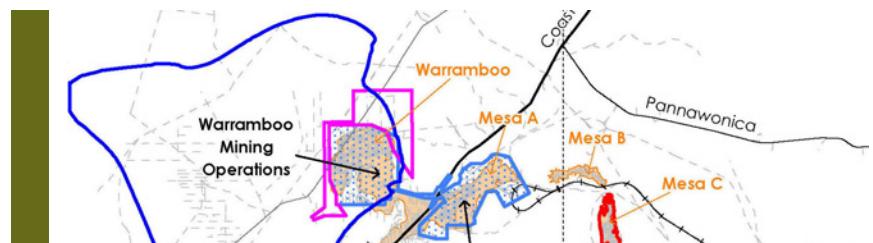




# Mesa A Hub: Warramboo and Mesa C Stygofauna Assessment



Prepared for Rio Tinto

October 2017





**Biota  
Environmental  
Sciences**

© Biota Environmental Sciences Pty Ltd 2017  
ABN 49 092 687 119  
Level 1, 228 Carr Place  
Leederville Western Australia 6007  
Ph: (08) 9328 1900 Fax: (08) 9328 6138

Job No.: 1080c

Prepared by: Jason Alexander

**Document Quality Checking History**

Version: A	Peer review:	Nicola Watson
Version: B	Director review:	Garth Humphreys
Version: B	Format review:	Fiona Hedley

Approved for issue: Garth Humphreys

This document has been prepared to the requirements of the client identified on the cover page and no representation is made to any third party. It may be cited for the purposes of scientific research or other fair use, but it may not be reproduced or distributed to any third party by any physical or electronic means without the express permission of the client for whom it was prepared or Biota Environmental Sciences Pty Ltd.

This report has been designed for double-sided printing. Hard copies supplied by Biota are printed on recycled paper.

This page intentionally blank

# Warramboo and Mesa C Stygofauna Assessment

## Contents

<b>1.0</b>	<b>Project Summary</b>	<b>9</b>
<b>2.0</b>	<b>Executive Summary</b>	<b>11</b>
<b>3.0</b>	<b>Introduction</b>	<b>13</b>
3.1	Project Background	13
3.2	Spatial Scales Used in this Report	13
3.3	Study Objectives and Scope	13
3.4	Purpose of the Report	15
3.5	Stygobitic Fauna Overview	15
<b>4.0</b>	<b>Methodology</b>	<b>17</b>
4.1	Desktop Review and Database Search	17
4.2	Habitat Characterisation	18
4.3	Sampling Methodology	19
4.4	Molecular Analysis	19
4.5	Categorisation of Conservation Significance	20
4.6	Survey Design	20
4.7	Survey Limitations	27
<b>5.0</b>	<b>Results</b>	<b>29</b>
5.1	Study Area Habitat Characterisation	29
5.2	Desktop Review	39
<b>6.0</b>	<b>Discussion</b>	<b>60</b>
6.1	Conservation Significance	60
6.2	Habitat Suitability	69
6.3	Conclusions	71
<b>7.0</b>	<b>Glossary</b>	<b>72</b>
<b>8.0</b>	<b>References</b>	<b>74</b>

### **Appendix 1**

Licence to take Fauna for Scientific Purposes

### **Appendix 2**

Molecular Reports

### **Appendix 3**

WAM SRE Categories

### **Appendix 4**

Report on the Morphological Identification of Collected Inermipes

### **Appendix 5**

Desktop Review; Study Comparison;

Stygobitic Fauna Species List; and Conservation Significance

## Appendix 6

### Raw Sampling Data (Warramboo and Mesa C)

#### Tables

Table 1.1: Summary of project specifications and limitations.	9
Table 4.1: Summary and location of database searches completed for the current scope.	17
Table 4.2: Conservation classification used within this report.	20
Table 4.3: Summary of field mobilisations completed for the Warramboo stygofauna study area.	20
Table 4.4: Location and summary of all phases of sites successfully sampled from Warramboo.	23
Table 4.5: Location and summary of Phase 1 sites successfully sampled at Mesa C.	25
Table 5.1: Mapped and inferred BWT geology of the study area.	34
Table 5.2: Prospectivity of the geological units within the study area to provide stygofauna habitat.	36
Table 5.3: Description of PECs overlapping the study area and desktop review boundaries.	36
Table 5.4: Summary of previous stygobitic fauna surveys within the study area.	39
Table 5.5: Summary of stygofauna records returned from database searches within the study area.	39
Table 5.6: Summary of morphological identifications and locations of desktop review specimens in relation to the Warramboo drawdown extent and buffer extent.	43
Table 5.7: Summary of morphological identifications and locations of desktop review specimens in relation to the Mesa C drawdown extent.	47
Table 5.8: Summary of higher order taxa collected from Warramboo during three phases of sampling.	49
Table 5.9: Taxonomic summary and locations of fauna identified from sampling within the Warramboo drawdown and buffer extents.	50
Table 5.10: Summary of higher order taxa collected from Mesa C during three phases of sampling.	55
Table 5.11: Taxonomic summary and locations of fauna identified from sampling within the Mesa C drawdown and buffer extents.	58
Table 6.1: Summary of species recorded from the Warramboo modelled drawdown and buffer extents during this survey and collated from the desktop review, including their distributions and WAM SRE status.	62
Table 6.2: Summary of species recorded from the Mesa C modelled drawdown extent during this survey and collated from the desktop review, including their distributions and WAM SRE status.	67
Table 6.3: Overall habitat suitability of the study area.	69

## Figures

Figure 3.1: Location of the modelled drawdown extent and study area in relation to Mesa A and Warramboo mining operations.	14
Figure 4.1: Climate and weather graph depicting long-term and monthly averages for the year preceding the final field mobilisation.	22
Figure 4.2: Location of stygofauna sites sampled at Warramboo in relation to sites sampled previously.	24
Figure 4.3: Location of stygofauna sites sampled at Mesa C in relation to sites sampled previously.	26
Figure 5.1: Water catchments, surface water drainage direction and aquifers within the study area.	30
Figure 5.2: Warramboo Modelled Robe Pisolite contours and thickness below the water table.	31
Figure 5.3: Cross-section of Warramboo showing water table in relation to geology. (Image supplied by Rio Tinto, cross-section location displayed in Figure 5.1).	32
Figure 5.4: Extent of the Robe Pisolite geology at Mesa C.	33
Figure 5.5: Cross-section of Mesa C showing water table in relation to geology and Robe River. (Image supplied by Rio Tinto; cross section location displayed in Figure 5.1).	34
Figure 5.6: Prospective stygofauna habitat within the study area in relation to sampled sites.	37
Figure 5.7: Location of PECs relevant to the current study area.	38
Figure 5.8: Location of higher order collections and sites sampled during previous studies within the study area.	41
Figure 5.9: Location of species previously recorded from within the buffered drawdown extent at Warramboo and their wider distribution within the study area – Map 1.	45
Figure 5.10: Location of species previously recorded from within the buffered drawdown extent at Warramboo and their wider distribution within the study area – Map 2.	46
Figure 5.11: Location of species previously recorded from within the buffered drawdown extent at Mesa C and their wider distribution within the study area.	48
Figure 5.12: Location of species collections from within the drawdown and buffer extents at Warramboo.	52
Figure 5.13: Excerpts of Bayesian analysis of CO1 haplotypes of the family Niphargidae (above), Paramelitidae (below) collected from Warramboo and Mesa C.	53
Figure 5.14: Excerpts of Bayesian analysis of CO1 haplotypes of the family Eriopisidae collected from Warramboo and Mesa C.	54
Figure 5.15: Location of species collections from within the drawdown and buffer extents at Mesa C.	59
Figure 6.1: Stygofauna (current and previous records) collection location in relation to habitat suitability within the study area.	70

This page intentionally blank.

# 1.0 Project Summary

In accordance with the Rio Tinto scope of work, Table 1.1 presents a summary of survey and project information.

Table 1.1: Summary of project specifications and limitations.

Project Name	Mesa A Hub: Warramboo and Mesa C Stygofauna Assessment
Level of Survey	Level 2 stygofauna survey
Location	Approximately 38 km west of Pannawonica township
Study Area Size	5,566.4 km <sup>2</sup>
Survey Timing	Surveys completed between June 2015 – March 2017
Relevant Regulatory Guidance Documents and Applicable Legislation	<ul style="list-style-type: none"> <li>• EPA Statement of Environmental Principles, Factors and Objectives (EPA 2016a);</li> <li>• Environmental Factor Guideline – Subterranean Fauna (EPA 2016b);</li> <li>• Technical Guidance - Subterranean fauna survey (EPA 2016c); and</li> <li>• Technical Guidance - Sampling methods for subterranean fauna (EPA 2016d).</li> </ul>
Key Survey Limitations	<ul style="list-style-type: none"> <li>• There is limited mapping of geological units below water table, with the exception of the Robe Pisolite.</li> <li>• A representative subset of 154 of the total of 178 Amphipoda specimens collected during this study were sequenced. Thirty-nine of the 154 specimens failed to yield a sequence, most often due to DNA degradation.</li> <li>• Most Amphipoda specimens were identified based on sequence data due to the predominance of juvenile and damaged specimens and some unresolved issues with past subterranean amphipod taxonomy, meaning that specimens were not resolved morphologically.</li> <li>• For most taxa, only adult specimens have diagnostic morphological characteristics necessary to be identified to species level and few adult specimens were obtained for most taxonomic groups.</li> <li>• Stygofauna sampling from sites within the drawdown extent at Warramboo was predominantly restricted to monitoring bores (sites with prefix MB) and water bores (sites with prefix WB), which are typically constructed with 1 mm slots in the casing, aimed at allowing the flow of water but limiting sediment ingress. This casing design can inhibit the movement of stygofauna with larger body morphologies and limit species recorded, thereby biasing the data. Reference sites were older and often large pastoral wells or uncased and thus likely to allow ingress of a wider range of stygofauna.</li> <li>• Conservation significance could not be assigned to taxa that were unable to be identified to species level (such as Amphipoda sp. 'indet' or Paramelitidae sp. 'indet') as these specimens may represent multiple species or may equate to a species already known elsewhere.</li> </ul>

This page intentionally blank.

## 2.0 Executive Summary

Rio Tinto is currently evaluating the development of a number of iron ore deposits within the Robe Valley, located in the Pilbara region of Western Australia. One such prospective development, the Mesa A Hub, is located within the western portion of the Robe Valley (approximately 45 km west of Pannawonica), and encompasses multiple proposed projects including Warramboo and Mesa C below water table mining. Mining of both the Warramboo and Mesa C deposits has the potential to impact local subterranean fauna communities (troglobitic and stygobitic fauna) that are known to be prevalent within the Robe Valley. To inform the assessment of these impacts, Rio Tinto commissioned Biota Environmental Sciences (Biota) to survey and assess the stygobitic fauna communities of Warramboo and Mesa C. This Level 2 survey comprised three phases of sampling at Warramboo (between June 2015 and December 2016), and two phases at Mesa C (between December 2016 and March 2017), as well as the completion of a desktop review collating previous relevant data from the wider area.

Twenty-five sites were sampled for stygofauna at Warramboo with 15 of the 25 sites repeat sampled in consecutive phases. Seven sites were sampled outside of the modelled drawdown extent and comprised mostly pastoral bores and wells and uncased drillholes. The remaining 18 sites were all located within the proposed drawdown extent and comprised mostly cased groundwater monitoring and water production bores. Twenty-three sites were sampled for stygofauna at Mesa C with nine sites sampled across both phases. Ten sampled sites were located outside the modelled drawdown extent, with the remaining 13 sites located within the drawdown extent.

The desktop review returned a total of 8,179 stygobitic fauna specimens recorded from the study area (a contextual area extending from Warramboo and Mesa C east to the headwaters of Bungaroo Creek) between 2002 and 2016, however 1,659 specimens were unable to be identified to species level. The remaining 6,520 specimens represented 128 distinct species.

Three species from the desktop review are currently listed as conservation significant. Two amphipod species, *Nedsia hurlberti* and *Nedsia sculptilis*, and the Blind Cave Eel, *Ophisternon candidum*, are Schedule 3 species in Western Australia. *Ophisternon candidum* is also listed as Vulnerable under the Environment Protection and Biodiversity Conservation Act 1999. None of these species have been recorded within the drawdown extents at Warramboo or Mesa C.

Seventy-five of the previously collected specimens collated during the desktop review came from within the drawdown extent at Warramboo. These represented 12 species from six orders and two phyla. The ostracod *Cypretta* sp. '4' is the only species from the desktop review results known solely from the within the Warramboo drawdown extent. The desktop review indicated that no stygobitic fauna were previously known from within the modelled drawdown extent at Mesa C.

A total of 369 stygofauna specimens were identified from the three phases of sampling at Warramboo, representing nine orders. Six species were recorded from within the drawdown extent at Warramboo and a further 19 from sampling within a buffer on the drawdown extent, which conservatively allows for uncertainty in the hydrogeological modelling.

A total of 276 stygofauna specimens were recorded from Mesa C sites during the two phases, representing eight orders. Two species were recorded from within the Mesa C drawdown extent and a further 19 were recorded from within the buffer on the drawdown extent.

From the combined desktop review and sampling results, a total of 18 species of stygofauna have been recorded from within the Warramboo drawdown extent, plus a further 53 from within the buffer on the drawdown extent; meaning a total of 71 stygal species are known from the maximal potential extent of the proposed drawdown at Warramboo. Sixteen of these species are categorised as being potential SRE species, based on WAM SRE guidelines. This includes four only known from the drawdown extent and an additional eight known only from the buffered drawdown extent. These species are mostly poorly represented in collections.

The combined Mesa C desktop review and sampling data show two species that are known from the drawdown extent, with a further 27 from the buffer extent, meaning a total of 29 species occur within the maximum potential drawdown area at Mesa C. Ten of these, including the two species from the drawdown extent, represent potential SRE species. The Seven of the potential SRE species are recorded only from the combined drawdown and buffer extents. The two species recorded from drawdown extent have been recorded elsewhere in the Robe Valley, however one is only recorded elsewhere within the buffer extent at Mesa C. The remaining three species are recorded from the wider study area or Pilbara bioregion.

Of the 5,566.4 km<sup>2</sup> study area, 252.6 km<sup>2</sup> represents high prospectivity habitat and 1,956 km<sup>2</sup> medium prospectivity, totalling almost 39.7% of the study area. Specimen collections were spatially distributed over all of the habitat prospectivity categories, with 45.2% of specimens recorded from groundwater in low prospectivity habitat. This is a function of the generally widespread nature of stygofauna habitat across at least a third of the study area. Considering this, and that at least 59 of the species recorded are widespread and occur in the wider Pilbara region, there is little evidence of significant barriers to dispersal across high and medium prospectivity stygofauna habitat at study area scale.

Given:

- what is currently known about the hydraulic connectedness hydrogeology of the study area;
- the extents of the proposal drawdown and the provisional buffer on that modelled extent at both Warramboo and Mesa C; and
- the wide spread species categorisation and distributions documented for 58 stygofauna species known from the combined drawdown and buffer extents at Warramboo and Mesa C,

it is likely that the 16 species that appear to be restricted to the combined drawdown and buffer extents at Warramboo and Mesa C are actually more widespread, and the result is an artefact of ecological sampling effects.

# 3.0 Introduction

## 3.1 Project Background

Rio Tinto is currently evaluating the development of a number of iron ore deposits within the Robe Valley, located in the Pilbara region of Western Australia. One such prospective development, the Mesa A Hub, is located within the western portion of the Robe Valley (approximately 45 km west of Pannawonica), and encompasses multiple proposed projects including Warramboo and Mesa C below water table (BWT) mining (Figure 3.1). Mining of the above water table Warramboo deposit is currently approved (EPA 2007), with the Mesa A Hub proposal entailing an expansion to current operations as well as mining BWT.

Mining of both the Warramboo and Mesa C deposits has the potential to impact local subterranean fauna communities (troglobitic and stygobitic fauna) that are known to be prevalent within the Robe Valley. To inform the assessment of these impacts, Rio Tinto wishes to build on the available information on these communities by collating existing data, determining knowledge gaps, and completing additional and baseline sampling at Waramboo and Mesa C, respectively.

As Rio Tinto proposes to mine below the water table at both Warramboo and Mesa C, lowering of the water table via dewatering will be required. Given this potential impact, Rio Tinto commissioned Biota Environmental Sciences (Biota) to survey and assess the stygobitic fauna communities of Warramboo and Mesa C. This level 2 survey comprised three phases of sampling at Warramboo, and two phases at Mesa C, as well as the completion of a desktop review collating previous relevant data from the wider study area.

## 3.2 Spatial Scales Used in this Report

For the purposes of this report, the following terms are used as defined below:

- |                 |   |
|-----------------|---|
| Study Area      | - The overall locality encompassing the drawdown extent, buffer extent and the desktop review (Figure 3.1).   |
| Drawdown Extent | - Refers to the area of modelled groundwater drawdown for both the Mesa C and Warramboo developments (Figure 3.1).  |
| Buffer Extent   | - Refers to the area covered by the 10 km buffer at Warramboo and Mesa C (Figure 3.1), to conservatively provision for uncertainty in the groundwater modelling of drawdown extent. |

## 3.3 Study Objectives and Scope

The scope of this study was to undertake an assessment of stygobitic fauna and habitat suitability within the study area. The key objectives of this study were as follows:

1. conduct a desktop review of relevant data available from the study area (Section 5.2);
2. conduct a multiple-phase sampling programme to document any stygofauna communities present within the drawdown extent and immediate surrounds (Section 5.2.4); and
3. assess the distribution of the recorded fauna in relation to the drawdown extent, place them into regional context, and discuss potential conservation significance (Section 5.2.5).

The study was planned and implemented as far as practicable in accordance with:

- EPA Statement of Environmental Principles, Factors and Objectives (EPA 2016a);
- Environmental Factor Guideline – Subterranean Fauna (EPA 2016b);
- Technical Guidance - Subterranean fauna survey (EPA 2016c); and
- Technical Guidance - Sampling methods for subterranean fauna (EPA 2016d).

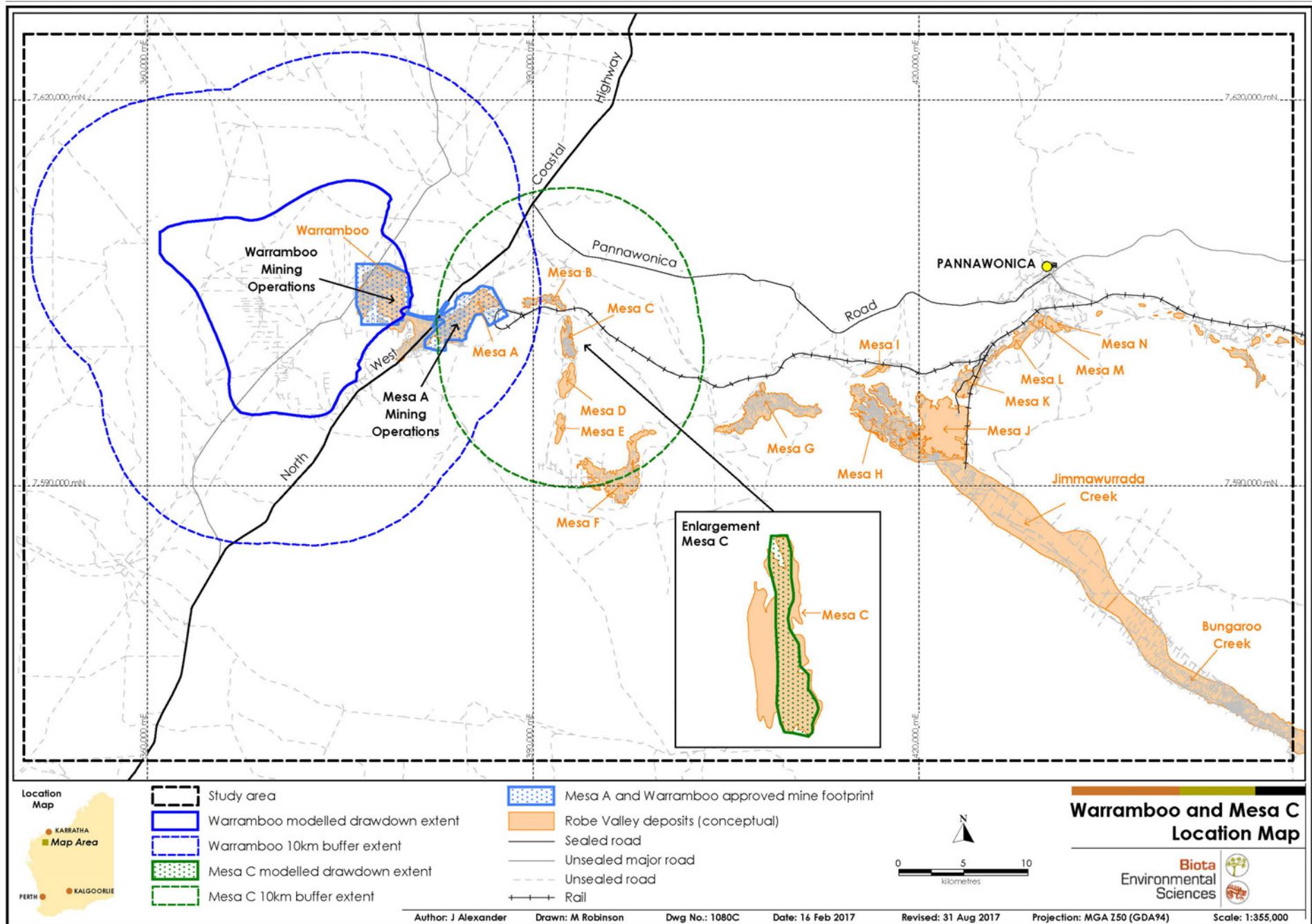


Figure 3.1: Location of the modelled drawdown extent and study area in relation to Mesa A and Warramboo mining operations.

