	28.7	26.7	26.1	24.2	24.2	25.8
BMR12177_21128_Indohya `sp. Biologic-PSEU183`	22.2	21.2	21.3	13.6	10.5	5.9	3.2	3.3		15.8	22.2	24.0	25.0	26.8	25.0	23.8	26.0	27.2	28.1	28.3	27.9	26.0	27.8	27.8	26.5	26.8	26.0	26.8	29.4	28.9	27.0	27.0	26.6	26.8	28.3	28.4	29.1	29.5	29.1	29.1	30.9	30.9	29.9	28.3	27.1	24.8	24.8	27.0
BMR11604_22083_Indohya `sp. Biologic-PSEU185`	22.1	19.8	18.8	15.7	16.8	17.6	15.9	15.7	15.8		20.6	25.3	27.5	26.4	25.3	23.8	26.0	26.0	27.4	27.3	27.3	25.3	27.1	27.2	27.4	27.4	27.0	28.1	28.4	29.0	27.5	27.5	27.1	27.7	28.3	27.5	30.1	29.1	29.9	29.0	30.4	30.7	28.0	27.8	27.5	26.4	26.9	28.2
OR067330_Indohya alexanderi	22.6	20.3	21.4	21.8	22.7	22.7	20.5	20.9	22.2	20.6		24.6	25.2	29.0	25.8	25.1	26.9	24.7	27.2	27.2	27.3	23.8	26.7	27.1	26.3	28.0	29.1	28.6	27.1	30.1	29.0	29.0	28.3	28.6	28.1	27.7	29.3	27.1	28.9	27.7	29.3	29.6	28.6	28.9	27.4	25.3	25.6	28.0
BMR05423_PP028613_20058_Austrohorus `sp. Biologic-PSEU060`	21.4	21.4	24.4	23.8	24.1	25.8	25.1	24.0	24.0	25.3	24.6		18.8	26.6	25.8	25.1	24.2	25.1	25.7	25.6	25.9	25.3	25.7	25.5	26.0	26.1	25.5	25.2	26.3	27.1	26.1	26.1	25.8	26.0	25.7	26.9	28.0	26.5	26.9	26.3	27.8	28.1	25.5	26.3	23.7	23.8	23.6	27.1
BMR13892_22082_Olpiidae `sp. Biologic-PSEU221`	24.4	24.6	27.3	24.9	25.8	26.6	25.6	24.6	25.0	27.5	25.2	18.8		28.9	26.2	25.8	25.1	26.2	27.1	27.0	27.4	25.3	27.2	27.4	27.4	27.8	26.8	28.1	27.4	28.3	29.8	29.8	29.6	29.2	28.1	29.8	28.6	29.1	30.1	28.9	29.8	30.2	29.0	28.3	27.5	26.9	26.7	28.9
BMR01147_OR940780_1811_Tyrannochthonius `sp. Biologic-PSEU014`	26.6	26.7	26.6	24.8	25.2	27.4	24.9	25.5	26.8	26.4	29.0	26.6	28.9		16.5	16.3	14.9	16.7	16.9	16.8	16.3	16.3	17.8	17.5	16.4	16.0	17.7	19.0	19.5	18.5	17.5	17.5	17.2	17.3	18.1	17.0	20.1	19.0	19.1	18.7	20.5	20.4	19.1	19.0	18.2	19.8	19.8	18.3
BMR12171_21128_Chthoniidae `sp. Biologic-PSEU188`	22.2	22.7	26.9	24.7	21.4	24.7	24.7	24.7	25.0	25.3	25.8	25.8	26.2	16.5		4.0	4.2	6.8	7.0	7.2	7.4	6.2	8.6	8.6	17.2	16.3	17.4	18.5	17.2	20.7	16.3	16.3	16.7	18.3	16.7	18.3	20.0	19.6	19.4	19.4	21.4	21.4	18.9	17.6	19.2	19.2	19.4	16.1
BMR12173_21128_Chthoniidae `sp. Biologic-PSEU188`	21.4	21.8	27.1	25.1	20.5	23.6	23.6	23.6	23.8	23.8	25.1	25.1	25.8	16.3	4.0		5.9	7.5	7.7	7.9	8.3	8.0	10.1	10.6	18.3	17.2	17.2	18.3	17.6	20.0	17.0	17.0	17.4	18.1	16.3	18.3	19.8	18.9	19.2	18.9	20.9	21.1	20.3	17.4	19.2	18.2	18.8	15.3
BMR12812_21128_Chthoniidae `sp. Biologic-PSEU188`	23.7	23.9	27.4	25.1	25.8	27.5	25.8	25.5	26.0	26.0	26.9	24.2	25.1	14.9	4.2	5.9		7.5	8.7	8.6	8.4	7.5	9.4	9.4	16.1	15.8	16.9	17.6	17.2	19.3	16.9	16.9	16.9	18.1	16.9	18.8	20.5	20.1	20.1	19.6	20.8	20.7	18.7	18.7	18.4	18.7	18.5	15.0
BMR12172_21128_Chthoniidae `sp. Biologic-PSEU188`	23.6	21.8	26.9	26.7	22.9	26.2	26.2	26.2	27.2	26.0	24.7	25.1	26.2	16.7	6.8	7.5	7.5		0.2	0.4	1.7	2.0	4.0	4.2	19.8	17.2	18.9	18.3	16.3	19.4	16.1	16.1	16.5	17.6	17.8	18.3	19.4	20.3	20.3	20.0	21.8	22.0	19.2	17.4	19.4	19.4	19.6	16.1
BMR13680_21128_Chthoniidae `sp. Biologic-PSEU188`	25.5	24.2	27.7	26.7	26.4	29.5	26.4	27.4	28.1	27.4	27.2	25.7	27.1	16.9	7.0	7.7	8.7	0.2		0.3	1.3	2.2	5.5	5.6	19.0	16.9	18.7	18.4	17.8	20.1	15.8	15.8	15.8	17.0	18.7	18.8	20.1	21.0	20.1	20.4	21.6	21.9	19.9	18.5	19.9	19.6	19.8	16.3
BMR13926_21128_Chthoniidae `sp. Biologic-PSEU188`	25.5	24.1	27.6	26.7	26.4	29.4	26.6	27.3	28.3	27.3	27.2	25.6	27.0	16.8	7.2	7.9	8.6	0.4	0.3		1.1	2.4	5.4	5.6	19.0	16.8	18.5	18.4	17.7	20.0	15.8	15.8	15.8	17.3	18.7	18.8	20.0	21.0	20.0	20.3	21.5	21.8	19.9	18.5	19.9	19.8	20.0	16.5
BMR12809_21128_Chthoniidae `sp. Biologic-PSEU188`	25.6	24.2	27.6	26.2	26.4	29.4	26.5	27.3	27.9	27.3	27.3	25.9	27.4	16.3	7.4	8.3	8.4	1.7	1.3	1.1		3.2	5.7	5.7	18.6	16.6	18.5	18.0	17.9	20.0	16.0	16.0	16.0	17.7	18.6	19.1	20.3	20.6	19.7	20.3	21.5	21.7	20.1	18.6	20.0	19.9	20.2	16.4
BMR12183_21128_Chthoniidae `sp. Biologic-PSEU188`	23.6	22.2	26.0	25.3	22.2	25.1	25.1	25.1	26.0	25.3	23.8	25.3	25.3	16.3	6.2	8.0	7.5	2.0	2.2	2.4	3.2		4.2	4.8	19.8	17.4	18.9	18.5	16.3	19.8	15.9	15.9	16.3	17.4	18.1	18.1	19.6	19.4	19.2	19.4	20.5	20.9	18.3	17.0	19.2	18.3	18.6	15.1
BMR13677_21128_Chthoniidae `sp. Biologic-PSEU188`	25.1	25.2	27.7	26.7	27.2	28.9	26.4	26.7	27.8	27.1	26.7	25.7	27.2	17.8	8.6	10.1	9.4	4.0	5.5	5.4	5.7	4.2		0.5	20.4	18.4	19.3	19.3	18.2	19.9	17.2	17.2	16.9	17.9	19.3	18.8	20.5	21.7	21.4	21.1	22.0	22.5	19.9	19.6	20.8	20.3	19.8	18.5
BMR13727_21128_Chthoniidae `sp. Biologic-PSEU188`	24.9	25.1	27.7	26.7	27.1	29.0	26.7	26.9	27.8	27.2	27.1	25.5	27.4	17.5	8.6	10.6	9.4	4.2	5.6	5.6	5.7	4.8	0.5		20.1	18.4	19.1	19.3	18.5	19.9	17.2	17.2	16.9	17.9	19.3	19.1	20.2	22.0	21.7	21.4	22.3	22.5	20.1	19.9	21.1	20.7	20.3	18.9
BMR12175_21128_Chthoniidae `sp. Biologic-PSEU186`	25.1	23.4	26.4	25.8	25.5	27.5	26.0	25.8	26.5	27.4	26.3	26.0	27.4	16.4	17.2	18.3	16.1	19.8	19.0	19.0	18.6	19.8	20.4	20.1		13.1	15.5	15.2	15.7	16.4	17.8	17.8	17.8	19.3	19.6	19.8	21.3	19.6	19.6	18.8	21.1	21.0	20.5	20.1	15.8	16.7	17.0	14.5
BMR12954_21128_Chthoniidae `sp. Biologic-PSEU192`	25.2	25.5	24.9	25.2	26.3	27.5	25.6	25.5	26.8	27.4	28.0	26.1	27.8	16.0	16.3	17.2	15.8	17.2	16.9	16.8	16.6	17.4	18.4	18.4	13.1		15.7	15.2	15.5	14.9	17.2	17.2	17.3	18.4	17.5	19.0	20.2	18.4	19.1	18.8	20.2	20.1	21.4	18.4	14.1	13.9	13.7	3.1
BMR11600_22083_Chthoniidae `sp. Biologic-PSEU189`	24.2	22.9	26.7	26.0	26.8	28.2	25.3	26.2	26.0	27.0	29.1	25.5	26.8	17.7	17.4	17.2	16.9	18.9	18.7	18.5	18.5	18.9	19.3	19.1	15.5	15.7		7.4	11.5	12.4	18.3	18.3	18.2	18.8	16.9	19.5	20.6	21.0	20.9	20.5	21.8	21.9	21.3	21.8	14.6	15.0	15.2	16.5
BMR11784_22083_Chthoniidae `sp. Biologic-PSEU187`	25.1	23.4	26.9	26.9	27.8	27.4	24.4	25.5	26.8	28.1	28.6	25.2	28.1	19.0	18.5	18.3	17.6	18.3	18.4	18.4	18.0	18.5	19.3	19.3	15.2	15.2	7.4		10.2	13.2	18.4	18.4	18.2	19.1	17.5	20.4	20.5	20.4	20.8	20.1	21.0	21.3	20.5	20.7	14.6	15.4	16.1	16.1
BMR11602_22083_Chthoniidae `sp. Biologic-PSEU190`	23.1	24.0	26.4	28.3	28.1	30.2	27.1	28.4	29.4	28.4	27.1	26.3	27.4	19.5	17.2	17.6	17.2	16.3	17.8	17.7	17.9	16.3	18.2	18.5	15.7	15.5	11.5	10.2		13.7	18.5	18.5	18.1	19.0	17.3	19.8	21.0	20.7	21.4	19.8	21.1	21.4	20.5	19.5	15.2	15.0	15.2	15.4
BMR11787_22083_Chthoniidae `sp. Biologic-PSEU194`	24.5	25.4	26.4	26.4	28.4	30.1	27.8	28.3	28.9	29.0	30.1	27.1	28.3	18.5	20.7	20.0	19.3	19.4	20.1	20.0	20.0	19.8	19.9	19.9	16.4	14.9	12.4	13.2	13.7		19.1	19.1	19.3	20.1	20.1	20.4	20.8	20.7	21.3	20.4	22.2	22.2	22.3	20.4	14.3	15.0	14.8	14.8
BMR12170_21128_Chthoniidae `sp. Biologic-PSEU191`	23.6	24.0	26.3	26.6	27.2	28.7	26.0	26.7	27.0	27.5	29.0	26.1	29.8	17.5	16.3	17.0	16.9	16.1	15.8	15.8	16.0	15.9	17.2	17.2	17.8	17.2	18.3	18.4	18.5	19.1		0.0	1.1	5.6	17.0	17.2	18.5	20.4	19.1	19.0	20.1	20.5	20.5	18.7	20.4	21.8	22.0	18.1
BMR12810_21128_Chthoniidae `sp. Biologic-PSEU191`	23.6	24.0	26.3	26.6	27.2	28.7	26.0	26.7	27.0	27.5	29.0	26.1	29.8	17.5	16.3	17.0	16.9	16.1	15.8	15.8	16.0	15.9	17.2	17.2	17.8	17.2	18.3	18.4	18.5	19.1	0.0		1.1	5.6	17.0	17.2	18.5	20.4	19.1	19.0	20.1	20.5	20.5	18.7	20.4	21.8	22.0	18.1
BMR12807_21128_Chthoniidae `sp. Biologic-PSEU191`	23.7	24.2	26.6	26.1	27.1	28.0	25.3	26.0	26.6	27.1	28.3	25.8	29.6	17.2	16.7	17.4	16.9	16.5	15.8	15.8	16.0	16.3	16.9	16.9	17.8	17.3	18.2	18.2	18.1	19.3	1.1	1.1		5.3	16.9	16.9	18.1	20.4	19.0	18.5	19.6	20.1	20.7	19.1	20.2	21.6	21.8	18.5
BMR12808_21128_Chthoniidae `sp. Biologic-PSEU191`	24.3	25.2	26.3	26.9	27.2	28.1	25.1	26.3	26.8	27.7	28.6	26.0	29.2	17.3	18.3	18.1	18.1	17.6	17.0	17.3	17.7	17.4	17.9	17.9	19.3	18.4	18.8	19.1	19.0	20.1	5.6	5.6	5.3		17.9	17.8	17.9	20.4	19.6	19.3	19.8	20.2	20.1	20.2	20.1	20.0	20.3	18.3
BMR05910_OR653772_20194_Chthoniidae `sp. Biologic-PSEU083`	23.3	24.2	26.3	26.6	27.1	29.8	27.5	28.1	28.3	28.3	28.1	25.7	28.1	18.1	16.7	16.3	16.9	17.8	18.7	18.7	18.6	18.1	19.3	19.3	19.6	17.5	16.9	17.5	17.3	20.1	17.0	17.0	16.9	17.9		19.1	20.7	20.1	19.5	18.2	19.6	19.8	19.9	20.2	18.5	20.0	20.3	16.5
BMR01100_MT052855_1845_Chthoniidae `sp. Biologic-PSEU009`	24.6	25.4	26.1	27.4	28.0	28.9	25.3	27.1	28.4	27.5	27.7	26.9	29.8	17.0	18.3	18.3	18.8	18.3	18.8	18.8	19.1	18.1	18.8	19.1	19.8	19.0	19.5	20.4	19.8	20.4	17.2	17.2	16.9	17.8	19.1		20.5	21.5	19.8	20.1	21.6	21.9	17.9	19.8	19.1	19.2	18.7	17.8
BMR01946_OR940765_1811_Chthoniidae `sp. Biologic-PSEU029`	26.1	25.8	27.1	29.5	28.0	28.9	25.6	27.5	29.1	30.1	29.3	28.0	28.6	20.1	20.0	19.8	20.5	19.4	20.1	20.0	20.3	19.6	20.5	20.2	21.3	20.2	20.6	20.5	21.0	20.8	18.5	18.5	18.1	17.9	20.7	20.5		21.5	21.6	20.5	22.3	22.6	20.4	20.5	20.4	21.8	21.6	21.4
BMR11990_21128_Chthoniidae `sp. Biologic-PSEU193`	26.9	27.4	29.0	27.9	27.1	28.3	26.9	28.3	29.5	29.1	27.1	26.5	29.1	19.0	19.6	18.9	20.1	20.3	21.0	21.0	20.6	19.4	21.7	22.0	19.6	18.4	21.0	20.4	20.7	20.7	20.4	20.4	20.4	20.4	20.1	21.5	21.5		5.9	4.8	7.5	7.8	19.0	21.2	19.8	19.4	19.2	19.2
BMR13676_21128_Chthoniidae `sp. Biologic-PSEU193`	26.9	26.7	28.6	27.8	29.0	30.5	27.1	28.7	29.1	29.9	28.9	26.9	30.1	19.1	19.4	19.2	20.1	20.3	20.1	20.0	19.7	19.2	21.4	21.7	19.6	19.1	20.9	20.8	21.4	21.3	19.1	19.1	19.0	19.6	19.5	19.8	21.6	5.9		3.3	6.8	7.1	18.2	20.5	20.5	20.0	19.8	20.0
BMR13681_21128_Chthoniidae `sp. Biologic-PSEU193`	26.6	26.3	28.4	28.1	29.0	29.9	26.7	28.4	29.1	29.0	27.7	26.3	28.9	18.7	19.4	18.9	19.6	20.0	20.4	20.3	20.3	19.4	21.1	21.4	18.8	18.8	20.5	20.1	19.8	20.4	19.0	19.0	18.5	19.3	18.2	20.1	20.5	4.8	3.3		4.6	4.9	17.6	20.5	19.3	18.3	18.1	20.0
BMR13726_21128_Chthoniidae `sp. Biologic-PSEU193`	28.1	28.0	29.8	29.6	30.7	31.8	29.1	30.4	30.9	30.4	29.3	27.8	29.8	20.5	21.4	20.9	20.8	21.8	21.6	21.5	21.5	20.5	22.0	22.3	21.1	20.2	21.8	21.0	21.1	22.2	20.1	20.1	19.6	19.8	19.6	21.6	22.3	7.5	6.8	4.6		0.6	19.3	21.6	19.8	18.9	19.2	21.1
BMR13925_21128_Chthoniidae `sp. Biologic-PSEU193`	28.3	28.0	29.8	29.5	30.5	31.9	29.5	30.5	30.9	30.7	29.6	28.1	30.2	20.4	21.4	21.1	20.7	22.0	21.9	21.8	21.7	20.9	22.5	22.5	21.0	20.1	21.9	21.3	21.4	22.2	20.5	20.5	20.1	20.2	19.8	21.9	22.6	7.8	7.1	4.9	0.6		19.5	21.7	20.1	19.6	19.8	21.6
BMR00220_MT044540_1749b_Chthoniidae `sp. Biologic-PSEU007`	25.4	25.7	26.6	28.3	29.3	30.2	27.3	28.7	29.9	28.0	28.6	25.5	29.0	19.1	18.9	20.3	18.7	19.2	19.9	19.9	19.9	20.1	18.3	19.9	20.1	20.5	21.4	21.3	20.5	20.5	22.3	20.5	20.5	20.7	20.1	19.9	17.9	20.4	19.0	18.2	17.6	19.3	19.5		19.8	20.8	20.3	20.0	22.5
BMR01112_MT052859_1845_Chthoniidae `sp. Biologic-PSEU006`	24.8	24.9	25.4	26.0	26.7	28.7	25.3	26.7	28.3	27.8	28.9	26.3	28.3	19.0	17.6	17.4	18.7	17.4	18.5	18.5	18.6	17.0	19.6	19.9	20.1	18.4	21.8	20.7	19.5	20.4	18.7	18.7	19.1	20.2	20.2	19.8	20.5	21.2	20.5	20.5	21.6	21.7	19.8		18.1	18.9	18.5	18.5
BMR12811_21128_Chthoniidae `sp. Biologic-PSEU195`	23.4	23.1	25.5	25.8	26.7	27.8	24.2	26.1	27.1	27.5	27.4	23.7	27.5	18.2	19.2	19.2	18.4	19.4	19.9	19.9	20.0	19.2	20.8	21.1	15.8	14.1	14.6	14.6	15.2	14.3	20.4	20.4	20.2	20.1	18.5	19.1	20.4	19.8	20.5	19.3	19.8	20.1	20.8	18.1		0.0	1.1	13.9
BMR12174_21128_Chthoniidae `sp. Biologic-PSEU195`	21.4	23.6	25.1	24.9	22.7	24.2	24.2	24.2	24.8	26.4	25.3	23.8	26.9	19.8	19.2	18.2	18.7	19.4	19.6	19.8	19.9	18.3	20.3	20.7	16.7	13.9	15.0	15.4	15.0	15.0	21.8	21.8	21.6	20.0	20.0	19.2	21.8	19.4	20.0	18.3	18.9	19.6	20.3	18.9	0.0		1.5	13.4
BMR12176_21128_Chthoniidae `sp. Biologic-PSEU195`	21.6	23.8	25.6	24.9	22.7	24.2	24.2	24.2	24.8	26.9	25.6	23.6	26.7	19.8	19.4	18.8	18.5	19.6	19.8	20.0	20.2	18.6	19.8	20.3	17.0	13.7	15.2	16.1	15.2	14.8	22.0	22.0	21.8	20.3	20.3	18.7	21.6	19.2	19.8	18.1	19.2	19.8	20.0	18.5	1.1	1.5		13.4
BMR12184_21128_Chthoniidae `sp. Biologic-PSEU192`	23.3	25.1	24.2	25.3	23.3	25.8	25.8	25.8	27.0	28.2	28.0	27.1	28.9	18.3	16.1	15.3	15.0	16.1	16.3	16.5	16.4	15.1	18.5	18.9	14.5	3.1	16.5	16.1	15.4	14.8	18.1	18.1	18.5	18.3	16.5	17.8	21.4	19.2	20.0	20.0	21.1	21.6	22.5	18.5	13.9	13.4	13.4	

3.1.4 Schizomida

Thirty-three schizomid specimens were successfully sequenced and resolved as two OTUs; *Draculoides* `sp. WAM-SCH067` and *Draculoides* `sp. Biologic-SCHI023` (Figure 3.4). The latter did not match any non-Study sequences and is restricted to the Study Area (Table 3.1). *Draculoides* `sp. Biologic-SCHI023` had intraspecific divergences of less than 4.1%, was more than 7.7% divergent from all other sequences in the analysis and had a linear range of 1.6 km (Table 3.1, Table 3.5).

Draculoides `sp. WAM-SCH067` matched non-Study sequences and had a linear range of 39.3 km (Table 3.1). The intraspecific divergences within this OTU, up to 6.9%, overlap with the divergence of *Draculoides* `sp. WAM-SCH067` from other sequences in the analysis (greater than 5.4%) (Table 3.5). Investigating the phylogeny determined there were potentially two OTUs within *Draculoides* `sp. WAM-SCH067`. Based on overlapping distributions of the lineages, we have kept *Draculoides* `sp. WAM-SCH067` as one OTU until more information is available (Table 3.5).