## 3.4 Purpose of the Report

The purpose of this report is to provide supporting information for the forthcoming environmental impact assessment (EIA) of proposed below water table mining and dewatering at both the Warramboo deposit and the Mesa C deposit.

This report presents the findings of the desktop review and documents the methodology, sampling effort and results of the stygobitic fauna survey completed within the study area. Both the field sampling and report are subject to specific limitations that are discussed in Section 4.7.

## 3.5 Stygobitic Fauna Overview

Australia was historically thought to lack habitat suitable for subterranean fauna. However studies in recent decades (mostly with an emphasis on EIA) have revealed Australia to be highly diverse in subterranean fauna, with numerous areas of interest throughout the continent (Guzik et al. 2010). In Western Australia, these zones of subterranean biodiversity can be found at Cape Range, Barrow Island, the Pilbara bioregion, the Yilgarn and the Nullarbor (Humphreys 2001a, Page et al. 2008, Guzik et al. 2010).

Surveys in the Pilbara have collected subterranean fauna from a range of geological units such as pisolithic iron formations, channel iron deposits, unconsolidated alluvium and sedimentary basalt (Marmonier et al. 1993, Biota 2004a, 2006a, 2010, 2011, 2013). This indicates that the suitability of subterranean fauna habitat is mostly a function of the availability of habitable space rather than a specific geological unit (Marmonier et al. 1993, Humphreys 1999, Biota 2006a),

Obligate subterranean fauna can be categorised into two distinct ecological groups:

1. Troglofauna - Survive only in air-filled cavities and interstices between the surface and the water table (not covered in this overview); and
2. Stygofauna – Which comprise aquatic taxa occurring in groundwater aquifers and subterranean water bodies.

Stygofaunal communities in Western Australia are predominantly Crustacean (e.g. Amphipoda, Isopoda, Decapoda, Syncarida, Ostracoda and Copepoda), however Annelida (e.g. Oligochaeta), Arachnida (e.g. Hydracarina) and Platyhelminthes are also commonly collected. Three species of stygofaunal vertebrates have been recorded from Australia. This includes two species of blind gudgeon (*Milyeringa veritas*, and *M. justitia*) as well as a Blind Cave Eel, *Ophisternon candidum* (Humphreys 2001b, DSEWPaC 2008, Foster and Humphreys 2011, Larson et al. 2013). The Blind Cave Eel has been recorded from Cape Range, Barrow Island and from the Bungaroo Valley, which falls within the study area of this report (Figure 3.1; Section 5.2) (Biota 2015a, 2016a).

This page intentionally blank.

# 4.0 Methodology

## 4.1 Desktop Review and Database Search

### 4.1.1 Review of Previous Stygofauna Surveys

A literature review was completed to identify relevant previous surveys from within the study area. This included searches of Biota's library database, GoogleScholar<sup>1</sup> and the EPA's website, in addition to the identification of previous surveys via database specimen records (Section 4.1.2). Reports and data supplied by Rio Tinto were also collated with the results of the literature search and reviewed.

### 4.1.2 Database Searches

The following databases were searched to assist with the compilation of a list of potential species for the study area:

1. NatureMap: a collaboration between the Department of Parks and Wildlife and the Western Australian Museum (WAM). This database represents the most comprehensive source of information on the distribution of Western Australia's fauna, comprising records from the Fauna Survey Returns database and WA Threatened Fauna Database (both maintained by the Department of Parks and Wildlife) and the WAM Specimen Database.
2. Atlas of Living Australia (ALA): a collaborative project between academic collecting institutions, private individual collectors and community groups. The atlas contains occurrence records, environmental data, images and the conservation status of species throughout Australia.
3. WAM's Crustacea database.
4. Department of Parks and Wildlife Pilbara Stygofauna Survey (PSS): results from a series of baseline stygofauna sampling carried out over the Pilbara region.
5. Biota Internal Database: This database includes all of the subterranean fauna data collected by Biota within Western Australia, including the majority of the collections from the Robe River valley locality.

Searches of the Department of Parks and Wildlife Priority Ecological Communities (PEC), Threatened Ecological Communities (TEC) and Environmentally Sensitive Areas databases were completed using the same bounding coordinates as the stygofauna database search (Table 4.1, Figure 3.1). Results for the desktop review are shown in Section 5.2.

Details of database searches conducted are summarised in Table 4.1, and Figure 3.1 shows the areas included in the searches.

Table 4.1: Summary and location of database searches completed for the current scope.

Database	Date	Search Target	Bounding Coordinates	
			Easting (m E)	Northing (m N)
Biota, NatureMap, ALA and PSS	23/01/17	Stygofauna	360500	7568700
			449050	7625135
WAM	11/11/15	Crustacea	393957	7607800
			376398	7599100
TECs and PECs	17/11/15	TECs and PECs	360500	7568700
			449050	7625135
Environmentally Sensitive areas	17/11/15	Environmentally Sensitive areas	360500	7568700
			449050	7625135

<sup>1</sup> <https://scholar.google.co.uk>

## 4.2 Habitat Characterisation

The likely habitats for stygofauna in the study area were initially characterised using a combination of regional information and site-specific geological data. Inputs considered in this process, where available, included:

1. the spatial extent of the study area in order to define the geological units that may be affected;
2. regional surface geology mapping;
3. hydrological and hydrogeological information, including the continuity of the aquifer and transmissivity of the aquifer substrate;
4. stratigraphic logging, images and information from drillholes in the study area;
5. previous sampling effort in the locality and the results of published and unpublished studies on stygobitic fauna communities; and
6. identification of rock types that have previously yielded stygofauna records from the study area and wider locality.

The habitat units identified through this process were assigned a likelihood to support stygal communities based on the above inputs, and then revisited on completion of the sampling component of this study, to further investigate if the spatial distribution of the fauna records provide support for the habitat model.

We have categorised the likelihood of the geological units within the study area to be a suitable habitat for stygofauna into Low, Moderate and High, based on the following characteristics:

- A) Presence of interstitial spaces or vugs.
- B) Continuity and transmissivity of the local occurrence of submerged geological units.
- C) The known occurrence of stygal communities from equivalent rock types during previous Pilbara surveys.
- D) Absence of large amounts of fine sediments such as clays, silts and sands within the geological unit description.
- E) Substrate permits inflow of surface water and nutrients infiltration.
- F) Substrate submerged below the water table.

Likelihood categories were then determined as follows:

- |        |  |
|--------|--|
| Low    | - Suitable geological unit may occur only above the water table within the study area. Rock type might have interstitial spaces (A) however may have high levels of fine sediments which reduce usability of spaces. Stygofauna not known from previous studies sampling of the same geology (C).  |
| Medium | - Unit likely partially or completely submerged below the water table (F). Presence of interstitial spaces (A), low numbers of stygofauna have been recorded from this geology previously (C). Small amounts of fine sedimented within the unit (D)  |
| High   | - Majority (five or six) categories confirmed for the geological unit, including the presence of continuous, transmissive aquifer (A, B). Geology sufficiently porous to allow nutrient infiltration from surface water runoff (E). Stygofauna routinely recorded from same rock type (D) and partially or completely submerged below the water table (F). |

Habitat suitability was visualised by plotting all stygofauna collections in the study area mapped within their prospectivity categories, using a 500 m buffer as a conservative extent for records. This allowed delineation of areas of highly prospective habitat with stygofauna records, from those without confirmed records but that are likely to be highly prospective based on geological knowledge. All areas within the buffer zones are treated as confirmed stygofauna habitat, while the area outside is inferred habitat.

## 4.3 Sampling Methodology

The Level 2 stygofauna survey was completed under “Licence to Take Fauna for Scientific Purposes” No. SF010296, SF10921 and 08-000238-1 issued to Jason Alexander (Appendix 1). Methodology and approach were consistent with those outlined in EPA Technical Guidance; Sampling Methods for Subterranean Fauna (EPA 2016e) and Technical Guidance: Subterranean Fauna Survey (EPA 2016c). Similar methodologies have been used in previous Robe Valley subterranean fauna assessments (Biota 2015a).

### 4.3.1 Stygofauna Sampling

Stygofauna were sampled using modified plankton haul nets, constructed from 70 µm plankton mesh, with 50 mm and 100 mm apertures attached to a stainless steel catch cylinder. Nets were lowered to the bottom of water bores and drill holes before being slowly hauled through the water column to the surface where the contents of the cylinder were flushed into a uniquely labelled container. Each monitoring site was sampled in this way a total of five times. On the final haul the net was agitated gently to stir the benthos layer and mobilise any fauna present for more effective specimen collecting. Specimens were stored in a shaded esky in order to keep the sample cool prior to sorting and identification.

Following sampling of each monitoring site, the nets were thoroughly rinsed with water, inspected and where possible, left to dry before using on another site. This prevented cross-contamination of specimens between sampling sites.

### 4.3.2 Data Management

Preliminary field identification of subterranean fauna occurred in-situ and comprised identification of specimens to order level, where possible, or separation of specimens into morphotypes. Sorting was completed using dissecting microscopes (Olympus SZ40 and SZ61, magnification up to 40x). Morphotypes were then assigned a unique number based on drillhole name, date and method of collection. Specimens were re-preserved in 100% ethanol once separated out into morphotypes, which allows for both morphological and molecular analyses.

## 4.4 Molecular Analysis

Molecular analysis of the order Amphipoda was conducted to determine the number of species present, and to compare the results with those obtained during previous surveys in the Robe Valley and with data from elsewhere in the Pilbara. Yvette Hitchen of Helix Molecular Solutions (Helix) completed the molecular sequencing. The collected specimens were sequenced for variation at the mitochondrial cytochrome oxidase subunit I gene (CO1; Appendix 2).

Dr Terrie Finston, Dr Oliver Berry (both of Helix; Appendix 2), Dr Karen Cullen (WAM), Dr Rachael King and Dr Steven Cooper (South Australian Museum) provided analysis and interpretation of the Amphipoda molecular data. The molecular analysis used was a preliminary neighbour-joining approach using representative sequences from regional context data sets, followed by a phylogenetic analysis using the sequence data from this study (Appendix 2). This resulted in amphipod specimens from the current survey being placed into genetic lineages, which also included specimens from collections elsewhere in the region. Determination of putative species was then inferred from these genetic lineages based on the level of divergence between lineages of the same group (such as order or family), giving consideration to the variation within each lineage, the spatial distribution of the records relative to available habitat information, and findings of past phylogenetic studies of the Amphipoda of the region (Finston and Johnson 2004, Finston et al. 2007, 2011).

It should be noted that detailed morphological analysis was not completed for the amphipod specimens and the phylogenetic analysis was based on sequence data from a single gene. Therefore, all species arrived at by this approach should be considered putative unless previously described and fully determined by taxonomic specialists.

## 4.5 Categorisation of Conservation Significance

For the purpose of this report, the conservation significance of identified stygofauna were categorised as per Table 4.2.

Table 4.2: Conservation classification used within this report.

Category	Description
Conservation Significant species	Species listed as Priority, Schedule or Vulnerable at State or Federal levels
Confirmed Short-range endemic (SRE) species *	Species where sufficient taxonomic expertise is available, and with adequate representation in WAM collections or genetic databases, that are known to be limited in distribution based on geological or hydrogeological characteristics
Potential SRE species *	Species where there is insufficient taxonomic knowledge or too limited a number of collections to determine SRE status. Habitat, morphology, molecular or taxonomic data deficient, but belonging to groups that may display short-range endemism
Widespread (not an SRE) species *	Well-collected species, that are typically taxonomically well resolved. Species are not confined by geological barriers.

\* Category based on WAM SRE guidelines (Appendix 3; WAM 2014)

## 4.6 Survey Design

### 4.6.1 Survey Timing and Personnel

After a ground-truthing reconnaissance in April 2015, three phases of stygofauna sampling were conducted at Warramboo between June 2015 and December 2016 (Table 4.3). Two phases of baseline stygofauna sampling were completed at Mesa C between December 2016 and March 2017 (Table 4.3).

Table 4.3: Summary of field mobilisations completed for the Warramboo stygofauna study area.

Mobilisation	Dates	Personnel	Purpose	Warramboo Phase	Mesa C Phase
1	23 <sup>rd</sup> – 28 <sup>th</sup> April, 2015	Jason Alexander, Michael Delaney	Field reconnaissance and ground truthing	-	-
2	3 <sup>rd</sup> – 7 <sup>th</sup> June, 2015	Jason Alexander and Penny Brooshoof	Stygofauna sampling	1	-
3	29 <sup>th</sup> September – 2 <sup>nd</sup> October, 2015	Jason Alexander and Penny Brooshoof	Stygofauna sampling	2	-
4	6 <sup>th</sup> – 11 <sup>th</sup> December, 2016	Nicola Watson and Jacinta King	Reference area stygofauna sampling (Warramboo). Baseline sampling (Mesa C)	3	1
5	7 <sup>th</sup> – 10 <sup>th</sup> March 2017	Jason Alexander and Michael Greenham	Baseline stygofauna sampling	-	2

The survey was managed by Jason Alexander, with Garth Humphreys, also of Biota, providing directional input. Where the state of collected specimens and taxonomic frameworks permitted, morphological identification of stygobitic copepod and ostracod specimens were completed by Bennelongia Environmental Consultants and Biota zoologists. Bennelongia and Adrian Pinder, of the Department of Biodiversity, Conservation and Attractions (DBCA), completed identifications of collected stygal oligochaetes. Tomislav Karanovic of the University of Tasmania completed identifications and a review of collected target harpacticoid copepods from the genus *Inermipus* (Appendix 4). Taxonomic names are as per WAM nomenclature and peer-reviewed published literature nomenclature standards.

## 4.6.2 Weather

Temperature and rainfall data were obtained from Mesa J mining operations approximately 29 km east of Mesa C. Long-term climatological data (rainfall data from 1971-2016, temperature data from 1971-2017) were obtained from the Bureau of Meteorology (BOM) weather station at Pannawonica (station number 5069, approximately 37 km east of the Mesa C).

Sampling occurred between June 2015 and March 2017. Several major rainfall events occurred during the sampling period, in addition to the 150 mm of rain that fell in the month prior to Warramboo Phase 1 sampling. Past observations suggest this approximate timing after significant rainfall creates suitable conditions for sampling (Biota 2006a).

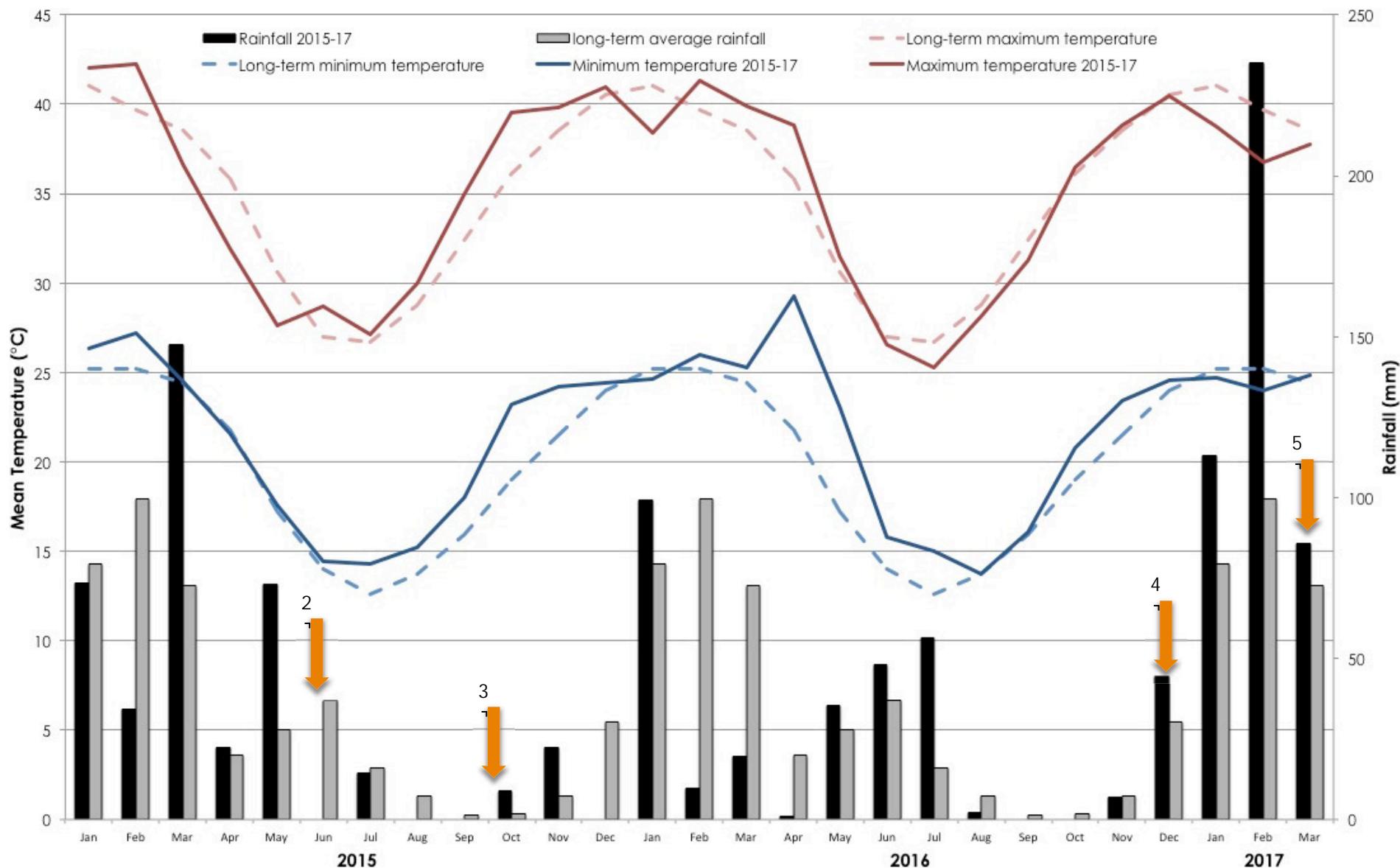


Figure 4.1: Climate and weather graph depicting long-term and monthly averages for the year preceding the final field mobilisation. (Long-term temperature data 1971-2005, rainfall data 1971-2014; arrows indicate field mobilisation timing as per Table 4.3)

## 4.6.3 Sampling Effort

### 4.6.3.1 Warramboo

Twenty-five sites were sampled for stygofauna at Warramboo over three phases of sampling (Table 4.4, Figure 4.2). Fifteen of the 25 sites were repeat sampled in consecutive phases. Seven sites were sampled outside of the modelled drawdown extent and comprised mostly pastoral bores and wells and uncased drillholes. The remaining 18 sites were all located within the drawdown extent and comprised mostly cased monitoring and water production bores. All sampled sites were located within the Warramboo buffer extent (Figure 4.2).

Table 4.4: Location and summary of all phases of sites successfully sampled from Warramboo.

Site Name	Easting (m E)	Northing (m N)	Drill Hole location*	Phases Sampled		
				1	2	3
Budgie Bore	382495	7615587	Outside	Yes	Yes	Yes
Camp Bore	382763	7612704	Outside	Yes	Yes	-
Daisy Well	381745	7617580	Outside	Yes	Yes	-
Huberts Bore	386148	7601259	Outside	-	-	Yes
MB13WARR001	377532	7604747	Inside	Yes	Yes	-
MB13WARR003	377714	7605478	Inside	Yes	Yes	-
MB13WARR004	378130	7605976	Inside	Yes	Yes	-
MB13WARR005	378947	7607019	Inside	Yes	Yes	-
MB13WARR006	379906	7607054	Inside	Yes	Yes	-
MB13WARR007	377024	7602548	Inside	Yes	Yes	-
MB13WARR010	377109	7605909	Inside	Yes	Yes	-
MB13WARR014	379420	7607022	Inside	Yes	Yes	-
MB16WARR005	375624	7603758	Inside	-	-	Yes
MB16WARR006	375082	7602835	Inside	-	-	Yes
MB16WARR009	374358	7600324	Inside	-	-	Yes
MB16WARR024	370153	7601558	Inside	-	-	Yes
MB16WARR040	374486	7601084	Inside	-	-	Yes
MEARC4193	370130	7599957	Inside	-	-	Yes
Queen Well	374567	7617795	Outside	Yes	Yes	-
RC12TOB0011	376164	7598699	Inside	-	-	Yes
RC13MEA0279	376781	7605110	Inside	Yes	Yes	-
RC13TOB0023	376172	7597836	Outside	-	-	Yes
TOBRC0009	380913	7600605	Outside	Yes	Yes	-
WB13WARR001	377525	7604736	Inside	-	Yes	-
WB13WARR003	377710	7605479	Inside	Yes	Yes	-

\* in relation to modelled drawdown extent

16      17      10

Coordinates in zone 50, datum GDA94

While not part of the Warramboo sampling, a further 23 sites were sampled during a similar time frame at nearby Mesa C (Section 4.6.3.2), the results of which provide context for the Warramboo study. Additionally, 53 groundwater bores (included in the desktop review) have previously been sampled in the Warramboo and Mesa A locality (Figure 4.2).

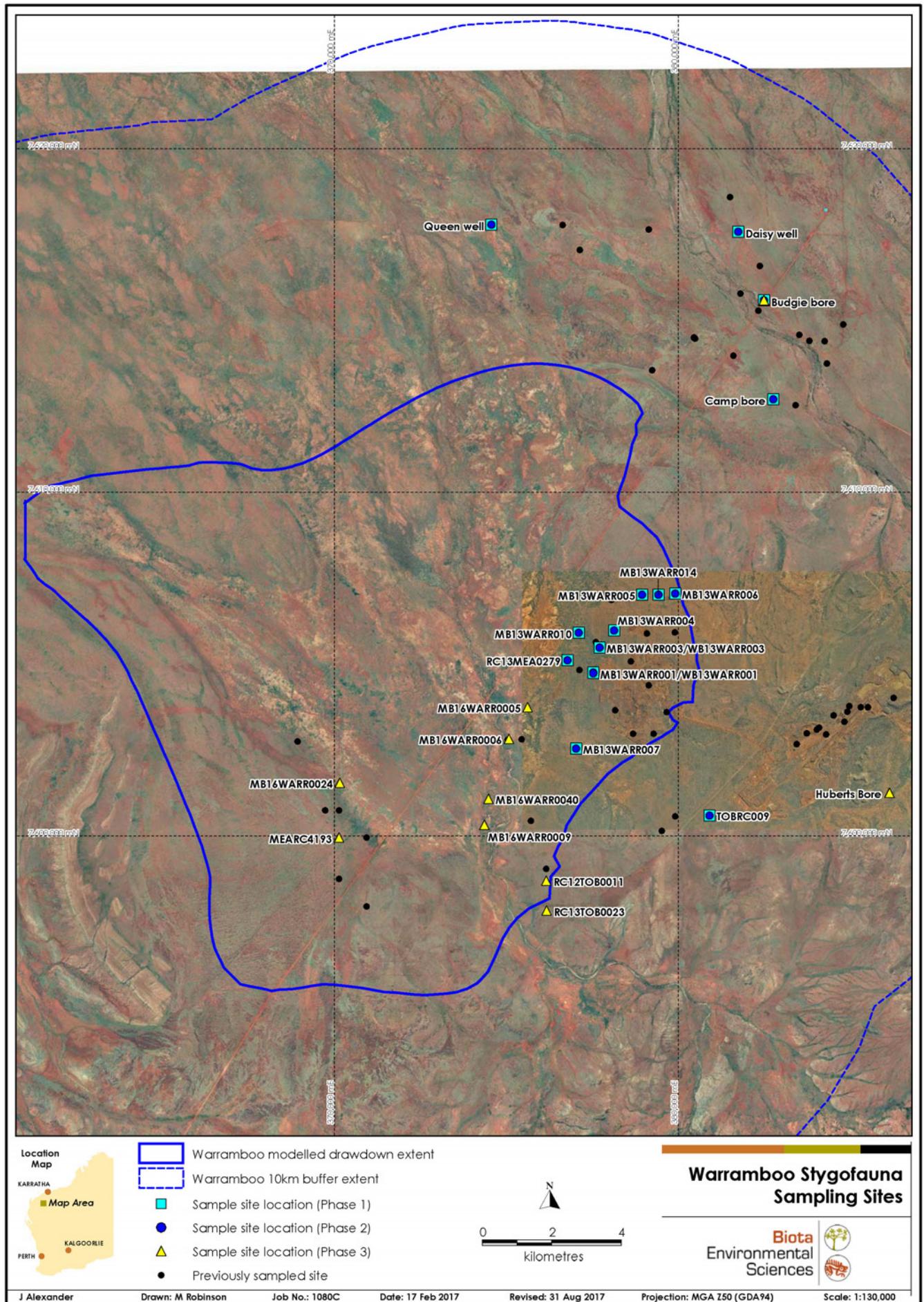


Figure 4.2: Location of stygofauna sites sampled at Warramboo in relation to sites sampled previously.

### 4.6.3.2 Mesa C

Twenty-three sites were sampled for stygofauna at Mesa C over two phases (Table 4.5, Figure 4.3). Nine sites were sampled across both phases (Table 4.5). Ten sampled sites were located outside the modelled drawdown extent, with the remaining 13 sites located within the drawdown extent. All sampled sites are located within the wider Mesa C buffer extent (Figure 4.3).

Table 4.5: Location and summary of Phase 1 sites successfully sampled at Mesa C.

Site Name	Easting (m E)	Northing (m N)	Drill Hole location*	Phases Sampled	
				1	2
Dave Bore	392512	7607436	Outside	Yes	Yes
Huberts Bore	386148	7601259	Outside	Yes	Yes
MB16MEC0008	393565	7600580	Outside		Yes
MB16MEC0009	393590	7601145	Outside		Yes
MEAWO4084	387068	7604793	Outside	Yes	
MEAWO4086	386829	7605287	Outside	Yes	Yes
MEAWO4087	386257	7605481	Outside	Yes	Yes
MEAWO4088	385478	7605097	Outside	Yes	Yes
MB15MEC0001	392991	7600257	Inside		Yes
MB16MEC0005	392760	7600523	Inside		Yes
MB16MEC0006	392454	7601078	Outside		Yes
MB16MEC0007	392713	7601954	Inside		Yes
RC15MEC0027	392792	7600255	Inside		Yes
RC15MEC0196	392838	7601494	Inside	Yes	
RC15MEC0200	392746	7602204	Inside		Yes
RC16MEC0092	392743	7601412	Inside	Yes	
RC16MEC0098	392791	7601469	Inside		Yes
RC16MEC0102	392790	7601511	Inside	Yes	Yes
RC16MEC0103	392387	7601451	Outside	Yes	
RC16MEC0129	392688	7601963	Inside	Yes	Yes
RC16MEC0177	392587	7602512	Inside		Yes
WB16MEC0001	392915	7601135	Inside	Yes	Yes
WB16MEC0002	392973	7600507	Inside	Yes	Yes
Total Sampled:				12	19

\* in relation to modelled drawdown extent

Coordinates in zone 50, datum GDA94

While not part of the Mesa C sampling, a further 25 sites were sampled during a similar time frame at nearby Warramboo (Section 4.6.3.1), the results of which provide context for the Mesa C sampling. Additionally, three groundwater bores (included in the desktop review) have previously been sampled in the Mesa C locality (Figure 4.3).

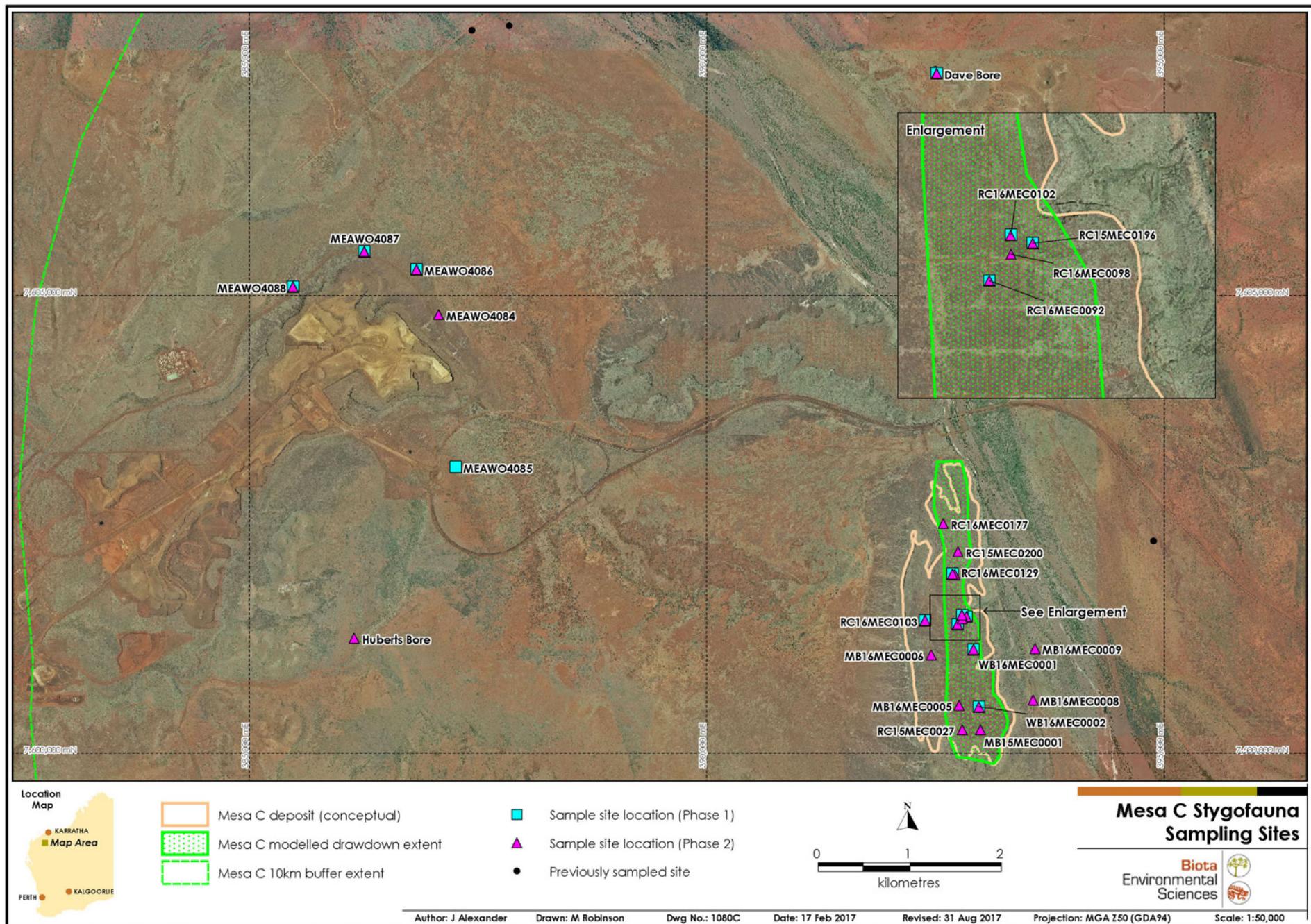


Figure 4.3: Location of stygofauna sites sampled at Mesa C in relation to sites sampled previously.

## 4.7 Survey Limitations

Several limitations apply to this study, some of which are common issues when working on subterranean fauna, rather than functions of this specific study. These limitations include:

1. There is limited mapping of geological units at below water table depths, with the exception of the Robe Pisolite. While we have made inferences where possible, using Yarraloola Conglomerate (provided by Rio Tinto) and surface geology layers (Alluvium) for habitat mapping within this report, the actual BWT extents of these geological units may differ. While there may be small pockets of other BWT geological units within the study area not outlined in this report, these geologies (Robe Pisolite, Yarraloola Conglomerate and Alluvium) are likely to represent the most pertinent geological units to study in respect of potential stygofauna habitat.
2. For several of the faunal groups there is a lack of adequate taxonomic framework and specialist expertise, both within Australia and internationally. This is particularly the case for the subterranean Platyhelminthes.
3. A representative subset of 154 of the total of 178 Amphipoda specimens collected during this study were sequenced. Thirty-nine of the 154 specimens failed to yield a sequence, most often due to DNA degradation.
4. Most Amphipoda specimens were identified based on sequence data due to the predominance of juvenile and damaged specimens and some unresolved issues from past subterranean amphipod taxonomy, meaning that specimens were not resolved morphologically. Previous studies within the Pilbara have found that current morphological identification keys for this group include some species that represent multiple taxa (Biota 2015b) and there are significant, and long-standing (Biota 2004b) issues associated with species-level morphological determinations in this order.
5. For most taxa, only adult specimens have the diagnostic morphological characteristics necessary to be identified to species level. As juvenile specimens are often collected, this limited the level to which many specimens could be identified (with the exception of the Amphipoda, where molecular methods were used to identify juvenile and damaged specimens to species level; see point 3 above).
6. Stygofauna sampling from sites within the drawdown extent at Warramboo was predominantly restricted to monitoring bores (sites with prefix MB) and water bores (sites with prefix WB), which are typically constructed with 1 mm slots in the casing, aimed at allowing the flow of water but limiting sediment ingress. This casing design can inhibit the movement of stygofauna with larger body morphologies and limit species recorded, thereby biasing the data. Sites outside the drawdown extent were older and often large pastoral wells or uncased and thus likely to allow ingress of a wider range of stygofauna.
7. Conservation significance could not be assigned to taxa that were unable to be identified to species level (such as Amphipoda sp. 'indet' or Paramelitidae sp. 'indet') as these specimens may represent multiple species or may equate to a species already known elsewhere.
8. Modelling for the drawdown extent at both Warramboo and Mesa C is ongoing and as such subsequent modelling may result in variations in the extent and magnitude of the drawdown extent considered in this report. In an attempt to mitigate this limitation, we have included within this report the 10 km buffer extent, which provides a conservative assessment of the drawdown for unlikely worst-case scenarios.

Despite these limitations, the study provides an assessment that meets current EPA guidance (Section 3.3) and is adequate to inform the forthcoming EIA for the Mesa A Hub proposal.

This page intentionally blank.

# 5.0 Results

## 5.1 Study Area Habitat Characterisation

Core habitat for subterranean fauna is primarily a function of available space and the potential for nutrient input from surface systems (Humphreys 1991, Wilkens et al. 2000, Biota and DC Blandford & Associates 2013). The following sections describe physical aspects relevant to the stygofauna communities pertinent to the current Warramboo and Mesa C study area (following the framework outlined in Section 4.2).

### 5.1.1 Warramboo Geology and Hydrology

The aquifer drawdown extent lies predominantly within the Onslow Coastal catchment, with the proposed drawdown extending marginally into the Robe River catchment to the northeast (Figure 5.1). The Warramboo area is characterised as a relatively flat, westward sloping coastal plain. There are two ephemeral watercourses within the area, the smaller of which, Warramboo Creek, flows northwest past the deposit (Rio Tinto 2010, 2015a). The larger of the two watercourses, the Robe River, flows through the area from southeast to northwest (Figure 5.1). There is currently an active borefield at Warramboo which is licenced for abstraction of three gigalitres of water annually (Rio Tinto 2015b).

The Robe Pisolite deposit at Warramboo lays 95% above the water table, which varies between 12 – 24 m below ground level (Rio Tinto 2010). Below water table, the Robe Pisolite is modelled as being up to 32 m thick within the drawdown extent (Figure 5.2, Figure 5.3). This is incised into the Yarraloola Conglomerate, which hosts most of the aquifer (Rio Tinto 2015a). Where the Robe Pisolite intersects the water table, water through-flow is largely unconfined due to the presence of solution cavities common in this geological unit.

The Robe Pisolite and Yarraloola Conglomerate is unconformably overlain by alluvium, which is largely above the water table at Warramboo and therefore mostly unsaturated (Rio Tinto 2015a) and not suitable as stygobitic fauna habitat.

Groundwater at Warramboo is recharged predominantly by direct infiltration from rainfall events and by stream flow generated from the wider catchment.

Physical characteristics indicate that the Yarraloola Conglomerate is likely to provide habitat for stygobitic fauna. This geological unit is transmissive and variably porous, and ranges between 10 - 80 m in thickness where occurring within the study area, typically extending below water table. This unit overlays the basal Ashburton Formation and is widespread within the west of the Robe Valley, with the inferred extent underlaying the entirety of the modelled aquifer drawdown extent area at Warramboo and extending southwest approximately 200 km coastally, almost to Cape Range (data supplied by Rio Tinto).

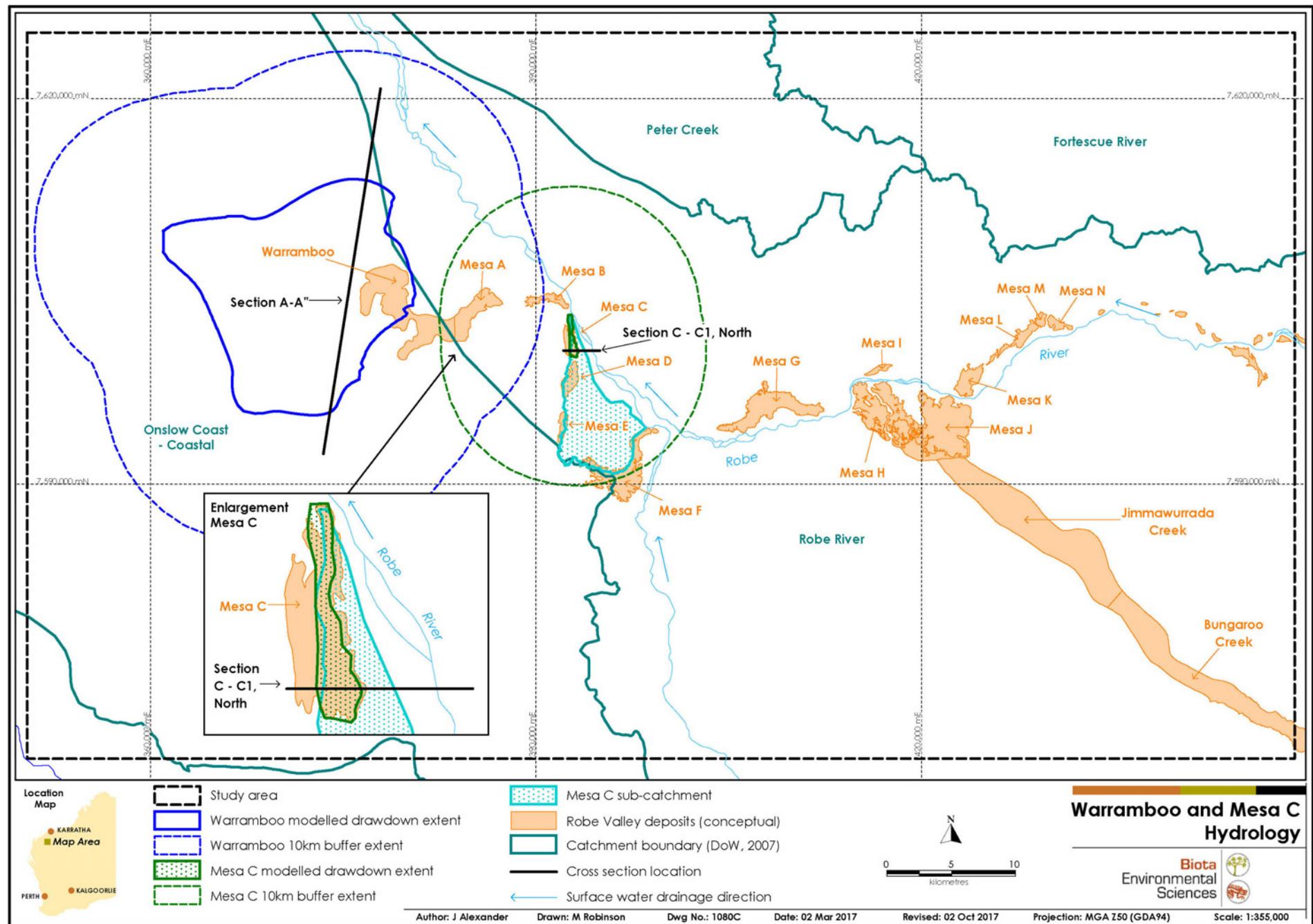


Figure 5.1: Water catchments, surface water drainage direction and aquifers within the study area.

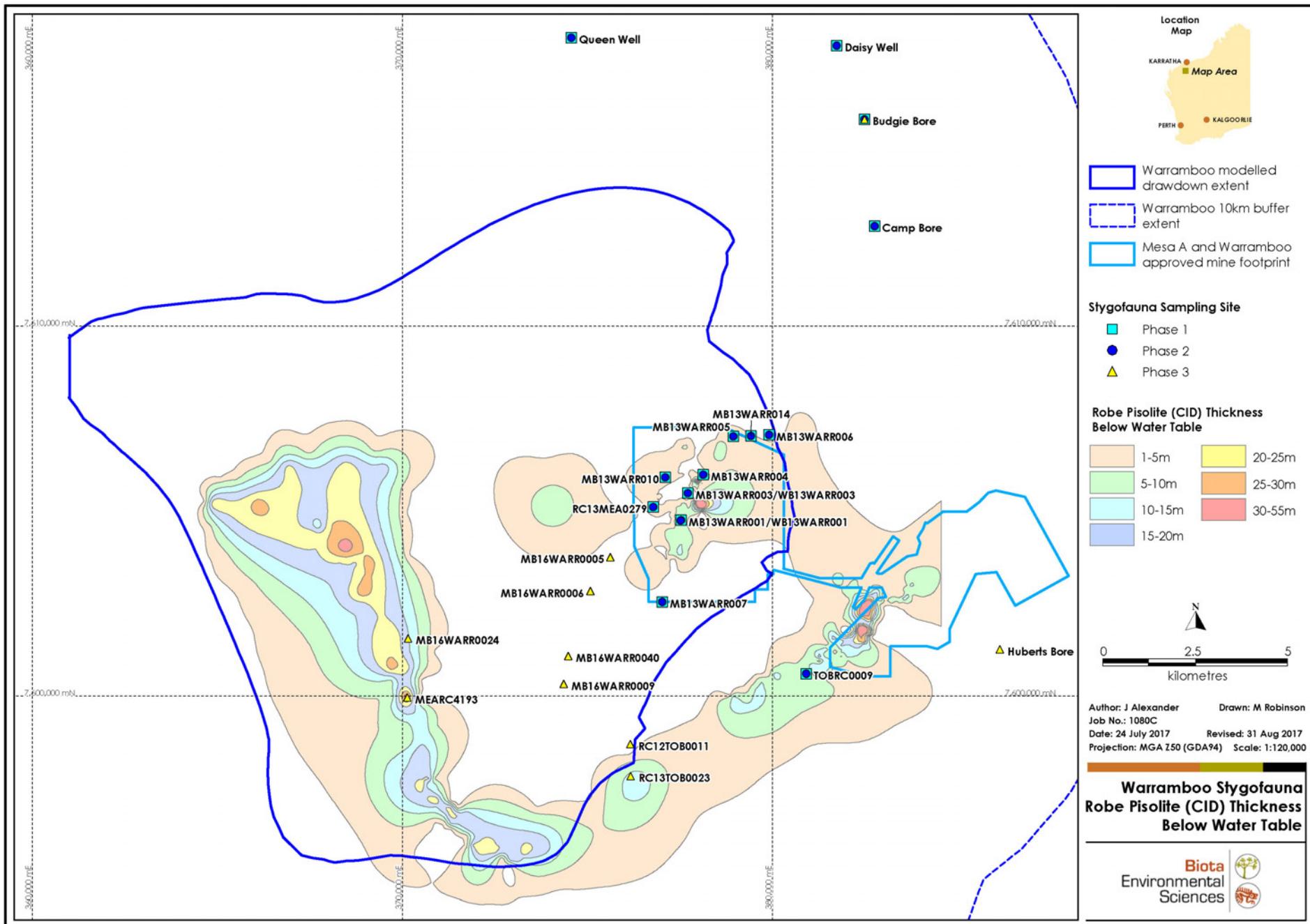


Figure 5.2: Warramboo Modelled Robe Pisolite contours and thickness below the water table.