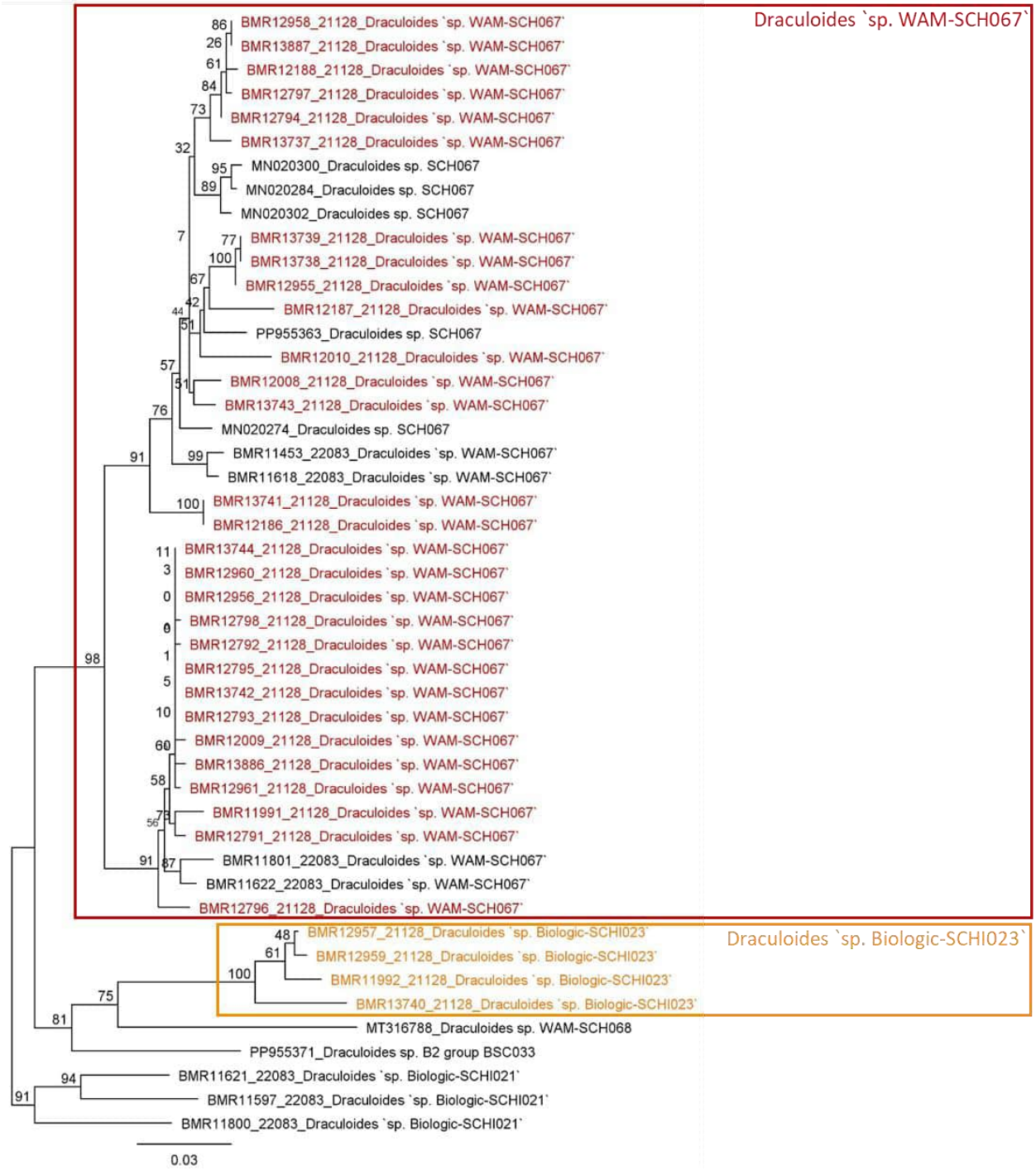

Figure 3.4. Phylogeny for the Schizomida dataset, with bootstrap values

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

COI Pairwise Distances (%)	BMR11453	BMR11618	BMR12008	BMR13743	BMR12188	BMR12794	BMR12797	BMR12958	BMR13887	BMR13737	MN020284	MN020300	MN020302	BMR12955	BMR13738	BMR13739	MN020274	PP955363	BMR13741	BMR12010	BMR11622	BMR12009	BMR12792	BMR12793	BMR12795	BMR12956	BMR12960	BMR13742	BMR13744	BMR12798	BMR12961	BMR13886	BMR12791	BMR11801	BMR12796	BMR11991	BMR12186	BMR12187	BMR11597	BMR11621	BMR11800	PP955371	MT316788	BMR11992	BMR12957	BMR12959	BMR13740
BMR11453_22083_Draculoides `sp. WAM-SCH067`		0.8	2.9	2.7	3.3	2.9	2.9	3.2	3.2	2.6	2.7	2.9	2.6	2.9	3.0	3.0	2.4	2.9	3.2	4.0	4.7	4.4	4.3	4.4	4.4	4.4	4.4	4.4	4.4	4.4	4.6	4.6	4.3	4.7	5.2	4.9	4.9	3.3	4.6	6.8	7.1	7.9	7.4	9.1	9.1	8.7	8.5	9.9
BMR11618_22083_Draculoides `sp. WAM-SCH067`	0.8		2.7	2.6	3.2	2.7	2.7	3.0	3.0	2.7	2.3	2.4	2.1	2.6	2.7	2.7	2.3	2.4	3.0	4.1	4.9	4.3	4.1	4.3	4.3	4.3	4.3	4.3	4.3	4.4	4.4	4.3	4.6	5.0	4.7	4.8	3.3	4.2	6.2	6.4	7.1	7.3	8.4	8.6	8.2	8.1	9.4
BMR12008_21128_Draculoides `sp. WAM-SCH067`	2.9	2.7		1.4	2.4	1.8	2.1	2.1	2.1	2.1	2.0	2.1	2.1	2.0	2.1	2.1	2.1	2.6	2.7	3.2	4.7	4.7	4.9	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.6	4.6	4.7	5.0	5.2	5.2	5.1	2.6	3.7	6.5	5.8	7.1	7.1	9.1	8.6	8.4	7.9	9.0
BMR13743_21128_Draculoides `sp. WAM-SCH067`	2.7	2.6	1.4		2.1	1.7	2.0	2.0	2.0	2.0	1.8	2.0	1.7	2.1	2.3	2.3	2.0	2.4	2.9	3.0	5.0	4.4	4.6	4.4	4.4	4.4	4.4	4.4	4.4	4.4	4.3	4.3	4.4	4.7	5.2	4.6	4.9	3.3	4.0	6.5	6.2	7.3	7.3	9.3	8.6	8.2	8.1	9.1
BMR12188_21128_Draculoides `sp. WAM-SCH067`	3.3	3.2	2.4	2.1		0.5	0.5	0.5	0.5	1.4	2.5	2.7	2.4	2.9	3.0	3.0	2.5	2.9	3.7	3.2	4.9	4.6	4.8	4.6	4.6	4.6	4.6	4.6	4.6	4.6	4.8	4.4	4.6	4.8	5.1	5.1	5.2	4.5	4.2	7.3	7.1	7.8	8.1	9.2	9.2	8.9	8.7	9.8
BMR12794_21128_Draculoides `sp. WAM-SCH067`	2.9	2.7	1.8	1.7	0.5		0.3	0.3	0.3	0.9	2.0	2.1	1.8	2.3	2.4	2.4	2.1	2.3	3.0	2.9	4.9	4.3	4.4	4.3	4.3	4.3	4.3	4.3	4.3	4.3	4.4	4.1	4.3	4.6	5.0	4.7	4.8	3.5	3.7	7.0	7.0	7.4	7.8	9.1	9.1	8.7	8.5	9.6
BMR12797_21128_Draculoides `sp. WAM-SCH067`	2.9	2.7	2.1	2.0	0.5	0.3		0.3	0.3	0.9	2.3	2.4	2.1	2.6	2.7	2.7	2.4	2.6	3.0	3.2	4.6	4.3	4.4	4.3	4.3	4.3	4.3	4.3	4.3	4.3	4.4	4.1	4.3	4.6	4.7	4.7	4.8	3.5	3.7	7.0	6.7	7.4	7.8	9.1	9.1	8.7	8.5	9.6
BMR12958_21128_Draculoides `sp. WAM-SCH067`	3.2	3.0	2.1	2.0	0.5	0.3	0.3		0.0	1.2	2.3	2.4	2.1	2.6	2.7	2.7	2.4	2.6	3.3	3.2	4.9	4.6	4.7	4.6	4.6	4.6	4.6	4.6	4.6	4.6	4.7	4.4	4.6	4.9	5.0	5.0	5.1	4.0	3.7	7.3	7.0	7.4	8.1	9.3	9.4	9.0	8.8	9.6
BMR13887_21128_Draculoides `sp. WAM-SCH067`	3.2	3.0	2.1	2.0	0.5	0.3	0.3	0.0		1.2	2.3	2.4	2.1	2.6	2.7	2.7	2.4	2.6	3.3	3.2	4.9	4.6	4.7	4.6	4.6	4.6	4.6	4.6	4.6	4.6	4.7	4.4	4.6	4.9	5.0	5.0	5.1	4.0	3.7	7.3	7.0	7.4	8.1	9.3	9.4	9.0	8.8	9.6
BMR13737_21128_Draculoides `sp. WAM-SCH067`	2.6	2.7	2.1	2.0	1.4	0.9	0.9	1.2	1.2		2.0	2.1	1.5	2.6	2.7	2.7	2.4	2.9	3.0	2.9	4.6	4.3	4.4	4.3	4.3	4.3	4.3	4.3	4.3	4.3	4.4	4.1	4.3	4.6	5.0	4.7	4.8	3.1	3.7	6.7	6.4	7.4	7.1	9.0	9.1	8.7	8.5	9.6
MN020284_Draculoides sp. SCH067	2.7	2.3	2.0	1.8	2.5	2.0	2.3	2.3	2.3	2.0		0.5	0.8	2.3	2.4	2.4	2.4	2.9	2.9	3.0	5.3	5.2	5.2	5.0	5.0	5.0	5.0	5.0	5.0	5.0	5.2	4.9	5.0	5.3	5.5	5.5	5.5	2.9	3.7	6.7	5.6	7.3	7.6	8.7	8.8	8.4	8.2	9.6
MN020300_Draculoides sp. SCH067	2.9	2.4	2.1	2.0	2.7	2.1	2.4	2.4	2.4	2.1	0.5		0.9	2.4	2.6	2.6	2.6	3.0	3.0	3.5	5.8	5.5	5.6	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.6	5.3	5.5	5.8	5.9	5.6	6.0	2.9	3.7	6.8	5.8	7.4	7.8	8.8	9.0	8.5	8.4	9.7
MN020302_Draculoides sp. SCH067	2.6	2.1	2.1	1.7	2.4	1.8	2.1	2.1	2.1	1.5	0.8	0.9		2.1	2.3	2.3	2.3	2.7	2.7	2.9	5.5	4.9	5.0	4.9	4.9	4.9	4.9	4.9	4.9	5.0	4.7	4.9	5.2	5.6	5.0	5.4	3.1	3.5	6.5	5.5	7.1	7.1	8.5	8.6	8.2	8.1	9.4
BMR12955_21128_Draculoides `sp. WAM-SCH067`	2.9	2.6	2.0	2.1	2.9	2.3	2.6	2.6	2.6	2.6	2.3	2.4	2.1		0.2	0.2	2.0	1.8	3.2	3.0	5.6	5.3	5.5	5.3	5.3	5.3	5.3	5.3	5.3	5.3	5.5	5.2	5.3	5.6	6.1	5.8	5.9	3.7	3.1	6.8	6.5	8.1	7.9	9.7	9.6	9.1	9.0	10.3
BMR13738_21128_Draculoides `sp. WAM-SCH067`	3.0	2.7	2.1	2.3	3.0	2.4	2.7	2.7	2.7	2.7	2.4	2.6	2.3	0.2		0.0	2.1	2.0	3.3	3.2	5.8	5.5	5.6	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.6	5.3	5.5	5.8	6.2	5.9	6.0	4.0	3.3	6.8	6.5	8.1	8.1	9.9	9.7	9.3	9.1	10.5
BMR13739_21128_Draculoides `sp. WAM-SCH067`	3.0	2.7	2.1	2.3	3.0	2.4	2.7	2.7	2.7	2.7	2.4	2.6	2.3	0.2	0.0		2.1	2.0	3.3	3.2	5.8	5.5	5.6	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.6	5.3	5.5	5.8	6.2	5.9	6.0	4.0	3.3	6.8	6.5	8.1	8.1	9.9	9.7	9.3	9.1	10.5
MN020274_Draculoides sp. SCH067	2.4	2.3	2.1	2.0	2.5	2.1	2.4	2.4	2.4	2.4	2.4	2.6	2.3	2.0	2.1	2.1		2.3	3.0	3.2	4.9	4.3	4.4	4.3	4.3	4.3	4.3	4.3	4.3	4.3	4.4	4.4	4.3	4.6	5.0	4.7	4.8	3.7	4.0	6.8	6.8	8.1	7.6	9.0	9.0	8.8	8.7	9.4
PP955363_Draculoides sp. SCH067	2.9	2.4	2.6	2.4	2.9	2.3	2.6	2.6	2.6	2.9	2.9	3.0	2.7	1.8	2.0	2.0	2.3		3.6	3.0	5.9	5.3	5.5	5.3	5.3	5.3	5.3	5.3	5.3	5.5	5.2	5.3	5.6	6.1	5.8	5.9	4.2	3.7	7.4	7.3	7.8	7.6	9.7	9.7	9.0	8.8	10.0
BMR13741_21128_Draculoides `sp. WAM-SCH067`	3.2	3.0	2.7	2.9	3.7	3.0	3.0	3.3	3.3	3.0	2.9	3.0	2.7	3.2	3.3	3.3	3.0	3.6		4.7	4.0	4.1	4.1	4.0	4.0	4.0	4.0	4.0	4.0	4.1	4.1	4.0	4.3	4.7	4.1	4.5	0.0	5.5	6.8	6.4	7.4	7.3	8.8	8.3	7.9	7.8	9.1
BMR12010_21128_Draculoides `sp. WAM-SCH067`	4.0	4.1	3.2	3.0	3.2	2.9	3.2	3.2	3.2	2.9	3.0	3.5	2.9	3.0	3.2	3.2	3.2	3.0	4.7		6.1	5.9	5.9	5.8	5.8	5.8	5.8	5.8	5.8	5.9	5.6	5.8	6.1	6.5	6.4	6.3	5.1	4.4	8.2	7.6	9.3	8.4	10.2	9.7	9.6	9.4	10.3
BMR11622_22083_Draculoides `sp. WAM-SCH067`	4.7	4.9	4.7	5.0	4.9	4.9	4.6	4.9	4.9	4.6	5.3	5.8	5.5	5.6	5.8	5.8	4.9	5.9	4.0	6.1		1.5	1.4	1.2	1.2	1.2	1.2	1.2	1.2	1.4	1.4	1.5	1.5	1.4	2.0	2.0	4.4	6.4	7.0	6.8	7.0	7.4	8.8	8.0	7.9	7.8	8.2
BMR12009_21128_Draculoides `sp. WAM-SCH067`	4.4	4.3	4.7	4.4	4.6	4.3	4.3	4.6	4.6	4.3	5.2	5.5	4.9	5.3	5.5	5.5	4.3	5.3	4.1	5.9	1.5		0.5	0.3	0.3	0.3	0.3	0.3	0.3	0.5	0.5	0.6	0.9	2.0	1.5	1.4	4.4	6.4	6.8	7.3	7.1	7.3	9.0	8.2	8.4	8.2	8.7
BMR12792_21128_Draculoides `sp. WAM-SCH067`	4.3	4.1	4.9	4.6	4.8	4.4	4.4	4.7	4.7	4.4	5.2	5.6	5.0	5.5	5.6	5.6	4.4	5.5	4.1	5.9	1.4	0.5		0.2	0.2	0.2	0.2	0.2	0.2	0.3	0.3	0.5	0.8	1.8	1.5	1.2	4.6	6.6	6.8	7.3	7.1	7.1	9.0	8.2	8.4	8.2	8.7
BMR12793_21128_Draculoides `sp. WAM-SCH067`	4.4	4.3	4.7	4.4	4.6	4.3	4.3	4.6	4.6	4.3	5.0	5.5	4.9	5.3	5.5	5.5	4.3	5.3	4.0	5.8	1.2	0.3	0.2		0.0	0.0	0.0	0.0	0.0	0.2	0.2	0.3	0.6	1.7	1.4	1.1	4.4	6.4	6.7	7.1	7.0	7.1	8.8	8.0	8.2	8.1	8.5
BMR12795_21128_Draculoides `sp. WAM-SCH067`	4.4	4.3	4.7	4.4	4.6	4.3	4.3	4.6	4.6	4.3	5.0	5.5	4.9	5.3	5.5	5.5	4.3	5.3	4.0	5.8	1.2	0.3	0.2	0.0		0.0	0.0	0.0	0.0	0.2	0.2	0.3	0.6	1.7	1.4	1.1	4.4	6.4	6.7	7.1	7.0	7.1	8.8	8.0	8.2	8.1	8.5
BMR12956_21128_Draculoides `sp. WAM-SCH067`	4.4	4.3	4.7	4.4	4.6	4.3	4.3	4.6	4.6	4.3	5.0	5.5	4.9	5.3	5.5	5.5	4.3	5.3	4.0	5.8	1.2	0.3	0.2	0.0	0.0		0.0	0.0	0.0	0.2	0.2	0.3	0.6	1.7	1.4	1.1	4.4	6.4	6.7	7.1	7.0	7.1	8.8	8.0	8.2	8.1	8.5
BMR12960_21128_Draculoides `sp. WAM-SCH067`	4.4	4.3	4.7	4.4	4.6	4.3	4.3	4.6	4.6	4.3	5.0	5.5	4.9	5.3	5.5	5.5	4.3	5.3	4.0	5.8	1.2	0.3	0.2	0.0	0.0	0.0		0.0	0.0	0.2	0.2	0.3	0.6	1.7	1.4	1.1	4.4	6.4	6.7	7.1	7.0	7.1	8.8	8.0	8.2	8.1	8.5
BMR13742_21128_Draculoides `sp. WAM-SCH067`	4.4	4.3	4.7	4.4	4.6	4.3	4.3	4.6	4.6	4.3	5.0	5.5	4.9	5.3	5.5	5.5	4.3	5.3	4.0	5.8	1.2	0.3	0.2	0.0	0.0	0.0	0.0		0.0	0.2	0.2	0.3	0.6	1.7	1.4	1.1	4.4	6.4	6.7	7.1	7.0	7.1	8.8	8.0	8.2	8.1	8.5
BMR13744_21128_Draculoides `sp. WAM-SCH067`	4.4	4.3	4.7	4.4	4.6	4.3	4.3	4.6	4.6	4.3	5.0	5.5	4.9	5.3	5.5	5.5	4.3	5.3	4.0	5.8	1.2	0.3	0.2	0.0	0.0	0.0	0.0	0.0		0.2	0.2	0.3	0.6	1.7	1.4	1.1	4.4	6.4	6.7	7.1	7.0	7.1	8.8	8.0	8.2	8.1	8.5
BMR12798_21128_Draculoides `sp. WAM-SCH067`	4.6	4.4	4.6	4.3	4.8	4.4	4.4	4.7	4.7	4.4	5.2	5.6	5.0	5.5	5.6	5.6	4.4	5.5	4.1	5.9	1.4	0.5	0.3	0.2	0.2	0.2	0.2	0.2	0.2		0.3	0.5	0.8	1.8	1.5	1.2	4.6	6.6	6.5	7.0	6.8	7.0	8.7	7.9	8.1	7.9	8.4
BMR12961_21128_Draculoides `sp. WAM-SCH067`	4.6	4.4	4.6	4.3	4.4	4.1	4.1	4.4	4.4	4.1	4.9	5.3	4.7	5.2	5.3	5.3	4.4	5.2	4.1	5.6	1.4	0.5	0.3	0.2	0.2	0.2	0.2	0.2	0.2	0.3		0.5	0.8	1.8	1.5	1.2	4.4	6.4	6.5	7.0	6.8	7.0	9.0	8.2	8.1	7.9	8.4
BMR13886_21128_Draculoides `sp. WAM-SCH067`	4.3	4.3	4.7	4.4	4.6	4.3	4.3	4.6	4.6	4.3	5.0	5.5	4.9	5.3	5.5	5.5	4.3	5.3	4.0	5.8	1.5	0.6	0.5	0.3	0.3	0.3	0.3	0.3	0.3	0.5	0.5		0.9	2.0	1.7	1.4	4.6	6.6	6.7	7.1	7.0	7.1	8.8	8.0	8.2	8.1	8.5
BMR12791_21128_Draculoides `sp. WAM-SCH067`	4.7	4.6	5.0	4.7	4.8	4.6	4.6	4.9	4.9	4.6	5.3	5.8	5.2	5.6	5.8	5.8	4.6	5.6	4.3	6.1	1.5	0.9	0.8	0.6	0.6	0.6	0.6	0.6	0.6	0.8	0.8	0.9		1.7	1.7	1.1	4.8	6.8	7.0	7.4	7.6	7.4	8.8	8.6	8.5	8.4	8.8
BMR11801_22083_Draculoides `sp. WAM-SCH067`	5.2	5.0	5.2	5.2	5.1	5.0	4.7	5.0	5.0	5.0	5.5	5.9	5.6	6.1	6.2	6.2	5.0	6.1	4.7	6.5	1.4	2.0	1.8	1.7	1.7	1.7	1.7	1.7	1.7	1.8	1.8	2.0	1.7		2.4	2.3	5.5	6.2	7.1	7.3	7.4	7.8	8.7	8.6	8.7	8.5	9.0
BMR12796_21128_Draculoides `sp. WAM-SCH067`	4.9	4.7	5.2	4.6	5.1	4.7	4.7	5.0	5.0	4.7	5.5	5.6	5.0	5.8	5.9	5.9	4.7	5.8	4.1	6.4	2.0	1.5	1.5	1.4	1.4	1.4	1.4	1.4	1.4	1.5	1.5	1.7	1.7	2.4		2.0	4.2	6.6	6.7	7.0	7.4	7.6	8.4	8.0	8.1	8.2	8.1
BMR11991_21128_Draculoides `sp. WAM-SCH067`	4.9	4.8	5.1	4.9	5.2	4.8	4.8	5.1	5.1	4.8	5.5	6.0	5.4	5.9	6.0	6.0	4.8	5.9	4.5	6.3	2.0	1.4	1.2	1.1	1.1	1.1	1.1	1.1	1.1	1.2	1.2	1.4	1.1	2.3	2.0		4.4	6.4	6.9	7.7	7.7	7.4	9.4	8.6	8.6	8.5	8.8
BMR12186_21128_Draculoides `sp. WAM-SCH067`	3.3	3.3	2.6	3.3	4.5	3.5	3.5	4.0	4.0	3.1	2.9	2.9	3.1	3.7	4.0	4.0	3.7	4.2	0.0	5.1	4.4	4.4	4.6	4.4	4.4	4.4	4.4	4.4	4.4	4.6	4.4	4.6	4.8	5.5	4.2	4.4		5.2	7.3	6.8	8.6	7.9	9.7	10.4	9.5	9.5	9.7
BMR12187_21128_Draculoides `sp. WAM-SCH067`	4.6	4.2	3.7	4.0	4.2	3.7	3.7	3.7	3.7	3.7	3.7	3.7	3.5	3.1	3.3	3.3	4.0	3.7	5.5	4.4	6.4	6.4	6.6	6.4	6.4	6.4	6.4	6.4	6.4	6.6	6.4	6.6	6.8	6.2	6.6	6.4	5.2		8.6	7.7	9.3	8.2	10.1	11.5	11.0	11.0	10.8
BMR11597_22083_Draculoides `sp. Biologic-SCHI021`	6.8	6.2	6.5	6.5	7.3	7.0	7.0	7.3	7.3	6.7	6.7	6.8	6.5	6.8	6.8	6.8	6.8	7.4	6.8	8.2	7.0	6.8	6.8	6.7	6.7	6.7	6.7	6.7	6.7	6.5	6.5	6.7	7.0	7.1	6.7	6.9	7.3	8.6		4.9	6.8	7.8	9.0	8.3	7.9	7.9	8.2
BMR11621_22083_Draculoides `sp. Biologic-SCHI021`	7.1	6.4	5.8	6.2	7.1	7.0	6.7	7.0	7.0	6.4	5.6	5.8	5.5	6.5	6.5	6.5	6.8	7.3	6.4	7.6	6.8	7.3	7.3	7.1	7.1	7.1	7.1	7.1	7.1	7.0	7.0	7.1	7.4	7.3	7.0	7.7	6.8	7.7	4.9		6.1	7.1	8.5	8.2	7.8	7.3	8.4
BMR11800_22083_Draculoides `sp. Biologic-SCHI021`	7.9	7.1	7.1	7.3	7.8	7.4	7.4	7.4	7.4	7.4	7.3	7.4	7.1	8.1	8.1	8.1	8.1	7.8	7.4	9.3	7.0	7.1	7.1	7.0	7.0	7.0	7.0	7.0	7.0	6.8	6.8	7.0	7.6	7.4	7.4	7.7	8.6	9.3	6.8	6.1		7.3	8.4	8.6	8.1	7.9	9.0
PP955371_Draculoides sp. B2 group BSC033	7.4	7.3	7.1	7.3	8.1	7.8	7.8	8.1	8.1	7.1	7.6	7.8	7.1	7.9	8.1	8.1	7.6	7.6	7.3	8.4	7.4	7.3	7.1	7.1	7.1	7.1	7.1	7.1	7.1	7.0	7.0	7.1	7.4	7.8	7.6	7.4	7.9	8.2	7.8	7.1	7.3		8.4	8.5	8.1	7.9	8.7
MT316788_Draculoides sp. WAM-SCH068	9.1	8.4	9.1	9.3	9.2	9.1	9.1	9.3	9.3	9.0	8.7	8.8	8.5	9.7	9.9	9.9	9.0	9.7	8.8	10.2	8.8	9.0	9.0	8.8	8.8	8.8	8.8	8.8	8.8	8.7	9.0	8.8	8.8	8.7	8.4	9.4	9.7	10.1	9.0	8.5	8.4	8.4		8.2	8.1	7.9	9.3
BMR11992_21128_Draculoides `sp. Biologic-SCHI023`	9.1	8.6	8.6	8.6	9.2	9.1	9.1	9.4	9.4	9.1	8.8	9.0	8.6	9.6	9.7	9.7	9.0	9.7	8.3	9.7	8.0	8.2	8.2	8.0	8.0	8.0	8.0	8.0	8.0	7.9	8.2	8.0	8.6	8.6	8.0	8.6	10.4	11.5	8.3	8.2	8.6	8.5	8.2		1.4	1.5	4.0
BMR12957_21128_Draculoides `sp. Biologic-SCHI023`	8.7	8.2	8.4	8.2	8.9	8.7	8.7	9.0	9.0	8.7	8.4	8.5	8.2	9.1	9.3	9.3	8.8	9.0	7.9	9.6	7.9	8.4	8.4	8.2	8.2	8.2	8.2	8.2	8.2	8.1	8.1	8.2	8.5	8.7	8.1	8.6	9.5	11.0	7.9	7.8	8.1	8.1	8.1	1.4		0.5	3.3
BMR12959_21128_Draculoides `sp. Biologic-SCHI023`	8.5	8.1	7.9	8.1	8.7	8.5	8.5	8.8	8.8	8.5	8.2	8.4	8.1	9.0	9.1	9.1	8.7	8.8	7.8	9.4	7.8	8.2	8.2	8.1	8.1	8.1	8.1	8.1	8.1	7.9	7.9	8.1	8.4	8.5	8.2	8.5	9.5	11.0	7.9	7.3	7.9	7.9	7.9	1.5	0.5		3.8
BMR13740_21128_Draculoides `sp. Biologic-SCHI023`	9.9	9.4	9.0	9.1	9.8	9.6	9.6	9.6	9.6	9.6	9.6	9.7	9.4	10.3	10.5	10.5	9.4	10.0	9.1	10.3	8.2	8.7	8.7	8.5	8.5	8.5	8.5	8.5	8.5	8.4	8.4	8.5	8.8	9.0	8.1	8.8	9.7	10.8	8.2	8.4	9.0	8.7	9.3	4.0	3.3	3.8	

3.1.5 Trombidiformes

Two mite specimens were successfully sequenced forming one OTU that matched non-Study sequences (Table 3.1, Figure 3.5). This OTU, Pezidae `sp. Biologic-ACAR003`, had intraspecific divergences less than 7.1%, was more than 25.4% divergent from all other sequences in the analysis, and had a linear range of 11.3 km (Table 3.1, Table 3.6).

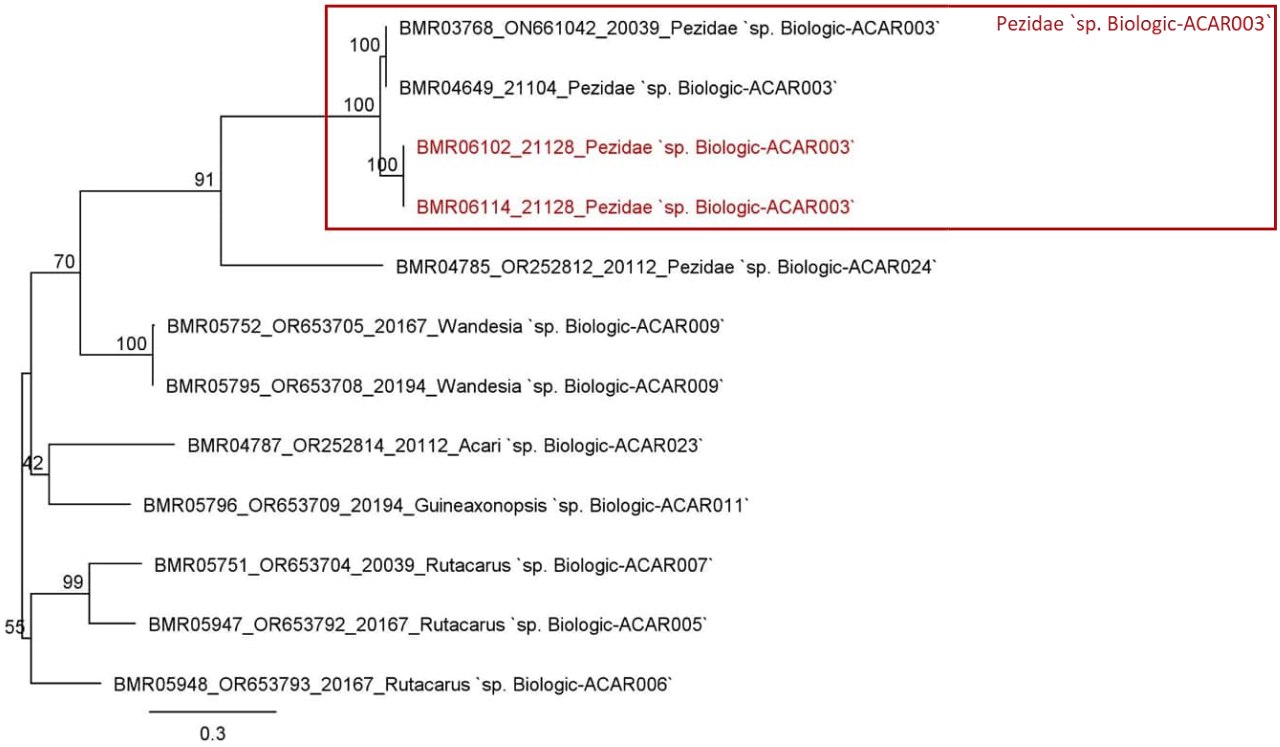

Figure 3.5. Phylogeny for the Trombidiformes dataset, with bootstrap values

Table 3.6: Pairwise distances (%) for the Trombidiformes dataset

COI Pairwise Distances (%)	BMR04787	BMR05947	BMR05948	BMR05796	BMR05752	BMR05795	BMR03768	BMR04649	BMR06102	BMR06114	BMR05751	BMR04785
BMR04787_OR252814_20112_Acari `sp. Biologic-ACAR023`		20.3	21.1	21.7	22.7	22.9	30.7	30.7	30.9	30.6	22.2	27.6
BMR05947_OR653792_20167_Rutacarus `sp. Biologic-ACAR005`	20.3		19.7	21.3	21.7	21.7	31.7	31.7	31.5	31.8	14.0	28.0
BMR05948_OR653793_20167_Rutacarus `sp. Biologic-ACAR006`	21.1	19.7		18.8	21.4	21.0	28.6	28.6	29.0	29.3	20.3	29.9
BMR05796_OR653709_20194_Guineaxonopsis `sp. Biologic-ACAR011`	21.7	21.3	18.8		20.8	20.7	27.9	27.9	28.2	28.3	22.5	28.8
BMR05752_OR653705_20167_Wandesia `sp. Biologic-ACAR009`	22.7	21.7	21.4	20.8		0.4	25.5	25.5	25.9	25.9	22.1	27.6
BMR05795_OR653708_20194_Wandesia `sp. Biologic-ACAR009`	22.9	21.7	21.0	20.7	0.4		25.7	25.7	26.1	26.2	22.0	27.0
BMR03768_ON661042_20039_Pezidae `sp. Biologic-ACAR003`	30.7	31.7	28.6	27.9	25.5	25.7		0.0	6.4	7.0	31.9	27.8
BMR04649_21104_Pezidae `sp. Biologic-ACAR003`	30.7	31.7	28.6	27.9	25.5	25.7	0.0		6.4	7.0	31.9	27.8
BMR06102_21128_Pezidae `sp. Biologic-ACAR003`	30.9	31.5	29.0	28.2	25.9	26.1	6.4	6.4		0.0	30.6	28.7
BMR06114_21128_Pezidae `sp. Biologic-ACAR003`	30.6	31.8	29.3	28.3	25.9	26.2	7.0	7.0	0.0		30.6	28.7
BMR05751_OR653704_20039_Rutacarus `sp. Biologic-ACAR007`	22.2	14.0	20.3	22.5	22.1	22.0	31.9	31.9	30.6	30.6		26.6
BMR04785_OR252812_20112_Pezidae `sp. Biologic-ACAR024`	27.6	28.0	29.9	28.8	27.6	27.0	27.8	27.8	28.7	28.7	26.6	

3.2 Chilopoda

Three centipede specimens were sequenced and resolved within two OTUs that matched non-Study sequences; *Cryptops* `sp. Biologic-CHIL048`and *Cormocephalus pyropygus* (Figure 3.6). *Cryptops* `sp. Biologic-CHIL048`matched sequences named *Cryptops* `sp. B07`, but as these sequences were named after the designation of the Biologic OTU *Cryptops* `sp. Biologic-CHIL048`the Biologic name was kept (Figure 3.6). The intraspecific distances within this OTU were up to 10.4%, which is considered to be acceptable with the current knowledge of this family (Wesener *et al.*, 2016) (Table 3.7). The divergence from all other sequences in the analysis was greater than 17.5%, and the linear range for *Cryptops* `sp. Biologic-CHIL048` was 56.1 km (Table 3.1, Table 3.7).

Two specimens matched the named species *Cormocephalus pyropygus,* with a linear range of 185.1 km (Table 3.1). The intraspecific divergences of this species were up to 16.5%, but this considerable divergence is noted in the species description and explained by morphological characteristics being relied upon for species delineation (Edgecombe *et al.*, 2019) (Table 3.7). *Cormocephalus pyropygus* was greater than 18.1% divergent compared to all other sequences in the analysis (Table 3.7). It is possible this species harbours undescribed species that are not yet resolvable using morphology.

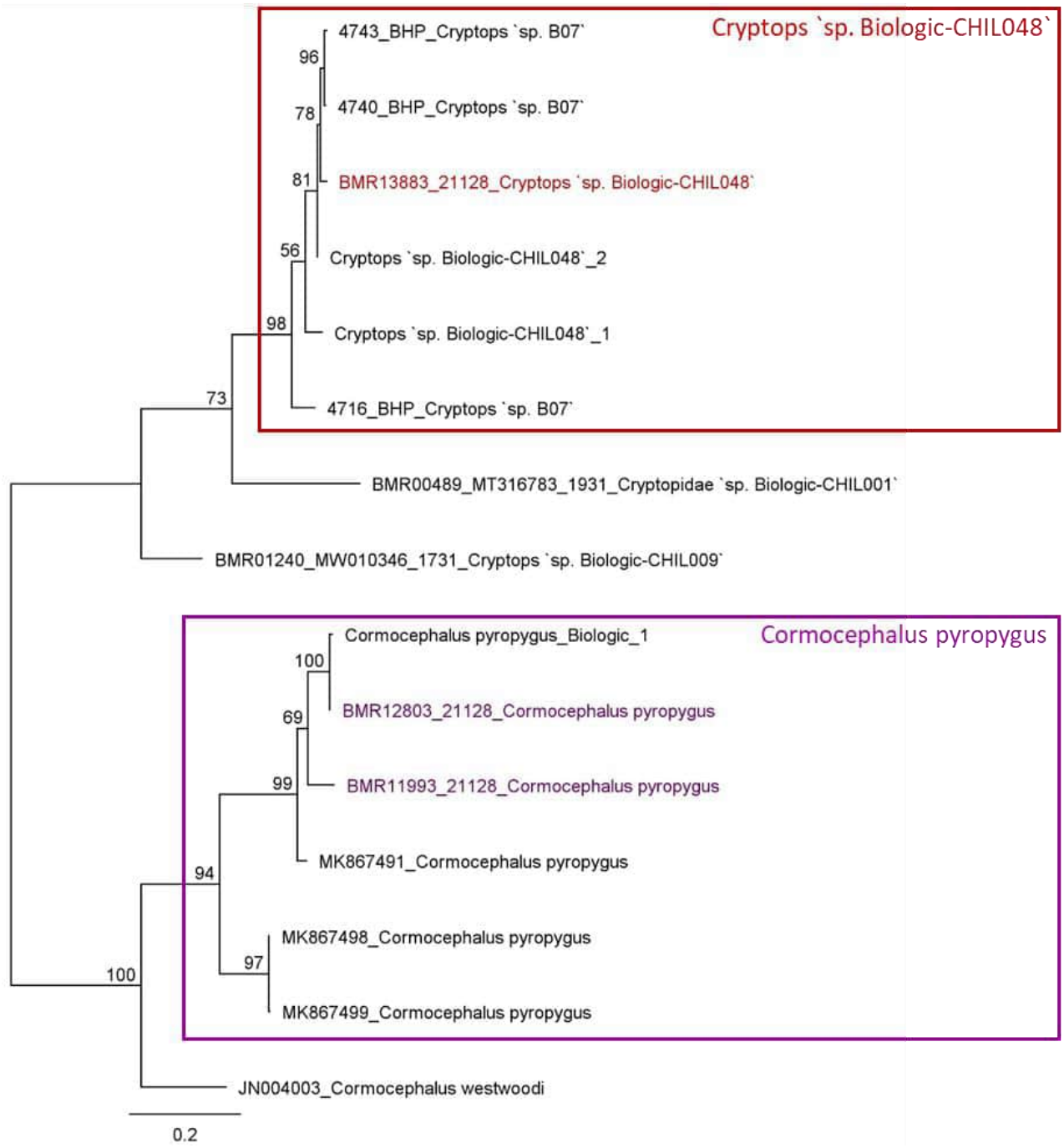

Figure 3.6. Phylogeny for the Chilopoda dataset, with bootstrap values

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

COI Pairwise Distances (%)	4716	4740	4743	Biologic-CHIL048_2	BMR13883	Biologic-CHIL048_1	BMR00489	BMR01240	BMR11993	BMR12803	C.pyropygus_Biologic_1	MK867491	MK867498	MK867499	JN004003
4716_BHP_Cryptops `sp. B07`		9.8	9.6	7.8	10.3	8.8	17.6	19.1	27.9	29.6	29.3	30.0	28.4	28.6	29.8
4740_BHP_Cryptops `sp. B07`	9.8		0.6	1.5	3.2	5.9	19.8	19.1	29.3	29.4	29.1	27.7	29.7	29.9	30.7
4743_BHP_Cryptops `sp. B07`	9.6	0.6		1.7	3.4	5.7	20.2	18.5	29.3	29.0	28.7	27.2	29.3	29.5	30.7
Cryptops `sp. Biologic-CHIL048`_2	7.8	1.5	1.7		3.3	5.1	18.4	19.0	28.5	28.2	28.0	28.1	28.1	28.3	29.2
BMR13883_21128_Cryptops `sp. Biologic-CHIL048`	10.3	3.2	3.4	3.3		6.5	19.6	19.8	29.3	28.7	28.4	28.7	28.7	28.8	28.7
Cryptops `sp. Biologic-CHIL048`_1	8.8	5.9	5.7	5.1	6.5		19.8	20.3	29.8	29.4	29.1	28.1	30.0	30.0	30.8
BMR00489_MT316783_1931_Cryptopidae `sp. Biologic-CHIL001`	17.6	19.8	20.2	18.4	19.6	19.8		21.0	27.6	27.2	27.1	28.7	25.7	25.8	26.2
BMR01240_MW010346_1731_Cryptops `sp. Biologic-CHIL009`	19.1	19.1	18.5	19.0	19.8	20.3	21.0		25.8	25.5	25.7	26.2	24.9	24.8	25.6
BMR11993_21128_Cormocephalus pyropygus	27.9	29.3	29.3	28.5	29.3	29.8	27.6	25.8		8.1	8.3	7.8	16.2	16.4	22.0
BMR12803_21128_Cormocephalus pyropygus	29.6	29.4	29.0	28.2	28.7	29.4	27.2	25.5	8.1		0.7	6.2	15.9	16.0	20.4
Cormocephalus pyropygus_Biologic_1	29.3	29.1	28.7	28.0	28.4	29.1	27.1	25.7	8.3	0.7		5.9	16.1	16.3	20.6
MK867491_Cormocephalus pyropygus	30.0	27.7	27.2	28.1	28.7	28.1	28.7	26.2	7.8	6.2	5.9		15.9	15.9	20.8
MK867498_Cormocephalus pyropygus	28.4	29.7	29.3	28.1	28.7	30.0	25.7	24.9	16.2	15.9	16.1	15.9		0.2	18.4
MK867499_Cormocephalus pyropygus	28.6	29.9	29.5	28.3	28.8	30.0	25.8	24.8	16.4	16.0	16.3	15.9	0.2		18.2
JN004003_Cormocephalus westwoodi	29.8	30.7	30.7	29.2	28.7	30.8	26.2	25.6	22.0	20.4	20.6	20.8	18.4	18.2	

3.3 Malacostraca

3.3.1 Amphipoda

Twenty-two amphipod specimens were resolved as four paramelitid OTUs, all matching non-Study sequences (Table 3.1, Figure 3.7). One OTU matched a described species, *Maarka weeliwollii*, which had a linear range of 84.1 km, intraspecific divergences less than 4.4% and was more than 15.9% divergent from all other sequences in the analysis (Table 3.1, Table 3.8).

Chydaekata `sp. E TLF-2008` is a well-established OTU, first published by Finston *et al.* (2007) and supported by numerous sequences in the Biologic database. In this analysis it was resolved with intraspecific divergences less than 0.6%, was greater than 19.8% divergent from all other sequences in the analysis and had a linear range of 50.3 km (Table 3.1, Table 3.8).

The final two OTUs, Paramelitidae `sp. Biologic-AMPH024`, and Paramelitidae `sp. Biologic-AMPH070`, had linear distances of 22.3 km and 14.8 km respectively (Table 3.1). These OTUs had intraspecific divergences of less than 3% and were more than 10.2% divergent from all other sequences in the analysis (Table 3.8).