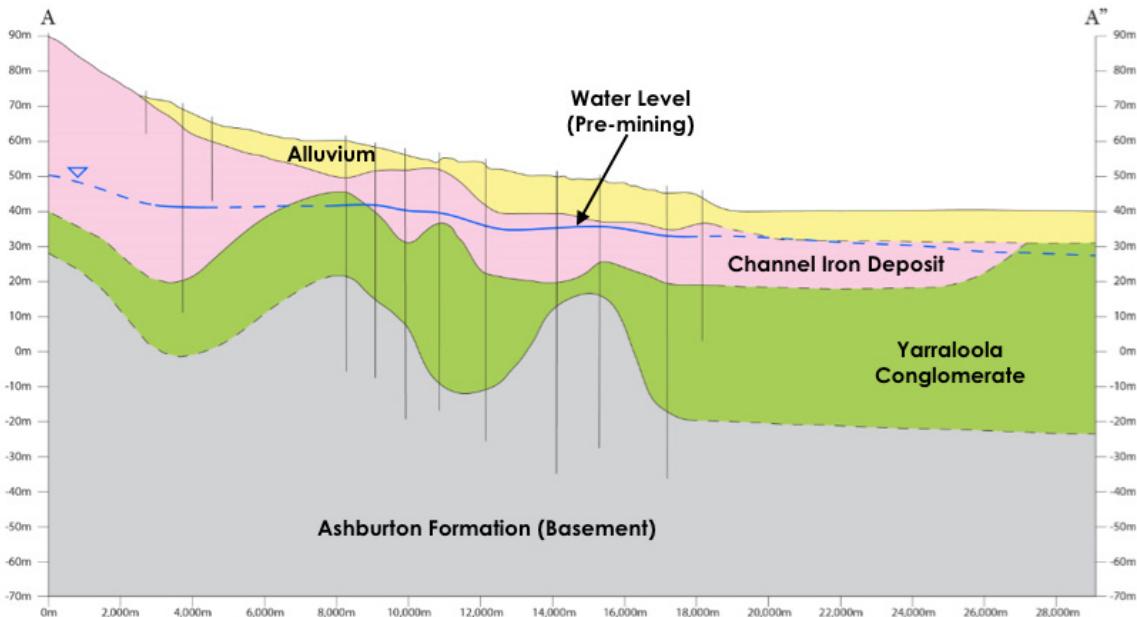


Figure 5.3: Cross-section of Warramboo showing water table in relation to geology.  
(Image supplied by Rio Tinto, cross-section location displayed in Figure 5.1).

#### 5.1.1.1 Hydrology and Geology of Mesa C

Mesa C forms part of the Deepdale group of Tertiary Pisolite deposits. The Robe Pisolite is channel fill within the palaeochannel of the original Robe River system deposited in the late Mesozoic to early Tertiary period. In the vicinity of Mesas A, B and C, the river is thought to have flowed across the broad Yarraloola Conglomerate Formation, with downward erosion into the conglomerate forming the river channel. Later erosion has resulted in a varying cover of alluvium, colluvium and aeolian sands. The more resilient iron rich channel fill remained as elongate topographic highs (mesas) along the current erosional surface. The mineralised sequence exhibits oolitic to pisolitic textures. Robe Pisolite generally outcrops as low mesa-form hills within the Robe Valley (data supplied by Rio Tinto).

The Mesa C deposit lies within the Mesa C sub-catchment, which is part of the broader Robe Valley catchment area (Figure 5.1, Figure 5.4). This sub-catchment is approximately 40 km<sup>2</sup> and confined to the south and west by other mesas and in the east by the Robe River (Figure 5.1; data supplied by Rio Tinto). Run-off from surface water on Mesa C drains from the mesa plateau on all sides and eventually contributes to the Robe River.

Modelling and hydro-geochemical data suggest that the Mesa C CID aquifer is principally isolated (Rio Tinto 2017), with the Robe Pisolite within the aquifer providing habitat for stygofauna. This aquifer geology is bounded in the west and south by the Ashburton Aquiclude and to the east and bottom by the low permeable Ashburton Aquitard (Figure 5.5). In the north the CID Aquifer may have some hydraulic connection with the Robe River Aquifer however minimal throughflow interaction is expected due to the clayey nature of the basal tertiary pisolite.

Recharge of the Mesa C aquifer is likely to occur at times of large rainfall events, which allows higher flowthrough of water from the Robe River. As the water table rises after rainfall, this flowthrough may become trapped within the confines of the Mesa C aquifer, which is then isolated when water levels drop below that of the bounding aquitard. Levels of direct rainfall infiltration is considered to be negligible (Rio Tinto 2017).

As the confined aquifer lies approximately 50 m below ground surface, the level of evapotranspiration from the aquifer is negligible. Throughflow water loss per year was estimated as being 175 ML per year (Rio Tinto 2017). Due to this low outflow, the chemistry of the Mesa C aquifer is stagnant with higher levels of sodium and chloride by comparison to the Robe alluvial aquifer (Rio Tinto 2017).

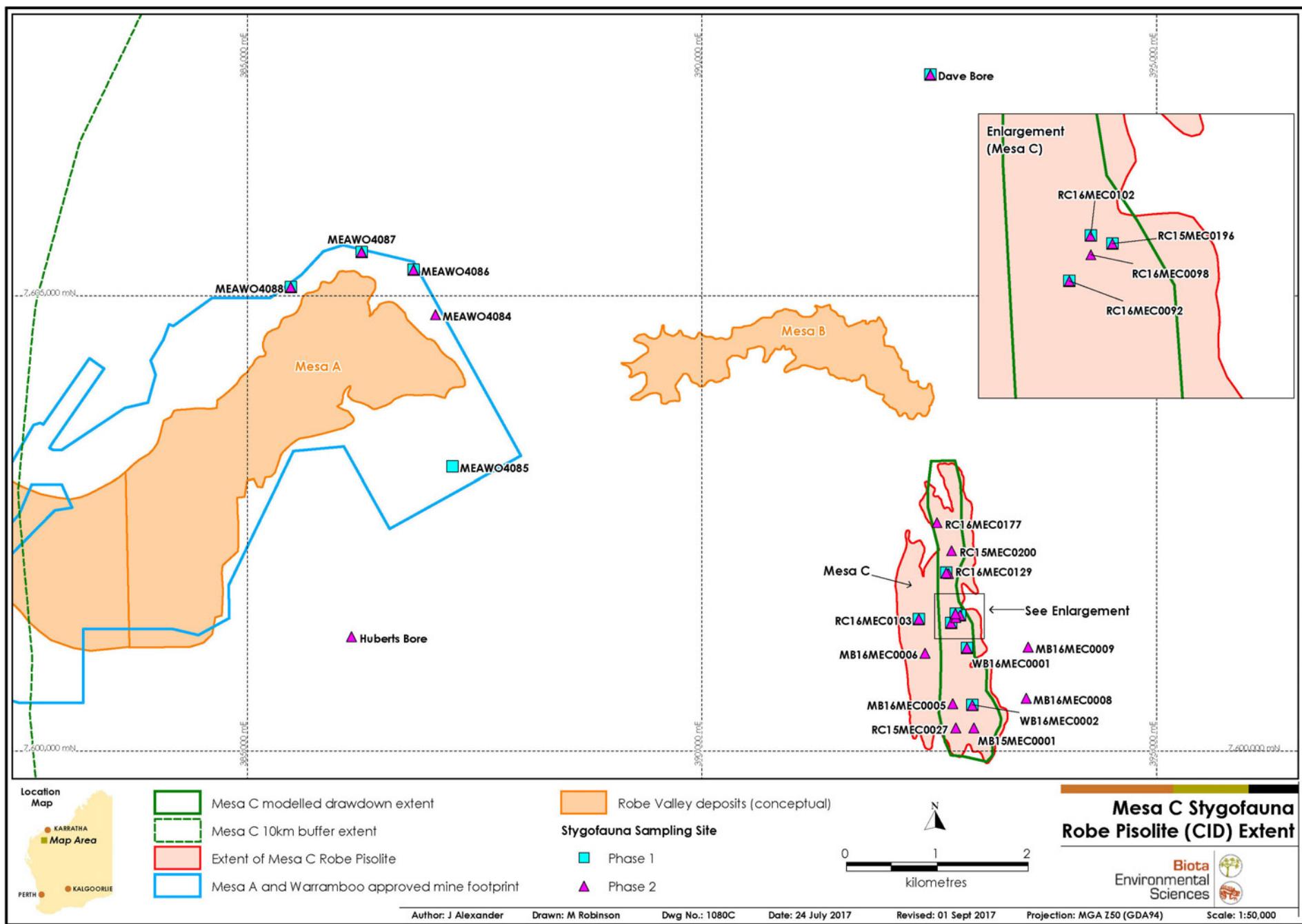


Figure 5.4: Extent of the Robe Pisolite geology at Mesa C.

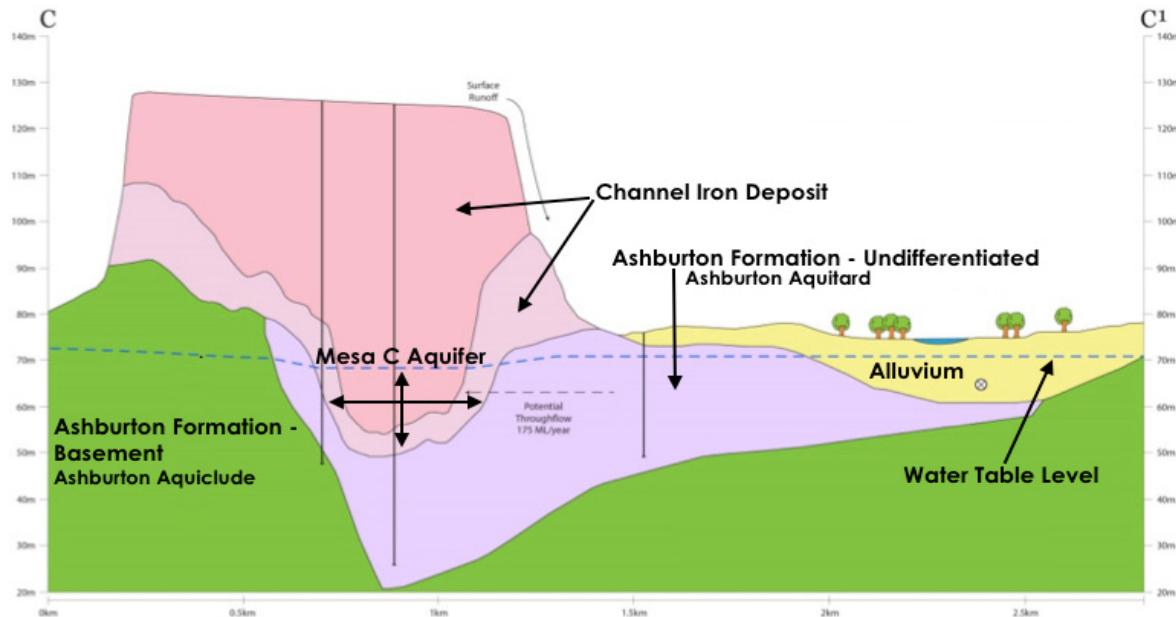


Figure 5.5: Cross-section of Mesa C showing water table in relation to geology and Robe River.  
(Image supplied by Rio Tinto; cross section location displayed in Figure 5.1).

### 5.1.2 Prospectivity of Habitat within the Study Area

While geological units have not been specifically mapped below water table (see Section 4.7), four key geological units occur BWT within the study area at Mesa C and Warramboo (Table 5.1). Multiple studies in the Pilbara region have previously found that transmissive geological units such as alluvium and pisolite (as occur within the study area; Table 5.1) are suitable habitat for stygofauna.

Table 5.1: Mapped and inferred BWT geology of the study area.

Geological Unit	Description	Habitat Suitability Characteristics (Section 4.2)
Alluvium	Unconsolidated fluvial deposits, mostly sand.	A, B, C, D, E, F
Yarraloola Conglomerate	Polymictic conglomerate, which typically consists of pebbles of chert, BIF and/or quartz in oxidised (limonitic), sandy clays. Predominantly below water table within the study area.	B, D, E, F
Ashburton Formation	Impermeable basement geological unit predominantly submerged within the study area.	B, F
Robe Pisolite (CID)	Pisolitic limonite deposits. Occurs along old river channels. Unit predominantly above water table.	A, B, C, D, E, F

Using the habitat suitability characteristics outlined in Section 4.2, the prospectivity of these geological units as stygofauna habitat was categorised (Table 5.1). Alluvium and Robe pisolite were categorised as highly prospective units and likely to provide primary habitat for stygofauna where below water table. Both the Robe Pisolate and alluvium geological units are also identified by the EPA as potential stygofauna habitat (EPA 2016e). The Yarraloola conglomerate is categorised as having medium habitat prospectivity when saturated (Figure 5.6).

The Ashburton formation is basement rock that represents an aquiclude, and is thereby likely to provide the greatest potential barrier to stygofauna distributions within the study area, and is low prospectivity habitat. This unit makes up 60.3% of the study area (Table 5.2, Figure 5.6).

Table 5.2: Prospective of the geological units within the study area to provide stygofauna habitat.

Habitat Prospective	Geological Unit	Proportion of survey area (%)
High	Robe Pisolite Alluvium *	4.5
Medium	Yarraloola Conglomerate ^	35.1
Low	Ashburton Formation	60.3

\* Saturated extent of unit not mapped and area based on surface geology (Geological Survey of Western Australia 1968).

^ Extent of unit inferred and provided by Rio Tinto.

### 5.1.3 TECs, PECs and Environmentally Sensitive Areas Database Search

Searches of the Department of Parks and Wildlife TEC, PEC and Environmentally Sensitive Areas database yielded a single PEC relevant to the current stygofauna study (Table 5.3, Figure 5.7). No TECs or environmentally sensitive areas were recorded from the search.

While no PECs relevant to stygofauna occur within either Warramboo or Mesa C drawdown extents, the wider study area boundary intersects the "Stygofaunal community of the Bungaroo Aquifer" PEC (Table 5.3, Figure 5.7). This PEC is categorised as Priority One; Poorly-known ecological community. This category is defined as:

"Ecological communities that are known from very few occurrences with a very restricted distribution (generally  $\leq 5$  occurrences or a total area of  $\leq 100\text{ha}$ ). Occurrences are believed to be under threat either due to limited extent, or being on lands under immediate threat (e.g. within agricultural or pastoral lands, urban areas, active mineral leases) or for which current threats exist. May include communities with occurrences on protected lands. Communities may be included if they are comparatively well-known from one or more localities but do not meet adequacy of survey requirements, and/or are not well defined, and appear to be under immediate threat from known threatening processes across their range."

Table 5.3: Description of PECs overlapping the study area and desktop review boundaries.

PEC Name	Description
Stygofaunal community of the Bungaroo aquifer	<p>A unique assemblage of aquatic subterranean fauna including eels, snails and other stygofauna.</p> <p>In their survey of Bungaroo, Bennelongia (2013) note "At least 28 stygofauna species of 10 higher level taxonomic groups were recorded (in their survey of the aquifer), including Rotifera, Gastropoda, Acariformes, Ostracoda and Isopoda, Oligochaeta, Copepoda, Syncarida, Amphipoda, and Nematoda. Eight of the stygofauna species collected are known to occur widely in the Pilbara, while another six occur widely in the Robe catchment. On the basis of existing data, 12 species are known only from within the Survey Area; this includes nine identified species and three taxa identified only to family or genus (the ranges of two nematodes and rotifers were not assessed).</p> <p>Based on existing information on the distributions of Pilbara stygofauna, it is unlikely that the 12 stygofauna species only known from the Survey Area are actually restricted to that area. However, a review of the ranges of taxonomically similar species suggested it is possible that five of the 12 species have ranges not much larger than the Survey Area.</p> <p>Habitat characterisation showed that the CID/alluvial aquifer in palaeochannels of the Robe and Bungaroo catchments, which occurs both upstream and downstream of the Survey Area potentially provides considerable habitat connectivity for stygofauna beyond the Survey Area and would appear to reduce the risk of any species being restricted to the Survey Area."</p>

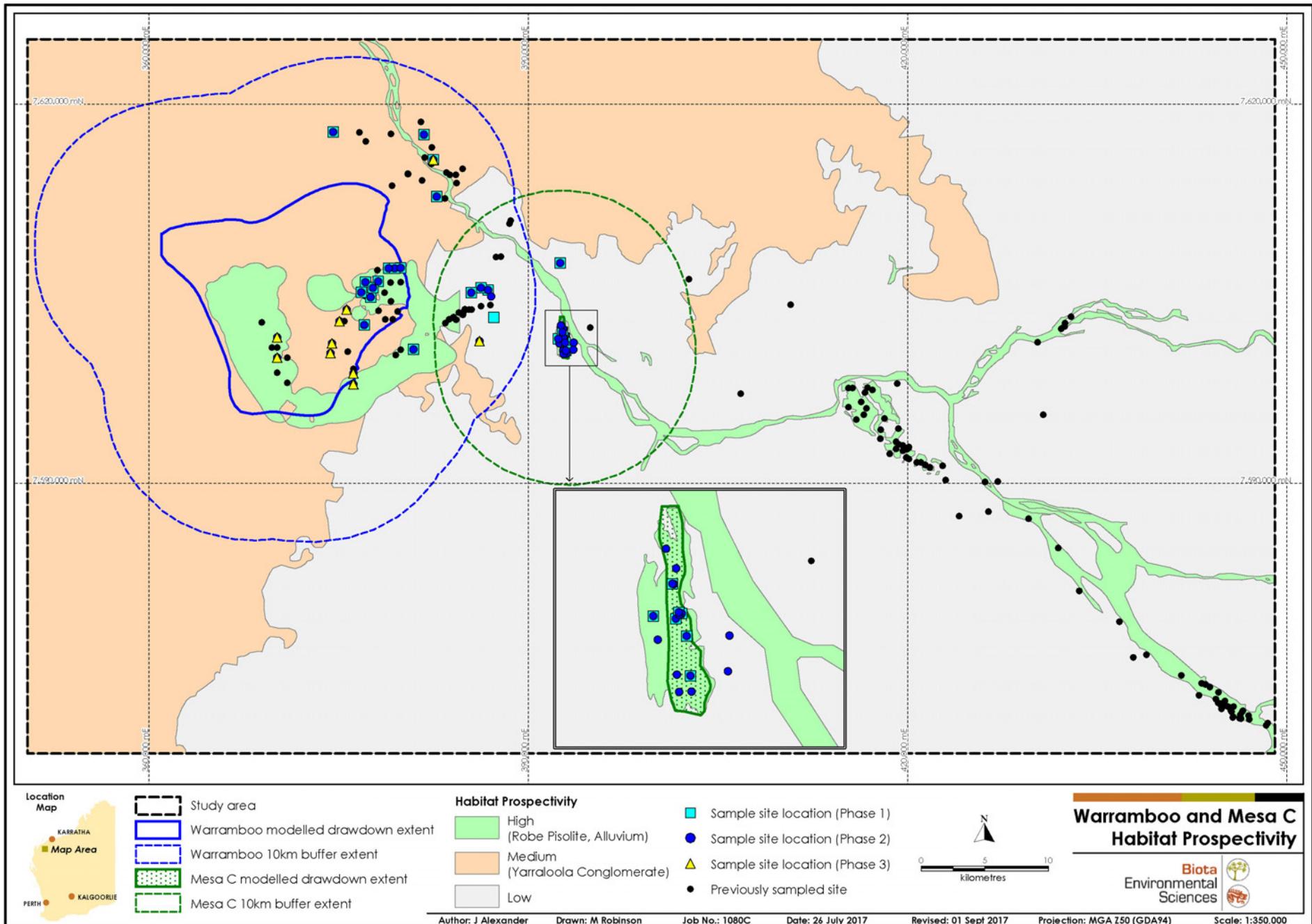


Figure 5.6: Prospective stygofauna habitat within the study area in relation to sampled sites.

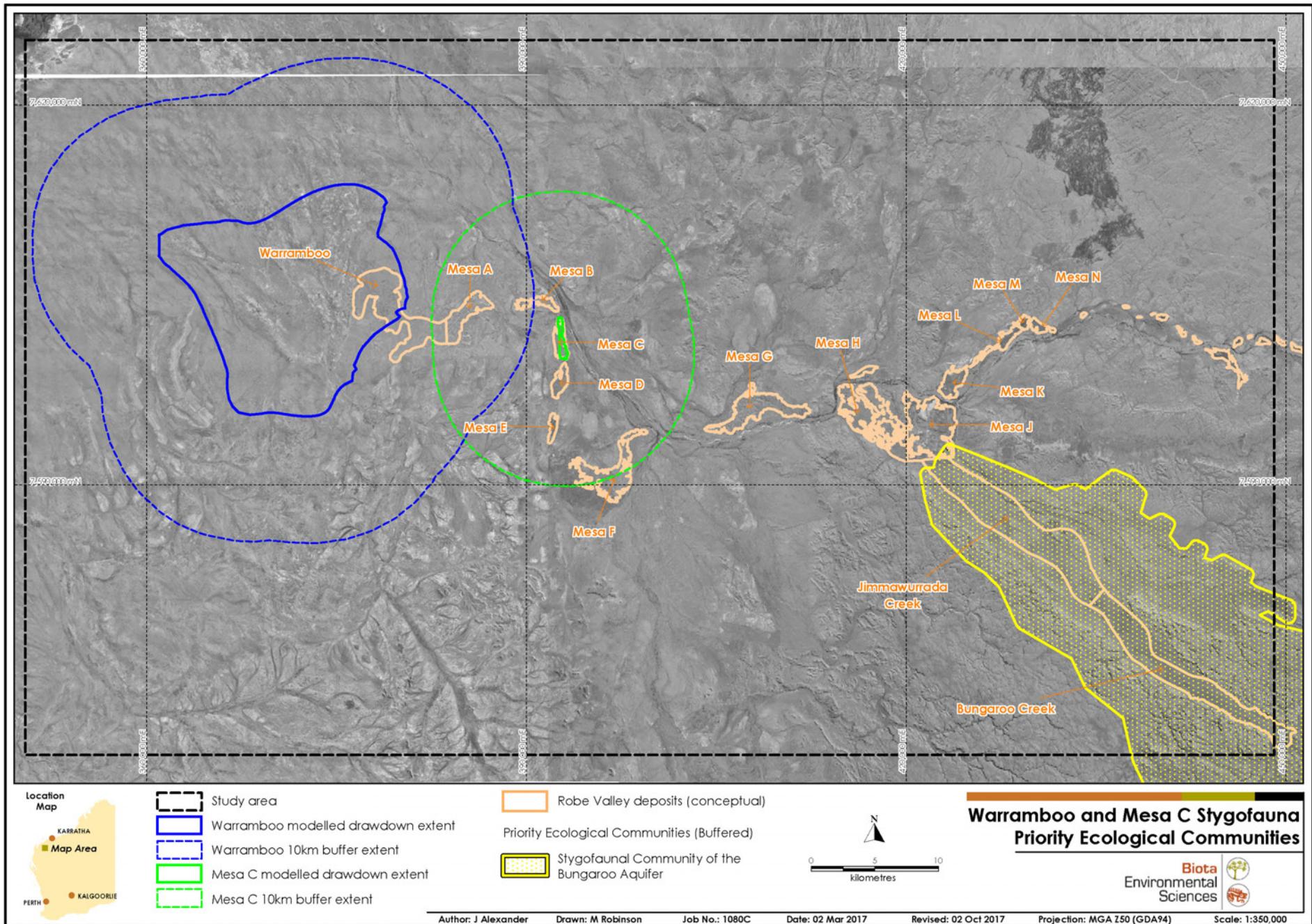


Figure 5.7: Location of PECs relevant to the current study area.

## 5.2 Desktop Review

### 5.2.1 Previous Relevant Surveys

A desktop review was completed to identify relevant previous records from the study area. Extensive stygobitic fauna sampling has been completed in the study area, however the majority of this sampling effort was localised to the Bungaroo Valley, where 19 phases of sampling have been completed (Table 5.4; Appendix 5). Few studies have focused on stygofauna within Mesa C and Warramboo specifically to date, however the then Department of Environment and Conservation (DEC) completed an overarching survey of stygofauna within the Pilbara (Halse et al. 2014), which overlaps these areas. Sampling for this study was completed between 2002 and 2005.

Table 5.4: Summary of previous stygobitic fauna surveys within the study area.

Report	Survey Timing
Halse et. al (2014) Department of Parks and Wildlife; Pilbara Regional Stygofauna Surveys	2002 - 2005
Biota (2004a) Mesa A and Bungaroo Creek Exploration Areas Subterranean Fauna Survey	2003
Biota (2006b) Mesa A / Warramboo and Yarraloola Borefield Development	2005
Biota (2015a) Bungaroo Subterranean Fauna Desktop Assessment	2003 – 2014
Biota (2016b) Bungaroo Coastal Waters Project Stygofauna Monitoring 2015	2015
Biota (2016a) Bungaroo Coastal Waters Project Stygofauna Monitoring 2016	2016
WAM (2017) Molecular analysis of Amphipoda from the Robe River Valley: Mesa H and Mesa B/C, Western Australia*	2016

\* Genetics report on amphipod specimens only. No sampling completed as part of the report.

Based on WAM, Biota and NatureMap and ALA database searches, a total of 8,179 stygobitic fauna specimens have previously been recorded from the study area, between 2002 and 2016, representing 176 taxa (Table 5.5). However only 128 taxa represented distinct species, with 46 representing indeterminate (damaged or juvenile) taxa.

Three species from the desktop review are currently listed as conservation significant. Two amphipod species, *Nedsia hurlberti* and *Nedsia sculptilis* and the Blind Cave Eel, *Ophisternon candidum*, are Schedule 3 species in Western Australia (Figure 5.8). *Ophisternon candidum* is also listed as Vulnerable Federally, under the Environment Protection and Biodiversity Conservation (EPBC) Act 1999.

Table 5.5: Summary of stygofauna records returned from database searches within the study area.

Taxonomy			Number Collated	Number Sites
Phylum	Class	Order (Common Name)		
Annelida	Oligochaeta	Indeterminate (Earthworm)	22	3
		Tubificida (Earthworm)	277	23
	Polychaeta	Phyllodocida (Polychaete worm)	1	1
		Aphaneura (Polychaete worm)	12	3
Arthropoda	Arachnida	Sarcoptiformes (Water mite)	28	6
		Trombidiformes (Water mite)	12	6
Chordata	Actinopterygii	Synbranchiformes (Blind cave eel) *	2	2
Crustacea	Copepoda	Calanoida (Calanoid copepod)	1288	38
		Cyclopoida (Cyclopoid copepod)	2025	76
		Harpacticoida (Harpacticoid copepod)	149	23
	Diplostraca	Cladocera (Water Flea)	2	2
	Malacostraca	Amphipoda (Sand hopper) *	1547	93
		Bathynellacea (Bathynellid)	33	15
		Isopoda (Slater)	43	8
		Thermosbaenacea (Thermosbaenacean)	573	19

Taxonomy			Number Collated	Number Sites
Phylum	Class	Order (Common Name)		
Crustacea	Ostracoda	Indeterminate (Seed shrimp)	132	5
		Podocopida (Seed shrimp)	623	34
Mollusca	Gastropoda	Basommatophora (Aquatic snail)	2	1
		Sorbeoconcha (Aquatic snail)	1195	5
Nematoda	Indeterminate	Indeterminate (Nematode worm)	32	5
Nemertea	Indeterminate	Indeterminate (Proboscis worm)	1	1
Platyhelminthes	Indeterminate	Indeterminate (Flatworm)	50	1
	Turbellaria	Indeterminate (Flatworm)	83	13
Protozoa	Indeterminate	Indeterminate (Protizoa)	15	3
Rotifera	Bdelloidea	Indeterminate (Rotifer)	20	4
		Philodinida (Rotifer)	12	1

\* Some species of these orders are of conservation significant (see Section 6.1).

A complete collation of the results from the desktop review, higher order collection locations and final species determination, where available, are provided in Appendix 5.

The following sections address only those results relevant to the modelled drawdown extent and the buffer extent. Indeterminate records are not discussed further (Section 4.7).

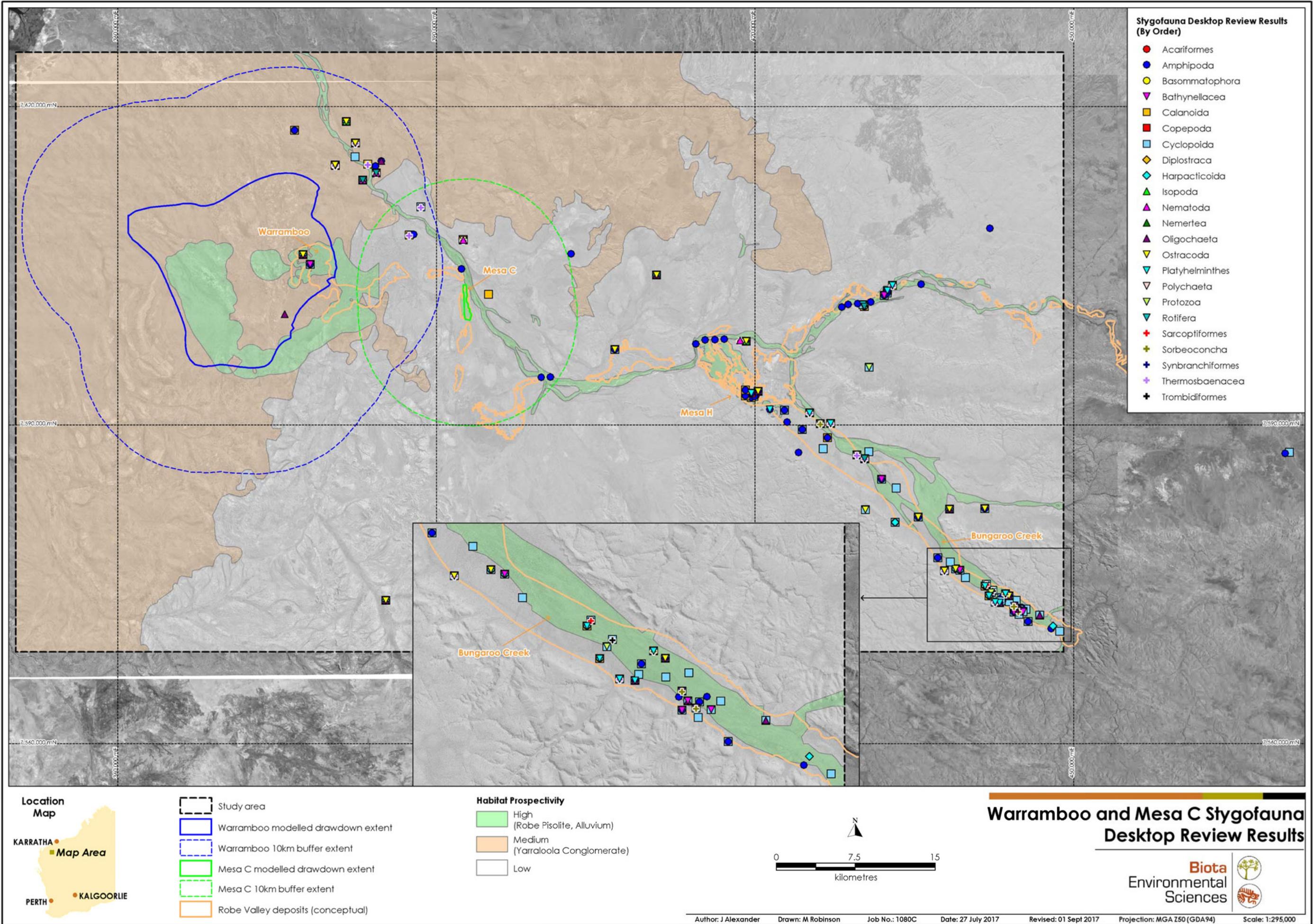


Figure 5.8: Location of higher order collections and sites sampled during previous studies within the study area.

## 5.2.2 Warramboo Historical Records

A total of 75 of the previously collected specimens collated during desktop review came from within the drawdown extent. All of those specimens were identified morphologically and were collected in 2002 and 2004. The previously collected specimens represented 12 stygobitic species from six orders and two phyla.

Eight of the 12 species previously recorded occur inside the drawdown extent but were also recorded from reference areas in the wider study area (Table 5.6, Figure 5.9, Figure 5.10). The four remaining species have only been recorded from within the drawdown extent based on the desktop review results for the study area. However, one of these, *Parapseudoleptomesochraturreei* was originally described from specimens in Turee Creek, approximately 291 km south east of Warramboo, which is outside the current study area (Karanovic 2006b). Likewise, *Bathynella* sp. 2 and *Phreodrilus* sp. 'WA32' have also been recorded from sites elsewhere in the Pilbara from the Pilbara Stygofauna Survey (sourced from publicly available PSS data).

A further 1,277 specimens belonging to 43 stygobitic species, including four species also recorded within the drawdown extent, were collated from records within the Warramboo buffer extent. Twenty-two of these species were recorded in reference areas within the wider study area.

## 5.2.3 Mesa C Historical Records

The desktop review indicated that no stygobitic fauna taxa were previously known from within the modelled drawdown extent at Mesa C (Table 5.7, Figure 5.11).

A total of 230 specimens belonging to 22 stygobitic species were recorded from the Mesa C buffer extent (Table 5.7, Figure 5.11). Of these species, 18 were also recorded in the wider study area.

Table 5.6: Summary of morphological identifications and locations of desktop review specimens in relation to the Warramboo drawdown extent and buffer extent.

Taxonomy				Collection Abundance and Distribution						
Class	Order	Family	Species	Within drawdown extent	(n)	Within Buffer Extent	(n)	Reference	(n)	
<b>Arthropoda</b>										
Arachnida	Sarcoptiformes	Indeterminate	Oribatida group 1	-		PSS016	16	PSS089*	1	
Arachnida	Sarcoptiformes	Indeterminate	Oribatida group 4	-		PSS015	1	-		
Arachnida	Trombidiformes	Arrenuridae	Arrenurus sp. 'nov. 2'	-		PSS016	3	-		
Arachnida	Trombidiformes	Mideopsidae	Guineaxonopsis sp. 'S1'	-		PSS015	1	-		
<b>Crustacea</b>										
Copepoda	Cyclopoida	Calanoida	Stygoridgewayia trispinosa	-		PSS015, PSS016, PSS017, PSS072, PSS073, PSS074, PSS075	481	31, BC156, BC186, BUNWE01, BUNWP0005, DD13MEH0007, JIMDR094, JIMWE004, JW021, JW024, RC13MEH0007, RC14MEH0018, RC14MEH0053, RR1, PSS088. PSS089*, PSS155, PSS158, PSS159, PSS160, PSS161	637	
		Cyclopidae	Apocylops dengizicus	-		PSS015	1	-		
			Diacyclops einslei	-		PSS017	10	-		
			Diacyclops humphreysi unispinosus	-		PSS016, PSS017, PSS072	98	PSS088. PSS089*, PSS159	34	
			Diacyclops sobeprolatus	PSS163, PSS164	3	-		BC186, BC434, BUNMD1227, PSS158, PSS375	34	
			Halicyclops rochai	-		PSS015, PSS016, PSS017, PSS072, PSS074	41	31, BC150, BC156, BC186, BC282, BC292, BC405, BC406, BUNMD0887, BUNWB09, BUNWB13, BUNWO1108, BUNWP0005, JIMWE004, JIMWE003, JW023, PSS088. PSS089*, PSS161, PSS201*, PZ10BUN003, RR1	516	
			Metacyclops pilbaricus	PSS163	35	-		BC228, BC292, BC401, BUNWB13	10	
			Microcyclops varicans	PSS164	1	PSS017	10	BC210, BUNWB08, D08BU021, Hyporheic 03, PSS017	84	
			Orbuscyclops westaustraliensis	-		PSS016, PSS072	5	-		
			Paracyclops chiltoni	-		Nr Five Mile Well*	2	-		
		Harpacticoida	Thermocyclops decipiens	-		BF 2-1	10	-		
			Ameiridae	Parapseudoleptomesochra tureei	PSS164	12	-	-		
			Stygonitocrella trispinosa	-		PSS015, PSS016, PSS072	28	PSS089*	4	
			Stygonitocrella unispinosa	PSS164	12	-		PSS088	4	
			Canthocamptidae	Elaphoidella humphreysi	-	PSS074, PSS075	3	BC1473, BC156, BC186, BUNWB09, BUNWB13, BUNWO0773, BUNWP0005, BUNWP0006, PSS089*, PSS157, PSS161	39	
		Ectinosomatidae	Pseudectinosoma galassiae	-		PSS015, PSS016, PSS072	13	-		
			Miraciidae	Schizopera roberiverensis	-	PSS015, PSS016	8	PSS089*	7	
Malacostraca	Amphipoda	Bogidiellidae	Bogidiellidae sp. '1'	-		PSS015, PSS072, PSS073, PSS074	10	PSS089*, PSS201*	11	
		Eriopisidae	Eriopisidae sp. 1 (PSS) (formerly Melitidae sp. 1 (PSS))	PSS163	1	PSS015, PSS075	3	BC1473, BC225, BC292, BC401, BC667, BUNWB10, JW021, JW023	14	
			Nedsia hurlberti	-		PSS015, PSS016, PSS017, PSS073	63	BC150, BC156, BC186, BC225, BC282, BC292, BUNDD1687, BUNWB13, JIMDD080, JIMDR094, JIMWE003, JIMWE004, JW021, JW023, JW024, PSS089*, PSS160, PZ10BUN022	239	
			Nedsia sp. 'AMM001/029/030'	-		Nr Five Mile Well*, RR3A	12	31, 32, 34, DD13MEH007, MCPE5, MCR3*, RC12JIM0019, RC13MEH0040, RC13MEH0041, RC13MEH0097, RC14MEH0018, RC14MEH0053, RR1, RRD4, RRU3, RRU6	56	
		Paramelitidae	Pilbarus millsii	-		PSS016	1	PSS089*, PSS159, PSS375	48	
		Syncarida	Bathynellidae	Bathynella sp. 2	PSS163	1	-	-		
			Parabathynellidae	Atopobathynella sp. 'A'	-	PSS015, PSS016	7	-		
		Isopoda	Cirolanidae	Haptolana yarraloola	-	PSS075	1	RR1, PSS089*,	6	
		Thermosbaenacea	Halosbaenidae	Halosbaena tulki	-	BHP Town Bore*, Nr Five Mile Well*, RR3A, RR1A, Woolshed Well, PSS015, PSS072, PSS073, PSS074	53	BC150, BC186, BC225, BC401, JW021, JW024, PSS089*, PSS161, PSS201*	504	
		Ostracoda	Podocopida	Candonidae	Areacandona astrepte	-	PSS015, PSS016	34	-	
			Areacandona scanloni		PSS164	5	PSS073	1	-	
			Areacandona sp. '4'		-	PSS015	1	-		
			Cypretta seurati		PSS164	1	-		BC282, PSS161	31
			Cypretta sp. 4		PSS164	1	-		-	
			Deminutiocandona aenigma		-	PSS016	2	-		

Taxonomy				Collection Abundance and Distribution					
Class	Order	Family	Species	Within drawdown extent (n)	Within Buffer Extent (n)	Reference	(n)		
Ostracoda	Podocopida	Candonidae	<i>Humphreyscandona fovea</i>	-	PSS017	10	JW021, PSS160	5	
			<i>Humphreyscandona imperfecta</i>	-	PSS016, PSS072, PSS075	10	87	1	
			<i>Humphreyscandona pilbarae</i>	-	PSS015, PSS017	4	-		
			<i>Humphreyscandona woutersi</i>	-	PSS017, PSS072, PSS073, PSS074, PSS075	182	PSS088, PSS089*, PSS161, PSS201*	26	
			<i>Meridiescandona</i> sp. '2'	-	PSS015, PSS016, PSS072, PSS074	34	-		
			<i>Origocandona</i> sp. '2'	-	PSS016	1	-		
			<i>Pilbaracandona rosa</i>	-	PSS072, PSS073, PSS075	6	PSS088, PSS160	13	
		Limnocytheridae	<i>Gomphodella hirsuta</i>	-	PSS015, PSS016	3	-		
Annelida									
Oligochaeta	Tubificida	Enchytraeidae	<i>Enchytraeus Pilbara</i> sp. '1'	-	PSS016	1	BC186	20	
			<i>Enchytraeus Pilbara</i> sp. '2'	-	PSS016	74	-		
		Phreodrilidae	<i>Phreodrilidae</i> sp. 'dissimilar ventral chaetae'	PSS164	2	PSS015, PSS016	25	BC401, BC434, JW023, PSS088	8
			<i>Phreodrilidae</i> sp. 'similar ventral chaetae'	-	PSS017	2	PSS155	6	
			<i>Phreodrilus</i> sp. 'WA32'	PSS164	1	-	-		
		Tubificidae	<i>Tubificidae</i> sp. '2A'	-	PSS016	20	PSS161	4	
Polychaeta	Phyllodocida	Nereididae	<i>Namanereis</i> sp. '1'	-	PSS016	1			
	Aphaneura	Aeolosomatidae	<i>Aeolosoma</i> sp. '3'	-	PSS017	3	PSS375	7	
Nematoda									
Indeterminate	Indeterminate	Indeterminate	<i>Nematoda</i> sp. '11'	-	PSS016	1	-		
			<i>Nematoda</i> sp. '2'	-	PSS015	1	-		
			<i>Nematoda</i> sp. '3'	-	PSS016	1	-		