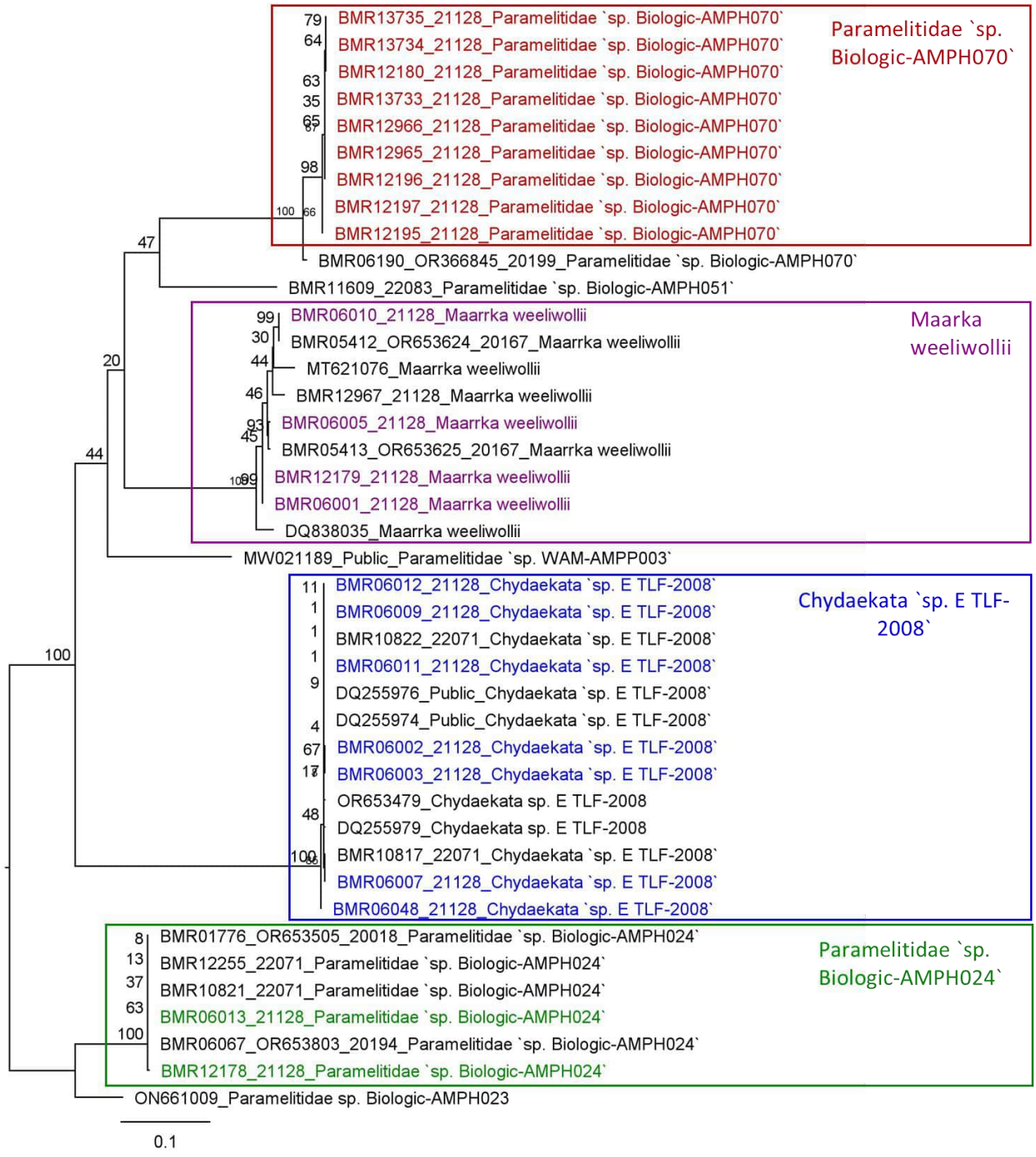

Figure 3.7. Phylogeny for the Amphipoda dataset, with bootstrap values

Table 3.8: Pairwise distances (%) for the Amphipoda dataset

COI Pairwise Distances (%)	BMR01776	BMR06013	BMR10821	BMR12255	BMR06067	BMR12178	ON669	BMR05412	BMR06010	BMR05413	BMR06005	BMR06001	BMR12179	BMR12967	MT621076	DQ838035	MW021189	BMR11609	BMR06190	BMR12180	BMR13734	BMR13735	BMR12196	BMR12965	BMR12966	BMR13733	BMR12195	BMR12197	BMR06002	BMR06003	BMR06009	BMR06011	BMR06012	BMR10822	DQ255974	DQ255976	BMR06007	BMR10817	DQ255979	OR653479	BMR06048
BMR01776_OR653505_20018_Paramelitidae `sp. Biologic-AMPH024`		0.0	0.0	0.0	0.1	0.2	10.3	20.1	20.1	20.2	20.1	20.1	20.1	20.4	20.3	21.1	19.8	19.8	18.9	19.6	19.5	19.5	19.4	19.3	19.3	19.3	19.2	19.2	22.8	22.8	22.9	22.9	22.9	22.9	22.9	22.9	22.9	22.9	22.8	22.9	22.9
BMR06013_21128_Paramelitidae `sp. Biologic-AMPH024`	0.0		0.0	0.0	0.1	0.2	10.3	20.1	20.1	20.2	20.1	20.1	20.1	20.4	20.3	21.1	19.8	19.8	18.9	19.6	19.5	19.5	19.4	19.3	19.3	19.3	19.2	19.2	22.8	22.8	22.9	22.9	22.9	22.9	22.9	22.9	22.9	22.9	22.8	22.9	22.9
BMR10821_22071_Paramelitidae `sp. Biologic-AMPH024`	0.0	0.0		0.0	0.1	0.2	10.3	20.1	20.1	20.2	20.1	20.1	20.1	20.4	20.3	21.1	19.8	19.8	18.9	19.6	19.5	19.5	19.4	19.3	19.3	19.3	19.2	19.2	22.8	22.8	22.9	22.9	22.9	22.9	22.9	22.9	22.9	22.9	22.8	22.9	22.9
BMR12255_22071_Paramelitidae `sp. Biologic-AMPH024`	0.0	0.0	0.0		0.1	0.2	10.3	20.1	20.1	20.2	20.1	20.1	20.1	20.4	20.3	21.1	19.8	19.8	18.9	19.6	19.5	19.5	19.4	19.3	19.3	19.3	19.2	19.2	22.8	22.8	22.9	22.9	22.9	22.9	22.9	22.9	22.9	22.9	22.8	22.9	22.9
BMR06067_OR653803_20194_Paramelitidae `sp. Biologic-AMPH024`	0.1	0.1	0.1	0.1		0.2	10.4	20.1	20.1	20.3	20.1	20.1	20.1	20.4	20.3	21.2	19.8	19.8	19.1	19.7	19.5	19.5	19.5	19.4	19.4	19.4	19.3	19.3	22.9	22.9	23.0	23.0	23.0	23.0	23.0	23.0	23.0	23.0	22.9	23.0	23.0
BMR12178_21128_Paramelitidae `sp. Biologic-AMPH024`	0.2	0.2	0.2	0.2	0.2		10.3	20.1	20.1	20.2	20.1	20.1	20.1	20.4	20.3	21.1	19.8	19.9	18.9	19.6	19.5	19.5	19.4	19.3	19.3	19.3	19.2	19.2	22.8	22.8	22.9	22.9	22.9	22.9	22.9	22.9	22.9	22.9	22.8	22.9	22.9
ON669_Paramelitidae sp. Biologic-AMPH023	10.3	10.3	10.3	10.3	10.4	10.3		19.5	19.5	20.8	20.7	20.7	20.7	20.8	19.6	21.7	17.3	19.5	18.3	17.8	18.7	18.7	17.6	18.5	18.5	18.5	17.4	17.4	21.7	21.7	21.7	21.7	21.7	21.7	21.7	21.7	21.7	21.7	21.6	21.7	21.7
BMR05412_OR653624_20167_Maarrka weeliwolllii	20.1	20.1	20.1	20.1	20.1	20.1	19.5		0.0	1.7	1.7	1.7	1.7	2.1	2.7	4.3	16.6	17.2	19.2	21.1	19.9	19.9	20.9	19.8	19.8	19.8	20.7	20.7	22.0	22.0	22.2	22.2	22.2	22.2	22.2	22.2	22.2	22.2	22.0	22.0	22.2
BMR06010_21128_Maarrka weeliwollii	20.1	20.1	20.1	20.1	20.1	20.1	19.5	0.0		1.7	1.7	1.7	1.7	2.1	2.7	4.3	16.6	17.2	19.2	21.1	19.9	19.9	20.9	19.8	19.8	19.8	20.7	20.7	22.0	22.0	22.2	22.2	22.2	22.2	22.2	22.2	22.2	22.2	22.0	22.0	22.2
BMR05413_OR653625_20167_Maarrka weeliwollii	20.2	20.2	20.2	20.2	20.3	20.2	20.8	1.7	1.7		0.3	0.9	0.9	2.3	3.5	3.5	17.5	17.5	19.6	21.6	20.7	20.7	21.4	20.5	20.5	20.5	21.1	21.1	22.8	22.8	22.9	22.9	22.9	22.9	22.9	22.9	22.9	22.9	22.8	22.8	22.9
BMR06005_21128_Maarrka weeliwollii	20.1	20.1	20.1	20.1	20.1	20.1	20.7	1.7	1.7	0.3		0.9	0.9	2.3	3.5	3.5	17.5	17.5	19.4	21.4	20.5	20.5	21.1	20.4	20.4	20.4	20.9	20.9	22.6	22.6	22.8	22.8	22.8	22.8	22.8	22.8	22.8	22.8	22.6	22.6	22.8
BMR06001_21128_Maarrka weeliwollii	20.1	20.1	20.1	20.1	20.1	20.1	20.7	1.7	1.7	0.9	0.9		0.0	2.6	3.8	2.6	17.0	17.2	19.2	21.1	20.2	20.2	20.9	20.1	20.1	20.1	20.7	20.7	22.5	22.5	22.6	22.6	22.6	22.6	22.6	22.6	22.6	22.6	22.5	22.5	22.6
BMR12179_21128_Maarrka weeliwollii	20.1	20.1	20.1	20.1	20.1	20.1	20.7	1.7	1.7	0.9	0.9	0.0		2.6	3.8	2.6	17.0	17.2	19.2	21.1	20.2	20.2	20.9	20.1	20.1	20.1	20.7	20.7	22.5	22.5	22.6	22.6	22.6	22.6	22.6	22.6	22.6	22.6	22.5	22.5	22.6
BMR12967_21128_Maarrka weeliwollii	20.4	20.4	20.4	20.4	20.4	20.4	20.8	2.1	2.1	2.3	2.3	2.6	2.6		3.6	5.2	17.5	18.1	20.3	22.2	21.0	21.0	22.0	20.8	20.8	20.8	21.8	21.8	22.8	22.8	22.9	22.9	22.9	22.9	22.9	22.9	22.9	22.9	22.8	22.8	22.9
MT621076_Maarrka weeliwollii	20.3	20.3	20.3	20.3	20.3	20.3	19.6	2.7	2.7	3.5	3.5	3.8	3.8	3.6		5.2	16.0	17.7	19.8	21.4	19.9	19.9	21.1	19.8	19.8	19.8	20.9	20.9	21.8	21.8	22.0	22.0	22.0	22.0	22.0	22.0	22.0	22.0	21.8	21.8	22.0
DQ838035_Maarrka weeliwollii	21.1	21.1	21.1	21.1	21.2	21.1	21.7	4.3	4.3	3.5	3.5	2.6	2.6	5.2	5.2		17.9	18.8	19.2	21.1	20.8	20.8	20.9	20.7	20.7	20.7	20.7	20.7	23.1	23.1	23.3	23.3	23.3	23.3	23.3	23.3	23.3	23.3	23.1	23.1	23.3
MW021189_Public_Paramelitidae `sp. WAM-AMPP003`	19.8	19.8	19.8	19.8	19.8	19.8	17.3	16.6	16.6	17.5	17.5	17.0	17.0	17.5	16.0	17.9		16.4	17.0	17.0	16.4	16.4	16.7	16.3	16.3	16.3	16.5	16.5	19.9	19.9	19.9	19.9	19.9	19.9	19.9	19.9	19.9	19.9	19.8	19.9	19.9
BMR11609_22083_Paramelitidae `sp. Biologic-AMPH051`	19.8	19.8	19.8	19.8	19.8	19.9	19.5	17.2	17.2	17.5	17.5	17.2	17.2	18.1	17.7	18.8	16.4		18.3	19.2	18.4	18.4	18.9	18.2	18.2	18.2	18.7	18.7	20.7	20.7	20.8	20.8	20.8	20.8	20.8	20.8	20.8	20.8	20.7	20.8	20.7
BMR06190_OR366845_20199_Paramelitidae `sp. Biologic-AMPH070`	18.9	18.9	18.9	18.9	19.1	18.9	18.3	19.2	19.2	19.6	19.4	19.2	19.2	20.3	19.8	19.2	17.0	18.3		2.9	2.9	2.9	2.6	2.6	2.6	2.6	2.4	2.4	19.4	19.4	19.6	19.6	19.6	19.6	19.6	19.6	19.6	19.6	19.4	19.6	19.4
BMR12180_21128_Paramelitidae `sp. Biologic-AMPH070`	19.6	19.6	19.6	19.6	19.7	19.6	17.8	21.1	21.1	21.6	21.4	21.1	21.1	22.2	21.4	21.1	17.0	19.2	2.9		0.0	0.0	0.2	0.2	0.2	0.2	0.4	0.4	20.3	20.3	20.3	20.3	20.3	20.3	20.3	20.3	20.3	20.3	20.5	20.3	20.0
BMR13734_21128_Paramelitidae `sp. Biologic-AMPH070`	19.5	19.5	19.5	19.5	19.5	19.5	18.7	19.9	19.9	20.7	20.5	20.2	20.2	21.0	19.9	20.8	16.4	18.4	2.9	0.0		0.0	0.2	0.2	0.2	0.2	0.4	0.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.6	21.3	21.3
BMR13735_21128_Paramelitidae `sp. Biologic-AMPH070`	19.5	19.5	19.5	19.5	19.5	19.5	18.7	19.9	19.9	20.7	20.5	20.2	20.2	21.0	19.9	20.8	16.4	18.4	2.9	0.0	0.0		0.2	0.2	0.2	0.2	0.4	0.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.6	21.3	21.3
BMR12196_21128_Paramelitidae `sp. Biologic-AMPH070`	19.4	19.4	19.4	19.4	19.5	19.4	17.6	20.9	20.9	21.4	21.1	20.9	20.9	22.0	21.1	20.9	16.7	18.9	2.6	0.2	0.2	0.2		0.0	0.0	0.0	0.2	0.2	20.5	20.5	20.5	20.5	20.5	20.5	20.5	20.5	20.5	20.3	20.5	20.3
BMR12965_21128_Paramelitidae `sp. Biologic-AMPH070`	19.3	19.3	19.3	19.3	19.4	19.3	18.5	19.8	19.8	20.5	20.4	20.1	20.1	20.8	19.8	20.7	16.3	18.2	2.6	0.2	0.2	0.2	0.0		0.0	0.0	0.2	0.2	21.6	21.6	21.6	21.6	21.6	21.6	21.6	21.6	21.6	21.4	21.4	21.4
BMR12966_21128_Paramelitidae `sp. Biologic-AMPH070`	19.3	19.3	19.3	19.3	19.4	19.3	18.5	19.8	19.8	20.5	20.4	20.1	20.1	20.8	19.8	20.7	16.3	18.2	2.6	0.2	0.2	0.2	0.0	0.0		0.0	0.2	0.2	21.6	21.6	21.6	21.6	21.6	21.6	21.6	21.6	21.6	21.4	21.4	21.4
BMR13733_21128_Paramelitidae `sp. Biologic-AMPH070`	19.3	19.3	19.3	19.3	19.4	19.3	18.5	19.8	19.8	20.5	20.4	20.1	20.1	20.8	19.8	20.7	16.3	18.2	2.6	0.2	0.2	0.2	0.0	0.0	0.0		0.2	0.2	21.6	21.6	21.6	21.6	21.6	21.6	21.6	21.6	21.6	21.4	21.4	21.4
BMR12195_21128_Paramelitidae `sp. Biologic-AMPH070`	19.2	19.2	19.2	19.2	19.3	19.2	17.4	20.7	20.7	21.1	20.9	20.7	20.7	21.8	20.9	20.7	16.5	18.7	2.4	0.4	0.4	0.4	0.2	0.2	0.2	0.2		0.0	20.3	20.3	20.3	20.3	20.3	20.3	20.3	20.3	20.3	20.0	20.3	20.0
BMR12197_21128_Paramelitidae `sp. Biologic-AMPH070`	19.2	19.2	19.2	19.2	19.3	19.2	17.4	20.7	20.7	21.1	20.9	20.7	20.7	21.8	20.9	20.7	16.5	18.7	2.4	0.4	0.4	0.4	0.2	0.2	0.2	0.2	0.0		20.3	20.3	20.3	20.3	20.3	20.3	20.3	20.3	20.3	20.0	20.3	20.0
BMR06002_21128_Chydaekata `sp. ETLF-2008`	22.8	22.8	22.8	22.8	22.9	22.8	21.7	22.0	22.0	22.8	22.6	22.5	22.5	22.8	21.8	23.1	19.9	20.7	19.4	20.3	21.4	21.4	20.5	21.6	21.6	21.6	20.3	20.3		0.0	0.2	0.2	0.2	0.2	0.2	0.2	0.3	0.3	0.3	0.3	0.5
BMR06003_21128_Chydaekata `sp. ETLF-2008`	22.8	22.8	22.8	22.8	22.9	22.8	21.7	22.0	22.0	22.8	22.6	22.5	22.5	22.8	21.8	23.1	19.9	20.7	19.4	20.3	21.4	21.4	20.5	21.6	21.6	21.6	20.3	20.3	0.0		0.2	0.2	0.2	0.2	0.2	0.2	0.3	0.3	0.3	0.3	0.5
BMR06009_21128_Chydaekata `sp. ETLF-2008`	22.9	22.9	22.9	22.9	23.0	22.9	21.7	22.2	22.2	22.9	22.8	22.6	22.6	22.9	22.0	23.3	19.9	20.8	19.6	20.3	21.4	21.4	20.5	21.6	21.6	21.6	20.3	20.3	0.2	0.2		0.0	0.0	0.0	0.0	0.0	0.2	0.2	0.2	0.2	0.3
BMR06011_21128_Chydaekata `sp. ETLF-2008`	22.9	22.9	22.9	22.9	23.0	22.9	21.7	22.2	22.2	22.9	22.8	22.6	22.6	22.9	22.0	23.3	19.9	20.8	19.6	20.3	21.4	21.4	20.5	21.6	21.6	21.6	20.3	20.3	0.2	0.2	0.0		0.0	0.0	0.0	0.0	0.2	0.2	0.2	0.2	0.3
BMR06012_21128_Chydaekata `sp. ETLF-2008`	22.9	22.9	22.9	22.9	23.0	22.9	21.7	22.2	22.2	22.9	22.8	22.6	22.6	22.9	22.0	23.3	19.9	20.8	19.6	20.3	21.4	21.4	20.5	21.6	21.6	21.6	20.3	20.3	0.2	0.2	0.0	0.0		0.0	0.0	0.0	0.2	0.2	0.2	0.2	0.3
BMR10822_22071_Chydaekata `sp. ETLF-2008`	22.9	22.9	22.9	22.9	23.0	22.9	21.7	22.2	22.2	22.9	22.8	22.6	22.6	22.9	22.0	23.3	19.9	20.8	19.6	20.3	21.4	21.4	20.5	21.6	21.6	21.6	20.3	20.3	0.2	0.2	0.0	0.0	0.0		0.0	0.0	0.2	0.2	0.2	0.2	0.3
DQ255974_Public_Chydaekata `sp. ETLF-2008`	22.9	22.9	22.9	22.9	23.0	22.9	21.7	22.2	22.2	22.9	22.8	22.6	22.6	22.9	22.0	23.3	19.9	20.8	19.6	20.3	21.4	21.4	20.5	21.6	21.6	21.6	20.3	20.3	0.2	0.2	0.0	0.0	0.0	0.0		0.0	0.2	0.2	0.2	0.2	0.3
DQ255976_Public_Chydaekata `sp. ETLF-2008`	22.9	22.9	22.9	22.9	23.0	22.9	21.7	22.2	22.2	22.9	22.8	22.6	22.6	22.9	22.0	23.3	19.9	20.8	19.6	20.3	21.4	21.4	20.5	21.6	21.6	21.6	20.3	20.3	0.2	0.2	0.0	0.0	0.0	0.0	0.0		0.2	0.2	0.2	0.2	0.3
BMR06007_21128_Chydaekata `sp. ETLF-2008`	22.9	22.9	22.9	22.9	23.0	22.9	21.7	22.2	22.2	22.9	22.8	22.6	22.6	22.9	22.0	23.3	19.9	20.8	19.6	20.3	21.4	21.4	20.5	21.6	21.6	21.6	20.3	20.3	0.3	0.3	0.2	0.2	0.2	0.2	0.2	0.2		0.0	0.3	0.3	0.5
BMR10817_22071_Chydaekata `sp. ETLF-2008`	22.9	22.9	22.9	22.9	23.0	22.9	21.7	22.2	22.2	22.9	22.8	22.6	22.6	22.9	22.0	23.3	19.9	20.8	19.6	20.3	21.4	21.4	20.5	21.6	21.6	21.6	20.3	20.3	0.3	0.3	0.2	0.2	0.2	0.2	0.2	0.2	0.0		0.3	0.3	0.5
DQ255979_Chydaekata sp. ETLF-2008	22.8	22.8	22.8	22.8	22.9	22.8	21.6	22.0	22.0	22.8	22.6	22.5	22.5	22.8	21.8	23.1	19.8	20.7	19.4	20.5	21.6	21.6	20.3	21.4	21.4	21.4	20.0	20.0	0.3	0.3	0.2	0.2	0.2	0.2	0.2	0.2	0.3	0.3		0.3	0.5
OR653479_Chydaekata sp. ETLF-2008	22.9	22.9	22.9	22.9	23.0	22.9	21.7	22.0	22.0	22.8	22.6	22.5	22.5	22.8	21.8	23.1	19.9	20.8	19.6	20.3	21.3	21.3	20.3	21.4	21.4	21.4	20.3	20.3	0.3	0.3	0.2	0.2	0.2	0.2	0.2	0.2	0.3	0.3	0.3		0.5
BMR06048_21128_Chydaekata `sp. ETLF-2008`	22.9	22.9	22.9	22.9	23.0	22.9	21.7	22.2	22.2	22.9	22.8	22.6	22.6	22.9	22.0	23.3	19.9	20.7	19.4	20.0	21.3	21.3	20.3	21.4	21.4	21.4	20.0	20.0	0.5	0.5	0.3	0.3	0.3	0.3	0.3	0.3	0.5	0.5	0.5	0.5	

3.3.2 Bathynellacea

Three Bathynellacea individuals were sequenced to form one parabathynellid OTU, matching non-Study sequences (Figure 3.8). *Atopobathynella* `sp. Biologic-PBAT019`had intraspecific divergences less than 6.5%, was more than 13.3% divergent from all other sequences in the analysis and had a linear distance of 81.4 km (Table 3.1, Table 3.9). This is an unusually large geographic distribution for *Atopobathynella* which includes the Turee Ck East subcatchment, Weeli Wolli subcatchment and the Gudai-Darri Fortescue River catchment.

There are two alternate hypotheses for this OTU. First, that there are distinct OTUs in what we are currently calling *Atopobathynella* `sp. Biologic-PBAT019 `. These OTUs would have intraspecific genetic distances of less than 4.7%, and interspecific distances of more than 6%. However, one of these four OTUs would still exhibit an unusual OTU distribution across two regional subcatchments (Turee Creek/Weeli Wolli Creek). The second hypothesis is that these sequences represent a single OTU. At this point we are cautiously grouping these sequences into a single OTU, with some preliminary morphological evidence suggesting they form a single taxon (G. Perina, pers comm)

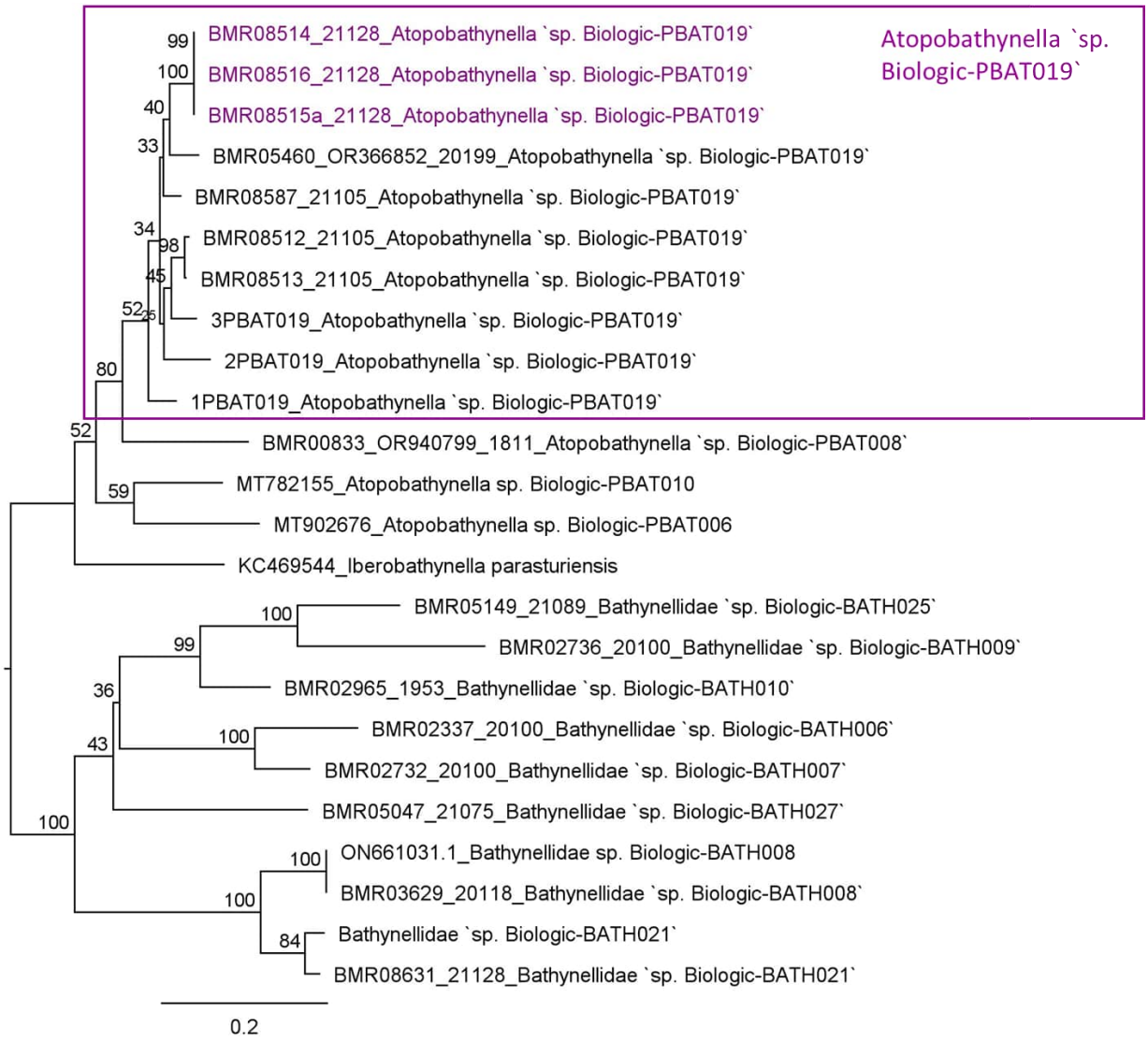

Figure 3.8. Phylogeny for the Bathynellacea dataset, with bootstrap values

Table 3.9: Pairwise distances (%) for the Bathynellacea dataset

COI Pairwise Distances (%)	KC469544	BMR08515a	1PBAT019	BMR08512	BMR08513	3PBAT019	BMR08587	BMR05460	BMR08514	BMR08516	2PBAT019	BMR00833	MT782155	MT902676	ON661031.1	BMR03629	Biologic-BATH021`	BMR08631	BMR05047	BMR02337	BMR02732	BMR02965	BMR02736	BMR05149
KC469544_Iberobathynella parasturiensis		13.9	14.5	16.0	16.1	16.6	15.2	16.6	15.7	15.7	16.6	19.0	17.5	19.9	24.7	24.7	25.4	25.1	24.3	26.1	27.5	24.3	26.4	25.5
BMR08515a_21128_Atopobathynella `sp. Biologic-PBAT019`	13.9		5.7	5.7	5.7	6.6	4.6	5.3	0.0	0.0	6.4	14.1	15.4	18.1	24.0	24.0	24.2	24.0	24.4	24.5	25.3	24.0	26.4	27.3
1PBAT019_Atopobathynella `sp. Biologic-PBAT019`	14.5	5.7		5.5	5.5	7.7	5.9	7.3	5.3	5.3	7.3	14.8	15.0	16.3	23.3	23.3	24.9	24.7	24.2	25.2	25.3	22.6	25.3	26.7
BMR08512_21105_Atopobathynella `sp. Biologic-PBAT019`	16.0	5.7	5.5		0.6	4.6	4.4	6.4	5.8	5.8	6.8	14.3	15.4	15.8	24.2	24.2	24.0	23.1	23.9	26.7	26.9	25.6	27.5	25.4
BMR08513_21105_Atopobathynella `sp. Biologic-PBAT019`	16.1	5.7	5.5	0.6		4.3	4.4	6.4	5.8	5.8	7.0	14.4	15.5	16.0	24.7	24.7	24.3	23.4	23.9	27.1	26.9	25.6	27.3	25.4
3PBAT019_Atopobathynella `sp. Biologic-PBAT019`	16.6	6.6	7.7	4.6	4.3		6.2	6.8	6.5	6.5	7.3	14.0	16.6	17.0	24.4	24.4	23.5	22.2	23.9	26.7	26.4	26.2	27.5	26.1
BMR08587_21105_Atopobathynella `sp. Biologic-PBAT019`	15.2	4.6	5.9	4.4	4.4	6.2		4.8	4.6	4.6	5.9	15.2	16.7	17.2	24.7	24.7	24.4	24.9	24.4	26.9	26.4	25.1	27.5	27.8
BMR05460_OR366852_20199_Atopobathynella `sp. Biologic-PBAT019`	16.6	5.3	7.3	6.4	6.4	6.8	4.8		5.6	5.6	8.5	14.7	16.4	17.6	24.9	24.9	23.2	22.5	23.7	26.7	26.4	26.4	28.0	25.8
BMR08514_21128_Atopobathynella `sp. Biologic-PBAT019`	15.7	0.0	5.3	5.8	5.8	6.5	4.6	5.6		0.0	7.3	13.4	15.2	16.7	24.0	24.0	22.9	22.0	23.3	26.0	25.3	25.8	26.4	24.9
BMR08516_21128_Atopobathynella `sp. Biologic-PBAT019`	15.7	0.0	5.3	5.8	5.8	6.5	4.6	5.6	0.0		7.3	13.4	15.2	16.7	24.0	24.0	22.9	22.0	23.3	26.0	25.3	25.8	26.4	24.9
2PBAT019_Atopobathynella `sp. Biologic-PBAT019`	16.6	6.4	7.3	6.8	7.0	7.3	5.9	8.5	7.3	7.3		14.0	16.7	18.1	23.8	23.8	23.5	23.6	25.2	26.7	26.0	25.1	26.7	25.4
BMR00833_OR940799_1811_Atopobathynella `sp. Biologic-PBAT008`	19.0	14.1	14.8	14.3	14.4	14.0	15.2	14.7	13.4	13.4	14.0		17.8	20.2	27.5	27.5	25.8	25.2	24.8	27.3	26.9	26.4	28.9	27.2
MT782155_Atopobathynella sp. Biologic-PBAT010	17.5	15.4	15.0	15.4	15.5	16.6	16.7	16.4	15.2	15.2	16.7	17.8		15.8	25.6	25.6	25.6	25.7	25.8	26.7	24.0	23.6	28.0	25.2
MT902676_Atopobathynella sp. Biologic-PBAT006	19.9	18.1	16.3	15.8	16.0	17.0	17.2	17.6	16.7	16.7	18.1	20.2	15.8		27.3	27.3	25.8	24.3	26.1	24.7	23.3	22.2	28.2	24.9
ON661031.1_Bathynellidae sp. Biologic-BATH008	24.7	24.0	23.3	24.2	24.7	24.4	24.7	24.9	24.0	24.0	23.8	27.5	25.6	27.3		0.0	11.5	11.2	23.1	25.1	26.4	21.4	28.0	25.3
BMR03629_20118_Bathynellidae `sp. Biologic-BATH008`	24.7	24.0	23.3	24.2	24.7	24.4	24.7	24.9	24.0	24.0	23.8	27.5	25.6	27.3	0.0		11.5	11.2	23.1	25.1	26.4	21.4	28.0	25.3
Bathynellidae `sp. Biologic-BATH021`	25.4	24.2	24.9	24.0	24.3	23.5	24.4	23.2	22.9	22.9	23.5	25.8	25.6	25.8	11.5	11.5		3.5	24.3	25.8	26.2	24.4	26.7	26.2
BMR08631_21128_Bathynellidae `sp. Biologic-BATH021`	25.1	24.0	24.7	23.1	23.4	22.2	24.9	22.5	22.0	22.0	23.6	25.2	25.7	24.3	11.2	11.2	3.5		24.0	25.1	26.4	24.0	26.4	25.4
BMR05047_21075_Bathynellidae `sp. Biologic-BATH027`	24.3	24.4	24.2	23.9	23.9	23.9	24.4	23.7	23.3	23.3	25.2	24.8	25.8	26.1	23.1	23.1	24.3	24.0		25.8	23.3	22.7	30.2	24.9
BMR02337_20100_Bathynellidae `sp. Biologic-BATH006`	26.1	24.5	25.2	26.7	27.1	26.7	26.9	26.7	26.0	26.0	26.7	27.3	26.7	24.7	25.1	25.1	25.8	25.1	25.8		14.8	21.5	24.0	26.4
BMR02732_20100_Bathynellidae `sp. Biologic-BATH007`	27.5	25.3	25.3	26.9	26.9	26.4	26.4	26.4	25.3	25.3	26.0	26.9	24.0	23.3	26.4	26.4	26.2	26.4	23.3	14.8		20.5	24.2	23.8
BMR02965_1953_Bathynellidae `sp. Biologic-BATH010`	24.3	24.0	22.6	25.6	25.6	26.2	25.1	26.4	25.8	25.8	25.1	26.4	23.6	22.2	21.4	21.4	24.4	24.0	22.7	21.5	20.5		23.1	19.8
BMR02736_20100_Bathynellidae `sp. Biologic-BATH009`	26.4	26.4	25.3	27.5	27.3	27.5	27.5	28.0	26.4	26.4	26.7	28.9	28.0	28.2	28.0	28.0	26.7	26.4	30.2	24.0	24.2	23.1		20.3
BMR05149_21089_Bathynellidae `sp. Biologic-BATH025`	25.5	27.3	26.7	25.4	25.4	26.1	27.8	25.8	24.9	24.9	25.4	27.2	25.2	24.9	25.3	25.3	26.2	25.4	24.9	26.4	23.8	19.8	20.3	

3.3.3 Isopoda

Eleven specimens were resolved as four OTUs, one of which matched non-Study sequences (Figure 3.9). Two specimens were identified as *Pygolabis weeliwolli*, a described species with intraspecific divergences less than 1%, was more than 21% divergent from all other sequences in the analysis and had a linear range of 28.1 km (Table 3.1, Table 3.10).

Six specimens were resolved as Oniscidea `sp. Biologic-ISOP152`, which had intraspecific divergences of less than 1%, was more than 19.8% divergent from all other sequences in the analysis and had a linear range of 3.4 km (Table 3.1, Table 3.10). *Troglarmadillo* `sp. Biologic-ISOP151`comprises two specimens with intraspecific divergences less than 0.3%, they were more than 9.8% divergent from other sequences in the analysis and had a linear range of 0 km (found in the same location) (Table 3.1, Table 3.10). The final OTU, Isopoda `sp. Biologic-ISOP153`was a singleton that was more than 19.4% divergent from all other sequences in the analysis (Table 3.1, Table 3.10).

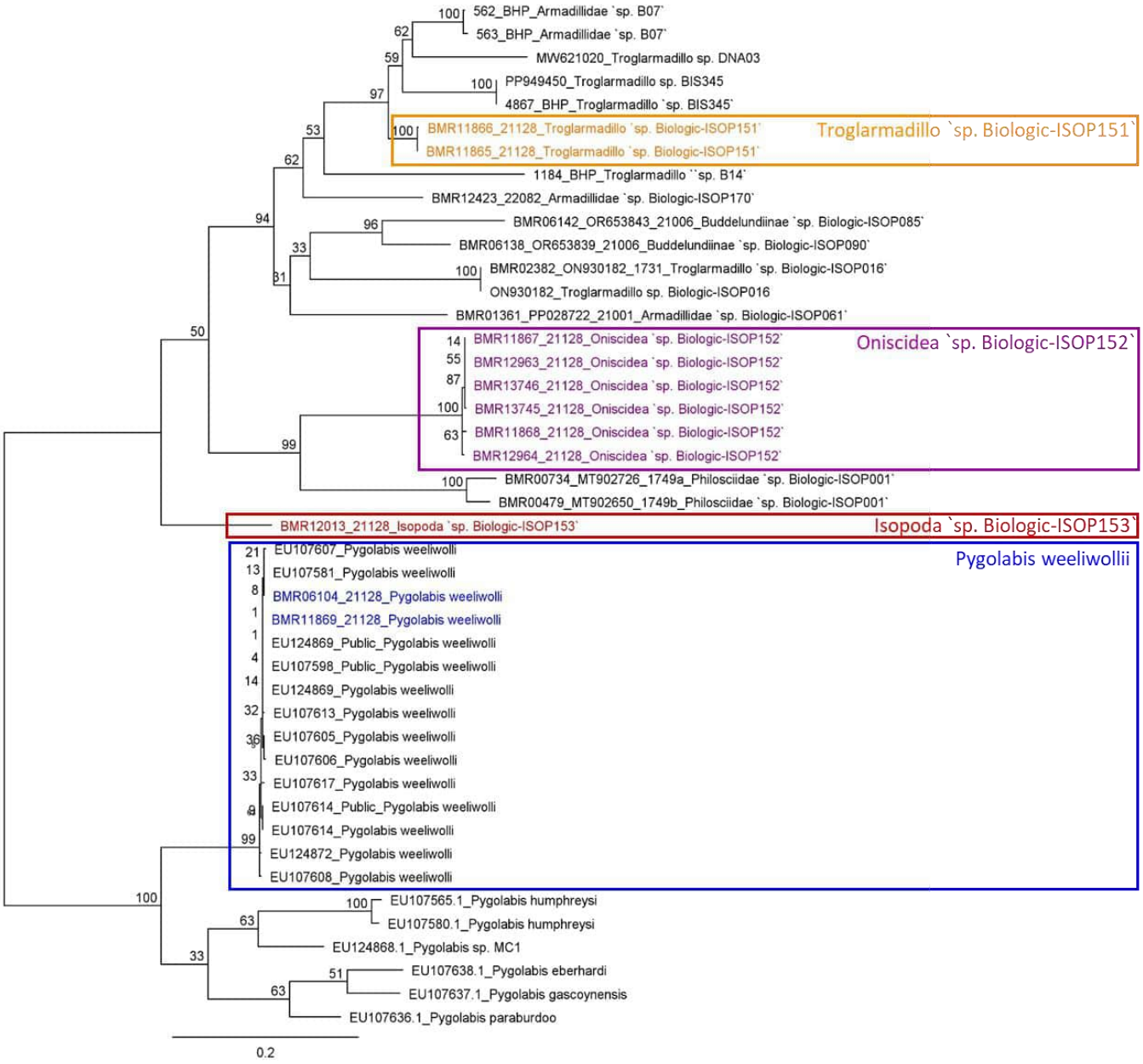

Figure 3.9. Phylogeny for the Isopoda dataset, with bootstrap values

Table 3.10: Pairwise distances (%) for the Isopoda dataset

COI Pairwise Distances (%)	562	563	BMR11865	BMR11866	4867	PP949450	MW621020	BMR12423	1184	BMR01361	BMR06138	BMR06142	BMR02382	ON930182	BMR12013	BMR00479	BMR00734	BMR11867	BMR12963	BMR13746	BMR13745	BMR12964	BMR11868	BMR06104	EU107581	BMR11869	EU107598	EU124869	EU124869	EU107607	EU107614	EU107605	EU107606	EU107613	EU107608	EU124872	EU107617
562_BHP_Armadillidae `sp. B07`		0.6	9.9	10.0	14.0	14.0	14.4	17.5	19.3	19.5	19.1	21.0	20.4	20.4	21.6	24.0	23.4	24.4	24.3	24.3	24.3	24.2	24.3	24.2	24.4	24.3	24.6	24.6	24.6	24.2	24.6	24.8	24.6	24.4	24.6	24.8	24.8
563_BHP_Armadillidae `sp. B07`	0.6		10.3	10.5	14.0	14.0	14.4	17.2	19.3	19.3	19.6	21.1	20.4	20.4	21.9	23.6	23.3	24.1	24.0	24.0	24.0	23.9	24.3	24.0	24.2	24.2	24.4	24.4	24.4	24.0	24.4	24.6	24.4	24.4	24.8	24.6	24.6
BMR11865_21128_Troglarmadillo `sp. Biologic-ISOP151`	9.9	10.3		0.2	12.3	12.3	14.3	17.0	18.6	19.0	18.5	21.1	18.7	18.7	19.5	22.9	22.6	23.7	23.6	23.6	23.6	23.4	23.7	25.1	25.3	25.2	25.5	25.5	25.5	25.5	25.1	25.3	25.1	25.3	25.1	25.3	25.3
BMR11866_21128_Troglarmadillo `sp. Biologic-ISOP151`	10.0	10.5	0.2		12.5	12.5	14.1	17.2	18.7	18.8	18.7	21.0	18.8	18.8	19.6	22.8	22.5	23.8	23.7	23.7	23.7	23.6	23.9	25.2	25.5	25.4	25.7	25.7	25.7	25.7	25.3	25.5	25.3	25.5	25.3	25.5	25.5
4867_BHP_Troglarmadillo `sp. BIS345`	14.0	14.0	12.3	12.5		0.0	16.1	18.5	20.4	21.3	19.8	21.4	21.4	21.4	21.4	22.5	23.1	23.4	23.3	23.3	23.3	23.1	23.4	23.3	23.5	23.4	23.7	23.7	23.7	23.7	23.3	23.9	23.7	23.5	23.5	23.5	23.1
PP949450_Troglarmadillo sp. BIS345	14.0	14.0	12.3	12.5	0.0		14.8	18.5	20.4	21.3	19.8	21.4	21.4	21.4	21.4	22.5	23.1	23.4	23.3	23.3	23.3	23.1	23.4	23.3	23.5	23.4	23.7	23.7	23.7	23.7	23.3	23.9	23.7	23.5	23.5	23.5	23.1
MW621020_Troglarmadillo sp. DNA03	14.4	14.4	14.3	14.1	16.1	14.8		19.0	21.5	21.9	21.9	20.8	20.1	20.1	22.3	22.2	22.5	25.5	25.4	25.4	25.4	25.4	25.5	26.0	25.0	26.1	25.1	25.1	25.1	25.1	24.8	25.3	25.1	25.0	25.1	25.0	25.1
BMR12423_22082_Armadillidae `sp. Biologic-ISOP170`	17.5	17.2	17.0	17.2	18.5	18.5	19.0		20.1	18.1	19.5	18.4	19.6	19.6	20.5	23.4	22.8	23.4	23.3	23.3	23.3	23.1	23.3	25.5	23.9	25.7	24.0	24.0	24.0	24.0	23.7	24.0	23.9	23.9	24.0	24.0	23.9
1184_BHP_Troglarmadillo ``sp. B14`	19.3	19.3	18.6	18.7	20.4	20.4	21.5	20.1		22.0	21.1	22.8	20.9	20.9	23.1	25.0	24.5	24.3	24.2	24.2	24.2	24.0	24.0	28.2	26.8	28.2	26.8	26.8	26.8	26.6	26.6	26.8	26.8	26.6	26.2	26.6	26.6
BMR01361_PP028722_21_Armadillidae `sp. Biologic-ISOP061`	19.5	19.3	19.0	18.8	21.3	21.3	21.9	18.1	22.0		18.2	18.5	21.0	21.0	21.0	22.6	22.9	24.1	24.0	24.0	24.2	23.9	23.7	26.0	25.9	26.1	26.0	26.0	26.0	25.7	26.0	26.2	26.0	26.0	26.2	26.4	26.0
BMR06138_OR653839_26_Buddelundiinae `sp. Biologic-ISOP090`	19.1	19.6	18.5	18.7	19.8	19.8	21.9	19.5	21.1	18.2		14.3	18.7	18.7	20.7	23.1	22.9	23.5	23.4	23.4	23.4	23.4	23.6	22.5	21.3	22.3	21.1	21.1	21.1	21.1	21.1	21.3	21.5	21.1	20.8	20.9	20.8
BMR06142_OR653843_26_Buddelundiinae `sp. Biologic-ISOP085`	21.0	21.1	21.1	21.0	21.4	21.4	20.8	18.4	22.8	18.5	14.3		21.1	21.1	22.3	23.9	25.1	26.9	26.7	26.7	26.7	27.1	27.2	23.1	22.0	23.3	22.2	22.2	22.2	21.9	22.2	22.2	22.0	22.2	22.2	22.6	22.2
BMR02382_ON930182_1731_Troglarmadillo `sp. Biologic-ISOP016`	20.4	20.4	18.7	18.8	21.4	21.4	20.1	19.6	20.9	21.0	18.7	21.1		0.0	22.3	25.1	24.9	24.7	24.6	24.6	24.8	24.3	24.8	23.7	23.1	23.7	23.1	23.1	23.1	23.0	23.0	23.3	23.3	23.1	23.0	23.1	23.1
ON930182_Troglarmadillo sp. Biologic-ISOP016	20.4	20.4	18.7	18.8	21.4	21.4	20.1	19.6	20.9	21.0	18.7	21.1	0.0		22.3	25.1	24.9	24.7	24.6	24.6	24.8	24.3	24.8	23.7	23.1	23.7	23.1	23.1	23.1	23.0	23.0	23.3	23.3	23.1	23.0	23.1	23.1
BMR12013_21128_Isopoda `sp. Biologic-ISOP153`	21.6	21.9	19.5	19.6	21.4	21.4	22.3	20.5	23.1	21.0	20.7	22.3	22.3	22.3		22.6	21.3	23.2	23.1	23.1	22.9	22.8	22.8	23.4	23.1	23.6	23.3	23.3	23.3	23.1	23.0	23.3	23.1	23.3	23.0	23.1	23.1
BMR00479_MT902650_1749b_Philosciidae `sp. Biologic-ISOP001`	24.0	23.6	22.9	22.8	22.5	22.5	22.2	23.4	25.0	22.6	23.1	23.9	25.1	25.1	22.6		5.8	20.0	19.9	19.9	19.9	20.1	20.5	25.5	25.9	25.7	26.0	26.0	26.0	26.0	26.0	26.2	26.0	26.0	26.4	26.2	26.2
BMR00734_MT902726_1749a_Philosciidae `sp. Biologic-ISOP001`	23.4	23.3	22.6	22.5	23.1	23.1	22.5	22.8	24.5	22.9	22.9	25.1	24.9	24.9	21.3	5.8		21.1	21.0	21.0	21.0	21.1	21.6	26.7	26.6	26.9	26.8	26.8	26.8	26.8	26.8	27.0	26.8	26.8	27.1	27.0	27.0
BMR11867_21128_Oniscidea `sp. Biologic-ISOP152`	24.4	24.1	23.7	23.8	23.4	23.4	25.5	23.4	24.3	24.1	23.5	26.9	24.7	24.7	23.2	20.0	21.1		0.1	0.1	0.3	0.6	0.9	26.6	26.2	26.7	26.4	26.4	26.4	26.0	26.0	26.5	26.4	26.2	26.4	26.4	26.2
BMR12963_21128_Oniscidea `sp. Biologic-ISOP152`	24.3	24.0	23.6	23.7	23.3	23.3	25.4	23.3	24.2	24.0	23.4	26.7	24.6	24.6	23.1	19.9	21.0	0.1		0.0	0.2	0.5	0.8	26.4	26.0	26.6	26.2	26.2	26.2	25.9	25.9	26.4	26.2	26.0	26.2	26.2	26.0
BMR13746_21128_Oniscidea `sp. Biologic-ISOP152`	24.3	24.0	23.6	23.7	23.3	23.3	25.4	23.3	24.2	24.0	23.4	26.7	24.6	24.6	23.1	19.9	21.0	0.1	0.0		0.2	0.5	0.8	26.4	26.0	26.6	26.2	26.2	26.2	25.9	25.9	26.4	26.2	26.0	26.2	26.2	26.0
BMR13745_21128_Oniscidea `sp. Biologic-ISOP152`	24.3	24.0	23.6	23.7	23.3	23.3	25.4	23.3	24.2	24.2	23.4	26.7	24.8	24.8	22.9	19.9	21.0	0.3	0.2	0.2		0.6	0.9	26.4	26.0	26.6	26.2	26.2	26.2	25.9	25.9	26.4	26.2	26.0	26.2	26.2	26.0
BMR12964_21128_Oniscidea `sp. Biologic-ISOP152`	24.2	23.9	23.4	23.6	23.1	23.1	25.4	23.1	24.0	23.9	23.4	27.1	24.3	24.3	22.8	20.1	21.1	0.6	0.5	0.5	0.6		0.6	26.7	26.4	26.9	26.6	26.6	26.6	26.2	26.2	26.8	26.6	26.4	26.6	26.6	26.4
BMR11868_21128_Oniscidea `sp. Biologic-ISOP152`	24.3	24.3	23.7	23.9	23.4	23.4	25.5	23.3	24.0	23.7	23.6	27.2	24.8	24.8	22.8	20.5	21.6	0.9	0.8	0.8	0.9	0.6		26.9	26.6	27.1	26.8	26.8	26.8	26.4	26.4	27.0	26.8	26.6	26.8	26.8	26.6
BMR06104_21128_Pygolabis weeliwolli	24.2	24.0	25.1	25.2	23.3	23.3	26.0	25.5	28.2	26.0	22.5	23.1	23.7	23.7	23.4	25.5	26.7	26.6	26.4	26.4	26.4	26.7	26.9		0.0	0.2	0.2	0.2	0.2	0.2	0.2	0.4	0.2	0.4	0.7	0.7	0.7
EU107581_Pygolabis weeliwolli	24.4	24.2	25.3	25.5	23.5	23.5	25.0	23.9	26.8	25.9	21.3	22.0	23.1	23.1	23.1	25.9	26.6	26.2	26.0	26.0	26.0	26.4	26.6	0.0		0.2	0.2	0.2	0.2	0.2	0.2	0.4	0.2	0.4	0.7	0.7	0.7
BMR11869_21128_Pygolabis weeliwolli	24.3	24.2	25.2	25.4	23.4	23.4	26.1	25.7	28.2	26.1	22.3	23.3	23.7	23.7	23.6	25.7	26.9	26.7	26.6	26.6	26.6	26.9	27.1	0.2	0.2		0.0	0.0	0.0	0.4	0.4	0.2	0.4	0.2	0.5	0.5	0.5
EU107598_Public_Pygolabis weeliwolli	24.6	24.4	25.5	25.7	23.7	23.7	25.1	24.0	26.8	26.0	21.1	22.2	23.1	23.1	23.3	26.0	26.8	26.4	26.2	26.2	26.2	26.6	26.8	0.2	0.2	0.0		0.0	0.0	0.4	0.4	0.2	0.4	0.2	0.5	0.5	0.5
EU124869_Public_Pygolabis weeliwolli	24.6	24.4	25.5	25.7	23.7	23.7	25.1	24.0	26.8	26.0	21.1	22.2	23.1	23.1	23.3	26.0	26.8	26.4	26.2	26.2	26.2	26.6	26.8	0.2	0.2	0.0	0.0		0.0	0.4	0.4	0.2	0.4	0.2	0.5	0.5	0.5
EU124869_Pygolabis weeliwolli	24.6	24.4	25.5	25.7	23.7	23.7	25.1	24.0	26.8	26.0	21.1	22.2	23.1	23.1	23.3	26.0	26.8	26.4	26.2	26.2	26.2	26.6	26.8	0.2	0.2	0.0	0.0	0.0		0.4	0.4	0.2	0.4	0.2	0.5	0.5	0.5
EU107607_Pygolabis weeliwolli	24.2	24.0	25.5	25.7	23.7	23.7	25.1	24.0	26.6	25.7	21.1	21.9	23.0	23.0	23.1	26.0	26.8	26.0	25.9	25.9	25.9	26.2	26.4	0.2	0.2	0.4	0.4	0.4	0.4		0.4	0.5	0.4	0.5	0.9	0.9	0.9
EU107614_Pygolabis weeliwolli	24.6	24.4	25.1	25.3	23.3	23.3	24.8	23.7	26.6	26.0	21.1	22.2	23.0	23.0	23.0	26.0	26.8	26.0	25.9	25.9	25.9	26.2	26.4	0.2	0.2	0.4	0.4	0.4	0.4	0.4		0.5	0.4	0.5	0.5	0.5	0.5
EU107605_Pygolabis weeliwolli	24.8	24.6	25.3	25.5	23.9	23.9	25.3	24.0	26.8	26.2	21.3	22.2	23.3	23.3	23.3	26.2	27.0	26.5	26.4	26.4	26.4	26.8	27.0	0.4	0.4	0.2	0.2	0.2	0.2	0.5	0.5		0.2	0.4	0.7	0.7	0.7
EU107606_Pygolabis weeliwolli	24.6	24.4	25.1	25.3	23.7	23.7	25.1	23.9	26.8	26.0	21.5	22.0	23.3	23.3	23.1	26.0	26.8	26.4	26.2	26.2	26.2	26.6	26.8	0.2	0.2	0.4	0.4	0.4	0.4	0.4	0.4	0.2		0.5	0.9	0.9	0.9
EU107613_Pygolabis weeliwolli	24.4	24.4	25.3	25.5	23.5	23.5	25.0	23.9	26.6	26.0	21.1	22.2	23.1	23.1	23.3	26.0	26.8	26.2	26.0	26.0	26.0	26.4	26.6	0.4	0.4	0.2	0.2	0.2	0.2	0.5	0.5	0.4	0.5		0.7	0.7	0.7
EU107608_Pygolabis weeliwolli	24.6	24.8	25.1	25.3	23.5	23.5	25.1	24.0	26.2	26.2	20.8	22.2	23.0	23.0	23.0	26.4	27.1	26.4	26.2	26.2	26.2	26.6	26.8	0.7	0.7	0.5	0.5	0.5	0.5	0.9	0.5	0.7	0.9	0.7		0.4	0.7
EU124872_Pygolabis weeliwolli	24.8	24.6	25.3	25.5	23.5	23.5	25.0	24.0	26.6	26.4	20.9	22.6	23.1	23.1	23.1	26.2	27.0	26.4	26.2	26.2	26.2	26.6	26.8	0.7	0.7	0.5	0.5	0.5	0.5	0.9	0.5	0.7	0.9	0.7	0.4		0.7
EU107617_Pygolabis weeliwolli	24.8	24.6	25.3	25.5	23.1	23.1	25.1	23.9	26.6	26.0	20.8	22.2	23.1	23.1	23.1	26.2	27.0	26.2	26.0	26.0	26.0	26.4	26.6	0.7	0.7	0.5	0.5	0.5	0.5	0.9	0.5	0.7	0.9	0.7	0.7	0.7	