\* located within the Mesa C buffer extent

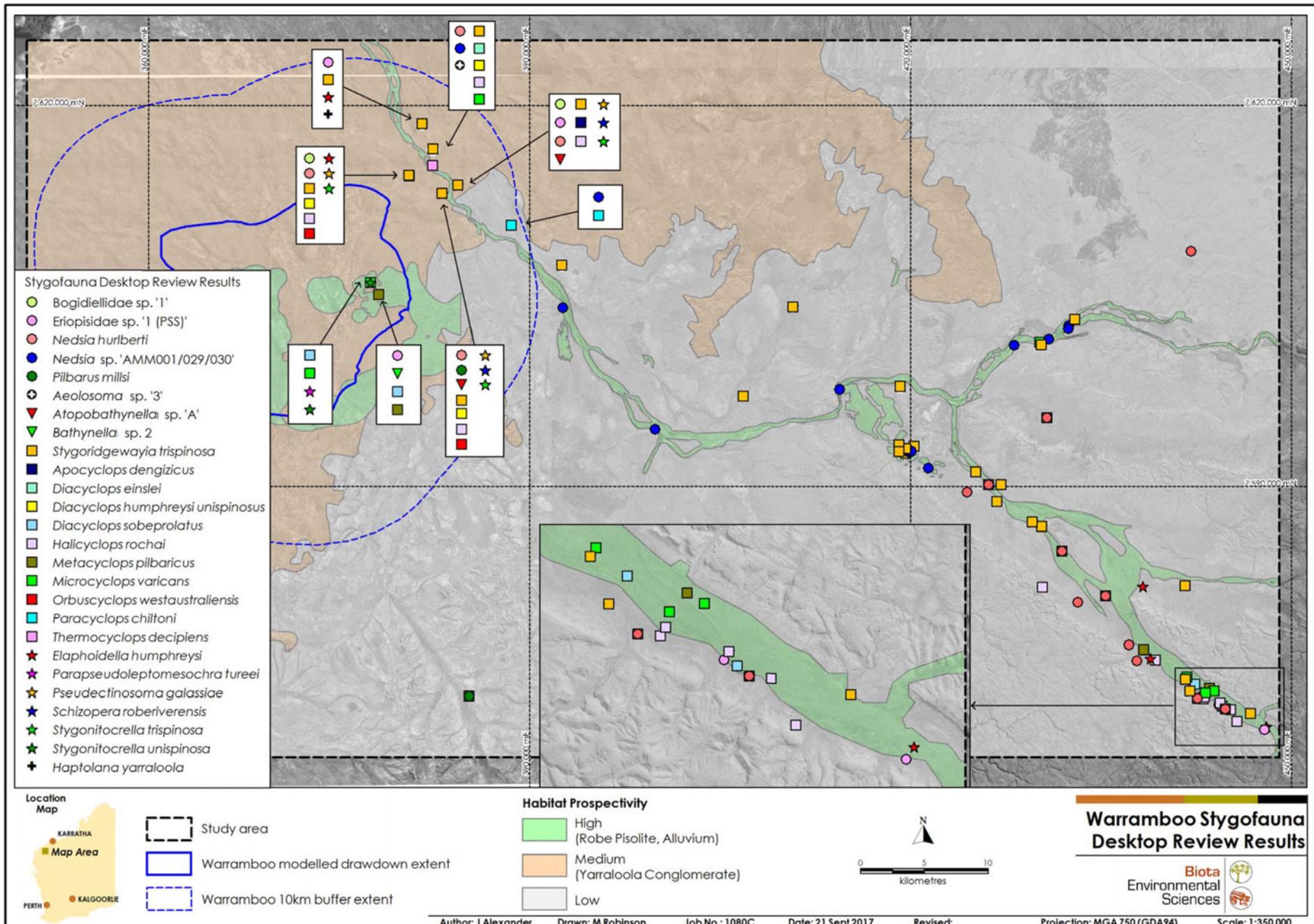


Figure 5.9: Location of species previously recorded from within the buffered drawdown extent at Warramboo and their wider distribution within the study area – Map 1.

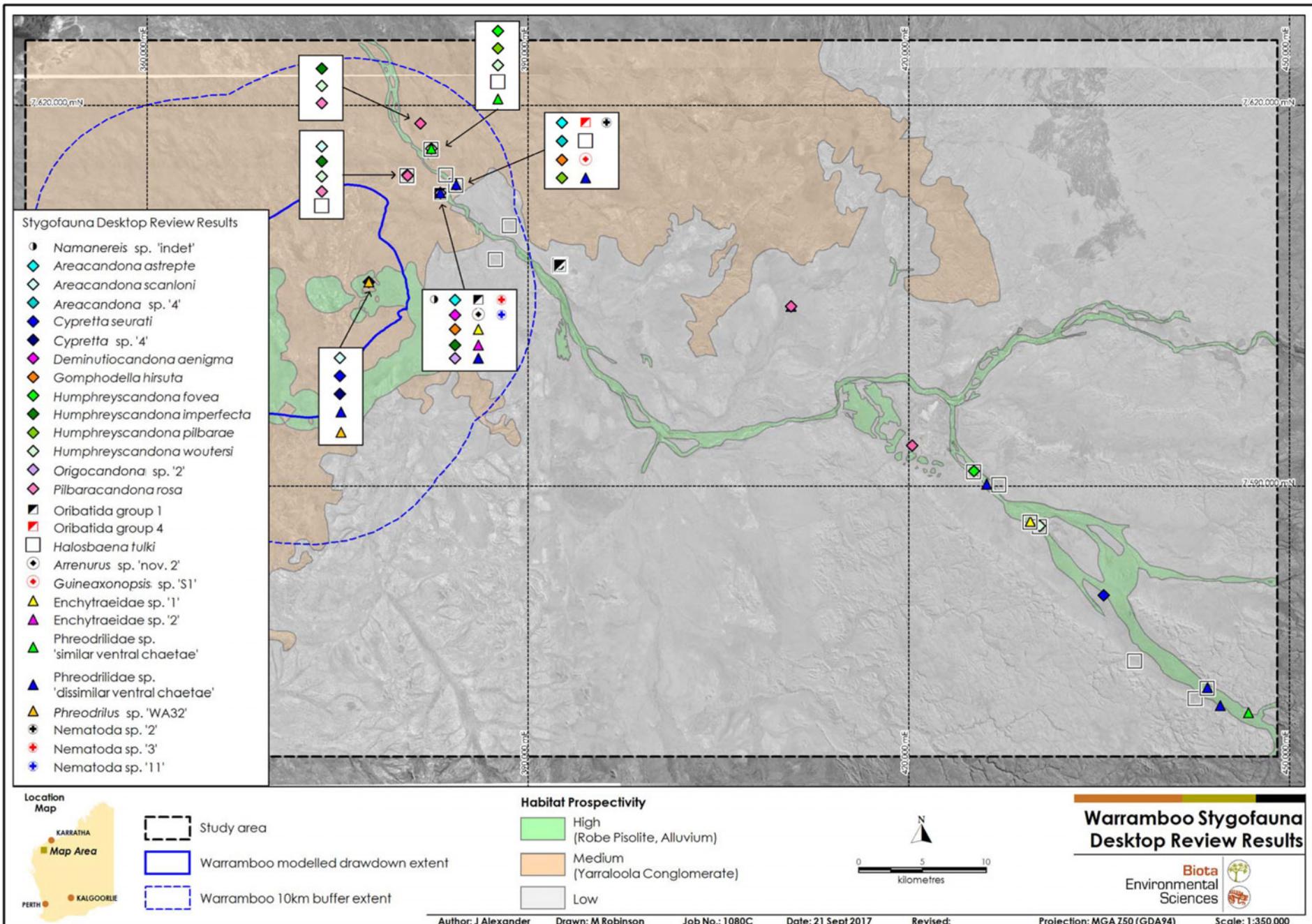


Figure 5.10: Location of species previously recorded from within the buffered drawdown extent at Warramboo and their wider distribution within the study area – Map 2.

Table 5.7: Summary of morphological identifications and locations of desktop review specimens in relation to the Mesa C drawdown extent.

Taxonomy				Collection Abundance and Distribution					
Class	Order	Family	Species	Within drawdown extent	(n)	Within Buffer Extent	(n)	Reference	(n)
<b>Arthropoda</b>									
Arachnida	Sarcoptiformes	Indeterminate	Oribatida group 1	-		PSS089	1	PSS016*	16
<b>Crustacea</b>									
Copepoda	Cyclopoida	Calanoida	Stygoridgewayia trispinosa	-		PSS089	73	31, BC156, BC186, BUNWE01, BUNWP0005, DD13MEH0007, JIMDR094, JIMWE004, JW021, JW024, RC13MEH0007, RC14MEH0018, RC14MEH0053, RR1, PSS088, PSS155, PSS158, PSS159, PSS160, PSS161, PSS015*, PSS016*, PSS017*, PSS072*, PSS073*, PSS074*, PSS075	1045
		Cyclopidae	Diacyclops humphreysi humphreysi	-		PSS089	5	BC019, BC1473, BC150, BC156, BC186, BC212, BC225, BC228, BC292, BC401, BC406, BC434, BC690, BUNDD1687, BUNMD1227, BUNWB13, BUNWO0773, BUNWO0774, BUNWO1104, BUNWO1105, BUNWO1108, BUNWP0005, BUNWP0006, BUWMD1500, J154, JIMWE003, JIMWE004, JW023, PSS375, PZ10BUN004, PZ10BUN022, PZ10BUN041, RC13MEH0007	764
			Diacyclops humphreysi unispinosus	-		PSS089	19	PSS088, PSS159, PSS016*, PSS017*, PSS072*	113
			Halicyclops rochai	-		PSS089, PSS201	3	31, BC150, BC156, BC186, BC282, BC292, BC405, BC406, BUNMD0887, BUNWB09, BUNWB13, BUNWO1108, BUNWP0005, JIMWE004, JIMWE003, JW023, PSS015*, PSS016*, PSS017*, PSS072*, PSS074*, PSS088, PSS089, PSS161, PSS201, PZ10BUN003, RR1	554
			Paracyclops chiltoni	-		Nr Five Mile Well*	2	-	
Harpacticoida	Canthocamptidae		Elaphoidella humphreysi	-		PSS089	3	BC1473, BC156, BC186, BUNWB09, BUNWB13, BUNWO0773, BUNWP0005, BUNWP0006, PSS074*, PSS075, PSS157, PSS161	39
	Miraciidae		Schizopera roberiverensis	-		PSS089	7	PSS015*, PSS016*	8
Malacostraca	Amphipoda	Bogidiellidae	Bogidiellidae sp. '1'	-		PSS089, PSS20	11	PSS015*, PSS072*, PSS073*, PSS074*	10
		Eriopisidae	Nedsia hurlberti	-		PSS089	3	BC150, BC156, BC186, BC225, BC282, BC292, BUNDD1687, BUNWB13, JIMDD080, JIMDR094, JIMWE003, JIMWE004, JW021, JW023, JW024, PSS015*, PSS016*, PSS017*, PSS073*, PSS160, PZ10BUN022	299
			Nedsia sp '24'	-		PSS201	1	PSS088	23
			Nedsia sp. 'AMM001/029/030'	-		Nr Five Mile Well*, MCPE5*, MCR3*	10	31, 32, 34, DD13MEH007, RC12JIM0019, RC13MEH0040, RC13MEH0041, RC13MEH0097, RC14MEH0018, RC14MEH0053, RR1, RR3A, RRD4, RRU3, RRU6	56
			Nedsia sp. 'AMM004'	-	200	2	87	5	
		Niphargidae	Niphargidae sp. 'AMN008'	-	200	3	-		
		Paramelitidae	Paramelitidae sp. '2'	-		PSS089, PSS201	5	BC1473, BC150, BC186, JIMDR094, JIMWE003, JIMWE004	25
			Pilbarus millsii	-		PSS089	10	PSS016*, PSS159, PSS375	38
	Isopoda	Cirolanidae	Haptolana yarraloola	-		PSS089	1	RR1, PSS075	6
			Kagalana tonde	-		PSS089	2	JW021, JW023, JW024, RR1	9
	Thermosbaenacea	Halosbaenidae	Halosbaena tulki	-		BHP Town Bore*, Nr Five Mile Well*, PSS089, PSS201	51	BC150, BC186, BC225, BC401, JW021, JW024, PSS161, RR3A, RR1A, Woolshed Well, PSS015*, PSS072*, PSS073*, PSS074*	506
Ostracoda	Podocopida	Candonidae	Humphreyscandona woutersi	-		PSS089, PSS201	15	PSS088, PSS161, PSS017*, PSS072*, PSS073*, PSS074*, PSS075	193
			Meridiescandona sp. '2'	-		PSS089	2	PSS015*, PSS016*, PSS072*, PSS074*	34
			Pilbaracandona sp. 'BOS526'	-		200	1	-	

\* located within the Warramboo buffer extent

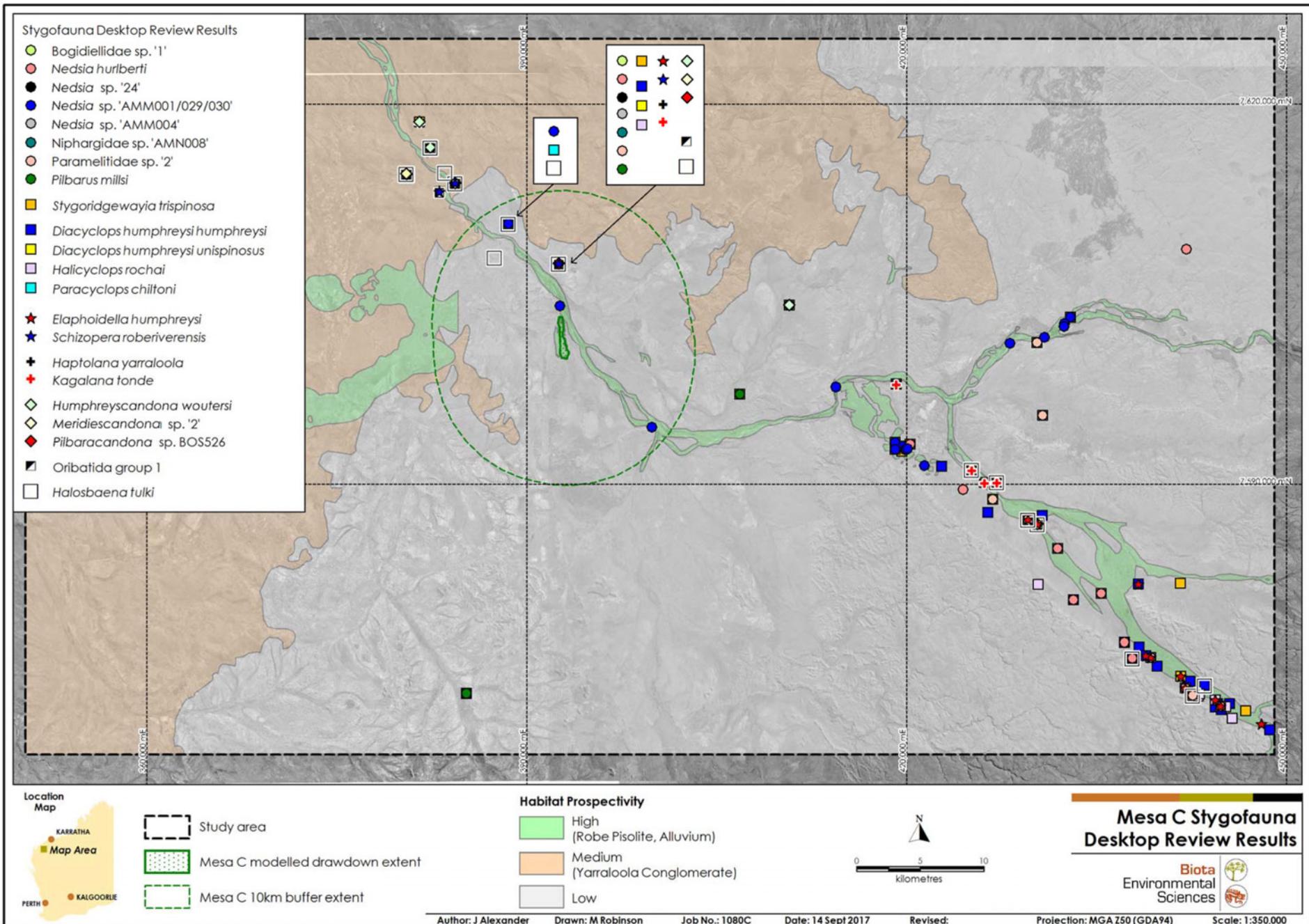


Figure 5.11: Location of species previously recorded from within the buffered drawdown extent at Mesa C and their wider distribution within the study area.

## 5.2.4 Survey Results

### 5.2.4.1 Warramboo

A total of 369 stygobitic fauna specimens were identified from the three phases of sampling and within the Warramboo drawdown and buffer extents (Table 5.8, Appendix 6). Nine orders were recorded, with the cyclopoid copepods and amphipods comprising 68.5% of total collections (36% and 32.5% respectively).

Table 5.8: Summary of higher order taxa collected from Warramboo during three phases of sampling.

Taxonomy			Number Collected	Number Sites
Phylum	Class	Order (Common Name)		
Annelida	Clitellata	Oligochaeta (Earthworms)	11	2
Crustacea	Copepoda	Calanoida (Calanoid Copepods)	28	2
		Cyclopoida (Cyclopoid Copepods)	133	5
		Harpacticoida (Harpacticoid Copepods)	4	1
		Amphipoda (Amphipods)	120	9
	Malacostraca	Isopoda (Slaters)	2	1
		Ostracoda (Ostracods)	1	1
		Syncarida (Bathynellids)	1	1
		Thermosbaenacea (Thermosbaenaceans)	69	3

A total of six species of stygofauna were recorded within the drawdown extent area at Warramboo, all of which belonged to the phylum Crustacea, with two species belonging to the class Copepoda, three species from the order Amphipoda and one from the order Bathynellacea.

Nineteen species were recorded within the buffer extent at Warramboo from seven orders. Details on the fauna collected are provided in the following sections.

#### Oligochaeta (Earthworms)

No oligochaetes were recorded from within the drawdown extent, however two species were identified from the buffer extent (Table 5.9, Figure 5.12). While not recorded previously within the study area, these species are widespread throughout the Pilbara and have been identified from sites in the eastern Pilbara during previous studies approximately 370 km east of Waramboo (Biota 2015b).

#### Copepoda (Calanoida, Cyclopoida and Harpacticoida)

Two morphologically identified species of copepod were collected from within the drawdown extent at Warramboo (Table 5.9, Figure 5.12). *Inermipes humphreysi* was recorded from one site within the Warramboo drawdown extent. This species is formally described from specimens from Barrow Island and is not restricted to the current study area (Appendix 4).

*Diacyclops humphreysi unispinosus* is also a previously described species recorded during the current survey from one site within the drawdown extent and two sites within the buffer extent, and is widespread within the Pilbara (Section 5.2.5).

Additionally, a further four copepod species were recorded from the Warramboo buffer extent. These species are all widespread throughout the study area (Appendix 5) and all previously described from specimens collected outside the buffer extent.

Table 5.9: Taxonomic summary and locations of fauna identified from sampling withing the Warramboo drawdown and buffer extents.

Taxonomy		Collection Abundance and Distribution				Previously Recorded elsewhere in the wider study area <sup>^</sup>
Family	Species	Within drawdown extent	(n)	Within Buffer Extent	(n)	
Oligochaeta (Earthworms)						
Naididae	Dero furcata	-		Daisy Well	4	No
	Pristina longiseta	-		Budgie Bore	7	No
Calanoida (Calanoid Copepods)						
Ridgewayiidae	Stygoridgewaya trispinosa	-		Budgie Bore, MEAWO4086*	28	Yes
Cyclopoida (Cyclopoid Copepods)						
Cyclopidae	Diacyclops humphreysi humphreysi	-		Camp Bore	15	Yes
	Diacyclops humphreysi unispinosus	RC13MEA0279	34	Budgie Bore, Camp Bore	59	Yes
	Microcyclops varicans	-		Budgie Bore	25	Yes
	Paracyclops chiltoni	-		Queen Well	21	Yes
Harpacticoida (Harpacticoid Copepods)						
Ameiridae	Inermipes humphreysi	RC13MEA0279	4	-		No
Amphipoda (Amphipods)						
Eriopisidae	Eriopisidae nov. gen. sp. 'AMM006'	-		RC13TOB0023, TOBRC0099	2	No
	Nedsia sp. 'AMM001/029/030'	-		Budgie Bore, Camp Bore	15	Yes
	Nedsia sp. 'AMM002'	-		Budgie Bore, Daisy Well	5	No
	Nedsia sp. 'AMM003'	MB13WARR010	3	-		No
	Nedsia sp. 'AMM005'	MB13WARR001	5	-		No
	Nedsia sp. 'AMM027'	-		Budgie Bore	1	No
	Nedsia sp. 'AMM028'	-		Budgie Bore	3	No
	Nedsia sp. 'AMM031'	-		Budgie Bore, MEAWO4086*	6	No
Niphargidae	Niphargidae sp. 'AMN001'	-		Budgie Bore	1	No
	Niphargidae sp. 'AMN008'	-		Budgie Bore, MEAWO4086*	12	Yes
Paramelitidae	Paramelitidae sp. 'AMP009'	-		Budgie Bore	1	No
	Paramelitidae sp. 'AMP023'	MB16WARR0009	54	TOBRC0009	12	No
Isopoda (Slaters)						
Cirolanidae	Haptolana yarraloola	-		Budgie Bore	2	Yes

Taxonomy		Collection Abundance and Distribution				Previously Recorded elsewhere in the wider study area^
Family	Species	Within drawdown extent	(n)	Within Buffer Extent	(n)	
Ostracoda (Ostracods)						
Candonidae	Humphreyscandona fovea	-		MEAWO4086*	1	Yes
Syncarida (Bathynellids)						
Parabathynellidae	Atopobathynella sp. 'B25'	MB16WARR0009	1	-		No
Thermosbaenacea (Thermosbaenaceans)						
Halosbaenidae	Halosbaena tulki	-		Budgie Bore	69	Yes

\* Sampled as part of Mesa C assessment (within both buffer extents)

^ See table 5.6, table 5.7 and appendices for historical collections within the study area.

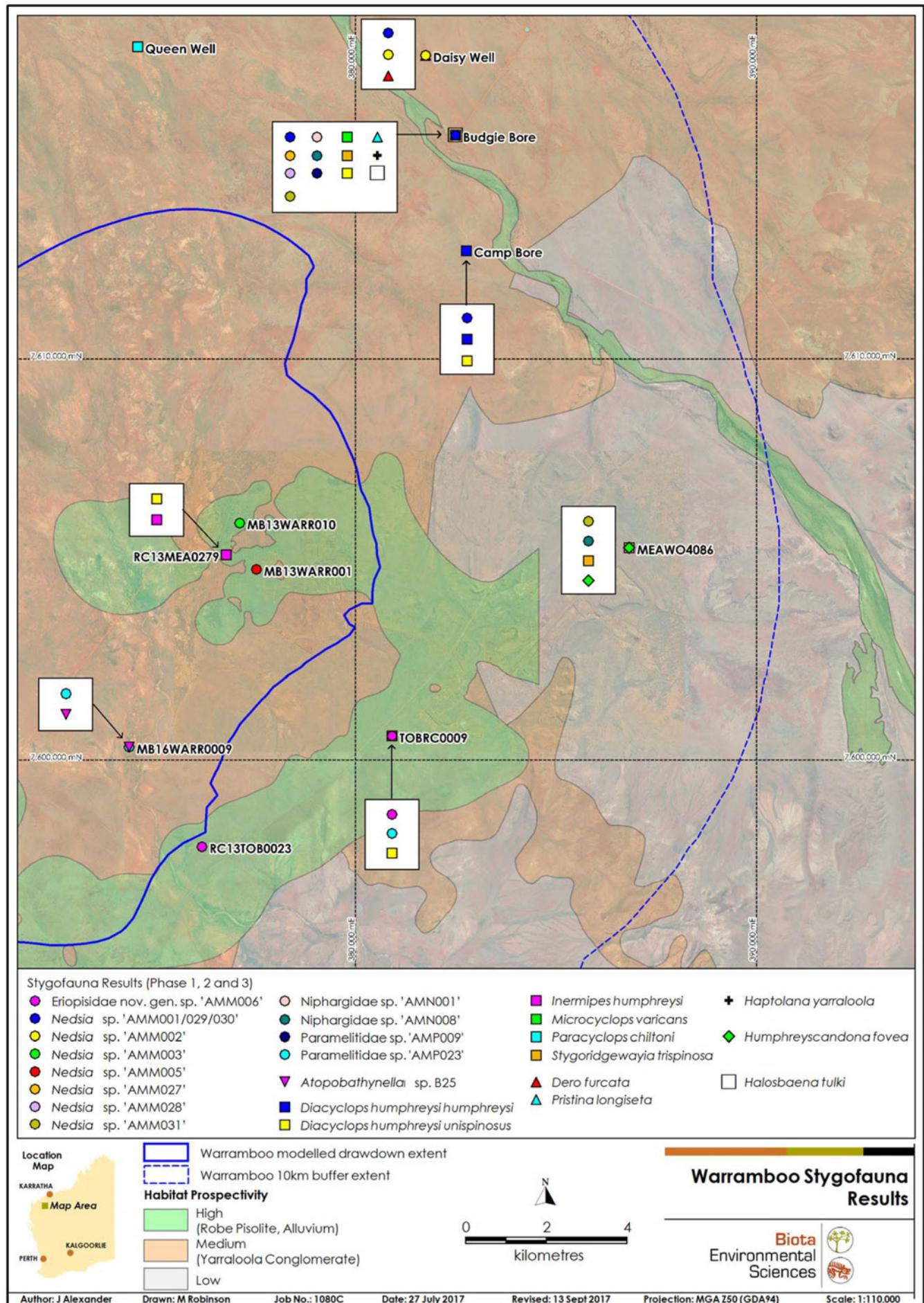


Figure 5.12: Location of species collections from within the drawdown and buffer extents at Warramboo.

### Order Amphipoda

Genetic analysis determined the presence of three lineages of Amphipoda from within the Warramboo drawdown extent and a further nine from the buffer extent. One lineage, Paramelitidae sp. 'AMP023', occurs within both the drawdown and buffer extents. For the purposes of this report, these lineages are considered to represent putative species (Table 5.9, Figure 5.12; Section 4.4; Appendix 2).

Eight of the identified species belonged to the family Eriopisidae, with two species each from the Niphargidae and Paramelitidae.

*Nedsia* sp. 'AMM003' and *Nedsia* sp. 'AMM005' are new species recorded only from within the modelled drawdown extent at Warramboo (Figure 5.12). During the current survey, Paramelitidae sp. 'AMP023' was recorded within the drawdown extent however was also previously known from a reference site. Additionally, Paramelitidae sp. 'AMP023' has been recorded outside the study area, approximately 102 km to north-northwest on Barrow Island (Section 5.2.5, Figure 5.13).

Of the remaining nine species recorded from the buffer extent, two species (*Nedsia* sp. 'AMM001/029/030' and *Niphargidae* sp. 'AMN008') were previously known from elsewhere in the study area (Figure 5.13, Figure 5.14). Paramelitidae sp. 'AMP009' has been recorded from Barrow Island (Figure 5.13). The remaining six species have not been recorded outside the buffer extent.

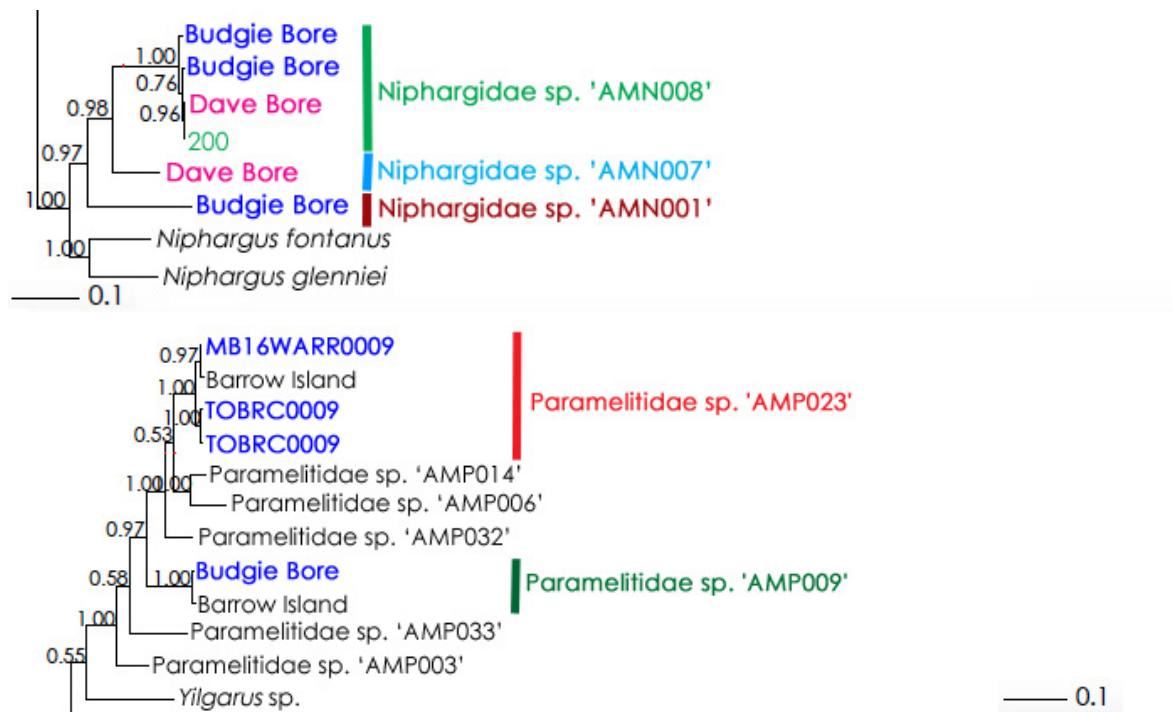


Figure 5.13: Excerpts of Bayesian analysis of CO1 haplotypes of the family Niphargidae (above), Paramelitidae (below) collected from Warramboo and Mesa C.  
(Numbers on major nodes correspond to posterior probabilities; values <50% are not shown. Stygal amphipod specimens collected from Warramboo are displayed in blue and Mesa C in pink. Reference specimens from GenBank displayed in black. Historically recorded specimens collected from within the buffer extent are displayed in green (Appendix 2). Coloured blocks indicate specimens belonging to a single species.)

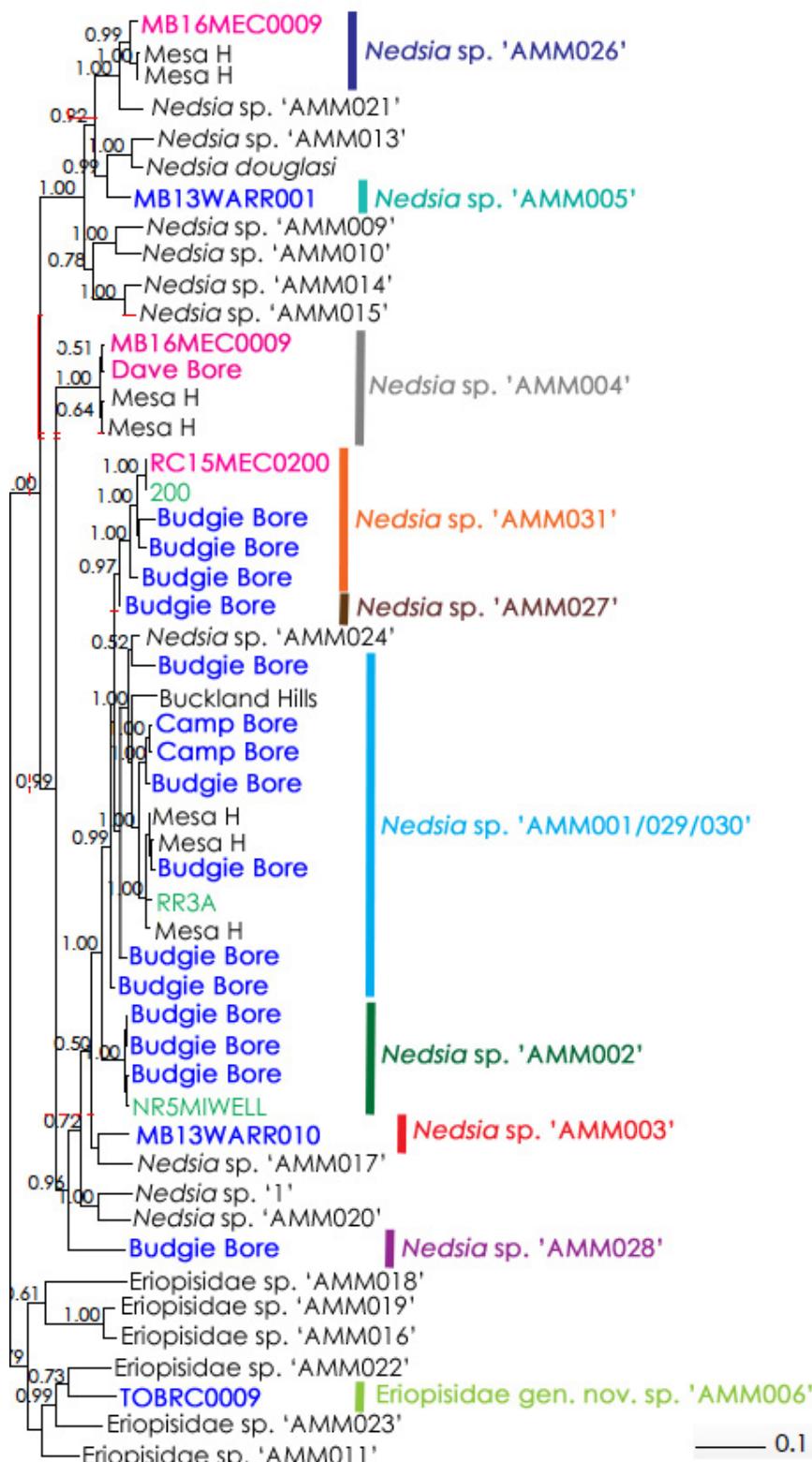


Figure 5.14: Excerpts of Bayesian analysis of CO1 haplotypes of the family Eriopisidae collected from Warramboo and Mesa C.

(Numbers on major nodes correspond to posterior probabilities; values <50% are not shown. Stygal amphipod specimens collected from Warramboo are displayed in blue and Mesa C in pink. Reference specimens from GenBank displayed in black. Historically recorded specimens collected from within the buffer extent are displayed in green (Appendix 2). Coloured blocks indicate specimens belonging to a single species.)

Order Isopoda

No isopods were recorded from within the drawdown extent at Warramboo (Table 5.9).

Two isopods from the family Cirolanidae, belonging to the species *Haptolana yarraloola*, were recorded from Budgie Bore, within the buffer extent. This species has also been recorded from Mesa H, within the study area and appears to be relatively widespread at local scale (Table 5.7, Appendix 5).

Order Ostracoda

No Ostracoda were recorded from within the drawdown extent at Warramboo (Table 5.9).

A single specimen belonging to the family Candonidae, belonging to the species *Humphreyscandona fovea*, was recorded from MEAWO4086, within the buffer extent (Table 5.9). This species was previously known from outside of the buffer extent from the portion of the Bungaroo Valley within the study area (Appendix 5). *H. fovea* was also originally described from specimens collected approximately 320 km northwest of Warramboo (Karanovic and Marmonier 2003).

Order Syncarida

A single specimen belonging to the order Bathynellacea (*Atopobathynella* sp. 'B25') was recorded from site MB16WARR0009 within the drawdown extent (Table 5.9, Figure 5.12). This specimen does not correspond to any described bathynellid taxa and is currently not known from any other location.

No additional Syncarida were recorded from the buffer extent.

Order Thermosbaenacea

No Thermosbaenacea were recorded from the drawdown extent at Warramboo (Table 5.9).

A total of 69 specimens of *Halosbaena tulki* were recorded from Budgie Bore during sampling at Warramboo. This species is widespread coastally, extending as far as Bungaroo (within the study area) however occurs at Cape range (approximately 190 km west) and Barrow Island.

Recent molecular work has indicated that this widespread species may actually represent a species complex containing at least five separate species that reflect local geography (Cape Range west, Cape Range east, Barrow Island, Pilbara low elevation and Pilbara high elevation) (Page et al. 2016).

## **5.2.5 Mesa C**

A total of 276 stygofauna specimens were recorded from Mesa C sites (Section 4.6.3.2) from two phases of sampling, representing eight orders (Table 5.10, Appendix 6). The copepod orders Cyclopoida and Harpacticoida were the greatest contributors to faunal composition comprising 26.1% and 18.5% of collections respectively.

Table 5.10: Summary of higher order taxa collected from Mesa C during three phases of sampling.

Taxonomy			Number Collected	Number Sites
Phylum	Class	Order (Common Name)		
Crustacea	Copepoda	Calanoida (Calanoid Copepods)	44	3
		Cyclopoida (Cyclopoid Copepods)	72	3
		Harpacticoida (Harpacticoid Copepods)	51	2
	Malacostraca	Amphipoda (Amphipods)	33	7
		Isopoda (Slaters)	1	1
		Ostracoda (Ostracods)	14	3
		Thermosbaenacea (Thermosbaenaceans)	43	2
Mollusca	Gastropoda	Sorbeoconcha (Aquatic Snails)	18	1

Two species were recorded from within the Mesa C drawdown extent and a further 19 were recorded from within the buffer extent. Details on the fauna collected are provided in the following sections.

#### Copepoda (Calanoida, Cyclopoida and Harpacticoida)

Eight species of copepod were collected from within the Mesa C buffer extent. This included one species of Calanoida, three Cyclopoida and four Harpacticoida. No copepods were identified from within the Mesa C drawdown extent (Table 5.11).

Of the eight species recorded from within the buffer extent, seven are also recorded from elsewhere in the study area (Appendix 5). *Megastygonitocrella unispinosa*, while not previously recorded within the study area, was originally described from specimens collected from a site along the Fortescue River, approximately 56 km north of Warramboo (Karanovic and Hancock 2009).

#### Order Amphipoda

Eight amphipod specimens were identified using genetic analysis from within the Mesa C drawdown extent. These specimens represented two species from the family Eriopisidae, *Nedsia* sp. 'AMM004' and *Nedsia* sp. 'AMM031' (Table 5.11, Figure 5.15), and both species were also collected from sites within the Mesa C buffer extent.

*Nedsia* sp. 'AMM004' differed by 9.4% from its closest related species, *Nedsia* sp. 'AMM031' and *Nedsia* sp. 'AMM024' (Figure 5.14, Appendix 2). Intraspecific variation between specimens of *Nedsia* sp. 'AMM004' recorded from Mesa C (MB16MEC0009) and Mesa H was very low at 0.3%. This low genetic variation over approximately 18 km indicates gene flow is currently ongoing amongst these *Nedsia* over at least this spatial extent.

*Nedsia* sp. 'AMM031' differed from the closest related species *Nedsia* sp. 'AMM001/029/030' (which is likely a species complex) by 3.9% (Figure 5.14, Appendix 2). Discussion with genetic and taxonomic specialists at Helix, WAM and the South Australian Museum have conservatively indicated this *Nedsia* sp. 'AMM031' is likely to be a distinct species from *Nedsia* sp. 'AMM001/029/030', however additional specimens and further analysis would be needed to more fully confirm this.

Three additional Amphipoda species were recorded from within the buffer extent (Table 5.11, Figure 5.15). These were *Niphargidae* sp. 'AMN007', a singleton collection from the buffer extent, *Eriopisidae* sp. 'AMM026' (which has previously been recorded from elsewhere in the study area; Table 5.11) and *Niphargidae* sp. 'AMN008'.

#### Order Isopoda

No isopods were recorded from within the drawdown extent at Mesa C (Table 5.11, Figure 5.15).

A single isopod from the family Cirolanidae, *Haptolana yarraloola*, was recorded from Dave Bore, within the buffer extent. This species has also been recorded from Mesa H, within the study area (Table 5.7, Appendix 5).

#### Order Ostracoda

No Ostracoda were recorded from within the drawdown extent at Mesa C (Table 5.11, Figure 5.15).

Three species of ostracoda were recorded from the buffer extent at Mesa C. One of these, *Humphreyscandona fovea*, is known from elsewhere in the study area at Bungaroo. The remaining two species, *Pilbaracandona* sp. BOS526 and *Areacandona* sp. BOS818, have distributions currently restricted to the buffer extent.

#### Order Thermosbaenacea

No Thermosbaenacea were recorded from the drawdown extent at Mesa C (Table 5.11, Figure 5.15).

A total of 43 specimens of *Halosbaena tulki* were recorded from Dave Bore and MB16MEC0009 during sampling at Mesa C. This species is widespread coastally, extending as far as Bungaroo (within the study area) and also occurs at Cape range and Barrow Island.

Order Sorbeoconcha

No aquatic snails were recorded from within the drawdown extent at Mesa C (Table 5.11).

Eighteen specimens belonging to the species Hydrobiidae sp. '3' were recorded from Dave Bore, within the Mesa C buffer extent. Only three of the recorded specimens were alive, with the remainder being empty shells.

Table 5.11: Taxonomic summary and locations of fauna identified from sampling within the Mesa C drawdown and buffer extents.

Taxonomy		Collection Abundance and Distribution				Recorded elsewhere in study area <sup>^</sup>
Family	Species	Within drawdown extent	(n)	Within Buffer Extent	(n)	
Calanoida (Calanoid Copepods)						
Ridgewayiidae	<i>Stygoridgewayia trispinosa</i>	-		Dave Bore, MB16MEC0008, MEAWO4086	44	Yes
Cyclopoida (Cyclopoid Copepods)						
Cyclopidae	<i>Diacyclops humphreysi humphreysi</i>	-		MB16MEC0009	1	Yes
	<i>Diacyclops humphreysi unispinosus</i>	-		Dave Bore, MB16MEC0009	56	Yes
	<i>Dussartcyclops uniarticulatus</i>	-		MB16MEC0008	15	Yes
Harpacticoida (Harpacticoid Copepods)						
Ameiridae	<i>Lucionitocrella yalleenensis</i>	-		MB16MEC0009	3	Yes
	<i>Megastygonitocrella unispinosa</i>	-		MB16MEC0008, MB16MEC0009	34	Yes
Canthocamptidae	<i>Elaphoidella humphreysi</i>	-		MB16MEC0008	10	Yes
Miraciidae	<i>Schizopera roberiverensis</i>	-		MB16MEC0008	4	Yes
Amphipoda (Amphipods)						
Eriopisidae	Eriopisidae sp. 'AMM026'	-		MB16MEC0009	7	Yes
	Nedsia sp. 'AMM004'	MB16MEC0007, RC15MEC0027, RC16MEC0102, WB16MEC0002	5	Dave Bore, MB16MEC0009	7	Yes
	Nedsia sp. 'AMM031'	RC15MEC0200	3	Dave Bore, MEAWO4086	3	No
Niphargidae	Niphargidae sp. 'AMN007'	-		Dave Bore	1	No
	Niphargidae sp. 'AMN008'	-		Dave Bore, MEAWO4086	7	No
Isopoda (Slaters)						
Cirolanidae	<i>Haptolana yarraloola</i>	-		Dave Bore	1	Yes
Ostracoda (Ostracods)						
Candonidae	<i>Areacandona</i> sp. BOS818	-		MB16MEC0008	1	No
	<i>Humphreyscandona fovea</i>	-		MEAWO4086	1	Yes
	<i>Pilbaracandona</i> sp. BOS526	-		Dave Bore	12	No
Thermosbaenacea (Thermosbaenaceans)						
Halosbaenidae	<i>Halosbaena tulki</i>	-		Dave Bore, MB16MEC0009	43	Yes
Sorbeoconcha (Aquatic snails)						
Hydrobiidae	Hydrobiidae sp. '3'	-		Dave Bore	18	No

\* Sampled as part of Mesa C assessment (within both buffer extents)

<sup>^</sup> See table 5.6 table 5.7 and appendices for historic collections within the study area.