3.4 Diplura

Eight dipluran specimens formed five OTUs, two of which matched non-Study sequences (Figure 3.10). Japygidae `sp. B34`and Japygidae `sp. DPL005`each matched non-Study sequences, the former with intraspecific divergences less than 1.8% and the latter with intraspecific divergences less than 5% (Table 3.11). Japygidae `sp. B34`was more than 7.8% divergent from all other sequences in the analysis with a linear range of 33.9 km (Table 3.1, Table 3.11). Japygidae `sp. DPL005`was more than 13.9% divergent from the other analysis sequences and had a linear range of 25.2 km (Table 3.1, Table 3.11).

The three remaining OTUs, Projapygidae `sp. Biologic-DIPL108`, Parajapygidae `sp. Biologic-DIPL090`and Parajapygidae `sp. Biologic-DIPL092`, were all singletons that were more than 13.7% divergent from all other sequences in the analysis (Table 3.1, Table 3.11).

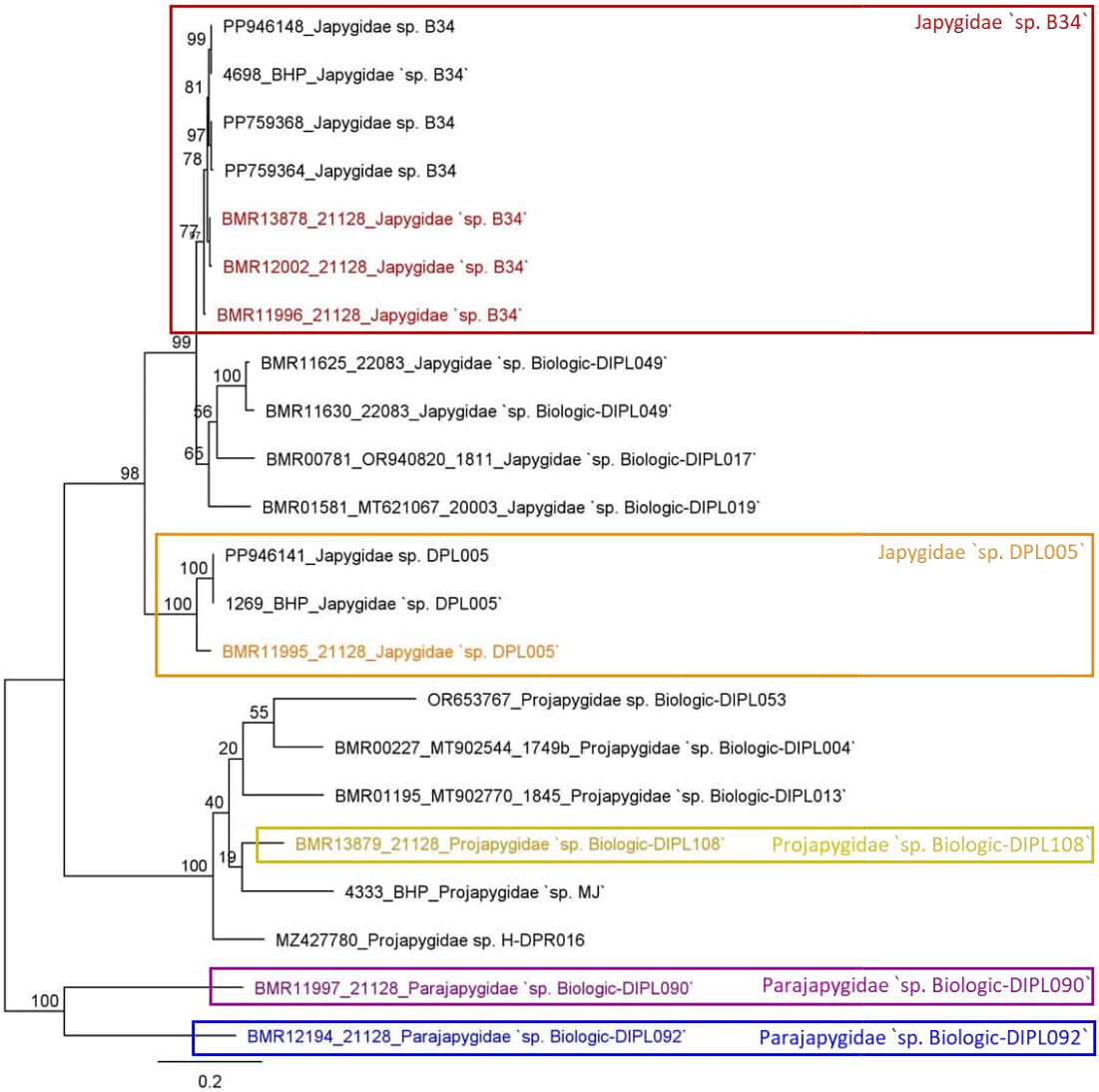

Figure 3.10. Phylogeny for the Diplura dataset, with bootstrap values

Table 3.11: Pairwise distances (%) for the Diplura dataset

COI Pairwise Distances (%)	PP946148	PP759368	PP759364	4698	BMR13878	BMR12002	BMR11996	BMR11630	BMR11625	BMR01581	BMR00781	PP946141	1269	BMR11995	OR653767	MZ427780	BMR13879	BMR00227	4333	BMR01195	BMR11997	BMR12194
PP946148_Japygidae sp. B34		0.9	1.2	0.0	1.2	1.5	1.5	9.4	9.0	10.2	9.1	14.4	14.5	14.1	23.8	22.7	23.2	24.7	25.8	22.6	25.5	25.8
PP759368_Japygidae sp. B34	0.9		0.3	1.0	1.2	1.5	1.5	9.3	8.8	9.4	9.1	14.6	15.0	14.1	24.0	22.1	23.3	24.8	25.4	22.5	25.0	25.5
PP759364_Japygidae sp. B34	1.2	0.3		1.2	1.4	1.7	1.7	9.4	9.0	9.6	9.3	14.9	15.2	14.3	24.2	22.1	23.1	24.6	25.5	22.3	25.1	25.5
4698_BHP_Japygidae `sp. B34`	0.0	1.0	1.2		1.3	1.6	1.6	9.4	8.9	10.1	9.2	14.7	14.7	14.2	24.1	23.4	23.4	24.9	26.0	22.8	25.5	25.6
BMR13878_21128_Japygidae `sp. B34`	1.2	1.2	1.4	1.3		0.3	1.2	8.7	8.2	9.7	8.8	14.9	14.9	14.1	24.0	22.6	23.7	25.1	26.0	22.2	25.3	25.6
BMR12002_21128_Japygidae `sp. B34`	1.5	1.5	1.7	1.6	0.3		1.5	8.7	8.2	10.0	9.1	14.9	14.9	14.0	24.3	22.8	24.0	25.4	26.1	22.3	25.5	25.6
BMR11996_21128_Japygidae `sp. B34`	1.5	1.5	1.7	1.6	1.2	1.5		8.7	7.9	9.1	8.8	14.6	14.6	14.3	23.7	23.4	23.4	24.6	26.0	22.5	25.1	26.0
BMR11630_22083_Japygidae `sp. Biologic-DIPL049`	9.4	9.3	9.4	9.4	8.7	8.7	8.7		1.8	10.3	9.7	16.7	16.7	16.1	24.5	24.2	25.4	25.4	26.7	24.2	25.0	26.2
BMR11625_22083_Japygidae `sp. Biologic-DIPL049`	9.0	8.8	9.0	8.9	8.2	8.2	7.9	1.8		9.6	9.4	16.7	16.7	16.1	24.5	24.5	25.8	25.5	27.4	24.6	25.1	26.0
BMR01581_MT621067_20003_Japygidae `sp. Biologic-DIPL019`	10.2	9.4	9.6	10.1	9.7	10.0	9.1	10.3	9.6		9.7	15.0	15.0	14.7	24.3	23.4	23.7	25.7	25.2	24.0	26.1	24.9
BMR00781_OR940820_1811_Japygidae `sp. Biologic-DIPL017`	9.1	9.1	9.3	9.2	8.8	9.1	8.8	9.7	9.4	9.7		16.1	16.1	15.4	22.6	24.9	23.9	26.3	26.6	23.1	25.1	25.8
PP946141_Japygidae sp. DPL005	14.4	14.6	14.9	14.7	14.9	14.9	14.6	16.7	16.7	15.0	16.1		0.0	4.9	24.5	21.8	23.6	23.4	25.4	23.9	27.5	26.2
1269_BHP_Japygidae `sp. DPL005`	14.5	15.0	15.2	14.7	14.9	14.9	14.6	16.7	16.7	15.0	16.1	0.0		4.9	24.5	22.4	23.6	23.4	25.4	23.9	27.5	26.3
BMR11995_21128_Japygidae `sp. DPL005`	14.1	14.1	14.3	14.2	14.1	14.0	14.3	16.1	16.1	14.7	15.4	4.9	4.9		24.2	22.6	23.6	25.5	24.6	22.3	27.1	25.3
OR653767_Projapygidae sp. Biologic-DIPL053	23.8	24.0	24.2	24.1	24.0	24.3	23.7	24.5	24.5	24.3	22.6	24.5	24.5	24.2		19.9	18.1	17.8	19.5	18.2	27.2	27.3
MZ427780_Projapygidae sp. H-DPR016	22.7	22.1	22.1	23.4	22.6	22.8	23.4	24.2	24.5	23.4	24.9	21.8	22.4	22.6	19.9		13.5	15.4	16.0	15.5	26.6	27.1
BMR13879_21128_Projapygidae `sp. Biologic-DIPL108`	23.2	23.3	23.1	23.4	23.7	24.0	23.4	25.4	25.8	23.7	23.9	23.6	23.6	23.6	18.1	13.5		13.8	15.0	15.5	28.1	27.3
BMR00227_MT902544_1749b_Projapygidae `sp. Biologic-DIPL004`	24.7	24.8	24.6	24.9	25.1	25.4	24.6	25.4	25.5	25.7	26.3	23.4	23.4	25.5	17.8	15.4	13.8		16.7	16.1	28.4	27.1
4333_BHP_Projapygidae `sp. MJ`	25.8	25.4	25.5	26.0	26.0	26.1	26.0	26.7	27.4	25.2	26.6	25.4	25.4	24.6	19.5	16.0	15.0	16.7		17.0	26.8	27.5
BMR01195_MT902770_1845_Projapygidae `sp. Biologic-DIPL013`	22.6	22.5	22.3	22.8	22.2	22.3	22.5	24.2	24.6	24.0	23.1	23.9	23.9	22.3	18.2	15.5	15.5	16.1	17.0		26.5	28.0
BMR11997_21128_Parajapygidae `sp. Biologic-DIPL090`	25.5	25.0	25.1	25.5	25.3	25.5	25.1	25.0	25.1	26.1	25.1	27.5	27.5	27.1	27.2	26.6	28.1	28.4	26.8	26.5		24.2
BMR12194_21128_Parajapygidae `sp. Biologic-DIPL092`	25.8	25.5	25.5	25.6	25.6	25.6	26.0	26.2	26.0	24.9	25.8	26.2	26.3	25.3	27.3	27.1	27.3	27.1	27.5	28.0	24.2	

3.5 Insecta

3.5.1 Blattodea

Seven cockroach specimens were sequenced successfully and identified as the described species *Nocticola cockingi* (Figure 3.11.1, Figure 3.12.2). These results are depicted within two phylogenies and the corresponding two pairwise distance tables because the Study specimens were sequenced using two sets of primers, LCO1490 and HCO2198 (Folmer *et al.*, 1994) and L2020 and H2619 (Yamauchi *et al.*, 2004). As these primers target separate gene regions, a phylogeny for each had to be created in order to display the data accurately (Figure 3.11.1, Figure 3.12.2, Table 3.12.1, Table 3.13.2).

Intraspecific divergences for *Nocticola cockingi* ranged from 0.4% to 12.3%, which is comparable to the upper threshold from the original description by Trotter et al. (Trotter *et al.*) (Table 3.12.1, Table 3.13.2). *Nocticola cockingi* was more than 15.8% divergent from all other sequences in the analyses, and had a linear range of 77.3 km (Table 3.1,Table 3.12.1, Table 3.13.2).

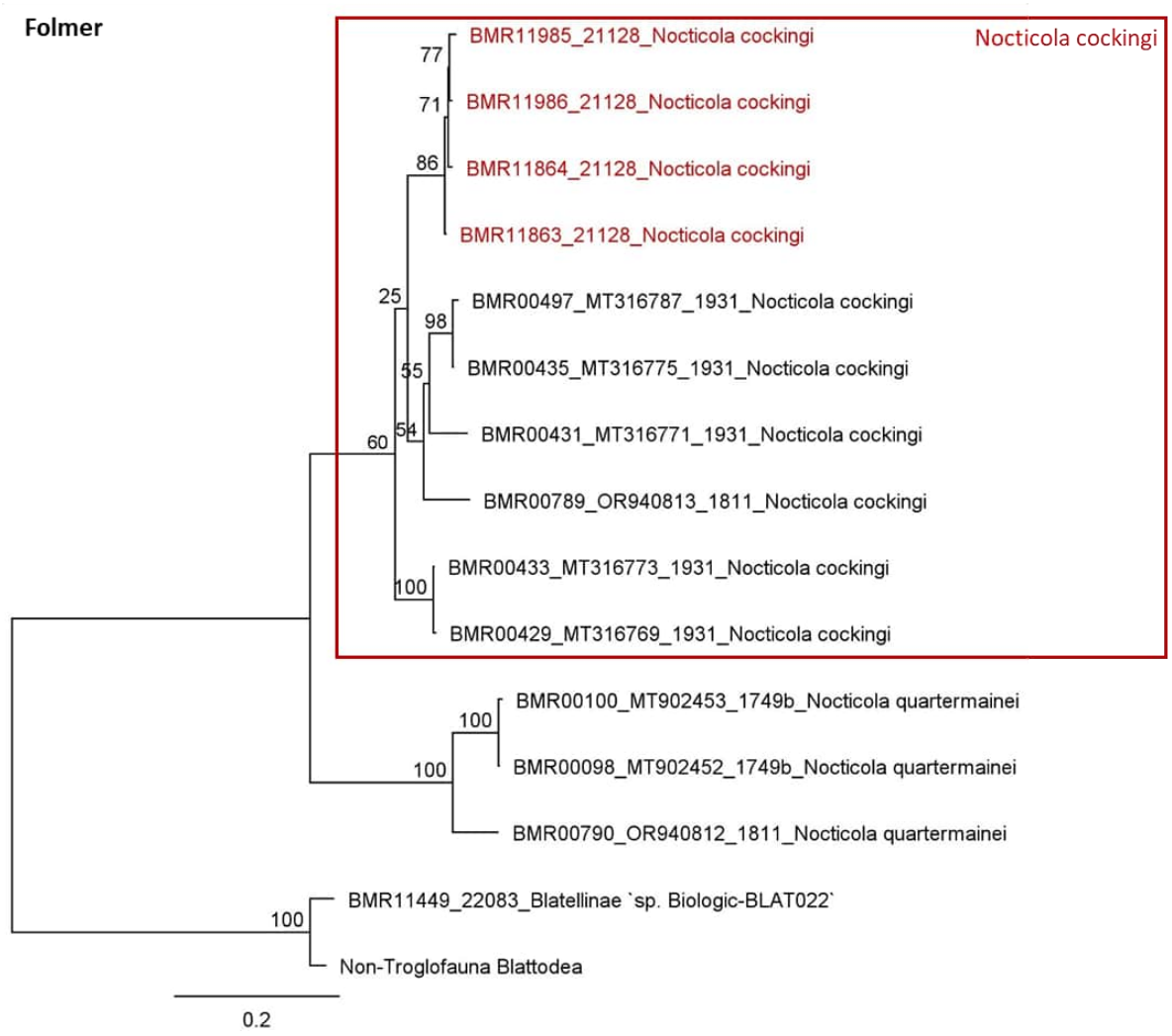

Figure 3.11.1 Phylogeny for the Blattodea dataset from Folmer *et al.* (1994) primers, with bootstrap values

Table 3.12.1: Pairwise distances (%) for the Blattodea (Folmer) dataset

COI Pairwise Distances (%)	BMR11449	Non-Troglofauna Blattodea	BMR11863	BMR11864	BMR11986	BMR11985	BMR00431	BMR00435	BMR00497	BMR00789	BMR00429	BMR00433	BMR00098	BMR00100	BMR00790
BMR11449_22083_Blatellinae `sp. Biologic-BLAT022`		4.3	23.6	23.6	23.9	23.8	23.6	23.8	24.0	23.9	23.9	24.3	25.8	25.8	23.7
Non-Troglofauna Blattodea	4.3		23.4	23.4	23.6	23.6	22.6	22.3	23.3	24.0	23.9	24.3	25.1	25.5	24.8
BMR11863_21128_Nocticola cockingi	23.6	23.4		1.1	1.1	1.5	8.8	8.5	8.8	9.3	8.5	8.5	17.6	17.6	17.0
BMR11864_21128_Nocticola cockingi	23.6	23.4	1.1		0.9	1.4	9.2	9.1	9.1	9.6	9.1	9.1	17.6	17.6	17.0
BMR11986_21128_Nocticola cockingi	23.9	23.6	1.1	0.9		1.1	9.3	9.1	9.3	9.6	9.0	9.0	18.0	18.0	17.4
BMR11985_21128_Nocticola cockingi	23.8	23.6	1.5	1.4	1.1		9.5	9.1	8.8	9.6	9.4	9.4	18.1	18.1	17.3
BMR00431_MT316771_1931_Nocticola cockingi	23.6	22.6	8.8	9.2	9.3	9.5		6.6	6.9	8.7	10.3	9.9	18.3	18.3	18.5
BMR00435_MT316775_1931_Nocticola cockingi	23.8	22.3	8.5	9.1	9.1	9.1	6.6		0.7	7.3	8.1	8.5	18.1	17.8	18.9
BMR00497_MT316787_1931_Nocticola cockingi	24.0	23.3	8.8	9.1	9.3	8.8	6.9	0.7		7.9	8.5	8.8	18.5	18.2	18.1
BMR00789_OR940813_1811_Nocticola cockingi	23.9	24.0	9.3	9.6	9.6	9.6	8.7	7.3	7.9		10.8	10.7	16.6	16.9	17.9
BMR00429_MT316769_1931_Nocticola cockingi	23.9	23.9	8.5	9.1	9.0	9.4	10.3	8.1	8.5	10.8		0.5	18.4	17.8	17.9
BMR00433_MT316773_1931_Nocticola cockingi	24.3	24.3	8.5	9.1	9.0	9.4	9.9	8.5	8.8	10.7	0.5		18.3	18.0	17.7
BMR00098_MT902452_1749b_Nocticola quartermainei	25.8	25.1	17.6	17.6	18.0	18.1	18.3	18.1	18.5	16.6	18.4	18.3		0.6	8.5
BMR00100_MT902453_1749b_Nocticola quartermainei	25.8	25.5	17.6	17.6	18.0	18.1	18.3	17.8	18.2	16.9	17.8	18.0	0.6		8.8
BMR00790_OR940812_1811_Nocticola quartermainei	23.7	24.8	17.0	17.0	17.4	17.3	18.5	18.9	18.1	17.9	17.9	17.7	8.5	8.8	

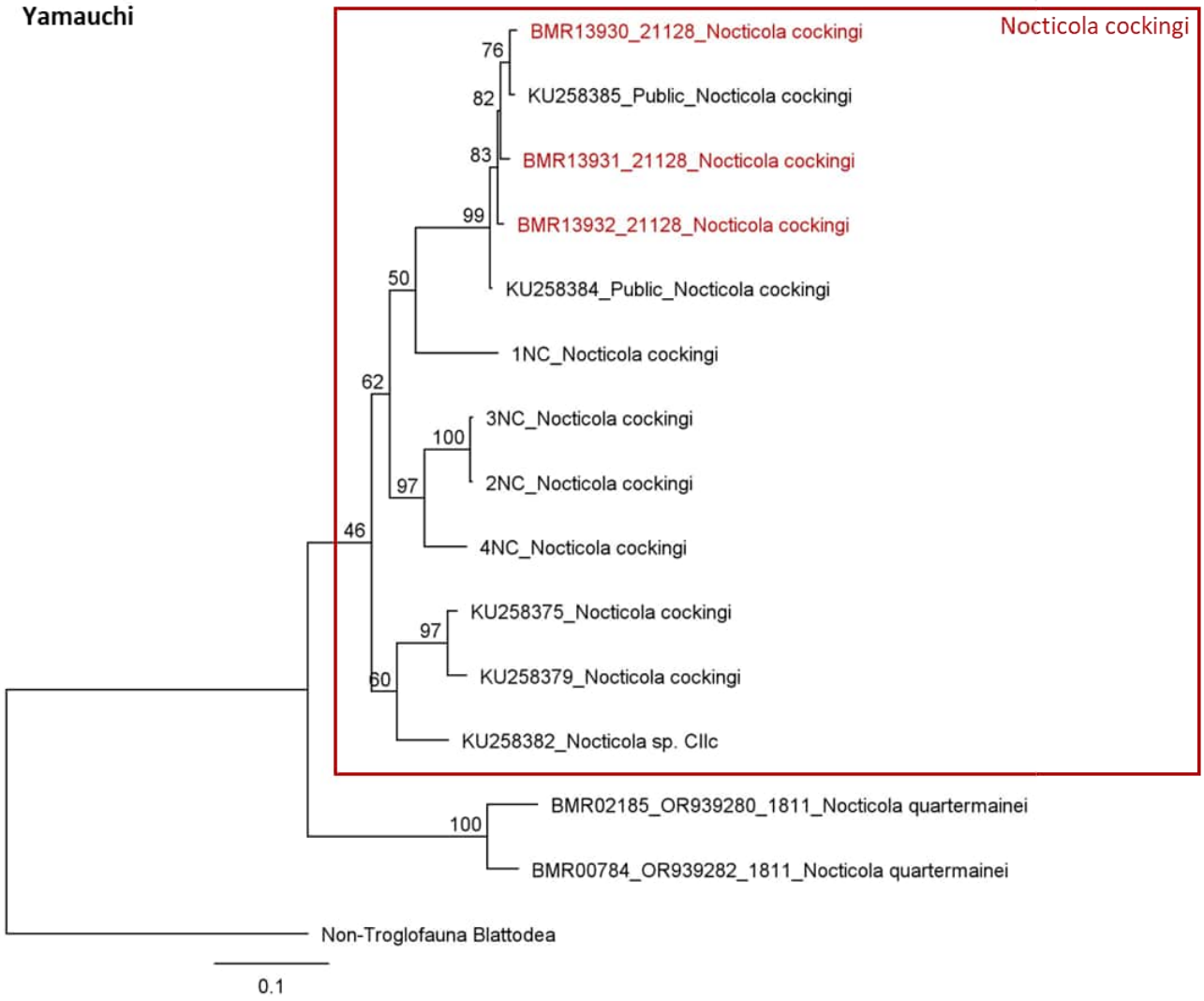

Figure 3.12.2 Phylogeny for the Blattodea dataset from Yamauchi *et al.* (2004) primers, with bootstrap values

Table 3.13.2: Pairwise distances (%) for the Blattodea (Yamauchi) dataset

COI Pairwise Distances (%)	KU258375	KU258379	KU258382	KU258384	BMR13932	BMR13931	KU258385	BMR13930	2NC	3NC	4NC	1NC	BMR02185	BMR00784	Non-Troglofauna Blattodea
KU258375_Nocticola cockingi		2.4	7.8	11.5	12.2	12.0	11.7	12.2	11.5	11.5	10.2	13.9	16.6	16.7	22.1
KU258379_Nocticola cockingi	2.4		8.4	11.0	11.7	12.0	10.9	11.5	11.5	11.5	10.5	13.5	16.9	16.7	21.7
KU258382_Nocticola sp. CIIc	7.8	8.4		11.0	11.7	11.7	10.9	11.4	10.7	10.7	11.5	13.2	16.2	15.9	23.4
KU258384_Public_Nocticola cockingi	11.5	11.0	11.0		1.3	1.8	2.1	2.5	12.2	12.2	11.7	12.1	17.7	17.0	22.7
BMR13932_21128_Nocticola cockingi	12.2	11.7	11.7	1.3		1.5	1.8	2.2	12.5	12.5	11.9	13.0	18.4	17.7	23.2
BMR13931_21128_Nocticola cockingi	12.0	12.0	11.7	1.8	1.5		2.0	1.7	13.0	13.0	12.2	13.2	18.2	17.6	23.1
KU258385_Public_Nocticola cockingi	11.7	10.9	10.9	2.1	1.8	2.0		1.0	12.4	12.4	12.0	13.5	18.0	17.4	22.9
BMR13930_21128_Nocticola cockingi	12.2	11.5	11.4	2.5	2.2	1.7	1.0		12.7	12.7	12.5	13.5	18.2	17.6	23.1
2NC_Nocticola cockingi	11.5	11.5	10.7	12.2	12.5	13.0	12.4	12.7		0.3	7.0	12.6	18.2	16.6	24.2
3NC_Nocticola cockingi	11.5	11.5	10.7	12.2	12.5	13.0	12.4	12.7	0.3		7.0	12.6	18.2	16.6	24.2
4NC_Nocticola cockingi	10.2	10.5	11.5	11.7	11.9	12.2	12.0	12.5	7.0	7.0		12.6	17.1	16.9	24.1
1NC_Nocticola cockingi	13.9	13.5	13.2	12.1	13.0	13.2	13.5	13.5	12.6	12.6	12.6		19.7	19.1	24.9
BMR02185_OR939280_1811_Nocticola quartermainei	16.6	16.9	16.2	17.7	18.4	18.2	18.0	18.2	18.2	18.2	17.1	19.7		6.1	24.1
BMR00784_OR939282_1811_Nocticola quartermainei	16.7	16.7	15.9	17.0	17.7	17.6	17.4	17.6	16.6	16.6	16.9	19.1	6.1		23.9
Non-Troglofauna Blattodea	22.1	21.7	23.4	22.7	23.2	23.1	22.9	23.1	24.2	24.2	24.1	24.9	24.1	23.9	

3.5.2 Coleoptera

Eleven Coleoptera specimens were resolved into six OTUs from four families, all matching non-Study sequences (Figure 3.13). The Curculionidae OTUs, *Cryptorhynchinae* `sp. B10` and Curculionidae `sp. B02`, had linear distances of 16.3 km and 39.9 km respectively (Table 3.1). *Cryptorhynchinae* `sp. B10` had intraspecific divergences less than 7.9% and was more than 17.1% divergent from all other sequences in the analysis (Table 3.14). Curculionidae `sp. B02` had intraspecific divergences less than 6.5% and was more than 10% divergent from all other sequences in the analysis (Table 3.14).

Pselaphinae `sp. Biologic-COLE008` and *Ptinella* `sp. Helix-CPT003` are both in the family Staphylinidae, with linear distances of 87 km and 456 km respectively (Table 3.1). Pselaphinae `sp. Biologic-COLE008` had intraspecific divergences less than 2.8% and was more than 10.1% divergent from the other sequences in the analysis (Table 3.14). *Ptinella* `sp. Helix-CPT003` had intraspecific divergences less than 3% and was more than 19.1% divergent from the other sequences in the analysis (Table 3.14).

Two specimens were resolved as described species *Typhlozuphium humicolum*, with intraspecific divergences less than 1%, divergences greater than 13.3% compared to other sequences in the analysis and a linear range of 29.0 km (Table 3.1, Table 3.14).

The final beetle specimen was resolved as Latridiidae `sp. Biologic-COLE052`. Though the study sequence matched this OTU, it also matched a sequence named informally as Carabidae `sp. Helix-C2` (Figure 3.13). From further analysis it was determined that the study sequence belonged to the family Latridiidae, and therefore the OTU Latridiidae `sp. Biologic-COLE052` was kept. The intraspecific divergences for this OTU were less than 4.9%, it was more than 19.4% divergent from all other sequences in the analysis and had a linear range of 381.5 km (Table 3.1, Table 3.14).

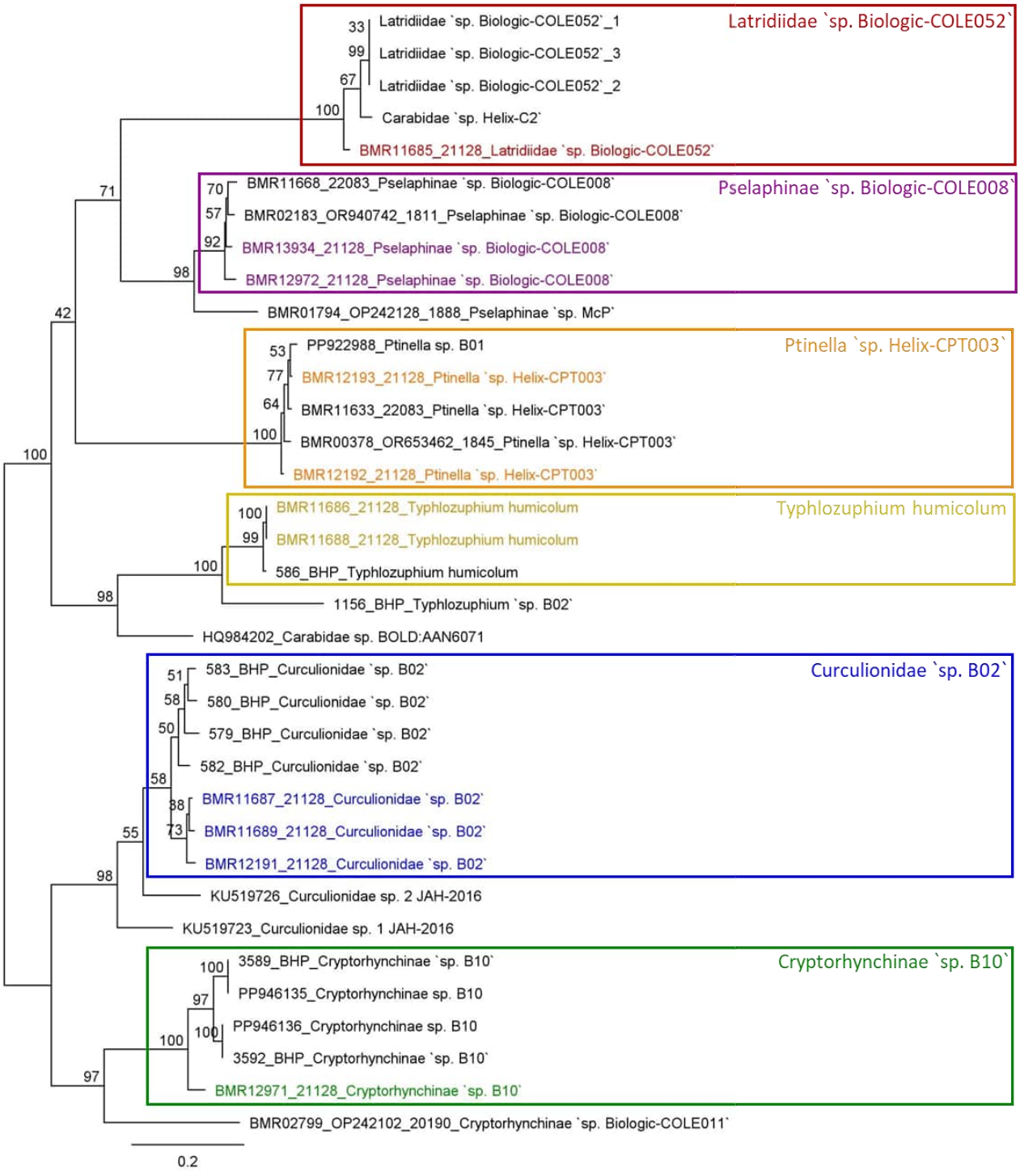

Figure 3.13. Phylogeny for the Coleoptera dataset, with bootstrap values

Table 3.14: Pairwise distances (%) for the Coleoptera dataset

COI Pairwise Distances (%)	579	580	583	582	BMR11687	BMR12191	BMR11689	KU519726	KU519723	BMR02799	BMR12971	3589	PP946135	3592	PP946136	586	BMR11686	BMR11688	1156	HQ984202	BMR01794	BMR02183	BMR13934	BMR11668	BMR12972	BMR00378	BMR11633	PP922988	BMR12192	BMR12193	BMR11685	Latridiidae `sp. Biologic-COLE052`_1	Latridiidae `sp. Biologic-COLE052`_2	Latridiidae `sp. Biologic-COLE052`_3	Carabidae `sp. Helix-C2`
579_BHP_Curculionidae `sp. B02`		4.0	3.2	4.6	6.1	6.2	6.2	11.6	12.2	19.3	19.3	21.4	21.2	21.6	21.3	23.6	23.6	23.6	25.2	20.5	22.5	20.7	20.5	20.0	20.5	24.0	23.4	23.3	23.9	26.2	25.6	24.4	24.4	24.4	24.2
580_BHP_Curculionidae `sp. B02`	4.0		2.6	4.1	6.2	6.4	6.2	12.2	11.7	19.5	19.8	22.3	22.1	22.1	21.7	23.4	24.0	24.0	24.8	20.8	22.0	21.1	20.4	20.8	20.5	24.5	23.9	23.7	24.4	25.8	26.2	24.5	24.5	24.5	24.5
583_BHP_Curculionidae `sp. B02`	3.2	2.6		4.3	5.6	5.8	6.2	11.4	11.4	18.7	18.7	21.6	21.2	21.8	21.3	22.6	22.6	22.6	24.3	19.9	21.6	19.9	19.5	19.6	19.6	23.9	23.3	23.1	23.7	25.8	26.2	24.7	24.7	24.7	24.4
582_BHP_Curculionidae `sp. B02`	4.6	4.1	4.3		5.2	5.8	5.7	10.6	12.8	19.3	19.6	22.9	22.7	22.1	21.7	24.3	24.9	24.9	24.8	20.8	21.7	20.7	19.9	20.3	20.7	23.4	23.1	22.9	23.4	24.9	26.4	25.1	25.1	25.1	25.3
BMR11687_21128_Curculionidae `sp. B02`	6.1	6.2	5.6	5.2		2.0	1.1	11.1	11.9	17.8	19.5	21.2	20.8	21.0	20.5	23.9	24.5	24.5	24.5	20.6	21.9	20.8	20.4	20.5	21.4	23.4	23.1	22.9	23.4	25.6	24.9	24.7	24.7	24.7	24.5
BMR12191_21128_Curculionidae `sp. B02`	6.2	6.4	5.8	5.8	2.0		2.5	11.2	12.4	18.0	19.6	22.6	22.1	22.3	21.8	24.3	24.6	24.6	25.4	20.8	22.4	21.2	20.4	20.5	21.2	24.3	23.8	23.3	23.7	26.2	26.0	25.0	25.0	25.0	25.4
BMR11689_21128_Curculionidae `sp. B02`	6.2	6.2	6.2	5.7	1.1	2.5		12.1	13.2	19.2	21.8	21.1	21.1	20.9	20.9	24.7	25.6	25.6	24.4	21.5	23.3	22.0	20.9	21.5	22.0	26.0	24.9	24.7	26.4	25.6	24.7	25.6	25.6	25.6	25.6
KU519726_Curculionidae sp. 2 JAH-2016	11.6	12.2	11.4	10.6	11.1	11.2	12.1		12.9	20.1	19.1	21.0	20.8	20.1	19.8	25.1	25.4	25.4	25.8	21.7	22.5	20.8	21.4	21.4	22.2	23.6	23.3	22.9	23.2	24.7	26.2	25.5	25.5	25.5	25.5
KU519723_Curculionidae sp. 1 JAH-2016	12.2	11.7	11.4	12.8	11.9	12.4	13.2	12.9		20.4	17.2	19.9	19.7	20.1	20.0	23.9	24.5	24.5	25.2	20.8	21.7	20.7	20.8	20.5	20.2	23.4	22.8	23.1	23.2	24.0	24.9	24.5	24.5	24.5	25.1
BMR02799_OP242102_20190_Cryptorhynchinae `sp. Biologic-COLE011`	19.3	19.5	18.7	19.3	17.8	18.0	19.2	20.1	20.4		17.3	20.7	20.8	20.1	20.0	23.7	23.7	23.7	25.2	22.9	20.5	21.6	21.7	22.5	22.6	23.6	23.1	23.9	23.2	25.6	27.3	25.8	25.8	25.8	25.5
BMR12971_21128_Cryptorhynchinae `sp. B10`	19.3	19.8	18.7	19.6	19.5	19.6	21.8	19.1	17.2	17.3		7.6	7.8	7.4	7.4	24.0	24.3	24.3	25.5	22.0	22.5	21.0	21.6	21.4	21.6	24.3	24.0	24.2	23.9	25.8	25.6	23.6	23.6	23.6	23.8
3589_BHP_Cryptorhynchinae `sp. B10`	21.4	22.3	21.6	22.9	21.2	22.6	21.1	21.0	19.9	20.7	7.6		0.0	3.9	3.9	26.9	27.1	27.1	27.1	25.1	23.6	23.6	23.6	22.7	23.6	26.9	27.1	26.9	27.6	26.9	26.0	25.3	25.3	25.3	26.2
PP946135_Cryptorhynchinae sp. B10	21.2	22.1	21.2	22.7	20.8	22.1	21.1	20.8	19.7	20.8	7.8	0.0		3.9	3.8	26.7	26.9	26.9	27.1	24.3	23.1	23.1	23.1	22.2	23.1	26.5	26.9	26.7	27.4	26.9	26.0	25.2	25.2	25.2	25.8
3592_BHP_Cryptorhynchinae `sp. B10`	21.6	22.1	21.8	22.1	21.0	22.3	20.9	20.1	20.1	20.1	7.4	3.9	3.9		0.0	27.7	27.9	27.9	27.9	25.7	24.5	24.5	24.5	24.0	24.0	26.6	26.9	26.6	26.9	26.7	27.1	26.4	26.4	26.4	26.6
PP946136_Cryptorhynchinae sp. B10	21.3	21.7	21.3	21.7	20.5	21.8	20.9	19.8	20.0	20.0	7.4	3.9	3.8	0.0		27.6	27.8	27.8	28.1	25.1	24.1	24.1	24.1	23.6	23.6	26.4	26.6	26.4	26.6	26.7	27.1	26.2	26.2	26.2	26.2
586_BHP_Typhlozuphium humicolum	23.6	23.4	22.6	24.3	23.9	24.3	24.7	25.1	23.9	23.7	24.0	26.9	26.7	27.7	27.6		0.9	0.9	13.4	15.6	19.6	21.3	21.1	21.2	21.9	21.9	22.3	22.3	22.1	23.6	22.2	22.9	22.9	22.9	22.6
BMR11686_21128_Typhlozuphium humicolum	23.6	24.0	22.6	24.9	24.5	24.6	25.6	25.4	24.5	23.7	24.3	27.1	26.9	27.9	27.8	0.9		0.0	13.7	15.6	20.2	21.6	21.7	21.5	22.3	22.0	22.5	22.5	22.5	24.0	21.8	23.3	23.3	23.3	22.9
BMR11688_21128_Typhlozuphium humicolum	23.6	24.0	22.6	24.9	24.5	24.6	25.6	25.4	24.5	23.7	24.3	27.1	26.9	27.9	27.8	0.9	0.0		13.7	15.6	20.2	21.6	21.7	21.5	22.3	22.0	22.5	22.5	22.5	24.0	21.8	23.3	23.3	23.3	22.9
1156_BHP_Typhlozuphium `sp. B02`	25.2	24.8	24.3	24.8	24.5	25.4	24.4	25.8	25.2	25.2	25.5	27.1	27.1	27.9	28.1	13.4	13.7	13.7		18.2	22.9	23.4	23.7	23.2	23.6	24.9	25.4	24.9	25.6	25.8	23.1	24.7	24.7	24.7	25.3
HQ984202_Carabidae sp. BOLD:AAN6071	20.5	20.8	19.9	20.8	20.6	20.8	21.5	21.7	20.8	22.9	22.0	25.1	24.3	25.7	25.1	15.6	15.6	15.6	18.2		19.7	19.4	19.7	19.1	20.6	21.1	21.5	20.9	21.6	23.3	23.1	22.0	22.0	22.0	22.0
BMR01794_OP242128_1888_Pselaphinae `sp. McP`	22.5	22.0	21.6	21.7	21.9	22.4	23.3	22.5	21.7	20.5	22.5	23.6	23.1	24.5	24.1	19.6	20.2	20.2	22.9	19.7		10.5	10.2	10.3	10.8	21.1	21.1	21.1	21.5	21.8	22.5	21.1	21.1	21.1	21.5
BMR02183_OR940742_1811_Pselaphinae `sp. Biologic-COLE008`	20.7	21.1	19.9	20.7	20.8	21.2	22.0	20.8	20.7	21.6	21.0	23.6	23.1	24.5	24.1	21.3	21.6	21.6	23.4	19.4	10.5		2.0	2.2	2.7	20.1	19.3	19.6	19.7	19.2	22.2	20.6	20.6	20.6	20.2
BMR13934_21128_Pselaphinae `sp. Biologic-COLE008`	20.5	20.4	19.5	19.9	20.4	20.4	20.9	21.4	20.8	21.7	21.6	23.6	23.1	24.5	24.1	21.1	21.7	21.7	23.7	19.7	10.2	2.0		2.4	2.6	20.5	19.9	20.1	20.2	19.8	21.8	20.2	20.2	20.2	19.5
BMR11668_22083_Pselaphinae `sp. Biologic-COLE008`	20.0	20.8	19.6	20.3	20.5	20.5	21.5	21.4	20.5	22.5	21.4	22.7	22.2	24.0	23.6	21.2	21.5	21.5	23.2	19.1	10.3	2.2	2.4		3.5	20.8	20.5	20.6	20.7	20.9	21.5	20.5	20.5	20.5	20.0
BMR12972_21128_Pselaphinae `sp. Biologic-COLE008`	20.5	20.5	19.6	20.7	21.4	21.2	22.0	22.2	20.2	22.6	21.6	23.6	23.1	24.0	23.6	21.9	22.3	22.3	23.6	20.6	10.8	2.7	2.6	3.5		21.3	20.7	20.8	21.2	20.7	21.6	20.2	20.2	20.2	20.4
BMR00378_OR653462_1845_Ptinella `sp. Helix-CPT003`	24.0	24.5	23.9	23.4	23.4	24.3	26.0	23.6	23.4	23.6	24.3	26.9	26.5	26.6	26.4	21.9	22.0	22.0	24.9	21.1	21.1	20.1	20.5	20.8	21.3		2.1	2.4	1.9	2.9	25.8	25.5	25.5	25.5	26.2
BMR11633_22083_Ptinella `sp. Helix-CPT003`	23.4	23.9	23.3	23.1	23.1	23.8	24.9	23.3	22.8	23.1	24.0	27.1	26.9	26.9	26.6	22.3	22.5	22.5	25.4	21.5	21.1	19.3	19.9	20.5	20.7	2.1		1.8	1.9	1.1	26.0	25.3	25.3	25.3	26.0
PP922988_Ptinella sp. B01	23.3	23.7	23.1	22.9	22.9	23.3	24.7	22.9	23.1	23.9	24.2	26.9	26.7	26.6	26.4	22.3	22.5	22.5	24.9	20.9	21.1	19.6	20.1	20.6	20.8	2.4	1.8		2.7	1.5	26.2	24.9	24.9	24.9	26.0
BMR12192_21128_Ptinella `sp. Helix-CPT003`	23.9	24.4	23.7	23.4	23.4	23.7	26.4	23.2	23.2	23.2	23.9	27.6	27.4	26.9	26.6	22.1	22.5	22.5	25.6	21.6	21.5	19.7	20.2	20.7	21.2	1.9	1.9	2.7		2.4	25.9	25.4	25.4	25.4	25.4
BMR12193_21128_Ptinella `sp. Helix-CPT003`	26.2	25.8	25.8	24.9	25.6	26.2	25.6	24.7	24.0	25.6	25.8	26.9	26.9	26.7	26.7	23.6	24.0	24.0	25.8	23.3	21.8	19.2	19.8	20.9	20.7	2.9	1.1	1.5	2.4		26.4	26.2	26.2	26.2	27.8
BMR11685_21128_Latridiidae `sp. Biologic-COLE052`	25.6	26.2	26.2	26.4	24.9	26.0	24.7	26.2	24.9	27.3	25.6	26.0	26.0	27.1	27.1	22.2	21.8	21.8	23.1	23.1	22.5	22.2	21.8	21.5	21.6	25.8	26.0	26.2	25.9	26.4		4.6	4.6	4.6	4.8
Latridiidae `sp. Biologic-COLE052`_1	24.4	24.5	24.7	25.1	24.7	25.0	25.6	25.5	24.5	25.8	23.6	25.3	25.2	26.4	26.2	22.9	23.3	23.3	24.7	22.0	21.1	20.6	20.2	20.5	20.2	25.5	25.3	24.9	25.4	26.2	4.6		0.0	0.0	2.9
Latridiidae `sp. Biologic-COLE052`_2	24.4	24.5	24.7	25.1	24.7	25.0	25.6	25.5	24.5	25.8	23.6	25.3	25.2	26.4	26.2	22.9	23.3	23.3	24.7	22.0	21.1	20.6	20.2	20.5	20.2	25.5	25.3	24.9	25.4	26.2	4.6	0.0		0.0	2.9
Latridiidae `sp. Biologic-COLE052`_3	24.4	24.5	24.7	25.1	24.7	25.0	25.6	25.5	24.5	25.8	23.6	25.3	25.2	26.4	26.2	22.9	23.3	23.3	24.7	22.0	21.1	20.6	20.2	20.5	20.2	25.5	25.3	24.9	25.4	26.2	4.6	0.0	0.0		2.9
Carabidae `sp. Helix-C2`	24.2	24.5	24.4	25.3	24.5	25.4	25.6	25.5	25.1	25.5	23.8	26.2	25.8	26.6	26.2	22.6	22.9	22.9	25.3	22.0	21.5	20.2	19.5	20.0	20.4	26.2	26.0	26.0	25.4	27.8	4.8	2.9	2.9	2.9	

3.5.3 Hemiptera

Five Hemiptera specimens were sequenced and identified as two OTUs, *Phaconeura* `sp. Biologic-HEMI003`and *Phaconeura* `sp. WAM-PHAC001` (Figure 3.14). *Phaconeura* `sp. WAM-PHAC001`had intraspecific divergences less than 1.1%, was more than 11.3% divergent from all other sequences in the analysis and had a linear range of 707.2 km (Table 3.1, Table 3.15). *Phaconeura* `sp. Biologic-HEMI003`had intraspecific divergences less than 9.6%, was more than 9.9% divergent from all other sequences in the analysis and had a linear range of 83.3 km (Table 3.1, Table 3.15). There is relatively high intraspecific variation within *Phaconeura* `sp. Biologic-HEMI003` sequences. This may result in the splitting of this OTU in future, but with the current information available we have kept the OTU as is.

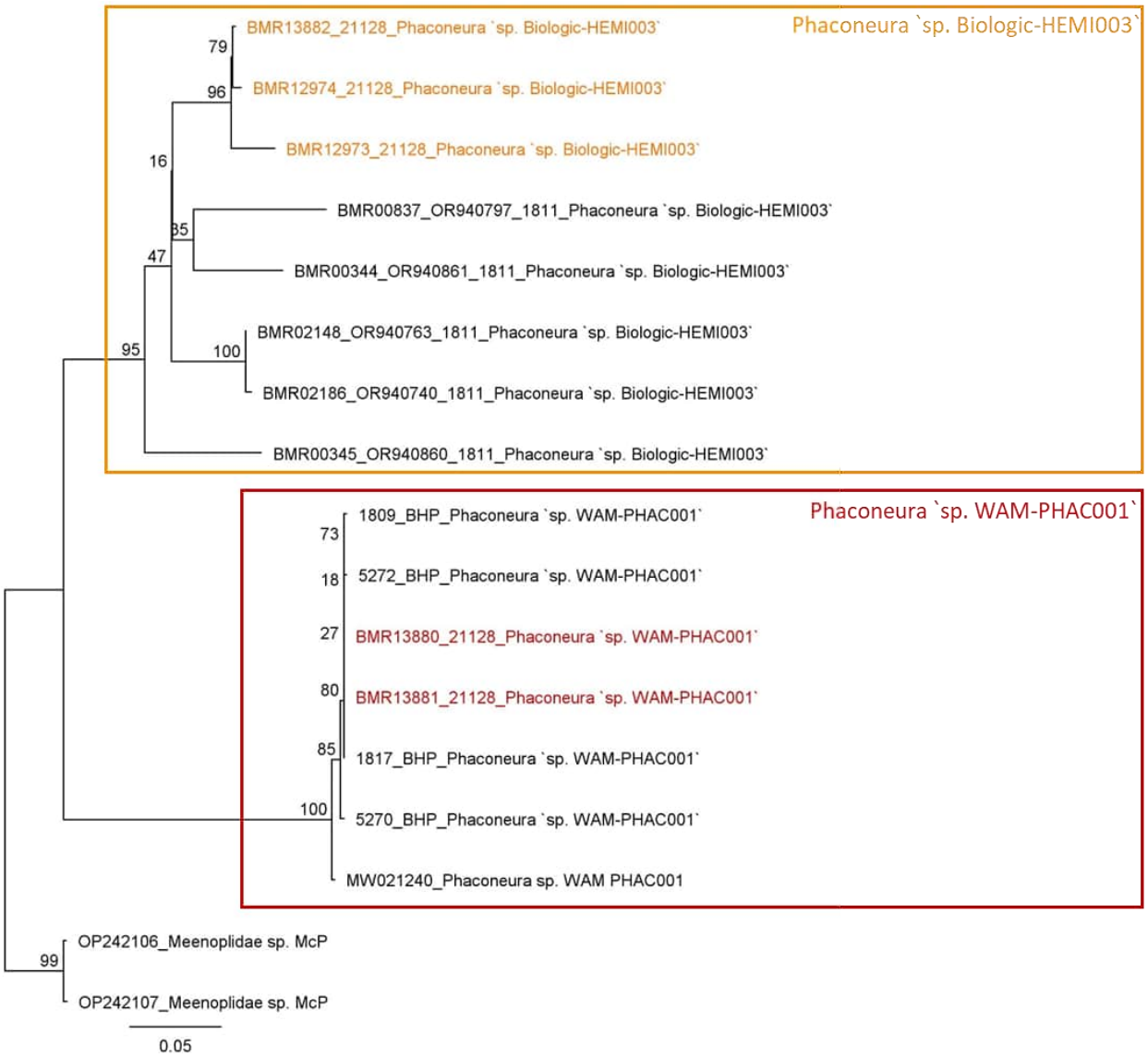

Figure 3.14. Phylogeny for the Hemiptera dataset, with bootstrap values

Table 3.15: Pairwise distances (%) for the Hemiptera dataset

COI Pairwise Distances (%)	1809	1817	BMR13880	BMR13881	5272	5270	MW021240	BMR00344	BMR02148	BMR02186	BMR12973	BMR12974	BMR13882	BMR00345	BMR00837	OP242106	OP242107
1809_BHP_Phaconeura `sp. WAM-PHAC001`		0.2	0.2	0.2	0.3	0.6	1.0	13.4	13.1	13.4	13.1	12.8	12.6	13.2	13.4	11.6	11.9
1817_BHP_Phaconeura `sp. WAM-PHAC001`	0.2		0.1	0.1	0.2	0.4	0.8	13.5	12.9	13.2	12.9	12.6	12.5	13.1	13.2	11.8	12.1
BMR13880_21128_Phaconeura `sp. WAM-PHAC001`	0.2	0.1		0.0	0.2	0.3	0.8	13.5	12.9	13.2	12.9	12.6	12.5	13.1	13.2	11.7	12.0
BMR13881_21128_Phaconeura `sp. WAM-PHAC001`	0.2	0.1	0.0		0.2	0.3	0.8	13.5	12.9	13.2	12.9	12.6	12.5	13.1	13.2	11.7	12.0
5272_BHP_Phaconeura `sp. WAM-PHAC001`	0.3	0.2	0.2	0.2		0.5	0.9	13.7	13.1	13.4	13.1	12.8	12.6	13.2	13.4	11.9	12.2
5270_BHP_Phaconeura `sp. WAM-PHAC001`	0.6	0.4	0.3	0.3	0.5		0.7	13.5	12.6	12.9	12.9	12.3	12.2	13.1	12.9	11.4	11.7
MW021240_Phaconeura sp. WAM PHAC001	1.0	0.8	0.8	0.8	0.9	0.7		13.5	12.6	12.9	12.6	12.3	12.2	12.8	12.9	11.4	11.7
BMR00344_OR940861_1811_Phaconeura `sp. Biologic-HEMI003`	13.4	13.5	13.5	13.5	13.7	13.5	13.5		7.0	7.3	7.9	6.7	7.0	8.7	7.9	11.1	10.8
BMR02148_OR940763_1811_Phaconeura `sp. Biologic-HEMI003`	13.1	12.9	12.9	12.9	13.1	12.6	12.6	7.0		0.3	6.4	5.6	5.6	8.2	8.1	10.0	10.0
BMR02186_OR940740_1811_Phaconeura `sp. Biologic-HEMI003`	13.4	13.2	13.2	13.2	13.4	12.9	12.9	7.3	0.3		6.7	5.9	5.9	8.5	8.2	10.2	10.2
BMR12973_21128_Phaconeura `sp. Biologic-HEMI003`	13.1	12.9	12.9	12.9	13.1	12.9	12.6	7.9	6.4	6.7		2.6	2.3	8.1	8.4	11.4	11.4
BMR12974_21128_Phaconeura `sp. Biologic-HEMI003`	12.8	12.6	12.6	12.6	12.8	12.3	12.3	6.7	5.6	5.9	2.6		0.6	7.6	7.9	10.8	10.5
BMR13882_21128_Phaconeura `sp. Biologic-HEMI003`	12.6	12.5	12.5	12.5	12.6	12.2	12.2	7.0	5.6	5.9	2.3	0.6		7.3	7.9	10.2	10.2
BMR00345_OR940860_1811_Phaconeura `sp. Biologic-HEMI003`	13.2	13.1	13.1	13.1	13.2	13.1	12.8	8.7	8.2	8.5	8.1	7.6	7.3		9.6	11.4	11.4
BMR00837_OR940797_1811_Phaconeura `sp. Biologic-HEMI003`	13.4	13.2	13.2	13.2	13.4	12.9	12.9	7.9	8.1	8.2	8.4	7.9	7.9	9.6		11.6	11.6
OP242106_Meenoplidae sp. McP	11.6	11.8	11.7	11.7	11.9	11.4	11.4	11.1	10.0	10.2	11.4	10.8	10.2	11.4	11.6		0.3
OP242107_Meenoplidae sp. McP	11.9	12.1	12.0	12.0	12.2	11.7	11.7	10.8	10.0	10.2	11.4	10.5	10.2	11.4	11.6	0.3	

3.5.4 Zygentoma

Seven Zygentoma specimens were sequenced and resolved as two OTUs, Atelurinae `sp. Biologic-ZYGE071`and *Trinemura* `sp. Biologic-ZYGE038` (Figure 3.15). Atelurinae `sp. Biologic-ZYGE071`did not match any non-Study sequences, had intraspecific divergences less than 2%, was more than 10.5% divergent from the other sequences in the analysis and had a linear range of 6 km (Table 3.1, Table 3.16).

Trinemura `sp. Biologic-ZYGE038`matched a non-Study sequence with intraspecific divergences less than 6.0% (Table 3.16). This OTU was more than 12% divergent from all other sequences in the analysis and had a linear range of 47.2 km (Table 3.1, Table 3.16).

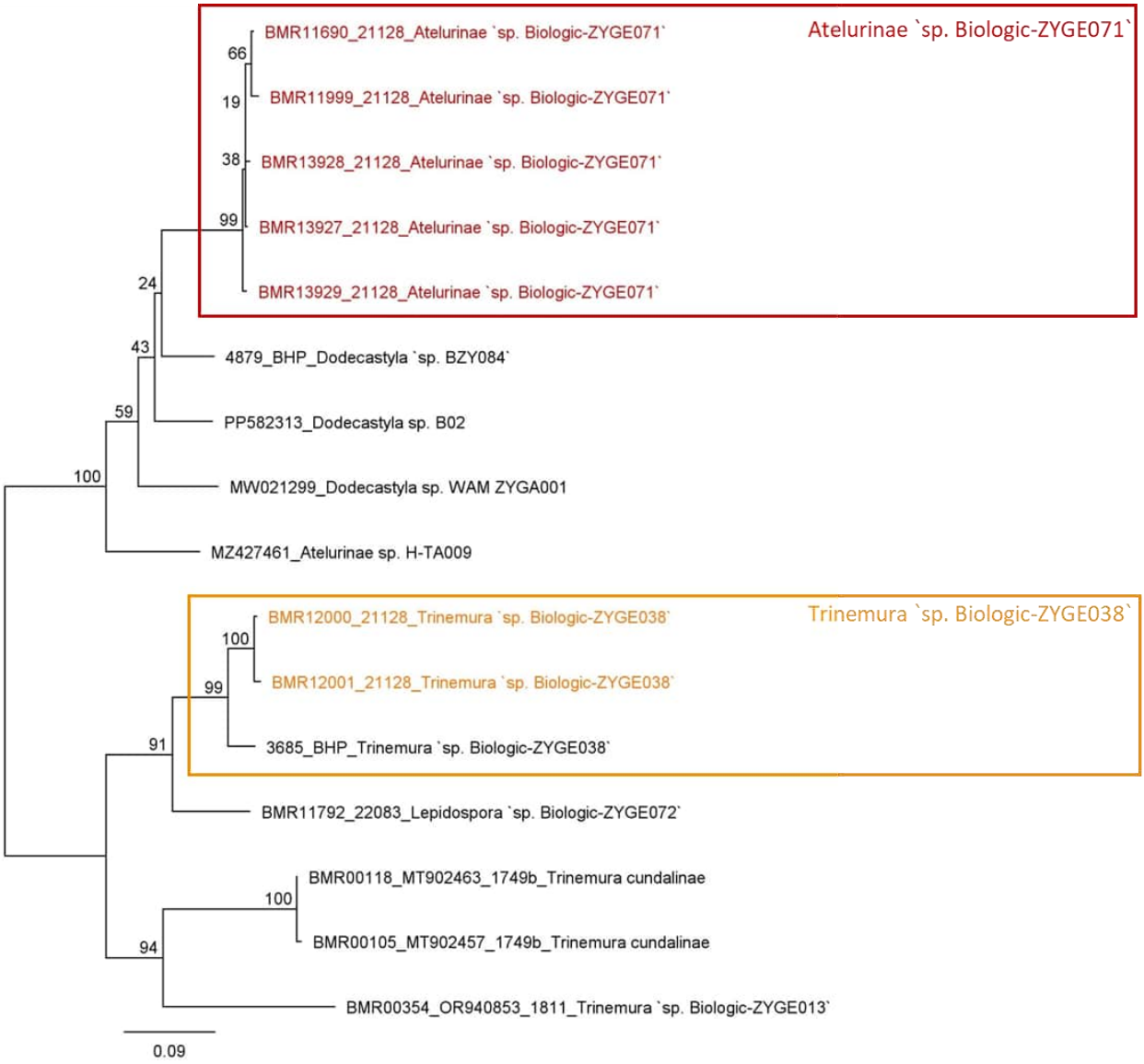

Figure 3.15. Phylogeny for the Zygentoma dataset, with bootstrap values

Table 3.16: Pairwise distances (%) for the Zygentoma dataset

COI Pairwise Distances (%)	BMR00105	BMR00118	BMR00354	BMR11792	3685	BMR12000	BMR12001	4879	PP582313	BMR11690	BMR11999	BMR13927	BMR13928	BMR13929	MW021299	MZ427461
BMR00105_MT902457_1749b_Trinemura cundalinae		0.5	17.8	17.4	18.3	17.3	17.2	22.0	23.4	23.3	24.4	23.3	23.3	23.6	20.8	21.9
BMR00118_MT902463_1749b_Trinemura cundalinae	0.5		17.3	17.6	18.5	17.2	17.0	22.5	23.9	23.8	24.9	23.8	23.8	24.0	21.1	22.4
BMR00354_OR940853_1811_Trinemura `sp. Biologic-ZYGE013`	17.8	17.3		18.7	18.5	18.4	19.0	24.0	24.7	23.8	24.0	23.8	24.0	24.4	23.4	26.1
BMR11792_22083_Lepidospora `sp. Biologic-ZYGE072`	17.4	17.6	18.7		13.1	12.1	12.4	23.5	20.4	22.8	22.4	22.8	23.2	23.0	20.7	20.8
3685_BHP_Trinemura `sp. Biologic-ZYGE038`	18.3	18.5	18.5	13.1		5.5	5.9	21.6	21.8	19.7	20.3	20.9	21.1	21.1	20.6	21.4
BMR12000_21128_Trinemura `sp. Biologic-ZYGE038`	17.3	17.2	18.4	12.1	5.5		0.9	22.9	21.7	22.0	22.8	21.6	22.2	21.8	20.5	22.4
BMR12001_21128_Trinemura `sp. Biologic-ZYGE038`	17.2	17.0	19.0	12.4	5.9	0.9		22.5	21.7	22.5	23.2	22.0	22.7	22.2	20.8	22.7
4879_BHP_Dodecastyla `sp. BZY084`	22.0	22.5	24.0	23.5	21.6	22.9	22.5		8.8	10.8	11.3	11.0	10.8	10.6	11.5	11.6
PP582313_Dodecastyla sp. B02	23.4	23.9	24.7	20.4	21.8	21.7	21.7	8.8		10.9	11.0	11.0	11.7	11.0	11.8	12.4
BMR11690_21128_Atelurinae `sp. Biologic-ZYGE071`	23.3	23.8	23.8	22.8	19.7	22.0	22.5	10.8	10.9		0.9	1.1	1.3	1.5	11.8	14.2
BMR11999_21128_Atelurinae `sp. Biologic-ZYGE071`	24.4	24.9	24.0	22.4	20.3	22.8	23.2	11.3	11.0	0.9		1.9	1.7	1.9	11.1	14.6
BMR13927_21128_Atelurinae `sp. Biologic-ZYGE071`	23.3	23.8	23.8	22.8	20.9	21.6	22.0	11.0	11.0	1.1	1.9		0.7	0.9	12.1	14.2
BMR13928_21128_Atelurinae `sp. Biologic-ZYGE071`	23.3	23.8	24.0	23.2	21.1	22.2	22.7	10.8	11.7	1.3	1.7	0.7		1.1	11.5	14.2
BMR13929_21128_Atelurinae `sp. Biologic-ZYGE071`	23.6	24.0	24.4	23.0	21.1	21.8	22.2	10.6	11.0	1.5	1.9	0.9	1.1		12.3	14.2
MW021299_Dodecastyla sp. WAM ZYGA001	20.8	21.1	23.4	20.7	20.6	20.5	20.8	11.5	11.8	11.8	11.1	12.1	11.5	12.3		14.0
MZ427461_Atelurinae sp. H-TA009	21.9	22.4	26.1	20.8	21.4	22.4	22.7	11.6	12.4	14.2	14.6	14.2	14.2	14.2	14.0	

3.6 Copepoda

Sisteen copepods were successfully sequenced to produce four OTUs within two orders, Cyclopoida and Harpacticoida (Table 2.1, Figure 3.16. Phylogeny for the Copepoda dataset, with bootstrap values. The cyclopoid OTU *Diacyclops* `sp. Biologic-CYCL037`matched non-Study sequences, one named the same and one informally named *Diacyclops humphreysi* sensu lato BCY059 (Figure 3.16. Phylogeny for the Copepoda dataset, with bootstrap values. Given that the latter sequence was more than 23% divergent from available, non-Study sequences of *Diacyclops humphreysi* and was not supported as this species within the phylogeny, we decided to retain the OTU *Diacyclops* `sp. Biologic-CYCL037` (Figure 3.16, Table 3.17). This OTU had intraspecific divergences less than 1.3%, was more than 19.2% divergent from all other sequences in the analysis and had a linear range of 29.3 km (Table 3.1, Table 3.17).

Of the harpacticoids, one was singletons that did not match any non-Study sequences; *Parastenocaris* `sp. Biologic-HARP032` (Figure 3.15). This OTU was more than 20.0% divergent from the other analysis sequences (Table 3.17). *Schizopera* `sp. Biologic-HARP031` matched non-Study sequences with intraspecific divergences less than 0.3%, was more than 20.1% divergent from all other sequences in the analysis and had a linear range of 2.9 km (Table 3.1, Table 3.17).

The final OTU, *Gordanitocrella* `sp. Biologic-HARP030`, did not match any non-Study sequences (Figure 3.15). It had intraspecific divergences of less than 7.7%, was more than 27.7% divergent compared to the other analysis sequences and had a linear range of 2.8 km (Table 3.1, Table 3.17). This OTU was morphologically identified as *Gordanitocrella trajani*, however there are no sequences for this species available for comparison. Therefore, though the morphological identification and distribution data for *Gordanitocrella trajani* makes it potentially synonymous with *Gordanitocrella* `sp. Biologic-HARP030` (Karanovic & Hancock, 2009), we have retained the latter name until more information is available.

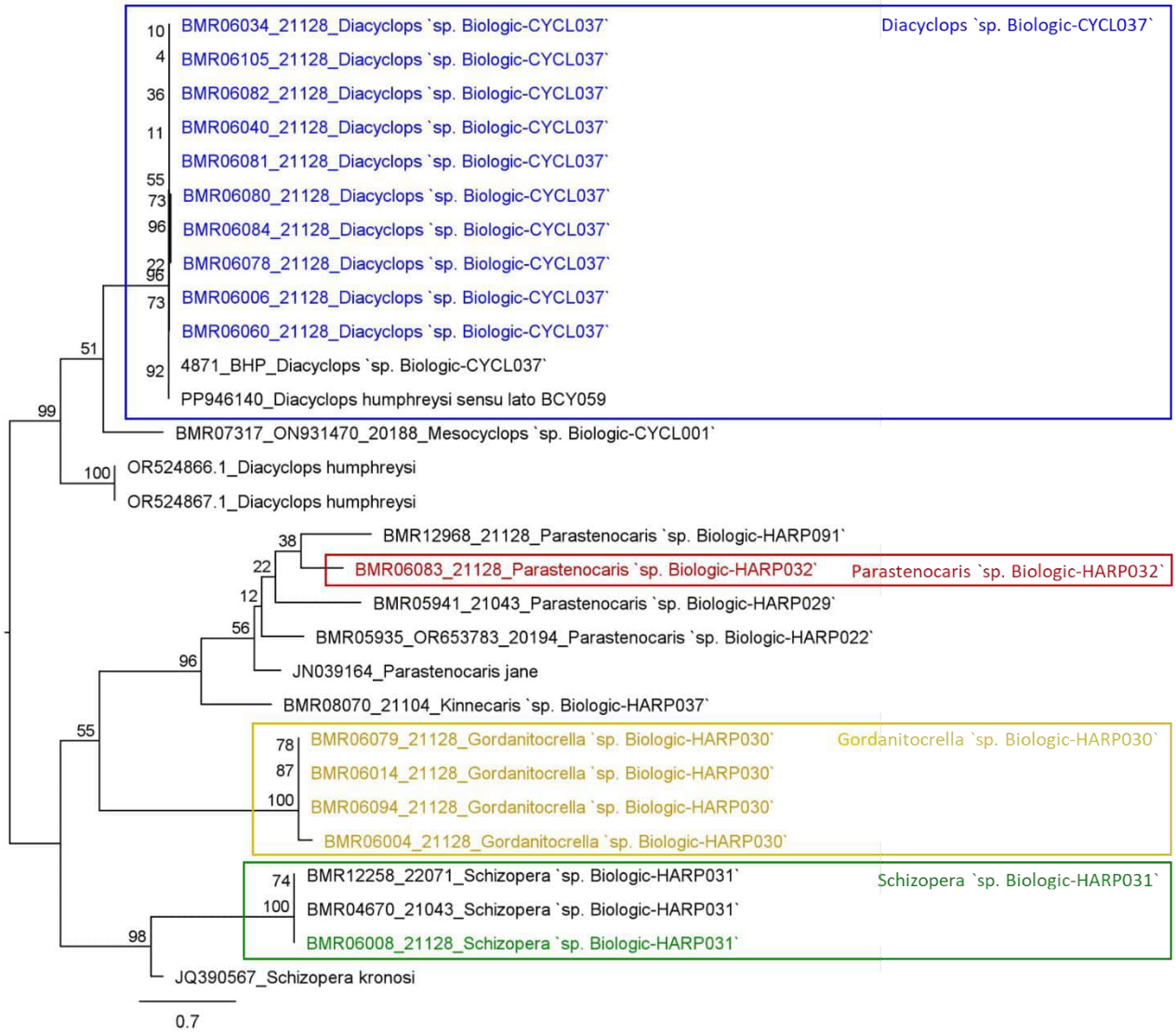

Figure 3.16. Phylogeny for the Copepoda dataset, with bootstrap values

Table 3.17: Pairwise distances (%) for the Copepoda dataset

COI Pairwise Distances (%)	4871	PP946140	BMR06006	BMR06060	BMR06034	BMR06040	BMR06081	BMR06082	BMR06105	BMR06078	BMR06080	BMR06084	BMR07317	OR524866.1	OR524867.1	BMR04670	BMR12258	BMR06008	JQ390567	BMR05935	JN039164	BMR06083	BMR12968	BMR05941	BMR08070	BMR06004	BMR06014	BMR06079	BMR06094
4871_BHP_Diacyclops `sp. Biologic-CYCL037`		0.0	0.4	0.4	0.2	0.2	0.2	0.2	0.2	1.2	1.1	1.1	19.3	23.3	23.3	28.3	28.3	28.1	25.8	32.0	32.2	31.0	32.8	33.9	32.6	30.0	30.4	30.5	30.8
PP946140_Diacyclops humphreysi sensu lato BCY059	0.0		0.4	0.4	0.2	0.2	0.2	0.2	0.2	1.2	1.1	1.1	19.4	23.3	23.3	28.1	28.1	27.9	25.8	32.1	32.2	31.0	32.9	33.9	32.6	30.0	30.4	30.5	30.8
BMR06006_21128_Diacyclops `sp. Biologic-CYCL037`	0.4	0.4		0.0	0.2	0.2	0.2	0.2	0.2	1.2	1.1	1.1	20.0	23.3	23.3	28.4	28.4	28.2	26.0	32.2	32.1	31.5	33.5	34.4	33.0	30.0	30.0	30.1	30.4
BMR06060_21128_Diacyclops `sp. Biologic-CYCL037`	0.4	0.4	0.0		0.2	0.2	0.2	0.2	0.2	1.2	1.1	1.1	20.0	23.3	23.3	28.4	28.4	28.2	26.0	32.2	32.1	31.5	33.5	34.4	33.0	30.0	30.0	30.1	30.4
BMR06034_21128_Diacyclops `sp. Biologic-CYCL037`	0.2	0.2	0.2	0.2		0.0	0.0	0.0	0.0	1.0	0.9	0.9	20.3	23.1	23.1	28.6	28.6	28.4	25.8	32.4	31.9	31.7	33.3	34.1	32.8	29.7	30.2	30.3	30.6
BMR06040_21128_Diacyclops `sp. Biologic-CYCL037`	0.2	0.2	0.2	0.2	0.0		0.0	0.0	0.0	1.0	0.9	0.9	20.3	23.1	23.1	28.6	28.6	28.4	25.8	32.4	31.9	31.7	33.3	34.1	32.8	29.7	30.2	30.3	30.6
BMR06081_21128_Diacyclops `sp. Biologic-CYCL037`	0.2	0.2	0.2	0.2	0.0	0.0		0.0	0.0	1.0	0.9	0.9	20.3	23.1	23.1	28.6	28.6	28.4	25.8	32.4	31.9	31.7	33.3	34.1	32.8	29.7	30.2	30.3	30.6
BMR06082_21128_Diacyclops `sp. Biologic-CYCL037`	0.2	0.2	0.2	0.2	0.0	0.0	0.0		0.0	1.0	0.9	0.9	20.3	23.1	23.1	28.6	28.6	28.4	25.8	32.4	31.9	31.7	33.3	34.1	32.8	29.7	30.2	30.3	30.6
BMR06105_21128_Diacyclops `sp. Biologic-CYCL037`	0.2	0.2	0.2	0.2	0.0	0.0	0.0	0.0		1.0	0.9	0.9	20.3	23.1	23.1	28.6	28.6	28.4	25.8	32.4	31.9	31.7	33.3	34.1	32.8	29.7	30.2	30.3	30.6
BMR06078_21128_Diacyclops `sp. Biologic-CYCL037`	1.2	1.2	1.2	1.2	1.0	1.0	1.0	1.0	1.0		0.1	0.1	20.5	23.3	23.3	29.4	29.4	29.2	26.2	31.8	31.1	31.4	32.7	34.0	31.8	29.2	29.6	29.7	30.1
BMR06080_21128_Diacyclops `sp. Biologic-CYCL037`	1.1	1.1	1.1	1.1	0.9	0.9	0.9	0.9	0.9	0.1		0.0	20.5	23.3	23.3	29.3	29.3	29.1	26.2	31.7	31.2	31.3	32.6	33.9	31.9	29.3	29.7	29.8	30.2
BMR06084_21128_Diacyclops `sp. Biologic-CYCL037`	1.1	1.1	1.1	1.1	0.9	0.9	0.9	0.9	0.9	0.1	0.0		20.5	23.3	23.3	29.3	29.3	29.1	26.2	31.7	31.2	31.3	32.6	33.9	31.9	29.3	29.7	29.8	30.2
BMR07317_ON931470_20188_Mesocyclops `sp. Biologic-CYCL001`	19.3	19.4	20.0	20.0	20.3	20.3	20.3	20.3	20.3	20.5	20.5	20.5		21.0	21.0	25.5	25.5	25.3	24.0	25.7	26.2	25.7	29.7	30.2	29.1	30.2	27.1	27.2	27.3
OR524866.1_Diacyclops humphreysi	23.3	23.3	23.3	23.3	23.1	23.1	23.1	23.1	23.1	23.3	23.3	23.3	21.0		0.0	29.5	29.5	29.4	25.4	29.7	26.9	29.5	32.3	30.0	31.1	30.6	29.1	29.2	29.4
OR524867.1_Diacyclops humphreysi	23.3	23.3	23.3	23.3	23.1	23.1	23.1	23.1	23.1	23.3	23.3	23.3	21.0	0.0		29.5	29.5	29.4	25.4	29.7	26.9	29.5	32.3	30.0	31.1	30.6	29.1	29.2	29.4
BMR04670_21043_Schizopera `sp. Biologic-HARP031`	28.3	28.1	28.4	28.4	28.6	28.6	28.6	28.6	28.6	29.4	29.3	29.3	25.5	29.5	29.5		0.0	0.2	20.3	27.2	23.7	26.0	30.1	26.9	28.6	30.8	29.3	29.3	29.2
BMR12258_22071_Schizopera `sp. Biologic-HARP031`	28.3	28.1	28.4	28.4	28.6	28.6	28.6	28.6	28.6	29.4	29.3	29.3	25.5	29.5	29.5	0.0		0.2	20.3	27.2	23.7	26.0	30.1	26.9	28.6	30.8	29.3	29.3	29.2
BMR06008_21128_Schizopera `sp. Biologic-HARP031`	28.1	27.9	28.2	28.2	28.4	28.4	28.4	28.4	28.4	29.2	29.1	29.1	25.3	29.4	29.4	0.2	0.2		20.2	27.4	23.9	25.8	29.9	26.7	28.9	30.6	29.1	29.1	29.0
JQ390567_Schizopera kronosi	25.8	25.8	26.0	26.0	25.8	25.8	25.8	25.8	25.8	26.2	26.2	26.2	24.0	25.4	25.4	20.3	20.3	20.2		27.5	26.5	24.3	30.8	27.3	28.0	29.7	29.5	29.6	29.5
BMR05935_OR653783_20194_Parastenocaris `sp. Biologic-HARP022`	32.0	32.1	32.2	32.2	32.4	32.4	32.4	32.4	32.4	31.8	31.7	31.7	25.7	29.7	29.7	27.2	27.2	27.4	27.5		16.9	18.8	22.2	21.6	23.6	29.1	28.6	28.7	29.1
JN039164_Parastenocaris jane	32.2	32.2	32.1	32.1	31.9	31.9	31.9	31.9	31.9	31.1	31.2	31.2	26.2	26.9	26.9	23.7	23.7	23.9	26.5	16.9		19.0	21.7	23.2	22.2	29.1	30.3	30.3	30.6
BMR06083_21128_Parastenocaris `sp. Biologic-HARP032`	31.0	31.0	31.5	31.5	31.7	31.7	31.7	31.7	31.7	31.4	31.3	31.3	25.7	29.5	29.5	26.0	26.0	25.8	24.3	18.8	19.0		20.1	22.9	23.1	29.3	27.8	27.9	28.0
BMR12968_21128_Parastenocaris `sp. Biologic-HARP091`	32.8	32.9	33.5	33.5	33.3	33.3	33.3	33.3	33.3	32.7	32.6	32.6	29.7	32.3	32.3	30.1	30.1	29.9	30.8	22.2	21.7	20.1		21.4	28.2	30.4	32.8	32.8	33.0
BMR05941_21043_Parastenocaris `sp. Biologic-HARP029`	33.9	33.9	34.4	34.4	34.1	34.1	34.1	34.1	34.1	34.0	33.9	33.9	30.2	30.0	30.0	26.9	26.9	26.7	27.3	21.6	23.2	22.9	21.4		25.3	31.9	32.2	32.3	32.3
BMR08070_21104_Kinnecaris `sp. Biologic-HARP037`	32.6	32.6	33.0	33.0	32.8	32.8	32.8	32.8	32.8	31.8	31.9	31.9	29.1	31.1	31.1	28.6	28.6	28.9	28.0	23.6	22.2	23.1	28.2	25.3		29.7	30.2	30.2	30.4
BMR06004_21128_Gordanitocrella `sp. Biologic-HARP030`	30.0	30.0	30.0	30.0	29.7	29.7	29.7	29.7	29.7	29.2	29.3	29.3	30.2	30.6	30.6	30.8	30.8	30.6	29.7	29.1	29.1	29.3	30.4	31.9	29.7		6.8	6.9	7.6
BMR06014_21128_Gordanitocrella `sp. Biologic-HARP030`	30.4	30.4	30.0	30.0	30.2	30.2	30.2	30.2	30.2	29.6	29.7	29.7	27.1	29.1	29.1	29.3	29.3	29.1	29.5	28.6	30.3	27.8	32.8	32.2	30.2	6.8		0.1	0.8
BMR06079_21128_Gordanitocrella `sp. Biologic-HARP030`	30.5	30.5	30.1	30.1	30.3	30.3	30.3	30.3	30.3	29.7	29.8	29.8	27.2	29.2	29.2	29.3	29.3	29.1	29.6	28.7	30.3	27.9	32.8	32.3	30.2	6.9	0.1		0.9
BMR06094_21128_Gordanitocrella `sp. Biologic-HARP030`	30.8	30.8	30.4	30.4	30.6	30.6	30.6	30.6	30.6	30.1	30.2	30.2	27.3	29.4	29.4	29.2	29.2	29.0	29.5	29.1	30.6	28.0	33.0	32.3	30.4	7.6	0.8	0.9	

3.7 Oligochaeta

Thirteen oligochaete specimens were successfully sequenced and resolved as five OTUs from three families; Naididae, Enchytraeidae, and Phreodrilidae (Figure 3.17). All matched non-Study sequences except one specimen, *Nais* `sp. Biologic-OLIG117`, which was more than 12.9% divergent from all other sequences in the analysis (Table 3.18). Before being sequenced, *Nais* `sp. Biologic-OLIG117` was morphologically identified as *Nais variabilis*, all of which were found from the same site. *Nais* `sp. Biologic-OLIG117` was compared to available sequences of *Nais variabilis* and was found to be 16-20% divergent from them. It should be noted that there is some uncertainty around the species concept of *Nais variabilis*. Sequences identified as *Nais variabilis* on GenBank form two lineages, ~10% divergent from each other, and it is therefore unlikely to represent a single species. All *Nais variabilis* specimens morphologically identified from this survey may represent *Nais* `sp. Biologic-OLIG117`, however, further molecular analyses would be required to confirm this.

The other naidid OTU, Naididae `sp. N1 LB-21015`, had intraspecific divergences less than 3.7%, was more than 18.7% divergent from the other sequences in the analysis and had a linear range of 13.1 km (Table 3.18).

Enchytraeidae `sp. E1 LB-2015`and Enchytraeidae `sp. E6 LB-2015`matched non-Study sequences with linear ranges of 398 km and 477.4 km respectively (Table 3.1). Enchytraeidae `sp. E1 LB-2015`had intraspecific divergences less than 6.6% and was more than 11.9% divergent from all other sequences in the analysis (Table 3.18). Enchytraeidae `sp. E6 LB-2015`had intraspecific divergences less than 7.9% and was more than 13% divergent from other analysis sequences (Table 3.18). Enchytraeidae `sp. E6 LB-2015` matched two informally named sequences that were well supported within this OTU with intraspecific divergences less than the typical 8% threshold we employ (Hebert *et al.*, 2003a), therefore these were included in the analysis and the Enchytraeidae `sp. E6 LB-2015`name was retained (Figure 3.17, Table 3.18).

Phreodrilidae `sp. P11 LB-2015`matched non-Study sequences with intraspecific divergences of less than 3.3%, was more than 19.4% divergent from other sequences in the analysis and had a linear range of 434.6 km (Table 3.1, Table 3.18).

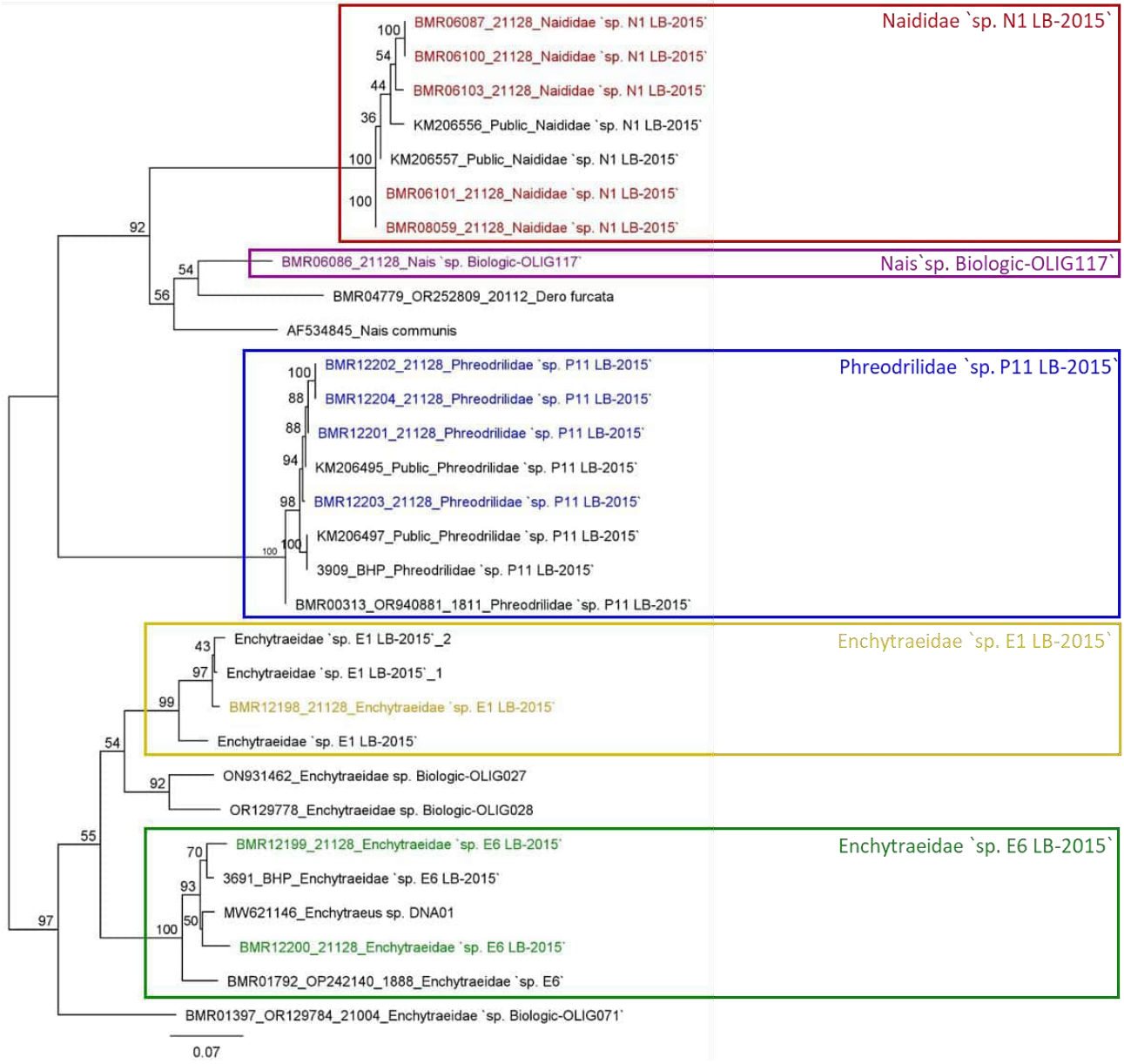

Figure 3.17. Phylogeny for the Oligochaeta dataset, with bootstrap values

Table 3.18: Pairwise distances (%) for the Oligochaeta dataset

COI Pairwise Distances (%)	BMR12198	Enchytraeidae `sp. E1 LB-2015`	Enchytraeidae `sp. E1 LB-2015`	Enchytraeidae `sp. E1 LB-2015`	OR129778	ON931462	BMR12200	BMR12199	MW621146	3691	BMR01792	BMR12204	BMR12202	BMR12203	BMR12201	KM206495	KM206497	3909	BMR00313	BMR06086	AF534845	BMR04779	BMR08059	BMR06101	BMR06103	BMR06100	BMR06087	KM206557	KM206556	BMR01397
BMR12198_21128_Enchytraeidae `sp. E1 LB-2015`		2.1	1.3	6.4	13.9	12.7	15.3	15.8	15.1	15.6	15.3	21.5	21.4	20.5	21.3	21.0	20.6	20.6	20.3	18.3	19.3	21.6	21.9	21.8	22.0	23.1	23.1	21.8	21.8	16.7
Enchytraeidae `sp. E1 LB-2015` _2	2.1		1.4	6.5	13.4	12.6	15.6	15.7	14.6	15.2	15.2	22.2	22.1	21.3	21.6	21.3	21.3	21.3	20.7	18.7	19.6	22.1	21.9	21.8	22.0	23.1	23.1	22.6	22.1	16.3
Enchytraeidae `sp. E1 LB-2015` _1	1.3	1.4		6.2	13.2	12.0	15.5	15.5	14.7	15.0	14.7	21.8	21.8	21.0	21.3	21.0	20.7	20.7	20.7	18.5	19.2	21.6	21.9	21.8	22.0	23.1	23.1	21.5	21.5	16.5
Enchytraeidae `sp. E1 LB-2015`	6.4	6.5	6.2		13.5	12.5	14.2	14.0	13.1	13.2	14.1	21.7	21.7	21.2	21.4	21.1	21.4	21.4	21.3	19.2	19.6	21.2	21.5	21.4	22.0	22.7	22.7	21.5	21.5	17.2
OR129778_Enchytraeidae sp. Biologic-OLIG028	13.9	13.4	13.2	13.5		8.2	15.6	15.1	14.3	14.9	14.7	20.9	20.7	20.1	20.5	20.4	20.7	20.7	19.8	19.2	20.2	20.3	22.4	22.2	22.5	22.7	22.7	21.2	20.9	15.9
ON931462_Enchytraeidae sp. Biologic-OLIG027	12.7	12.6	12.0	12.5	8.2		15.8	14.8	15.0	14.1	14.3	20.5	20.4	19.6	19.9	19.8	19.6	19.6	19.5	20.9	20.7	21.4	23.7	23.6	23.8	24.4	24.4	22.9	22.6	17.0
BMR12200_21128_Enchytraeidae `sp. E6 LB-2015`	15.3	15.6	15.5	14.2	15.6	15.8		4.2	3.8	3.8	7.8	21.5	21.5	21.0	21.6	21.4	21.6	21.6	21.0	22.5	22.1	23.0	22.6	22.5	22.7	23.3	23.3	23.8	23.2	17.6
BMR12199_21128_Enchytraeidae `sp. E6 LB-2015`	15.8	15.7	15.5	14.0	15.1	14.8	4.2		3.7	2.8	6.8	21.4	21.4	21.1	21.6	21.3	21.7	21.7	20.8	22.0	22.6	21.7	22.6	22.5	22.7	23.3	23.3	24.4	23.8	17.6
MW621146_Enchytraeus sp. DNA01	15.1	14.6	14.7	13.1	14.3	15.0	3.8	3.7		2.6	6.2	22.3	22.1	21.5	22.2	21.9	21.7	21.7	21.0	21.6	21.5	22.6	22.4	22.2	22.5	23.1	23.1	24.1	23.5	17.8
3691_BHP_Enchytraeidae `sp. E6 LB-2015`	15.6	15.2	15.0	13.2	14.9	14.1	3.8	2.8	2.6		5.6	21.2	21.1	20.4	21.1	20.8	21.0	21.0	20.5	21.8	21.7	21.9	21.9	21.8	22.0	22.7	22.7	23.8	23.2	17.2
BMR01792_OP242140_1888_Enchytraeidae `sp. E6`	15.3	15.2	14.7	14.1	14.7	14.3	7.8	6.8	6.2	5.6		22.9	22.8	22.1	22.8	22.5	21.7	21.7	21.6	22.2	21.7	20.7	23.0	23.1	23.8	24.0	24.0	23.8	23.8	17.8
BMR12204_21128_Phreodrilidae `sp. P11 LB-2015`	21.5	22.2	21.8	21.7	20.9	20.5	21.5	21.4	22.3	21.2	22.9		0.0	1.1	0.8	1.1	2.5	2.5	3.2	22.9	22.0	22.8	24.6	24.4	24.4	25.1	25.1	24.4	23.8	21.6
BMR12202_21128_Phreodrilidae `sp. P11 LB-2015`	21.4	22.1	21.8	21.7	20.7	20.4	21.5	21.4	22.1	21.1	22.8	0.0		1.1	0.6	0.9	2.3	2.3	3.1	22.9	22.0	22.8	24.6	24.4	24.4	25.1	25.1	24.4	23.8	21.6
BMR12203_21128_Phreodrilidae `sp. P11 LB-2015`	20.5	21.3	21.0	21.2	20.1	19.6	21.0	21.1	21.5	20.4	22.1	1.1	1.1		0.8	0.5	1.2	1.2	2.0	22.2	21.3	22.3	24.6	24.4	24.4	25.1	25.1	24.1	23.5	20.9
BMR12201_21128_Phreodrilidae `sp. P11 LB-2015`	21.3	21.6	21.3	21.4	20.5	19.9	21.6	21.6	22.2	21.1	22.8	0.8	0.6	0.8		0.3	1.7	1.7	2.5	22.9	21.8	22.8	24.6	24.4	24.4	25.1	25.1	24.4	23.8	21.6
KM206495_Public_Phreodrilidae `sp. P11 LB-2015`	21.0	21.3	21.0	21.1	20.4	19.8	21.4	21.3	21.9	20.8	22.5	1.1	0.9	0.5	0.3		1.3	1.4	2.1	22.4	21.4	22.5	24.0	24.2	24.2	24.9	24.9	24.1	23.5	21.1
KM206497_Public_Phreodrilidae `sp. P11 LB-2015`	20.6	21.3	20.7	21.4	20.7	19.6	21.6	21.7	21.7	21.0	21.7	2.5	2.3	1.2	1.7	1.3		0.0	2.3	21.9	21.3	22.5	24.2	24.4	24.4	24.7	24.7	24.1	23.5	21.1
3909_BHP_Phreodrilidae `sp. P11 LB-2015`	20.6	21.3	20.7	21.4	20.7	19.6	21.6	21.7	21.7	21.0	21.7	2.5	2.3	1.2	1.7	1.4	0.0		2.3	22.0	21.3	22.5	24.6	24.4	24.4	24.7	24.7	24.1	23.5	21.1
BMR00313_OR940881_1811_Phreodrilidae `sp. P11 LB-2015`	20.3	20.7	20.7	21.3	19.8	19.5	21.0	20.8	21.0	20.5	21.6	3.2	3.1	2.0	2.5	2.1	2.3	2.3		22.7	21.0	22.1	24.8	24.7	24.7	25.3	25.3	24.1	23.5	20.5
BMR06086_21128_Nais `sp. Biologic-OLIG117`	18.3	18.7	18.5	19.2	19.2	20.9	22.5	22.0	21.6	21.8	22.2	22.9	22.9	22.2	22.9	22.4	21.9	22.0	22.7		13.0	13.2	18.8	19.6	19.4	19.6	19.6	19.8	20.1	19.2
AF534845_Nais communis	19.3	19.6	19.2	19.6	20.2	20.7	22.1	22.6	21.5	21.7	21.7	22.0	22.0	21.3	21.8	21.4	21.3	21.3	21.0	13.0		15.9	19.3	19.8	20.7	21.1	21.1	19.5	19.8	19.2
BMR04779_OR252809_20112_Dero furcata	21.6	22.1	21.6	21.2	20.3	21.4	23.0	21.7	22.6	21.9	20.7	22.8	22.8	22.3	22.8	22.5	22.5	22.5	22.1	13.2	15.9		21.0	20.9	21.1	21.4	21.4	21.5	21.2	18.7
BMR08059_21128_Naididae `sp. N1 LB-2015`	21.9	21.9	21.9	21.5	22.4	23.7	22.6	22.6	22.4	21.9	23.0	24.6	24.6	24.6	24.6	24.0	24.2	24.6	24.8	18.8	19.3	21.0		0.1	3.0	3.0	3.0	0.8	3.6	21.7
BMR06101_21128_Naididae `sp. N1 LB-2015`	21.8	21.8	21.8	21.4	22.2	23.6	22.5	22.5	22.2	21.8	23.1	24.4	24.4	24.4	24.4	24.2	24.4	24.4	24.7	19.6	19.8	20.9	0.1		2.9	2.9	2.9	0.6	3.4	21.6
BMR06103_21128_Naididae `sp. N1 LB-2015`	22.0	22.0	22.0	22.0	22.5	23.8	22.7	22.7	22.5	22.0	23.8	24.4	24.4	24.4	24.4	24.2	24.4	24.4	24.7	19.4	20.7	21.1	3.0	2.9		1.9	1.9	2.8	2.5	21.8
BMR06100_21128_Naididae `sp. N1 LB-2015`	23.1	23.1	23.1	22.7	22.7	24.4	23.3	23.3	23.1	22.7	24.0	25.1	25.1	25.1	25.1	24.9	24.7	24.7	25.3	19.6	21.1	21.4	3.0	2.9	1.9		0.1	2.2	2.6	21.8
BMR06087_21128_Naididae `sp. N1 LB-2015`	23.1	23.1	23.1	22.7	22.7	24.4	23.3	23.3	23.1	22.7	24.0	25.1	25.1	25.1	25.1	24.9	24.7	24.7	25.3	19.6	21.1	21.4	3.0	2.9	1.9	0.1		2.2	2.6	21.8
KM206557_Public_Naididae `sp. N1 LB-2015`	21.8	22.6	21.5	21.5	21.2	22.9	23.8	24.4	24.1	23.8	23.8	24.4	24.4	24.1	24.4	24.1	24.1	24.1	24.1	19.8	19.5	21.5	0.8	0.6	2.8	2.2	2.2		2.6	21.4
KM206556_Public_Naididae `sp. N1 LB-2015`	21.8	22.1	21.5	21.5	20.9	22.6	23.2	23.8	23.5	23.2	23.8	23.8	23.8	23.5	23.8	23.5	23.5	23.5	23.5	20.1	19.8	21.2	3.6	3.4	2.5	2.6	2.6	2.6		20.4
BMR01397_OR129784_21004_Enchytraeidae `sp. Biologic-OLIG071`	16.7	16.3	16.5	17.2	15.9	17.0	17.6	17.6	17.8	17.2	17.8	21.6	21.6	20.9	21.6	21.1	21.1	21.1	20.5	19.2	19.2	18.7	21.7	21.6	21.8	21.8	21.8	21.4	20.4	

3.8 Ostracoda

Thirteen ostracod specimens were sequenced and resolved as four OTUs that all matched non-Study sequences, two of which are named species (Figure 3.18. Phylogeny for the Ostracoda dataset, with bootstrap values *Notacandona boultoni* and *Notacandona modesta* had linear ranges of 38.9 km and 12.1 km respectively (Table 3.1). *Notacandona boultoni* had intraspecific divergences less than 8.5% and was more than 14.5% divergent from all other sequences in the analysis (Table 3.19). *Notacandona modesta* had intraspecific divergences less than 1.5% and was more than 14.8% divergent from the other analysis sequences (Table 3.19).

Meridiescandona `sp. Biologic-OSTR057` was morphologically identified as *Meridiescandona marillanae,* but as there were no sequences available for this species to provide a comparison an OTU name was assigned. This OTU had intraspecific divergences of less than 1.2%, was more than 9.6% divergent from all other sequences in the analysis and had a linear range of 18.4 km (Table 3.1, Table 3.19).

The final ostracod OTU, *Gomphodella* `sp. Biologic-OSTR078`, matched non-Study sequences with a linear range of 1.5 km (Table 3.1). The intraspecific divergences for *Gomphodella* `sp. Biologic-OSTR078`were less than 3% and it was more than 12.5% divergent from all other sequences in the analysis (Table 3.19).

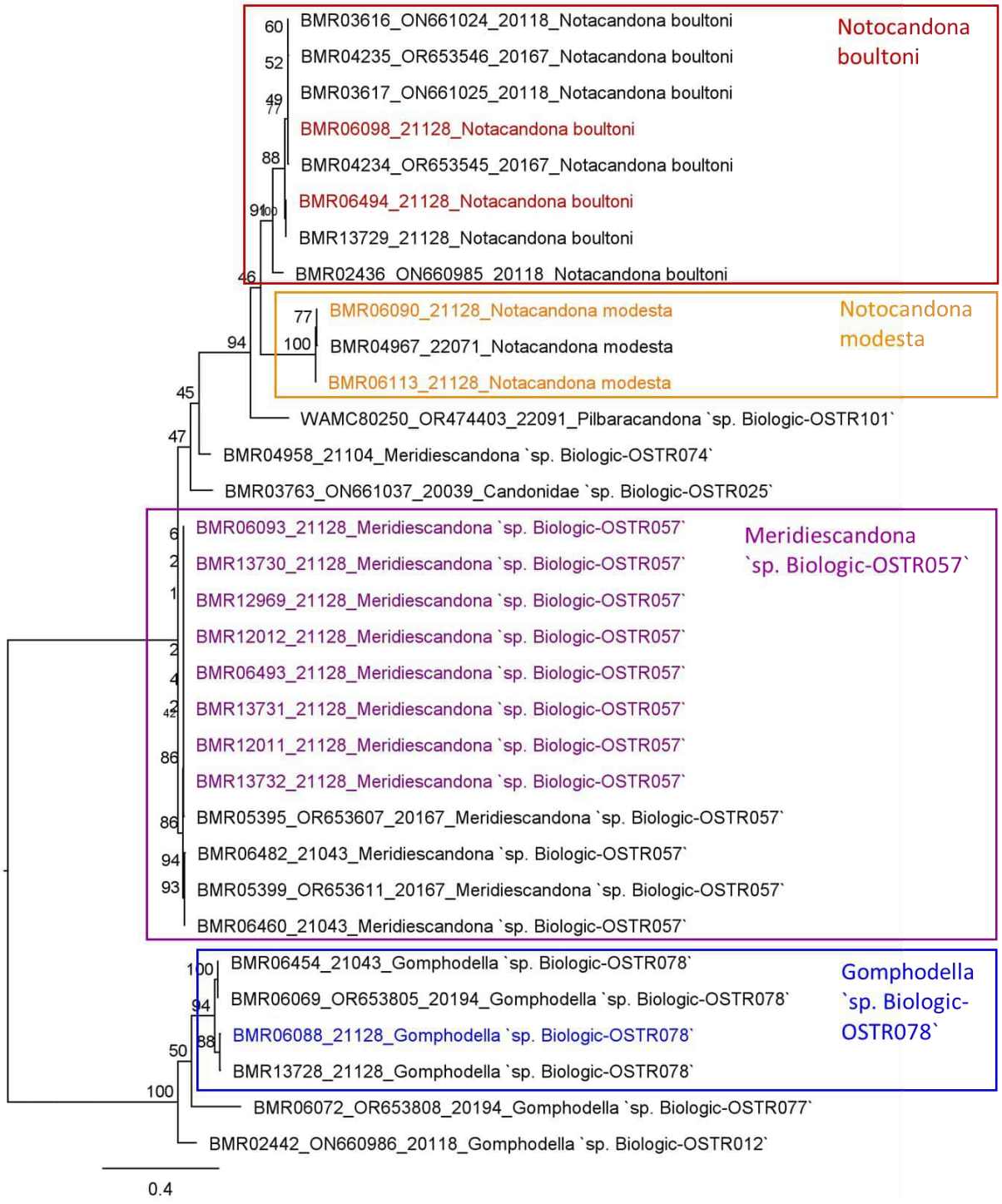

Figure 3.18. Phylogeny for the Ostracoda dataset, with bootstrap values

Table 3.19: Pairwise distances (%) for the Ostracoda dataset

COI Pairwise Distances (%)	BMR02436	BMR03616	BMR03617	BMR04234	BMR06098	BMR04235	BMR06494	BMR13729	WAMC80250	BMR04967	BMR06113	BMR06090	BMR03763	BMR04958	BMR05395	BMR06093	BMR06493	BMR12011	BMR12012	BMR12969	BMR13730	BMR13731	BMR13732	BMR05399	BMR06460	BMR06482	BMR02442	BMR06069	BMR06454	BMR06088	BMR13728	BMR06072
BMR02436_ON660985_20118_Notacandona boultoni		8.4	7.3	7.1	7.4	7.5	6.8	6.8	14.9	15.6	14.9	15.8	18.1	15.9	17.1	16.9	16.9	16.9	16.9	16.9	16.9	16.9	16.9	16.2	16.4	16.3	29.7	31.2	29.8	31.2	31.2	29.4
BMR03616_ON661024_20118_Notacandona boultoni	8.4		0.0	0.2	0.1	0.4	1.8	1.8	15.9	15.9	15.6	16.2	18.1	15.4	15.6	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.6	29.5	29.3	29.3	29.7	29.5	30.8
BMR03617_ON661025_20118_Notacandona boultoni	7.3	0.0		0.2	0.1	0.4	1.4	1.4	14.7	16.1	15.6	16.4	19.2	16.3	16.4	16.3	16.3	16.3	16.3	16.3	16.3	16.3	16.3	15.8	15.4	16.0	30.9	31.0	29.3	31.5	31.2	30.8
BMR04234_OR653545_20167_Notacandona boultoni	7.1	0.2	0.2		0.2	0.6	1.5	1.5	14.6	16.0	15.4	16.3	19.1	16.4	16.6	16.4	16.4	16.4	16.4	16.4	16.4	16.4	16.4	16.0	15.6	16.1	30.7	30.9	29.1	31.3	31.0	30.6
BMR06098_21128_Notacandona boultoni	7.4	0.1	0.1	0.2		0.4	1.4	1.4	14.8	16.2	15.7	16.5	19.3	16.3	16.5	16.3	16.3	16.3	16.3	16.3	16.3	16.3	16.3	15.9	15.5	16.0	30.9	31.1	29.4	31.5	31.2	30.9
BMR04235_OR653546_20167_Notacandona boultoni	7.5	0.4	0.4	0.6	0.4		1.9	1.9	15.6	16.1	15.5	16.3	19.5	16.6	16.7	16.7	16.7	16.7	16.7	16.7	16.7	16.7	16.7	16.2	15.8	16.4	31.0	31.2	29.5	31.7	31.3	31.7
BMR06494_21128_Notacandona boultoni	6.8	1.8	1.4	1.5	1.4	1.9		0.0	14.7	16.0	15.6	16.3	19.5	16.4	17.2	17.0	17.0	17.0	17.0	17.0	17.0	17.0	17.0	16.3	15.9	16.4	31.5	31.3	29.5	31.8	31.5	30.8
BMR13729_21128_Notacandona boultoni	6.8	1.8	1.4	1.5	1.4	1.9	0.0		14.7	16.0	15.6	16.3	19.5	16.4	17.2	17.0	17.0	17.0	17.0	17.0	17.0	17.0	17.0	16.3	15.9	16.4	31.5	31.3	29.5	31.8	31.5	30.8
WAMC80250_OR474403_22091_Pilbaracandona `sp. Biologic-OSTR101`	14.9	15.9	14.7	14.6	14.8	15.6	14.7	14.7		17.5	17.6	17.9	20.4	17.2	19.3	19.1	19.1	19.1	19.1	19.1	19.1	19.1	19.1	19.1	18.1	19.3	29.8	30.5	27.5	29.8	29.8	28.2
BMR04967_22071_Notacandona modesta	15.6	15.9	16.1	16.0	16.2	16.1	16.0	16.0	17.5		0.9	0.9	20.4	18.8	19.0	19.1	19.1	19.1	19.1	19.1	19.1	19.1	19.1	18.8	19.2	19.0	31.0	31.6	30.0	31.6	31.9	29.7
BMR06113_21128_Notacandona modesta	14.9	15.6	15.6	15.4	15.7	15.5	15.6	15.6	17.6	0.9		1.4	21.6	20.5	19.5	19.7	19.7	19.7	19.7	19.7	19.7	19.7	19.7	19.4	19.4	19.6	29.7	29.7	29.7	30.2	30.4	30.0
BMR06090_21128_Notacandona modesta	15.8	16.2	16.4	16.3	16.5	16.3	16.3	16.3	17.9	0.9	1.4		20.8	19.1	18.9	19.1	19.1	19.1	19.1	19.1	19.1	19.1	19.1	18.9	19.2	19.1	31.2	31.8	30.2	31.8	32.1	29.8
BMR03763_ON661037_20039_Candonidae `sp. Biologic-OSTR025`	18.1	18.1	19.2	19.1	19.3	19.5	19.5	19.5	20.4	20.4	21.6	20.8		10.9	10.4	10.3	10.3	10.3	10.3	10.3	10.3	10.3	10.3	10.7	9.9	10.9	29.7	30.2	28.2	29.9	29.6	30.4
BMR04958_21104_Meridiescandona `sp. Biologic-OSTR074`	15.9	15.4	16.3	16.4	16.3	16.6	16.4	16.4	17.2	18.8	20.5	19.1	10.9		10.2	10.3	10.3	10.3	10.3	10.3	10.3	10.3	10.3	10.5	9.7	10.6	28.1	30.5	28.9	30.4	30.1	29.1
BMR05395_OR653607_20167_Meridiescandona `sp. Biologic-OSTR057`	17.1	15.6	16.4	16.6	16.5	16.7	17.2	17.2	19.3	19.0	19.5	18.9	10.4	10.2		0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.9	0.7	1.1	27.4	28.1	26.0	28.4	28.4	28.6
BMR06093_21128_Meridiescandona `sp. Biologic-OSTR057`	16.9	15.4	16.3	16.4	16.3	16.7	17.0	17.0	19.1	19.1	19.7	19.1	10.3	10.3	0.2		0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.8	0.4	0.9	27.4	28.3	26.2	28.6	28.6	28.9
BMR06493_21128_Meridiescandona `sp. Biologic-OSTR057`	16.9	15.4	16.3	16.4	16.3	16.7	17.0	17.0	19.1	19.1	19.7	19.1	10.3	10.3	0.2	0.0		0.0	0.0	0.0	0.0	0.0	0.0	0.8	0.4	0.9	27.4	28.3	26.2	28.6	28.6	28.9
BMR12011_21128_Meridiescandona `sp. Biologic-OSTR057`	16.9	15.4	16.3	16.4	16.3	16.7	17.0	17.0	19.1	19.1	19.7	19.1	10.3	10.3	0.2	0.0	0.0		0.0	0.0	0.0	0.0	0.0	0.8	0.4	0.9	27.4	28.3	26.2	28.6	28.6	28.9
BMR12012_21128_Meridiescandona `sp. Biologic-OSTR057`	16.9	15.4	16.3	16.4	16.3	16.7	17.0	17.0	19.1	19.1	19.7	19.1	10.3	10.3	0.2	0.0	0.0	0.0		0.0	0.0	0.0	0.0	0.8	0.4	0.9	27.4	28.3	26.2	28.6	28.6	28.9
BMR12969_21128_Meridiescandona `sp. Biologic-OSTR057`	16.9	15.4	16.3	16.4	16.3	16.7	17.0	17.0	19.1	19.1	19.7	19.1	10.3	10.3	0.2	0.0	0.0	0.0	0.0		0.0	0.0	0.0	0.8	0.4	0.9	27.4	28.3	26.2	28.6	28.6	28.9
BMR13730_21128_Meridiescandona `sp. Biologic-OSTR057`	16.9	15.4	16.3	16.4	16.3	16.7	17.0	17.0	19.1	19.1	19.7	19.1	10.3	10.3	0.2	0.0	0.0	0.0	0.0	0.0		0.0	0.0	0.8	0.4	0.9	27.4	28.3	26.2	28.6	28.6	28.9
BMR13731_21128_Meridiescandona `sp. Biologic-OSTR057`	16.9	15.4	16.3	16.4	16.3	16.7	17.0	17.0	19.1	19.1	19.7	19.1	10.3	10.3	0.2	0.0	0.0	0.0	0.0	0.0	0.0		0.0	0.8	0.4	0.9	27.4	28.3	26.2	28.6	28.6	28.9
BMR13732_21128_Meridiescandona `sp. Biologic-OSTR057`	16.9	15.4	16.3	16.4	16.3	16.7	17.0	17.0	19.1	19.1	19.7	19.1	10.3	10.3	0.2	0.0	0.0	0.0	0.0	0.0	0.0	0.0		0.8	0.4	0.9	27.4	28.3	26.2	28.6	28.6	28.9
BMR05399_OR653611_20167_Meridiescandona `sp. Biologic-OSTR057`	16.2	15.4	15.8	16.0	15.9	16.2	16.3	16.3	19.1	18.8	19.4	18.9	10.7	10.5	0.9	0.8	0.8	0.8	0.8	0.8	0.8	0.8	0.8		0.0	0.2	27.4	28.3	26.2	28.6	28.6	28.9
BMR06460_21043_Meridiescandona `sp. Biologic-OSTR057`	16.4	15.4	15.4	15.6	15.5	15.8	15.9	15.9	18.1	19.2	19.4	19.2	9.9	9.7	0.7	0.4	0.4	0.4	0.4	0.4	0.4	0.4	0.4	0.0		0.2	25.6	26.2	26.2	26.7	26.4	28.9
BMR06482_21043_Meridiescandona `sp. Biologic-OSTR057`	16.3	15.6	16.0	16.1	16.0	16.4	16.4	16.4	19.3	19.0	19.6	19.1	10.9	10.6	1.1	0.9	0.9	0.9	0.9	0.9	0.9	0.9	0.9	0.2	0.2		27.5	28.4	26.4	28.7	28.7	29.1
BMR02442_ON660986_20118_Gomphodella `sp. Biologic-OSTR012`	29.7	29.5	30.9	30.7	30.9	31.0	31.5	31.5	29.8	31.0	29.7	31.2	29.7	28.1	27.4	27.4	27.4	27.4	27.4	27.4	27.4	27.4	27.4	27.4	25.6	27.5		12.8	12.6	12.9	12.9	15.2
BMR06069_OR653805_20194_Gomphodella `sp. Biologic-OSTR078`	31.2	29.3	31.0	30.9	31.1	31.2	31.3	31.3	30.5	31.6	29.7	31.8	30.2	30.5	28.1	28.3	28.3	28.3	28.3	28.3	28.3	28.3	28.3	28.3	26.2	28.4	12.8		0.0	2.9	2.9	15.0
BMR06454_21043_Gomphodella `sp. Biologic-OSTR078`	29.8	29.3	29.3	29.1	29.4	29.5	29.5	29.5	27.5	30.0	29.7	30.2	28.2	28.9	26.0	26.2	26.2	26.2	26.2	26.2	26.2	26.2	26.2	26.2	26.2	26.4	12.6	0.0		2.2	2.4	15.0
BMR06088_21128_Gomphodella `sp. Biologic-OSTR078`	31.2	29.7	31.5	31.3	31.5	31.7	31.8	31.8	29.8	31.6	30.2	31.8	29.9	30.4	28.4	28.6	28.6	28.6	28.6	28.6	28.6	28.6	28.6	28.6	26.7	28.7	12.9	2.9	2.2		0.3	14.5
BMR13728_21128_Gomphodella `sp. Biologic-OSTR078`	31.2	29.5	31.2	31.0	31.2	31.3	31.5	31.5	29.8	31.9	30.4	32.1	29.6	30.1	28.4	28.6	28.6	28.6	28.6	28.6	28.6	28.6	28.6	28.6	26.4	28.7	12.9	2.9	2.4	0.3		14.8
BMR06072_OR653808_20194_Gomphodella `sp. Biologic-OSTR077`	29.4	30.8	30.8	30.6	30.9	31.7	30.8	30.8	28.2	29.7	30.0	29.8	30.4	29.1	28.6	28.9	28.9	28.9	28.9	28.9	28.9	28.9	28.9	28.9	28.9	29.1	15.2	15.0	15.0	14.5	14.8	

3.9 Pauropoda

Eleven Pauropoda specimens were successfully sequenced to produce eight OTUs, two of which matched non-Study sequences (Figure 3.19). Pauropoda `sp. Biologic-PAUR072`, Pauropoda `sp. Biologic-PAUR073`, Pauropoda `sp. Biologic-PAUR075`, Pauropoda `sp. Biologic-PAUR085`, Pauropoda `sp. Biologic-PAUR086`and Pauropoda `sp. Biologic-PAUR087`were all singletons, each with more than 16% divergence from all other sequences in the analysis (Table 3.20).

Pauropoda `sp. Biologic-PAUR074` matched non-Study sequences with a linear range of 33.6 km (Table 3.1). The intraspecific divergences for this OTU were less than 0.6%, and the divergence from all other analysis sequences was greater than 16.1% (Table 3.20).

Three Pauropoda specimens were resolved as *Decapauropus* `sp. WAM-PAUD002`. This OTU had intraspecific divergences less than 5.3%, was more than 17.5% divergent from all sequences in the analysis and had a linear range of 228.5 km (Table 3.1).

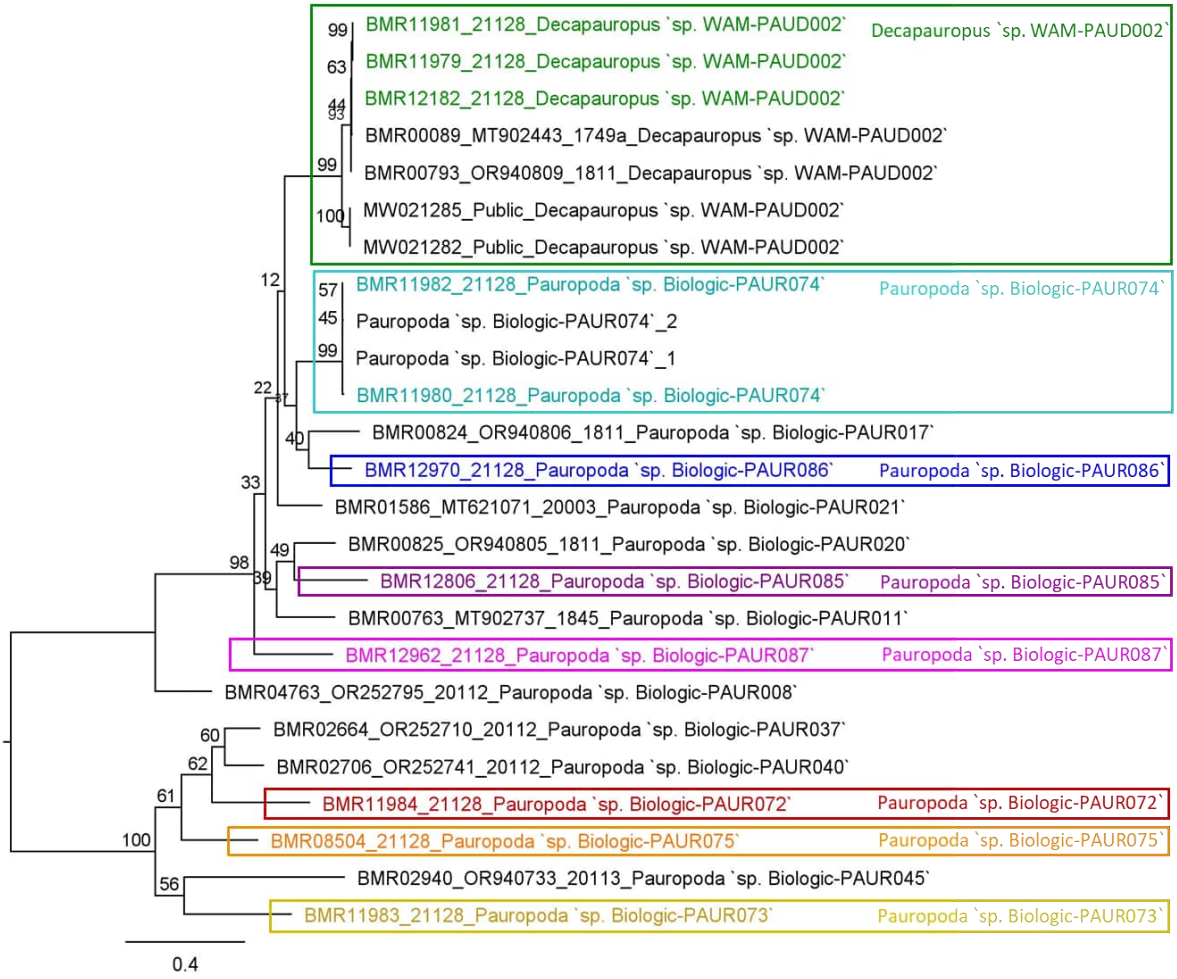

Figure 3.19. Phylogeny for the Pauropoda dataset, with bootstrap values

Table 3.20: Pairwise distances (%) for the Pauropoda dataset

COI Pairwise Distances (%)	MW021285	MW021282	BMR12182	BMR00793	BMR00089	BMR11981	BMR11979	BMR00825	Biologic-PAUR074_2	BMR11982	Biologic-PAUR074_1	BMR11980	BMR12970	BMR00824	BMR01586	BMR00763	BMR12806	BMR12962	BMR04763	BMR11984	BMR02706	BMR02664	BMR08504	BMR11983	BMR02940
MW021285_Public_Decapauropus `sp. WAM-PAUD002`		0.0	4.9	4.7	5.0	5.2	5.1	18.4	18.2	19.4	18.1	18.4	19.0	17.6	17.9	20.7	20.9	21.1	24.7	35.7	33.9	33.5	33.3	35.7	37.1
MW021282_Public_Decapauropus `sp. WAM-PAUD002`	0.0		4.9	4.7	5.0	5.2	5.1	18.4	18.2	19.4	18.1	18.4	19.0	17.6	17.9	20.7	20.9	21.1	24.7	35.7	33.9	33.5	33.3	35.7	37.1
BMR12182_21128_Decapauropus `sp. WAM-PAUD002`	4.9	4.9		0.2	0.2	0.3	0.2	18.2	17.9	19.4	17.8	18.1	18.2	18.7	18.3	20.2	19.8	22.5	24.2	35.2	33.3	32.6	32.8	35.5	36.3
BMR00793_OR940809_1811_Decapauropus `sp. WAM-PAUD002`	4.7	4.7	0.2		0.3	0.5	0.3	18.4	17.8	19.2	17.6	17.9	18.4	18.8	18.2	20.4	20.0	22.7	24.2	35.4	33.1	32.6	32.8	35.7	36.5
BMR00089_MT902443_1749a_Decapauropus `sp. WAM-PAUD002`	5.0	5.0	0.2	0.3		0.5	0.3	18.4	18.1	19.4	17.9	18.2	18.4	18.8	18.5	20.4	19.8	22.5	24.4	35.4	33.4	32.6	32.8	35.5	36.3
BMR11981_21128_Decapauropus `sp. WAM-PAUD002`	5.2	5.2	0.3	0.5	0.5		0.0	17.9	18.2	19.4	18.1	17.9	18.8	19.0	18.6	20.4	19.8	22.5	24.7	35.2	33.5	32.6	32.8	35.4	36.3
BMR11979_21128_Decapauropus `sp. WAM-PAUD002`	5.1	5.1	0.2	0.3	0.3	0.0		17.9	18.1	19.4	17.9	17.9	18.7	18.9	18.5	20.4	19.8	22.5	24.6	35.2	33.4	32.6	32.8	35.4	36.2
BMR00825_OR940805_1811_Pauropoda `sp. Biologic-PAUR020`	18.4	18.4	18.2	18.4	18.4	17.9	17.9		21.3	23.1	21.1	21.0	20.8	19.5	19.8	19.1	19.8	21.4	24.5	35.7	33.3	34.6	34.4	36.3	34.2
Pauropoda `sp. Biologic-PAUR074` _2	18.2	18.2	17.9	17.8	18.1	18.2	18.1	21.3		0.0	0.2	0.5	16.4	17.6	16.8	20.5	21.1	22.7	25.0	34.6	32.8	32.6	35.0	36.0	35.1
BMR11982_21128_Pauropoda `sp. Biologic-PAUR074`	19.4	19.4	19.4	19.2	19.4	19.4	19.4	23.1	0.0		0.0	0.2	18.0	20.0	19.1	22.0	21.1	22.7	27.5	34.6	35.0	32.6	35.0	36.8	37.0
Pauropoda `sp. Biologic-PAUR074` _1	18.1	18.1	17.8	17.6	17.9	18.1	17.9	21.1	0.2	0.0		0.3	16.2	17.5	16.6	20.4	21.1	22.7	25.2	34.7	33.0	32.6	35.0	36.2	35.3
BMR11980_21128_Pauropoda `sp. Biologic-PAUR074`	18.4	18.4	18.1	17.9	18.2	17.9	17.9	21.0	0.5	0.2	0.3		16.5	17.8	16.9	20.4	21.4	22.9	25.7	34.9	33.1	32.6	35.0	35.9	35.1
BMR12970_21128_Pauropoda `sp. Biologic-PAUR086`	19.0	19.0	18.2	18.4	18.4	18.8	18.7	20.8	16.4	18.0	16.2	16.5		16.1	18.1	20.2	21.1	21.1	25.3	34.9	32.3	33.2	36.3	34.7	34.3
BMR00824_OR940806_1811_Pauropoda `sp. Biologic-PAUR017`	17.6	17.6	18.7	18.8	18.8	19.0	18.9	19.5	17.6	20.0	17.5	17.8	16.1		16.8	19.1	23.3	22.7	24.7	34.4	30.7	32.8	36.3	35.4	35.0
BMR01586_MT621071_20003_Pauropoda `sp. Biologic-PAUR021`	17.9	17.9	18.3	18.2	18.5	18.6	18.5	19.8	16.8	19.1	16.6	16.9	18.1	16.8		17.9	24.3	22.1	23.5	33.1	30.2	29.6	34.5	36.4	35.2
BMR00763_MT902737_1845_Pauropoda `sp. Biologic-PAUR011`	20.7	20.7	20.2	20.4	20.4	20.4	20.4	19.1	20.5	22.0	20.4	20.4	20.2	19.1	17.9		22.7	22.0	27.2	33.3	34.3	33.7	34.1	36.3	35.1
BMR12806_21128_Pauropoda `sp. Biologic-PAUR085`	20.9	20.9	19.8	20.0	19.8	19.8	19.8	19.8	21.1	21.1	21.1	21.4	21.1	23.3	24.3	22.7		21.8	29.5	34.8	35.2	33.7	35.0	35.9	35.9
BMR12962_21128_Pauropoda `sp. Biologic-PAUR087`	21.1	21.1	22.5	22.7	22.5	22.5	22.5	21.4	22.7	22.7	22.7	22.9	21.1	22.7	22.1	22.0	21.8		24.9	31.5	32.8	31.1	33.7	35.0	36.3
BMR04763_OR252795_20112_Pauropoda `sp. Biologic-PAUR008`	24.7	24.7	24.2	24.2	24.4	24.7	24.6	24.5	25.0	27.5	25.2	25.7	25.3	24.7	23.5	27.2	29.5	24.9		31.2	27.4	30.4	32.2	32.1	31.7
BMR11984_21128_Pauropoda `sp. Biologic-PAUR072`	35.7	35.7	35.2	35.4	35.4	35.2	35.2	35.7	34.6	34.6	34.7	34.9	34.9	34.4	33.1	33.3	34.8	31.5	31.2		19.9	18.5	24.7	25.2	26.3
BMR02706_OR252741_20112_Pauropoda `sp. Biologic-PAUR040`	33.9	33.9	33.3	33.1	33.4	33.5	33.4	33.3	32.8	35.0	33.0	33.1	32.3	30.7	30.2	34.3	35.2	32.8	27.4	19.9		13.7	20.5	25.8	26.7
BMR02664_OR252710_20112_Pauropoda `sp. Biologic-PAUR037`	33.5	33.5	32.6	32.6	32.6	32.6	32.6	34.6	32.6	32.6	32.6	32.6	33.2	32.8	29.6	33.7	33.7	31.1	30.4	18.5	13.7		18.5	25.6	26.2
BMR08504_21128_Pauropoda `sp. Biologic-PAUR075`	33.3	33.3	32.8	32.8	32.8	32.8	32.8	34.4	35.0	35.0	35.0	35.0	36.3	36.3	34.5	34.1	35.0	33.7	32.2	24.7	20.5	18.5		25.6	25.8
BMR11983_21128_Pauropoda `sp. Biologic-PAUR073`	35.7	35.7	35.5	35.7	35.5	35.4	35.4	36.3	36.0	36.8	36.2	35.9	34.7	35.4	36.4	36.3	35.9	35.0	32.1	25.2	25.8	25.6	25.6		25.8
BMR02940_OR940733_20113_Pauropoda `sp. Biologic-PAUR045`	37.1	37.1	36.3	36.5	36.3	36.3	36.2	34.2	35.1	37.0	35.3	35.1	34.3	35.0	35.2	35.1	35.9	36.3	31.7	26.3	26.7	26.2	25.8	25.8	

3.10 Symphyla

Three symphylan specimens were sequenced and resolved as three OTUs, all singletons (Table 3.1,

Figure 3.20). *Hanseniella* `sp. Biologic-SYMP077`, *Hanseniella* `sp. Biologic-SYMP088` and Scolopendrellidae `sp. Biologic-SYMP089`were all more than 15.3% divergent from the other analysis sequences (Table 3.21).

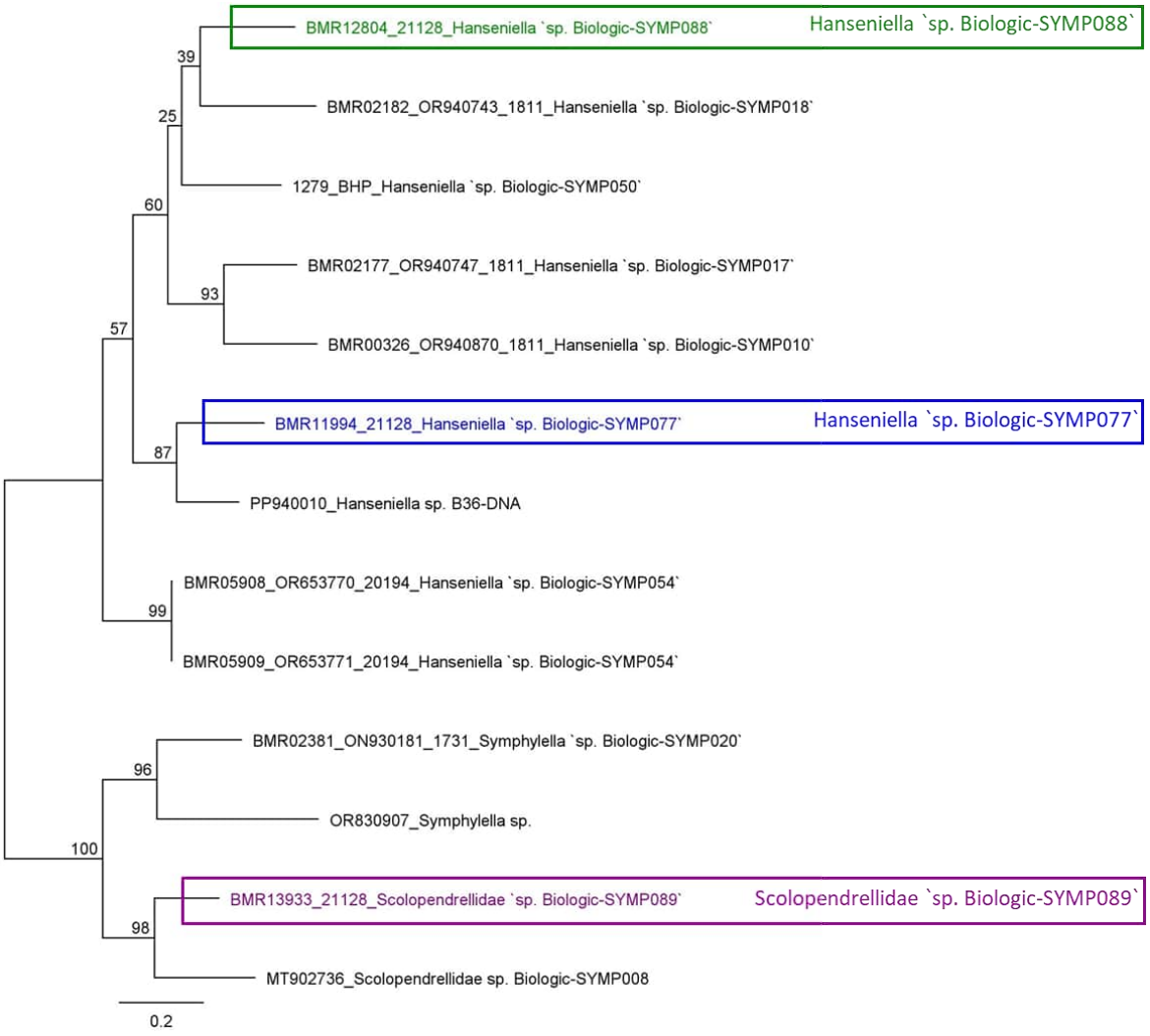

Figure 3.20: Phylogeny for the Symphyla dataset, with bootstrap values

Table 3.21: Pairwise distances (%) for the Symphyla dataset

COI Pairwise Distances (%)	1279	BMR02182	BMR05908	BMR05909	BMR12804	BMR00326	BMR02177	BMR11994	PP940010	BMR02381	OR830907	BMR13933	MT902736
1279_BHP_Hanseniella `sp. Biologic-SYMP050`		17.8	17.9	17.8	18.4	19.3	18.8	21.4	18.8	26.3	25.8	24.7	26.6
BMR02182_OR940743_1811_Hanseniella `sp. Biologic-SYMP018`	17.8		17.9	18.1	18.5	19.8	19.8	21.1	18.3	27.2	26.1	26.8	24.8
BMR05908_OR653770_20194_Hanseniella `sp. Biologic-SYMP054`	17.9	17.9		0.2	19.3	18.6	19.7	18.8	18.9	23.3	25.2	24.2	22.9
BMR05909_OR653771_20194_Hanseniella `sp. Biologic-SYMP054`	17.8	18.1	0.2		19.1	18.8	19.6	18.7	18.9	23.4	25.2	24.0	22.9
BMR12804_21128_Hanseniella `sp. Biologic-SYMP088`	18.4	18.5	19.3	19.1		19.0	19.1	21.4	18.3	26.1	26.4	24.6	26.7
BMR00326_OR940870_1811_Hanseniella `sp. Biologic-SYMP010`	19.3	19.8	18.6	18.8	19.0		16.9	21.1	19.4	26.0	27.7	26.4	25.2
BMR02177_OR940747_1811_Hanseniella `sp. Biologic-SYMP017`	18.8	19.8	19.7	19.6	19.1	16.9		19.8	19.4	26.4	28.0	26.3	26.4
BMR11994_21128_Hanseniella `sp. Biologic-SYMP077`	21.4	21.1	18.8	18.7	21.4	21.1	19.8		15.5	25.7	28.4	25.8	25.5
PP940010_Hanseniella sp. B36-DNA	18.8	18.3	18.9	18.9	18.3	19.4	19.4	15.5		23.9	24.2	23.5	26.7
BMR02381_ON930181_1731_Symphylella `sp. Biologic-SYMP020`	26.3	27.2	23.3	23.4	26.1	26.0	26.4	25.7	23.9		19.0	19.3	21.9
OR830907_Symphylella sp.	25.8	26.1	25.2	25.2	26.4	27.7	28.0	28.4	24.2	19.0		21.4	22.0
BMR13933_21128_Scolopendrellidae `sp. Biologic-SYMP089`	24.7	26.8	24.2	24.0	24.6	26.4	26.3	25.8	23.5	19.3	21.4		15.4
MT902736_Scolopendrellidae sp. Biologic-SYMP008	26.6	24.8	22.9	22.9	26.7	25.2	26.4	25.5	26.7	21.9	22.0	15.4	

4 Summary

Using well-established DNA extraction and sequencing methods, this molecular systematics analysis designated 70 distinct OTU/species to 220 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:

- Araneae (COI): 5 OTUs, none matching non-Study sequences
- Palpigrades (COI): 3 OTUs, none matching non-Study sequences
- Pseudoscorpiones (COI): 8 OTUs, none matching non-Study sequences
- Schizomida (COI): 2 OTUs, 1 matching non-Study sequences,
- Trombidiformes (mites) (COI): 1 OTU, matching non-Study sequences,
- Chilopoda (COI): 2 OTUs, both matching non-Study sequences,
- Amphipoda (COI): 4 OTUs, all matching non-Study sequences,
- Bathynellacea (COI): 1 OTUs, matching non-Study sequences,
- Isopoda (COI): 4 OTUs, 1 matching non-Study sequences,
- Diplura (COI): 5 OTUs, 2 matching non-Study sequences,
- Blattodea (COI): 1 OTU matching non-Study sequences,
- Coleoptera (COI): 6 OTUs, all matching non-Study sequences,
- Hemiptera (COI): 2 OTUs, both matching non-Study sequences,
- Zygentoma (COI): 2 OTUs, one matching non-Study sequences,
- Copepoda (COI): 4 OTUs, 1 matching non-Study sequences,
- Oligochaeta (COI): 5 OTUs, 4 matching non-Study sequences,
- Ostracoda (COI): 4 OTUs, three matching non-Study sequences,
- Pauropoda (COI): 8 OTUs, 2 matching non-Study sequences, and
- Symphyla (COI): 3 OTUs, none matching non-Study sequences.

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Appendix A: Specimen Data

BMR	Unique ID code	Site	Dec_Lat	Dec_Long	Coll_Date	Coll_Method	Lowest_ID_Legacy	OTU_Name	Reaction_State
Arachnida: Araneae									
BMR11674	19788	EPS0882R	-22.92637869	119.1651973	23/11/2022	Scrape	Araneae `sp. indet.`	Araneae `sp. Biologic-ARAN093`	PASS
BMR11681	23804	EPS1078R	-22.91021369	119.187025	25/06/2023	Haul-Scrape	Araneae `sp. indet.`	Araneae `sp. Biologic-ARAN092`	PASS
BMR11672	23720	EPS0247R	-22.90789748	119.1447726	28/06/2023	Scrape	Araneae `sp. indet.`	Araneae `sp. Biologic-ARAN094`	PASS
BMR11673	23783	EPS0589R	-22.91329065	119.1300942	28/06/2023	Scrape	Araneae `sp. indet.`	Araneae `sp. Biologic-ARAN094`	PASS
BMR11682	23842	EPS1078R	-22.91021369	119.187025	7/09/2023	Haul-Scrape	Araneae `sp. indet.`	Araneae `sp. Biologic-ARAN092`	PASS
BMR11671	23571	EPS0879R	-22.91012696	119.1636964	7/09/2023	Haul-Scrape	Araneae `sp. indet.`	Araneae `sp. Biologic-ARAN094`	PASS
BMR12976	29459	EPS1109R	-22.91302888	119.1914424	13/04/2024	Haul-Scrape	Araneae `sp. indet.`	Araneae `sp. Biologic-ARAN093`	PASS
BMR12800	30568	EPS0887R	-22.9241214	119.1651045	16/04/2024	Scrape	Araneae `sp. indet.`	Araneae `sp. Biologic-ARAN093`	PASS
BMR12799	30442	EPS0589R	-22.91329065	119.1300942	17/04/2024	Scrape	Araneae `sp. indet.`	Araneae `sp. Biologic-ARAN094`	PASS
BMR13885	30289	EPS0779R	-22.91874663	119.151627	16/06/2024	Scrape	Araneae `sp. indet.`	Araneae `sp. Biologic-ARAN094`	PASS
BMR11684	23220	EPS0580R	-22.90428085	119.1285337	28/06/2023	Scrape	Oonopidae `sp. indet.`	Araneae `sp. Biologic-ARAN094`	PASS
BMR12802	30534	EPS0747R	-22.91288182	119.1481004	15/04/2024	Scrape	Gnaphosidae `sp. indet.`	Araneae `sp. Biologic-ARAN094`	PASS
Arachnida: Araneae: Oonopidae									
BMR12801	19547	EPS0768R	-22.91456082	119.1505381	15/11/2022	Trap	Oonopidae `sp. indet.`	*Prethopalpus* `sp. Biologic-ARAN115`	PASS
Arachnida: Araneae: Orsolobidae									
BMR11987	22330	EPS0864R	-22.90766357	119.1634402	28/06/2023	Haul-Scrape	Araneomorphae `sp. indet.`	Orsolobidae `sp. Biologic-ARAN091`	PASS
BMR13884	30240	EPS0590R	-22.91283213	119.1300751	17/06/2024	Scrape	Araneae `sp. indet.`	Orsolobidae `sp. Biologic-ARAN091`	PASS

BMR	Unique ID code	Site	Dec_Lat	Dec_Long	Coll_Date	Coll_Method	Lowest_ID_Legacy	OTU_Name	Reaction_State
Arachnida: Palpigrades									
BMR12006	20336	EPS0867R	-22.92314615	119.1637328	17/11/2022	Scrape	Palpigradi `sp. indet.`	Palpigradi `sp. Biologic-PALP077`	PASS
BMR12007	19246	EPS1097R	-22.91107989	119.190051	17/11/2022	Haul-Scrape	Palpigradi `sp. indet.`	Palpigradi `sp. Biologic-PALP077`	PASS
BMR12005	18845	EPS0949R	-22.92634136	119.1710392	23/11/2022	Scrape	Palpigradi `sp. indet.`	Palpigradi `sp. Biologic-PALP077`	PASS
BMR12181	26517	EPS1109R	-22.91302888	119.1914424	25/06/2023	Haul-Scrape	Palpigradi `sp. indet.`	Palpigradi `sp. Biologic-PALP075`	PASS
BMR12975	21822	EPS1121R	-22.91293158	119.1927415	25/06/2023	Haul-Scrape	Palpigradi `sp. indet.`	Palpigradi `sp. Biologic-PALP077`	PASS
BMR12003	23879	EPS0852R	-22.91976268	119.1614348	27/06/2023	Scrape	Palpigradi `sp. indet.`	Palpigradi `sp. Biologic-PALP077`	PASS
BMR12805	26874	EPS0768R	-22.91456082	119.1505381	15/04/2024	Scrape	Palpigradi `sp. indet.`	Palpigradi `sp. Biologic-PALP086`	PASS
BMR12004	21953	EPS0894R	-22.92100666	119.1651356	26/06/2023	Scrape	Palpigradi `sp. indet.`	Palpigradi `sp. Biologic-PALP077`	PASS
BMR12977	29540	EPS0220R	-22.91066292	119.1520275	27/06/2023	Haul-Scrape	Palpigradi `sp. indet.`		FAIL; contamination
Arachnida: Pseudoscorpiones: Chthoniidae									
BMR12170	19433	EPS0768R	-22.91456082	119.1505381	15/11/2022	Trap	Chthoniidae `sp. indet.`	Chthoniidae `sp. Biologic-PSEU191`	PASS
BMR12953	20157	EPS0793R	-22.91278351	119.1530593	15/11/2022	Scrape	Chthoniidae `sp. indet.`		FAIL; PCR
BMR12172	19552	EPS1046R	-22.9137965	119.1832267	17/11/2022	Trap	Chthoniidae `sp. indet.`	Chthoniidae `sp. Biologic-PSEU188`	PASS
BMR12183	26508	EPS1121R	-22.91293158	119.1927415	17/11/2022	Trap	Chthoniidae `sp. indet.`	Chthoniidae `sp. Biologic-PSEU188`	PASS
BMR13680	19428	EPS1054R	-22.9114708	119.1842253	17/11/2022	Trap	Chthoniidae `sp. indet.`	Chthoniidae `sp. Biologic-PSEU188`	PASS
BMR13681	19791	EPS0776R	-22.90895849	119.1505245	18/11/2022	Haul-Scrape	Chthoniidae `sp. indet.`	Chthoniidae `sp. Biologic-PSEU193`	PASS
BMR13726	26429	EPS0247R	-22.90789748	119.1447726	18/11/2022	Scrape	Lagynochthonius `sp. indet.`	Chthoniidae `sp. Biologic-PSEU193`	PASS

BMR	Unique ID code	Site	Dec_Lat	Dec_Long	Coll_Date	Coll_Method	Lowest_ID_Legacy	OTU_Name	Reaction_State
BMR12171	19550	EPS0946R	-22.92775196	119.170999	23/11/2022	Trap	Chthoniidae `sp. indet.`	Chthoniidae `sp. Biologic-PSEU188`	PASS
BMR12173	20339	EPS0894R	-22.92100666	119.1651356	23/11/2022	Scrape	Chthoniidae `sp. indet.`	Chthoniidae `sp. Biologic-PSEU188`	PASS
BMR13926	23840	EPS1078R	-22.91021369	119.187025	25/06/2023	Haul-Scrape	Chthoniidae `sp. indet.`	Chthoniidae `sp. Biologic-PSEU188`	PASS
BMR12812	24101	EPS0920R	-22.92119538	119.1680299	26/06/2023	Trap	Chthoniidae `sp. indet.`	Chthoniidae `sp. Biologic-PSEU188`	PASS
BMR12184	26522	EPS0991R	-22.92042333	119.1754824	26/06/2023	Scrape	Chthoniidae `sp. indet.`	Chthoniidae `sp. Biologic-PSEU192`	PASS
BMR13727	21336	EPS0927R	-22.91056568	119.168107	27/06/2023	Haul-Scrape	Chthoniidae `sp. indet.`	Chthoniidae `sp. Biologic-PSEU188`	PASS
BMR12807	23817	EPS0767R	-22.91513697	119.1505255	27/06/2023	Scrape	Chthoniidae `sp. indet.`	Chthoniidae `sp. Biologic-PSEU191`	PASS
BMR12810	24173	EPS0768R	-22.91456082	119.1505381	27/06/2023	Trap	Tyrannochthonius `sp. indet.`	Chthoniidae `sp. Biologic-PSEU191`	PASS
BMR12174	23762	EPS0746R	-22.91333363	119.1481428	27/06/2023	Scrape	Chthoniidae `sp. indet.`	Chthoniidae `sp. Biologic-PSEU195`	PASS
BMR12811	22347	EPS0794R	-22.91238685	119.1534738	27/06/2023	Scrape	Chthoniidae `sp. indet.`	Chthoniidae `sp. Biologic-PSEU195`	PASS
BMR12175	23882	EPS0864R	-22.90766357	119.1634402	28/06/2023	Haul-Scrape	Chthoniidae `sp. indet.`	Chthoniidae `sp. Biologic-PSEU186`	PASS
BMR12808	23491	EPS0639R	-22.90928794	119.1385232	28/06/2023	Scrape	Chthoniidae `sp. indet.`	Chthoniidae `sp. Biologic-PSEU191`	PASS
BMR11990	26956	EPS0580R	-22.90428085	119.1285337	28/06/2023	Scrape	Chthoniidae `sp. indet.`	Chthoniidae `sp. Biologic-PSEU193`	PASS
BMR13925	24040	EPS0630R	-22.9083716	119.1376455	28/06/2023	Trap	Lagynochthonius `sp. indet.`	Chthoniidae `sp. Biologic-PSEU193`	PASS
BMR12176	23535	EPS0731R	-22.91925833	119.1461644	29/06/2023	Scrape	Lagynochthonius `sp. indet.`	Chthoniidae `sp. Biologic-PSEU195`	PASS
BMR12809	23155	EPS1109R	-22.91302888	119.1914424	7/09/2023	Haul-Scrape	Chthoniidae `sp. indet.`	Chthoniidae `sp. Biologic-PSEU188`	PASS

BMR	Unique ID code	Site	Dec_Lat	Dec_Long	Coll_Date	Coll_Method	Lowest_ID_Legacy	OTU_Name	Reaction_State
BMR13677	30602	EPS0928R	-22.90970443	119.1680652	15/04/2024	Scrape	Tyrannochthonius `sp. indet.`	Chthoniidae `sp. Biologic-PSEU188`	PASS
BMR12954	30565	EPS0882R	-22.92637869	119.1651973	16/04/2024	Scrape	Lagynochthonius `sp. indet.`	Chthoniidae `sp. Biologic-PSEU192`	PASS
BMR13676	30299	EPS0590R	-22.91283213	119.1300751	17/06/2024	Scrape	Lagynochthonius `sp. indet.`	Chthoniidae `sp. Biologic-PSEU193`	PASS
Arachnida: Pseudoscorpiones: Hyidae									
BMR12185	26519	EPS0746R	-22.91333363	119.1481428	16/11/2022	Trap	*Indohya* `sp. indet.`	*Indohya* `sp. Biologic-PSEU183`	PASS
BMR13725	17942	EPS1078R	-22.91021369	119.187025	17/11/2022	Haul-Scrape	*Indohya* `sp. indet.`		FAIL; contamination
BMR12177	23548	EPS0887R	-22.9241214	119.1651045	26/06/2023	Scrape	*Indohya* `sp. indet.`	*Indohya* `sp. Biologic-PSEU183`	PASS
BMR11989	26136	EPS0746R	-22.91333363	119.1481428	27/06/2023	Scrape	*Indohya* `sp. indet.`	*Indohya* `sp. Biologic-PSEU183`	PASS
BMR11988	23612	EPS0247R	-22.90789748	119.1447726	28/06/2023	Scrape	*Indohya* `sp. indet.`	*Indohya* `sp. Biologic-PSEU184`	PASS
BMR13678	24452	EPS1158R	-22.91236883	119.1973108	12/04/2024	Haul-Scrape	*Indohya* `sp. indet.`		FAIL; contamination
BMR13679	30403	EPS0794R	-22.91238685	119.1534738	15/04/2024	Scrape	*Indohya* `sp. indet.`	*Indohya* `sp. Biologic-PSEU183`	PASS
Arachnida: Schizomida: Hubbardiidae									
BMR12955	30136	EPS0603R	-22.91354369	119.1322318	15/11/2022	Trap	*Draculoides* `sp. indet.`	*Draculoides* `sp. WAM-SCH067`	PASS
BMR13738	18965	EPS0589R	-22.91329065	119.1300942	15/11/2022	Trap	*Draculoides* `sp. indet.`	*Draculoides* `sp. WAM-SCH067`	PASS
BMR12188	26511	EEX0050	-22.91389969	119.1631614	16/11/2022	Trap	*Draculoides* `sp. indet.`	*Draculoides* `sp. WAM-SCH067`	PASS
BMR12009	19431	EPS1142R	-22.91418314	119.1958637	17/11/2022	Trap	*Draculoides* `sp. indet.`	*Draculoides* `sp. WAM-SCH067`	PASS
BMR12798	18882	EEX0053	-22.91558429	119.185477	17/11/2022	Trap	*Draculoides* `sp. indet.`	*Draculoides* `sp. WAM-SCH067`	PASS
BMR12956	30235	EEX0108	-22.91309982	119.1916159	17/11/2022	Trap	*Draculoides* `sp. indet.`	*Draculoides* `sp. WAM-SCH067`	PASS

BMR	Unique ID code	Site	Dec_Lat	Dec_Long	Coll_Date	Coll_Method	Lowest_ID_Legacy	OTU_Name	Reaction_State
BMR12008	18851	EPS0507R	-22.90477233	119.1126427	18/11/2022	Trap	*Draculoides* `sp. indet.`	*Draculoides* `sp. WAM-SCH067	PASS
BMR12187	26515	EPS0244R	-22.90702231	119.1447432	18/11/2022	Trap	*Draculoides* `sp. indet.`	*Draculoides* `sp. WAM-SCH067	PASS
BMR12186	26527	EPS0946R	-22.92775196	119.170999	23/11/2022	Trap	*Draculoides* `sp. indet.`	*Draculoides* `sp. WAM-SCH067	PASS
BMR13741	19851	EPS0948R	-22.92689879	119.1709948	23/11/2022	Haul-Scrape	*Draculoides* `sp. indet.`	*Draculoides* `sp. WAM-SCH067	PASS
BMR11992	24265	EPS0991R	-22.92042333	119.1754824	26/06/2023	Trap	*Draculoides* `sp. indet.`	*Draculoides* `sp. Biologic-SCHI023`	PASS
BMR12957	29868	EPS0866R	-22.92359269	119.1637482	26/06/2023	Scrape	*Draculoides* `sp. indet.`	*Draculoides* `sp. Biologic-SCHI023`	PASS
BMR12959	30206	EPS0938R	-22.92101687	119.1696434	26/06/2023	Scrape	*Draculoides* `sp. indet.`	*Draculoides* `sp. Biologic-SCHI023`	PASS
BMR11991	23295	EPS0960R	-22.9098705	119.1712543	27/06/2023	Scrape	*Draculoides* `sp. indet.`	*Draculoides* `sp. WAM-SCH067	PASS
BMR12958	30332	EPS0747R	-22.91288182	119.1481004	27/06/2023	Scrape	*Draculoides* `sp. indet.`	*Draculoides* `sp. WAM-SCH067	PASS
BMR13739	24779	EPS0590R	-22.91283213	119.1300751	28/06/2023	Trap	*Draculoides* `sp. indet.`	*Draculoides* `sp. WAM-SCH067	PASS
BMR12010	23156	EPS0643R	-22.92028805	119.1407631	29/06/2023	Scrape	*Draculoides* `sp. indet.`	*Draculoides* `sp. WAM-SCH067	PASS
BMR13743	30081	EPS0548R	-22.90435338	119.1258289	12/04/2024	Trap	*Draculoides* `sp. indet.`	*Draculoides* `sp. WAM-SCH067	PASS
BMR12792	28120	EPS1109R	-22.91302888	119.1914424	13/04/2024	Haul-Scrape	*Draculoides* `sp. indet.`	*Draculoides* `sp. WAM-SCH067	PASS
BMR12793	30393	EPS1121R	-22.91293158	119.1927415	13/04/2024	Haul-Scrape	*Draculoides* `sp. indet.`	*Draculoides* `sp. WAM-SCH067	PASS
BMR12795	30531	EPS1130R	-22.91512395	119.1943932	13/04/2024	Scrape	*Draculoides* `sp. indet.`	*Draculoides* `sp. WAM-SCH067`	PASS
BMR12960	29845	EPS1078R	-22.91021369	119.187025	13/04/2024	Haul-Scrape	*Draculoides* `sp. indet.`	*Draculoides* `sp. WAM-SCH067`	PASS

BMR	Unique ID code	Site	Dec_Lat	Dec_Long	Coll_Date	Coll_Method	Lowest_ID_Legacy	OTU_Name	Reaction_State
BMR12961	30315	EEX0046	-22.91477458	119.1912693	13/04/2024	Roots	*Draculoides* `sp. indet.`	*Draculoides* `sp. WAM-SCH067`	PASS
BMR13744	30195	EEX0052	-22.91430702	119.1788248	14/04/2024	Trap	*Draculoides* `sp. indet.`	*Draculoides* `sp. WAM-SCH067`	PASS
BMR13886	29633	EPS0273R	-22.91316015	119.175498	14/04/2024	Trap	*Draculoides* `sp. indet.`	*Draculoides* `sp. WAM-SCH067`	PASS
BMR12791	26783	EPS0927R	-22.91056568	119.168107	15/04/2024	Haul-Scrape	*Draculoides* `sp. indet.`	*Draculoides* `sp. WAM-SCH067`	PASS
BMR12794	30404	EPS0767R	-22.91513697	119.1505255	15/04/2024	Scrape	*Draculoides* `sp. indet.`	*Draculoides* `sp. WAM-SCH067`	PASS
BMR12796	30543	EPS0787R	-22.91028126	119.1520036	15/04/2024	Scrape	*Draculoides* `sp. indet.`	*Draculoides* `sp. WAM-SCH067`	PASS
BMR12797	30762	EPS0794R	-22.91238685	119.1534738	15/04/2024	Scrape	*Draculoides* `sp. indet.`	*Draculoides* `sp. WAM-SCH067`	PASS
BMR13742	29842	EPS0779R	-22.91874663	119.151627	15/04/2024	Trap	*Draculoides* `sp. indet.`	*Draculoides* `sp. WAM-SCH067`	PASS
BMR13887	29549	EPS0746R	-22.91333363	119.1481428	15/04/2024	Trap	*Draculoides* `sp. indet.`	*Draculoides* `sp. WAM-SCH067`	PASS
BMR13737	30480	EPS0261R	-22.91411426	119.1432186	16/04/2024	Scrape	*Draculoides* `sp. indet.`	*Draculoides* `sp. WAM-SCH067`	PASS
BMR13740	29560	EPS0852R	-22.91976268	119.1614348	16/06/2024	Scrape	*Draculoides* `sp. indet.`	*Draculoides* `sp. Biologic-SCHI023`	PASS
Arachnida: Trombidiformes: Pezidae									
BMR06102	16095	GWB0032S	-22.91732353	119.2056657	2022-05-14	Haul	Pezidae sp.	Pezidae `sp. Biologic-ACAR003`	PASS
BMR06114	16106	GWB0032S	-22.91732353	119.2056657	2022-05-14	Haul	Halacaridae sp.	Pezidae `sp. Biologic-ACAR003`	PASS
BMR06099	16158	GWB0032S	-22.91732353	119.2056657	2022-05-14	Haul	Halacaridae sp.		FAIL; contamination
Chilopoda: Scolopendropmorpha: Cryptopidae									
BMR13883	29543	EPS0852R	-22.91976268	119.1614348	16/06/2024	Scrape	*Cryptops* `sp. indet.`	*Cryptops* `sp. Biologic-CHIL048`	PASS
Chilopoda: Scolopendropmorpha: Scolopendridae									

BMR	Unique ID code	Site	Dec_Lat	Dec_Long	Coll_Date	Coll_Method	Lowest_ID_Legacy	OTU_Name	Reaction_State
BMR11993	23564	EPS0894R	-22.92100666	119.1651356	26/06/2023	Scrape	*Cryptops* `sp. indet.`	*Cormocephalus pyropygus*	PASS
BMR12803	30362	EPS0920R	-22.92119538	119.1680299	14/04/2024	Haul-Scrape	*Cryptops* `sp. indet.`	*Cormocephalus pyropygus*	PASS
Malacostraca: Amphipoda: Paramelitidae									
BMR12197	26523	EPS0864R	-22.90766357	119.1634402	16/11/2022	Haul-Scrape	Paramelitidae `sp. U3 plumose setae short dist. segm.`	Paramelitidae `sp. Biologic-AMPH070`	PASS
BMR12196	26528	EPS1098R	-22.91055114	119.1899658	17/11/2022	Haul-Scrape	Paramelitidae `sp. U3 plumose setae short dist. segm.`	Paramelitidae `sp. Biologic-AMPH070`	PASS
BMR12179	19950	HEOP0478	-22.90399946	119.2150008	24/11/2022	Haul	*Maarrka* `sp. indet.`	*Maarrka weeliwollii*	PASS
BMR12180	23589	EPS1158R	-22.91236883	119.1973108	15/06/2023	Haul-Scrape	Paramelitidae `sp. indet.`	Paramelitidae `sp. Biologic-AMPH070`	PASS
BMR12965	30104	EPS1098R	-22.91055114	119.1899658	25/06/2023	Haul-Scrape	Paramelitidae `sp. indet.`	Paramelitidae `sp. Biologic-AMPH070`	PASS
BMR12195	26532	EPS0305R	-22.90866634	119.1663828	28/06/2023	Haul-Scrape	Paramelitidae `sp. indet.`	Paramelitidae `sp. Biologic-AMPH070`	PASS
BMR12178	21583	HEOP0478	-22.90399946	119.2150008	7/09/2023	Haul	Paramelitidae `sp. indet.`	Paramelitidae `sp. Biologic-AMPH024`	PASS
BMR13733	25848	EPS0306R	-22.91103853	119.1934837	12/04/2024	Haul	Paramelitidae `sp. indet.`	Paramelitidae `sp. Biologic-AMPH070`	PASS
BMR13734	27948	EPS1158R	-22.91236883	119.1973108	12/04/2024	Haul-Scrape	Paramelitidae `sp. indet.`	Paramelitidae `sp. Biologic-AMPH070`	PASS
BMR13735	30423	EPS1158R	-22.91236883	119.1973108	12/04/2024	Haul-Scrape	Paramelitidae `sp. indet.`	Paramelitidae `sp. Biologic-AMPH070`	PASS
BMR12966	30121	EPS1098R	-22.91055114	119.1899658	13/04/2024	Haul-Scrape	Paramelitidae `sp. indet.`	Paramelitidae `sp. Biologic-AMPH070`	PASS
BMR06007	16183	GWB0016S	-22.93165729	119.1848459	2022-05-12	Haul	Paramelitidae sp. `U3 plumose setae`	*Chydaekata* `sp. E TLF-2008`	PASS
BMR06012	15166	GWB0016S	-22.93165729	119.1848459	2022-05-12	Haul	*Chydaekata* sp.	*Chydaekata* `sp. E TLF-2008`	PASS
BMR06010	15634	GWB0017S	-22.91870963	119.2006409	2022-05-12	Haul	*Maarrka weeliwollii*	*Maarrka weeliwollii*	PASS

BMR	Unique ID code	Site	Dec_Lat	Dec_Long	Coll_Date	Coll_Method	Lowest_ID_Legacy	OTU_Name	Reaction_State
BMR06013	16181	GWB0017S	-22.91870963	119.2006409	2022-05-12	Haul	Paramelitidae sp. `U3 plumose setae`	Paramelitidae `sp. Biologic-AMPH024`	PASS
BMR06002	14501	HEOP0478	-22.90399946	119.2150008	2022-05-13	Haul	*Chydaekata* sp.	*Chydaekata* `sp. E TLF-2008`	PASS
BMR06003	16116	HEOP0478	-22.90399946	119.2150008	2022-05-13	Haul	Paramelitidae sp.	*Chydaekata* `sp. E TLF-2008`	PASS
BMR06011	14382	HEOP0478	-22.90399946	119.2150008	2022-05-13	Haul	*Chykdaekata*? sp.	*Chydaekata* `sp. E TLF-2008`	PASS
BMR06001	16178	HEOP0478	-22.90399946	119.2150008	2022-05-13	Haul	*Maarrka weeliwollii*	*Maarrka weeliwollii*	PASS
BMR06048	16148	GWB0032S	-22.91732353	119.2056657	2022-05-14	Haul	Paramelitidae sp. `U3 plumose setae`	*Chydaekata* `sp. E TLF-2008`	PASS
BMR06005	15438	GWB0032S	-22.91732353	119.2056657	2022-05-14	Haul	*Maarrka weeliwollii*	*Maarrka weeliwollii*	PASS
BMR06009	15343	Old BHP Camp	-22.91445062	119.2098208	2022-05-16	Haul	Paramelitidae sp.	Chydaekata `sp. E TLF-2008`	PASS
Malacostraca: Bathynellacea: Parabathynellidae									
BMR08514	19951	EPS0879R	-22.91012696	119.1636964	16/11/2022	Haul-Scrape	*Atopobathynella* `sp. indet.`	*Atopobathynella* `sp. Biologic-PBAT019`	PASS
BMR08515	19952	EPS0879R	-22.91012696	119.1636964	16/11/2022	Haul-Scrape	*Atopobathynella* `sp. indet.`	*Atopobathynella* `sp. Biologic-PBAT019`	PASS
BMR08516	19953	EPS0879R	-22.91012696	119.1636964	16/11/2022	Haul-Scrape	*Atopobathynella* `sp. indet.`	*Atopobathynella* `sp. Biologic-PBAT019`	PASS
Malacostraca: Isopoda: Armadillidae									
BMR11867	19148	EPS0622R	-22.91735359	119.1372821	15/11/2022	Trap	Philosciidae `sp. indet.`	Oniscidea `sp. Biologic-ISOP152`	PASS
BMR12964	30096	EPS0261R	-22.91411426	119.1432186	15/11/2022	Scrape	Philosciidae `sp. indet.`	Oniscidea `sp. Biologic-ISOP152`	PASS
BMR13746	19614	EPS0768R	-22.91456082	119.1505381	15/11/2022	Trap	Philosciidae `sp. indet.`	Oniscidea `sp. Biologic-ISOP152`	PASS
BMR12963	29874	EPS0244R	-22.90702231	119.1447432	18/11/2022	Trap	Philosciidae `sp. indet.`	Oniscidea `sp. Biologic-ISOP152`	PASS
BMR11868	20458	EPS0903R	-22.92564248	119.1662038	23/11/2022	Trap	Philosciidae `sp. indet.`	Oniscidea `sp. Biologic-ISOP152`	PASS

BMR	Unique ID code	Site	Dec_Lat	Dec_Long	Coll_Date	Coll_Method	Lowest_ID_Legacy	OTU_Name	Reaction_State
BMR13745	17662	EPS0824R	-22.91631828	119.1562195	23/11/2022	Trap	Philosciidae `sp. indet.`	Oniscidea `sp. Biologic-ISOP152`	PASS
BMR12013	21395	EPS0927R	-22.91056568	119.168107	27/06/2023	Haul-Scrape	Philosciidae `sp. indet.`	Isopoda `sp. Biologic-ISOP153`	PASS
Malacostraca: Isopoda: Armadillidae									
BMR11865	21876	EPS0819R	-22.92037716	119.1565295	27/06/2023	Scrape	*Troglarmadillo* `sp. indet.`	*Troglarmadillo* `sp. Biologic-ISOP151`	PASS
BMR11866	24767	EPS0819R	-22.92037716	119.1565295	27/06/2023	Trap	*Troglarmadillo* `sp. indet.`	*Troglarmadillo* `sp. Biologic-ISOP151`	PASS
Malacostraca: Isopoda: Tainisopidae									
BMR11869	23575	HEOP0478	-22.90399946	119.2150008	15/06/2023	Haul	*Pygolabis* `sp. indet.`	*Pygolabis weeliwolli*	PASS
BMR06104	16165	HEOP0478	-22.90399946	119.2150008	2022-05-13	Haul	*Pygolabis weeliwolli*	*Pygolabis weeliwolli*	PASS
Entognatha: Diplura: Japygidae									
BMR12002	23691	EPS0946R	-22.92775196	119.170999	26/06/2023	Haul-Scrape	Diplura `sp. indet.`	Japygidae `sp. B34`	PASS
BMR11995	21644	EPS0879R	-22.91012696	119.1636964	27/06/2023	Haul-Scrape	Japygidae `sp. indet.`	Japygidae `sp. DPL005`	PASS
BMR11996	26099	EPS0864R	-22.90766357	119.1634402	28/06/2023	Haul-Scrape	Japygidae `sp. indet.`	Japygidae `sp. B34`	PASS
BMR13878	29559	EPS0866R	-22.92359269	119.1637482	16/06/2024	Scrape	Japygidae `sp. indet.`	Japygidae `sp. B34`	PASS
Entognatha: Diplura: Parajapygidae									
BMR12194	26531	EPS0857R	-22.91008237	119.1607299	16/11/2022	Haul-Scrape	Diplura `sp. indet.`	Parajapygidae `sp. Biologic-DIPL092`	PASS
BMR11997	22210	EPS0864R	-22.90766357	119.1634402	28/06/2023	Haul-Scrape	Parajapygidae	Parajapygidae `sp. Biologic-DIPL090`	PASS
Entognatha: Diplura: Projapygidae									
BMR13747	20274	EPS0305R	-22.90866634	119.1663828	16/11/2022	Trap	Projapygidae `sp. indet.`		FAIL; bad sequence
BMR13879	30215	EPS0779R	-22.91874663	119.151627	16/06/2024	Scrape	Diplura `sp. indet.`	Projapygidae `sp. Biologic-DIPL108`	PASS
Insecta: Blattodea: Nocticolidae									
BMR11864	20037	EPS1109R	-22.91302888	119.1914424	17/11/2022	Haul-Scrape	*Nocticola* `sp. indet.`	*Nocticola cockingi*	PASS

BMR	Unique ID code	Site	Dec_Lat	Dec_Long	Coll_Date	Coll_Method	Lowest_ID_Legacy	OTU_Name	Reaction_State
BMR13932	23828	EPS0946R	-22.92775196	119.170999	26/06/2023	Haul-Scrape	*Nocticola* `sp. indet.`	*Nocticola cockingi*	PASS
BMR13930	23310	EPS0960R	-22.9098705	119.1712543	27/06/2023	Scrape	*Nocticola* `sp. indet.`	*Nocticola cockingi*	PASS
BMR11863	23547	EPS0864R	-22.90766357	119.1634402	28/06/2023	Haul-Scrape	*Nocticola* `sp. indet.`	*Nocticola cockingi*	PASS
BMR11985	26945	EPS0639R	-22.90928794	119.1385232	28/06/2023	Scrape	*Nocticola* `sp. indet.`	*Nocticola cockingi*	PASS
BMR11986	26913	EPS0589R	-22.91329065	119.1300942	28/06/2023	Scrape	*Nocticola* `sp. indet.`	*Nocticola cockingi*	PASS
BMR13931	23506	EPS0639R	-22.90928794	119.1385232	28/06/2023	Scrape	*Nocticola* `sp. indet.`	*Nocticola cockingi*	PASS
Insecta: Coleoptera									
BMR12190	26524	EPS1137R	-22.91192876	119.1944822	16/11/2022	Trap	Coleoptera `sp. indet.`		FAIL; bad seq
Insecta: Coleoptera: Carabidae									
BMR11685	19737	EPS0768R	-22.91456082	119.1505381	15/11/2022	Trap	Coleoptera `sp. indet.`	Latridiidae `sp. Biologic-COLE052`	PASS
BMR11686	18879	EPS0590R	-22.91283213	119.1300751	15/11/2022	Scrape	Coleoptera `sp. indet.`	*Typhlozuphium humicolum*	PASS
BMR11688	23584	EPS0588R	-22.91372819	119.1301664	28/06/2023	Scrape	Zuphiini `sp. indet.`	*Typhlozuphium humicolum*	PASS
Insecta: Coleoptera: Curculionidae									
BMR12971	30070	EPS1160R	-22.91572752	119.1987251	16/05/2022	Haul-Scrape	Curculionidae `sp. indet.`	Cryptorhynchinae `sp. B10`	PASS
BMR11687	22095	EPS1075R	-22.91126021	119.1870942	25/06/2023	Haul-Scrape	Curculionidae `sp. indet.`	Curculionidae `sp. B02`	PASS
BMR12191	26516	EPS0866R	-22.92359269	119.1637482	26/06/2023	Scrape	Curculionidae `sp. indet.`	Curculionidae `sp. B02`	PASS
BMR11689	23153	EPS0580R	-22.90428085	119.1285337	28/06/2023	Scrape	Curculionidae `sp. indet.`	Curculionidae `sp. B02`	PASS
Insecta: Coleoptera: Staphylinidae									
BMR12192	26487	EPS1121R	-22.91293158	119.1927415	17/11/2022	Trap	Staphylinidae `sp. indet.`	*Ptinella* `sp. Helix-CPT003`	PASS
BMR12193	26426	EPS1109R	-22.91302888	119.1914424	25/06/2023	Trap	Staphylinidae `sp. indet.`	*Ptinella* `sp. Helix-CPT003`	PASS
BMR12972	30223	EPS0767R	-22.91513697	119.1505255	27/06/2023	Scrape	Pselaphinae `sp. indet.`	Pselaphinae `sp. Biologic-COLE008`	PASS
BMR13934	24188	EPS0630R	-22.9083716	119.1376455	28/06/2023	Trap	Pselaphinae `sp. indet.`	Pselaphinae `sp. Biologic-COLE008`	PASS
Insecta: Hemiptera: Meenoplidae									

BMR	Unique ID code	Site	Dec_Lat	Dec_Long	Coll_Date	Coll_Method	Lowest_ID_Legacy	OTU_Name	Reaction_State
BMR12973	30077	EPS0776R	-22.90895849	119.1505245	18/11/2022	Haul-Scrape	Meenoplidae `sp. indet.`	*Phaconeura* `sp. Biologic-HEMI003`	PASS
BMR13882	19735	EPS0638R	-22.90968804	119.13882	18/11/2022	Scrape	Meenoplidae `sp. indet.`	*Phaconeura* `sp. Biologic-HEMI003`	PASS
BMR13880	21890	EEX0046	-22.91477458	119.1912693	25/06/2023	Scrape	Meenoplidae `sp. indet.`	*Phaconeura* `sp. WAM-PHAC001`	PASS
BMR12974	30267	EEX0050	-22.91389969	119.1631614	27/06/2023	Scrape	Meenoplidae `sp. indet.`	*Phaconeura* `sp. Biologic-HEMI003`	PASS
BMR13881	23615	EEX0711	-22.92025135	119.142678	29/06/2023	Scrape	Meenoplidae `sp. indet.`	*Phaconeura* `sp. WAM-PHAC001`	PASS
Insecta: Zygentoma: Nicoletiidae									
BMR11999	18903	EPS0243R	-22.90705156	119.1378101	18/11/2022	Trap	Atelurinae `sp. indet.`	Atelurinae `sp. Biologic-ZYGE071`	PASS
BMR13928	20518	EPS0977R	-22.92358135	119.1741229	24/11/2022	Scrape	Atelurinae `sp. indet.`	Atelurinae `sp. Biologic-ZYGE071`	PASS
BMR11690	23675	EPS1109R	-22.91302888	119.1914424	25/06/2023	Haul-Scrape	Atelurinae `sp. indet.`	Atelurinae `sp. Biologic-ZYGE071`	PASS
BMR13927	23858	EPS0852R	-22.91976268	119.1614348	27/06/2023	Scrape	Atelurinae `sp. indet.`	Atelurinae `sp. Biologic-ZYGE071`	PASS
BMR12001	23664	EPS0747R	-22.91288182	119.1481004	27/06/2023	Scrape	Nicoletiidae `sp. indet.`	*Trinemura* `sp. Biologic-ZYGE038`	PASS
BMR12000	23129	EPS0725R	-22.91189079	119.1443074	29/06/2023	Scrape	Lepidospora `sp. indet.`	*Trinemura* `sp. Biologic-ZYGE038`	PASS
BMR13929	29554	EPS0866R	-22.92359269	119.1637482	16/06/2024	Scrape	Atelurinae `sp. indet.`	Atelurinae `sp. Biologic-ZYGE071`	PASS
Maxillopoda: Cyclopoida: Cyclopidae									
BMR06078	15076	GWB0017S	-22.91870963	119.2006409	2022-05-12	Haul	*Diacyclops* cf. *humphreysi*	*Diacyclops* `sp. Biologic-CYCL037`	PASS
BMR06080	16154	GWB0016S	-22.93165729	119.1848459	2022-05-12	Haul	*Diacyclops* cf. *cockingi*	*Diacyclops* `sp. Biologic-CYCL037`	PASS
BMR06006	15097	HEOP0478	-22.90399946	119.2150008	2022-05-13	Haul	*Diacyclops* nr. *humphreysi*	*Diacyclops* `sp. Biologic-CYCL037`	PASS

BMR	Unique ID code	Site	Dec_Lat	Dec_Long	Coll_Date	Coll_Method	Lowest_ID_Legacy	OTU_Name	Reaction_State
BMR06060	15263	HEOP0478	-22.90399946	119.2150008	2022-05-13	Haul	*Diacyclops* cf. *cockingi*	*Diacyclops* `sp. Biologic-CYCL037`	PASS
BMR06081	16275	GWB0032D	-22.91733125	119.2057016	2022-05-13	Haul	*Diacyclops* cf. *humphreysi*	*Diacyclops* `sp. Biologic-CYCL037`	PASS
BMR06105	16159	GWB0032D	-22.91733125	119.2057016	2022-05-13	Haul	Cyclopoida sp.	*Diacyclops* `sp. Biologic-CYCL037`	PASS
BMR06034	15154	GWB0032S	-22.91732353	119.2056657	2022-05-14	Haul	*Diacyclops* cockingi	*Diacyclops* `sp. Biologic-CYCL037`	PASS
BMR06040	15642	GWB0032S	-22.91732353	119.2056657	2022-05-14	Haul	Cyclopoida sp.	*Diacyclops* `sp. Biologic-CYCL037`	PASS
BMR06082	16152	GWB0032S	-22.91732353	119.2056657	2022-05-14	Haul	*Diacyclops* cf. *humphreysi*	*Diacyclops* `sp. Biologic-CYCL037`	PASS
BMR06084	15285	GWB0017D	-22.91870713	119.2006338	2022-05-14	Haul	*Diacyclops* sp.	*Diacyclops* `sp. Biologic-CYCL037`	PASS
Maxillopoda: Harpacticoida: Ameiridae									
BMR06004	16288	GWB0016S	-22.93165729	119.1848459	2022-05-12	Haul	*Gordanitocrella trajani*	*Gordanitocrella* `sp. Biologic-HARP030`	PASS
BMR06079	16084	GWB0032D	-22.91733125	119.2057016	2022-05-13	Haul	Harpacticoida sp.	*Gordanitocrella* `sp. Biologic-HARP030`	PASS
BMR06094	16296	GWB0032D	-22.91733125	119.2057016	2022-05-13	Haul	*Gordanitocrella trajani*	*Gordanitocrella* `sp. Biologic-HARP030`	PASS
BMR06014	16147	GWB0032S	-22.91732353	119.2056657	2022-05-14	Haul	*Gordanitocrella trajani*	*Gordanitocrella* `sp. Biologic-HARP030`	PASS
Maxillopoda: Harpacticoida: Miraciidae									
BMR06008	15088	GWB0032S	-22.91732353	119.2056657	2022-05-14	Haul	*Schizopera* sp.	*Schizopera* `sp. Biologic-HARP031`	PASS
Maxillopoda: Harpacticoida: Parastenocarididae									
BMR06083	16297	GWB0032S	-22.91732353	119.2056657	2022-05-14	Haul	*Parastenocaris* sp.	*Parastenocaris* `sp. Biologic-HARP032`	PASS
Clitellata: Enchytraeida: Enchytraeidae									
BMR12199	19849	EEX0046	-22.91477458	119.1912693	17/11/2022	Scrape	Enchytraeidae `sp. indet.`	Enchytraeidae `sp. E6 LB-2015`	PASS

BMR	Unique ID code	Site	Dec_Lat	Dec_Long	Coll_Date	Coll_Method	Lowest_ID_Legacy	OTU_Name	Reaction_State
BMR12198	19609	EPS0869R	-22.92232929	119.1637156	23/11/2022	Trap	Enchytraeidae `sp. indet.`	Enchytraeidae `sp. Biologic-OLIG159	PASS
BMR12200	26520	EPS0857R	-22.91008237	119.1607299	7/09/2023	Haul-Scrape	Enchytraeidae `sp. indet.`	Enchytraeidae `sp. E6 LB-2015`	PASS
Clitellata: Tubificida: Phreodrilidae									
BMR12202	26512	EPS1096R	-22.91140943	119.1900193	17/11/2022	Haul-Scrape	Phreodrilidae `sp. 1 bifid-1 single-pointed`	Phreodrilidae `sp. P11 LB-2015`	PASS
BMR12201	26533	Old BHP Camp	-22.91445062	119.2098208	15/06/2023	Haul	Naididae `sp. indet.`	Phreodrilidae `sp. P11 LB-2015`	PASS
BMR12203	26506	EPS1098R	-22.91055114	119.1899658	25/06/2023	Haul-Scrape	Phreodrilidae `sp. 1 bifid-1 single-pointed`	Phreodrilidae `sp. P11 LB-2015`	PASS
BMR12204	23179	EPS1097R	-22.91107989	119.190051	25/06/2023	Haul-Scrape	Phreodrilidae `sp. 1 bifid-1 single-pointed`	Phreodrilidae `sp. P11 LB-2015`	PASS
BMR06096	15221	Old BHP Camp	-22.91445062	119.2098208	2022-05-16	Haul	Phreodrilidae `1 bifid-1 single-pointed`		FAIL; bad seq
BMR06437	17711	Old BHP Camp	-22.91445062	119.2098208	2022-05-16	Haul	Phreodrilidae `1 bifid-1 single-pointed`		FAIL; PCR
Clitellata: Tubificida: Naididae									
BMR08059	26507	Old BHP Camp	-22.91445062	119.2098208	15/06/2023	Haul	Phreodrilidae `sp. 1 bifid-1 single-pointed`	Naididae `sp. N1 LB-2015`	PASS
BMR06086	15389	GWB0016S	-22.93165729	119.1848459	2022-05-12	Haul	*Nais variabilis*	*Nais* `sp. Biologic-OLIG117`	PASS
BMR06103	14430	GWB0032D	-22.91733125	119.2057016	2022-05-13	Haul	*Pristina jenkinae*	Naididae `sp. N1 LB-2015`	PASS
BMR06087	15265	GWB0017D	-22.91870713	119.2006338	2022-05-14	Haul	*Pristina jenkinae*	Naididae `sp. N1 LB-2015`	PASS
BMR06100	16096	GWB0032S	-22.91732353	119.2056657	2022-05-14	Haul	*Pristina jenkinae*	Naididae `sp. N1 LB-2015`	PASS
BMR06101	15455	Old BHP Camp	-22.91445062	119.2098208	2022-05-16	Haul	*Pristina jenkinae*	Naididae `sp. N1 LB-2015`	PASS
Ostracoda: Podocopida: Candonidae									
BMR12011	21778	HEOP0478	-22.90399946	119.2150008	24/11/2022	Haul	*Meridiescandona* `sp. indet.`	*Meridiescandona* `sp. Biologic-OSTR057`	PASS
BMR12012	21587	HEOP0478	-22.90399946	119.2150008	24/11/2022	Haul	*Meridiescandona* `sp. indet.`	*Meridiescandona* `sp. Biologic-OSTR057`	PASS

BMR	Unique ID code	Site	Dec_Lat	Dec_Long	Coll_Date	Coll_Method	Lowest_ID_Legacy	OTU_Name	Reaction_State
BMR13730	22632	HEOP0478	-22.90399946	119.2150008	7/09/2023	Haul	Candonidae `sp. indet.`	*Meridiescandona* `sp. Biologic-OSTR057`	PASS
BMR13732	26811	HEOP0478	-22.90399946	119.2150008	12/04/2024	Haul	Candonidae `sp. indet.`	*Meridiescandona* `sp. Biologic-OSTR057`	PASS
BMR06098	16186	GWB0017S	-22.91870963	119.2006409	2022-05-12	Haul	*Notacandona boultoni*	*Notacandona boultoni*	PASS
BMR06090	16097	GWB0016S	-22.93165729	119.1848459	2022-05-12	Haul	*Notacandona modesta*	*Notacandona modesta*	PASS
BMR06493	18438	HEOP0478	-22.90399946	119.2150008	2022-05-13	Haul	*Meridiescandona marillanae*	*Meridiescandona* `sp. Biologic-OSTR057`	PASS
BMR06494	18462	GWB0032S	-22.91732353	119.2056657	2022-05-14	Haul	*Notacandona boultoni*	*Notacandona boultoni*	PASS
BMR06113	16182	GWB0032S	-22.91732353	119.2056657	2022-05-14	Haul	*Notacandona modesta*	*Notacandona modesta*	PASS
BMR06093	16283	Old BHP Camp	-22.91445062	119.2098208	2022-05-16	Haul	*Meridiescandona marillanae*	*Meridiescandona* `sp. Biologic-OSTR057`	PASS
BMR13731	23149	EPS1109R	-22.91302888	119.1914424	2023-09-07	Haul-Scrape	*Meridiescandona marillanae*	*Meridiescandona* `sp. Biologic-OSTR057`	PASS
BMR12969	30074	HEOP0478	-22.90399946	119.2150008	2024-04-12	Haul	*Meridiescandona marillanae*	*Meridiescandona* `sp. Biologic-OSTR057`	PASS
Ostracoda: Podocopida: Darwinulidae									
BMR06091	16260	GWB0016S	-22.93165729	119.1848459	2022-05-12	Haul	*Vestalenula* sp.		FAIL; contamination
Ostracoda: Podocopida: Limnocytheridae									
BMR06088	16279	GWB0032S	-22.91732353	119.2056657	2022-05-14	Haul	*Notacandona boultoni*	*Gomphodella* `sp. Biologic-OSTR078`	PASS
BMR06112	16089	GWB0032S	-22.91732353	119.2056657	2022-05-14	Haul	*Gomphodella yandii*		FAIL; PCR
Pauropoda: Tetramerocerata									
BMR08504	26567	EPS0883R	-22.92602224	119.1651974	23/11/2022	Scrape	Pauropoda `sp. indet.`	Pauropoda `sp. Biologic-PAUR075`	PASS
BMR11984	27030	EPS1097R	-22.91107989	119.190051	25/06/2023	Haul-Scrape	Pauropoda `sp. indet.`	Pauropoda `sp. Biologic-PAUR072`	PASS
BMR11982	23651	EPS0887R	-22.9241214	119.1651045	26/06/2023	Scrape	Pauropoda `sp. indet.`	Pauropoda `sp. Biologic-PAUR074`	PASS

BMR	Unique ID code	Site	Dec_Lat	Dec_Long	Coll_Date	Coll_Method	Lowest_ID_Legacy	OTU_Name	Reaction_State
BMR11983	23652	EEX0050	-22.91389969	119.1631614	27/06/2023	Scrape	Pauropoda `sp. indet.`	Pauropoda `sp. Biologic-PAUR073`	PASS
BMR11980	21603	EPS0244R	-22.90702231	119.1447432	28/06/2023	Scrape	Pauropoda `sp. indet.`	Pauropoda `sp. Biologic-PAUR074`	PASS
BMR12806	27596	EPS0813R	-22.90960775	119.1552994	15/04/2024	Haul-Scrape	Pauropoda `sp. indet.`	Pauropoda `sp. Biologic-PAUR085`	PASS
BMR12970	29557	EPS0928R	-22.90970443	119.1680652	15/04/2024	Trap	Pauropoda `sp. indet.`	Pauropoda `sp. Biologic-PAUR086`	PASS
BMR12962	30483	EPS0927R	-22.91056568	119.168107	15/04/2024	Haul-Scrape	Pauropoda `sp. indet.`	Pauropoda `sp. Biologic-PAUR087`	PASS
Pauropoda: Tetramerocerata: Pauropodidae									
BMR11979	19798	EPS0984R	-22.9138975	119.174093	24/11/2022	Haul-Scrape	Pauropoda `sp. indet.`	*Decapauropus* `sp. WAM-PAUD002`	PASS
BMR12182	26518	EPS1075R	-22.91126021	119.1870942	25/06/2023	Haul-Scrape	Pauropoda `sp. indet.`	*Decapauropus* `sp. WAM-PAUD002`	PASS
BMR11981	22680	EPS1109R	-22.91302888	119.1914424	7/09/2023	Haul-Scrape	Pauropoda `sp. indet.`	*Decapauropus* `sp. WAM-PAUD002`	PASS
Symphyla: Cephalostigmata: Scolopendrellidae									
BMR13933	30319	EPS0894R	-22.92100666	119.1651356	16/06/2024	Scrape	Symphyla `sp. indet.`	Scolopendrellidae `sp. Biologic-SYMP089`	PASS
Symphyla: Cephalostigmata: Scutigerellidae									
BMR11994	19059	EPS0971R	-22.92003887	119.1724571	23/11/2022	Scrape	Hanseniella `sp. indet.`	*Hanseniella* `sp. Biologic-SYMP077`	PASS
BMR12804	27581	EPS0927R	-22.91056568	119.168107	15/04/2024	Haul-Scrape	Scutigerellidae `sp. indet.`	*Hanseniella* `sp. Biologic-SYMP088`	PASS