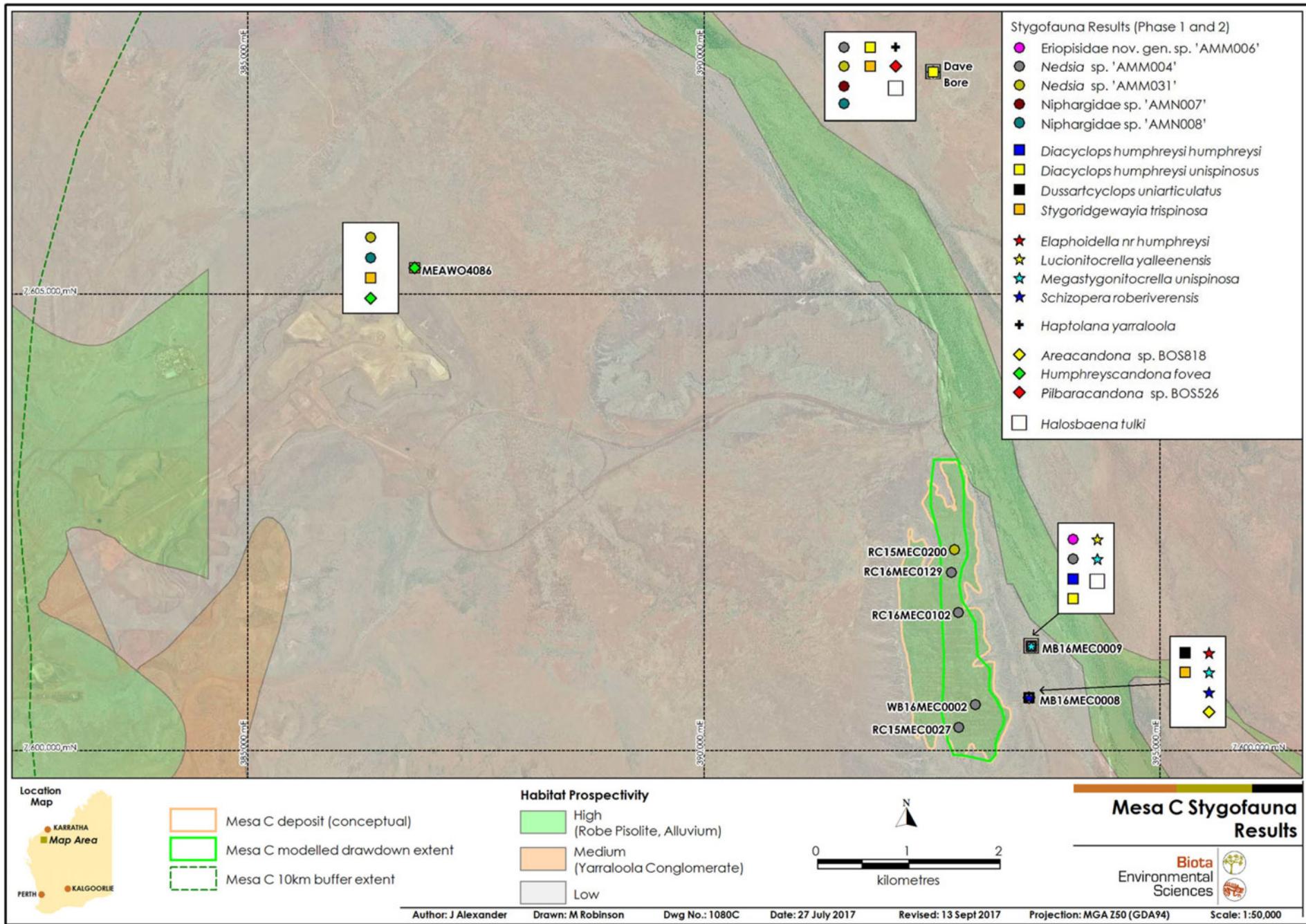


Figure 5.15: Location of species collections from within the drawdown and buffer extents at Mesa C.

# 6.0 Discussion

## 6.1 Conservation Significance

The following three species of known conservation significance have been recorded from the study area:

- *Ophisternon candidum* (Blind Cave Eel) – Stygal eel collected from Bungaroo in the east of the study area (Figure 3.1). This species is also known from Cape Range, approximately 192 km northwest of Warramboo. Listed as vulnerable federally under the EPBC Act 1999 and as Schedule 3 in Western Australia;
- *Nedsia sculptilis* – Amphipoda species previously collected from the Bungaroo Valley within the study area, which was originally described on the basis of morphology (Bradbury and Williams 1996). Listed as Schedule 3 in Western Australia; and
- *Nedsia hurlberti* – Amphipoda species previously collected from the Bungaroo Valley within the study area, which was originally described on the basis of morphology (Bradbury and Williams 1996). Listed as Schedule 3 in Western Australia.

While these species were noted in the desktop review, and are relevant to the wider study area, no records of these species have been obtained from either the Warramboo or Mesa C drawdown extent areas. However, *Nedsia sculptilis* and *Nedsia hurlberti* were described solely on the basis of morphology with no genetic analysis completed as part of their formal description (Bradbury and Williams 1996), whereas specimens from this study were identified based on molecular analysis. Multiple studies in the Pilbara have indicated that some morphologically described amphipod species may represent species complexes. Equally, past difficulties have arisen with resolving Amphipoda taxonomic boundaries based on morphology alone, where differences in characters has actually represented variation within a species rather than delineating separate species (Biota 2001). The large number of specimens that are juvenile and damaged, and are therefore not informative to morphological analysis, compounds these issues; reducing the power of morphological approaches and limiting determinations of species distribution based on this. Given these considerations, genetic analysis is likely to be more effective and objective approach to assigning species, reviewing distributions, and thereby assessing conservation significance of putative species within this group.

### 6.1.1 Warramboo

Overall 71 stygofauna species were recorded in total as occurring within the combined drawdown and buffer extent areas (Table 6.1). None of these species are listed as conservation significant or categorised as confirmed SRE species using WAM SRE guidelines (Appendix 3).

Eighteen species of stygofauna were recorded and collated from within the Warramboo drawdown extent. Sixty species were recorded from within the buffer extent. Seven of these species occurred within both the drawdown extent and buffer extent.

Sixteen species from the buffer and drawdown extents are categorised as being potential SRE species based on available information. Five of these were recorded from within the drawdown extent, with four of those species currently only known from the drawdown extent. The remaining 11 species were recorded from the buffer extent, with eight of the 11 recorded only from within the buffer extent. These species are mostly poorly represented in collections, with three species (*Atopobathynella* sp. 'B25', *Cyprætta* sp. '4' and *Niphargidae* sp. 'AMN001') represented by singleton records (Table 6.1).

Four potential SRE species were collated from records also outside the study area, with *Humphreyscandona imperfecta*, *Humphreyscandona pilbarae* and *Origocandona* sp. '2' recorded from the Fortecue River north of Warramboo, and *Phreodrilus* sp. 'WA32', collected from west of Warramboo (Table 6.1). Despite being recorded outside the study area, these species are conservatively retained as potential SRE species as they are known from limited collections and distributions.

Of the 60 species recorded from within the buffer extent, 49 are considered widespread, based on WAM SRE guidelines, as they are recorded in multiple locations throughout the Pilbara or other locations (such as Barrow Island; Table 6.1).

Table 6.1: Summary of species recorded from the Warramboo modelled drawdown and buffer extents during this survey and collated from the desktop review, including their distributions and WAM SRE status.

Species Name	Collected From		Collection Representation (Total number sites)*	New Species	Singleton Record	SRE Sub Categories ^	Notes
	Drawdown Extent	Buffer Extent					
<b>Potential SRE Species</b>							
<i>Atopobathynella</i> sp. 'B25'	X	-	Poor (Poor)	X	X	A, C	Known only from the drawdown extent
<i>Cyprætta</i> sp. '4'	X	-	Poor (Poor)	-	X	A, C	Known only from the drawdown extent
<i>Nedsia</i> sp. 'AMM003'	X	-	Poor (Poor)	X	-	A, D	Known only from the drawdown extent
<i>Nedsia</i> sp. 'AMM005'	X	-	Poor (Poor)	X	-	A, D	Known only from the drawdown extent
<i>Phreodrilus</i> sp. 'WA32'	X	-	Poor (Poor)	-	-	A, C	Also recorded from one PSS site approximately 50 km west of Warramboo drawdown extent
<i>Eriopisidae</i> nov. gen. sp. 'AMM006'	-	X	Poor (Poor)	X	-	A, D	Known only from buffer extent
<i>Humphreyscandona imperfecta</i>	-	X	Good (Poor)	-	-	C	Also collected from Fortescue River site approximately 58 km north of Warramboo.
<i>Humphreyscandona pilbara</i> e	-	X	Poor (Poor)	-	-	C	Also collected from Fortescue River site approximately 51 km north west of Warramboo.
<i>Meridiescandona</i> sp. '2'	-	X	Poor (Poor)	-	-	A, C	Known only from buffer extent
<i>Nedsia</i> sp. 'AMM002'	-	X	Poor (Poor)	X	-	A, D	Known only from buffer extent
<i>Nedsia</i> sp. 'AMM027'	-	X	Poor (Poor)	X	-	A, D	Known only from buffer extent
<i>Nedsia</i> sp. 'AMM028'	-	X	Poor (Poor)	X	-	A, D	Known only from buffer extent
<i>Nedsia</i> sp. 'AMM031'	-	X	Poor (Poor)	X	-	A, D	Known only from buffer extent
<i>Niphargidae</i> sp. 'AMN001'	-	X	Poor (Poor)	X	X	A, D	Known only from buffer extent
<i>Niphargidae</i> sp. 'AMN008'	-	X	Fair (Poor)	-	-	A, D	Known only from buffer extent
<i>Origocandona</i> sp. '2'	-	X	Poor (Poor)	-	-	A, C	Also collected from Fortescue River site approximately 58 km north of Warramboo.
<b>Widespread</b>							
<i>Areacandona scanloni</i>	X	X	Good (Fair)	-	-	C	Widespread collections within the PSS
<i>Diacyclops humphreysi unispinosus</i>	X	X	Good (Fair)	-	-	C	Described from specimens on Barrow Island (Karanovic 2006b)
<i>Diacyclops sobeprolatus</i>	X	X	Good (Good)	-	-	C	Described from specimens near Newman (Karanovic 2006b)
<i>Eriopisidae</i> sp. 1 (PSS)	X	X	Good (Good)	-	-	A, C	Widespread collections within the PSS
<i>Microcyclops varicans</i>	X	X	Good (Good)	-	-	C	Described from specimens in the Eastern Pilbara and near Fortescue (Karanovic 2006b)
<i>Paramelitidae</i> sp 'AMP023'	X	X	Good (Poor)	-	-	A, C	Recorded also on Barrow Island

Species Name	Collected From		Collection Representation (Total number sites)*	New Species	Singleton Record	SRE Sub Categories ^	Notes
<i>Phreodrilidae</i> sp. 'dissimilar ventral chaetae'	X	X	Good (Good)	-	-	C	Also occurs in the east Pilbara (Biota 2015b)
<i>Bathynella</i> sp. '2'	X	-	Fair (Fair)	-	-	A, C	Widespread collections within the PSS
<i>Cyprætta seurati</i>	X	-	Good (Good)	-	-	C	Widespread collections within the PSS.
<i>Inermipes humphreysi</i>	X	-	Fair (Fair)	-	-	A, B, C, E	Known from the Warramboo drawdown extent and Barrow Island (Appendix 4)
<i>Metacyclops pilbaricus</i>	X	-	Good (Fair)	-	-	C	Described from specimens near Newman (Karanovic 2006b), Eastern Pilbara.
<i>Parapseudoleptomesochra tureei</i>	X	-	Poor (Poor)	-	-	A, C	Also located at Turee Creek approximately 291 km south east of Warramboo (Karanovic 2006b)
<i>Stygonitocrella unispinosa</i>	X	-	Good (Good)	-	-	A, C	Described from the Robe Valley and North of the study area (Karanovic 2006b). Widespread collections within the PSS
<i>Arrenurus</i> sp. 'nov. 2'	-	X	Poor (Poor)	-	-	A, C	Also recorded from PSS028, approximately 372 km north east of Warramboo
<i>Aeolosoma</i> sp. '3'	-	X	Fair (Poor)	-	-	C	Widespread collections within the PSS
<i>Apocyclops dengizicus</i>	-	X	Good (Good)	-	-	C	Cosmopolitan species
<i>Areacandona astrepte</i>	-	X	Good (Poor)	-	-	C	Widespread collections within the PSS
<i>Areacandona</i> sp. '4'	-	X	Poor (Poor)	-	-	C	Widespread collections within the PSS
<i>Atopobathynella</i> sp. 'A'	-	X	Fair (Poor)	-	-	C	Widespread collections within the PSS
<i>Bogidiellidae</i> sp. '1'	-	X	Good (Good)	-	-	C	Widespread collections within the PSS
<i>Deminutiocandona aenigma</i>	-	X	Good (Poor)	-	-	C	Also collected from site PSS365 approximately 175km south of Warramboo
<i>Dero furcate</i>	-	X	Good (Good)	-	-	C	Widespread collections within the PSS and subsequent sampling (Biota 2015b)
<i>Diacyclops einslei</i>	-	X	Fair (Poor)	-	-	A, C	Described from outside the study area (De Laurentiis et al. 1999)
<i>Diacyclops humphreysi humphreysi</i>	-	X	Good (Good)	-	-	C	Widespread collections within the PSS and subsequent sampling (Biota 2015b)
<i>Elaphoidella humphreysi</i>	-	X	Good (Good)	-	-	C	Widespread collections within the PSS
<i>Enchytraeus Pilbara</i> sp. '1'	-	X	Good (Good)	-	-	C	Widespread collections within the PSS and subsequent sampling (Biota 2015b).
<i>Enchytraeus Pilbara</i> sp. '2'	-	X	Good (Good)	-	-	C	Widespread collections within the PSS and subsequent sampling (Biota 2015b).

Species Name	Collected From		Collection Representation (Total number sites)*	New Species	Singleton Record	SRE Sub Categories ^	Notes
<i>Gomphodella hirsuta</i>	-	X	Good (Good)	-	-	C	Widespread throughout the Pilbara and described from eastern Pilbara specimens (Karanovic 2006a)
<i>Guineaxonopsis</i> sp. 'S1'	-	X	Fair (Poor)	-	-	A, C	Also recorded from eastern Pilbara (Biota 2015b).
<i>Halicyclops rochai</i>	-	X	Good (Good)	-	-	C	Described from the Robe Valley and North of the study area (De Laurentiis et al. 1999). Widespread collections within the PSS
<i>Halosbaena tulki</i>	-	X	Good (Good)	-	-	C	Widespread coastally, Collected throughout the study area, Cape Range and Barrow Island.
<i>Haptolana yarraloola</i>	-	X	Poor (Poor)	-	-	C	Collections within the Robe Valley, also collected from PSS173 approximately 210 km south west of Warramboo
<i>Humphreyscandona fovea</i>	-	X	Good (Fair)	-	-	C	Widespread collections within the PSS
<i>Humphreyscandona woutersi</i>	-	X	Good (Good)	-	-	C	Widespread collections within the PSS
<i>Namanereis</i> sp. '1'	-	X	Fair (Poor)	-	-	A, C	Widespread collections within the PSS
<i>Nedsia hurlberti</i>	-	X	Good (Good)	-	-	C	Widespread collections within the PSS and Robe Valley
<i>Nedsia</i> sp. 'AMM001/029/030'	-	X	Fair (Fair)	-	-	C	Widespread collections within the Robe Valley
<i>Nematoda</i> sp. '11'	-	X	Poor (Poor)	-	X	A, C	Recorded only from PSS016
<i>Nematoda</i> sp. '2'	-	X	Fair (Poor)	-		A, C	Widespread collections within the PSS
<i>Nematoda</i> sp. '3'	-	X	Poor (Poor)	-	X	A, C	Recorded only from PSS016
<i>Orbuscyclops westaustraliensis</i>	-	X	Poor (Poor)	-	-	C	Widespread collections within the PSS
Oribatida group 1	-	X	Good (Fair)	-	-	A, C	Widespread collections within the PSS
Oribatida group 4	-	X	Poor (Poor)	-	-	A, C	Recorded from one other site in the PSS approximately 602 km east of Warramboo
<i>Paracyclops chiltoni</i>	-	X	Poor (Poor)	-	-	C	Widespread collections within the PSS
<i>Paramelitidae</i> sp. 'AMP009'	-	X	Good (Fair)	-	-	A, D	Recorded also on Barrow Island
<i>Phreodrilid</i> sp. 'similar ventral chaetae'	-	X	Good (Good)	-	-	C	Widespread collections within the PSS and subsequent sampling (Biota 2015b)
<i>Pilbaracandona rosa</i>	-	X	Good (Good)	-	-	C	Recorded also on Barrow Island
<i>Pilbarus millsi</i>	-	X	Good (Good)	-	-	C	Widespread collections within the PSS and Robe Valley
<i>Pristina longiseta</i>	-	X	Good (Good)	-	-	C	Widespread collections within the PSS and subsequent sampling (Biota 2015b)
<i>Pseudectinosoma galassiae</i>	-	X	Good (Fair)	-	-	C	Widespread collections within the PSS
<i>Schizopera roberiverensis</i>	-	X	Good (Poor)	-	-	C	Widespread collections within the PSS

Species Name	Collected From		Collection Representation (Total number sites)*	New Species	Singleton Record	SRE Sub Categories ^	Notes
<i>Stygonitocrella trispinosa</i>	-	X	Good (Good)	-	-	C	Widespread collections within the PSS
<i>Stygoridgegwayia trispinosa</i>	-	X	Good (Good)	-	-	C	Widespread collections within the PSS and subsequent sampling (Biota 2015b)
<i>Thermocyclops decipiens</i>	-	X	Good (Good)	-	-	C	Cosmopolitan species
Tubificidae sp. '2A'	-	X	Good (Poor)	-	-	C	Widespread collections within the PSS

\* Within the predicted drawdown extent

\* Poor: <10 specimens/sites, Fair: 10 – 25, Good: >25 (estimated from available data).

^ A. Data Deficient, B. Habitat Indicators, C. Morphology indicators, D. Molecular Evidence, E. Research and Expertise (more detail in Appendix 3)

## 6.1.2 Mesa C

Two species of amphipod were recorded from the Mesa C drawdown extent during sampling with a further 27 species recorded from the buffer extent (29 in total; Table 6.2). None of these species are listed as conservation significant or categorised as confirmed SRE species using WAM SRE guidelines (Appendix 3).

Ten species are considered to represent potential SRE species, with two occurring both within the drawdown and buffer extents, *Nedsia* sp. 'AMM004' and *Nedsia* sp. 'AMM031'. *Nedsia* sp. 'AMM004' is widespread within the Robe Valley, occurring also at Mesa H however *Nedsia* sp. 'AMM031' is only recorded from within the drawdown and buffer extents. Of the the remaining eight species recorded from the buffer extent, two represent singleton records, with six species currently unrecorded outside the buffer extent. *Lucionitocrella yalleenensis* and *Megastygonitocrella unispinosa* were recorded from sites outside the current study area, however they are conservatively retained here as potential SRE species as they are only known from limited collections and distributions (Table 6.2).

Nineteen of the collated species were categorised as widespread. These species were predominantly morphologically identified and well represented within collections and literature. Seventeen of these species were widespread in PSS collections, with formal descriptions arising from those collections.

Table 6.2: Summary of species recorded from the Mesa C modelled drawdown extent during this survey and collated from the desktop review, including their distributions and WAM SRE status.

Species Name	Collected From		Collection Representation (Total number sites)*	New Species	Singleton Record	SRE Sub Categories ^	Notes
	Drawdown Extent	Buffer Extent					
<b>Potential SRE Species</b>							
<i>Nedisia sp. 'AMM004'</i>	X	X	Poor (Poor)	X	-	A, D	Also recorded from Mesa H
<i>Nedisia sp. 'AMM031'</i>	X	X	Poor (Poor)	X	-	A, D	Known only from drawdown and buffer extent
<i>Areacandona sp. BOS818</i>	-	X	Poor (Poor)	-	X	A, C	Singleton record known only from Mesa C buffer extent.
<i>Dussartcycllops uniarticulatus</i>	-	X	Poor (Poor)	-	-	A, C	Known only from Mesa C buffer extent.
<i>Lucionitocrella yalleenensis</i>	-	X	Poor (Poor)	-	-	A, C	Described from site approximately 78 km east of Mesa C (Karanovic and Hancock 2009).
<i>Megastygonitocrella unispinosa</i>	-	X	Fair (Poor)	-	-	C	Also recorded from Robe River site approximately 47 km north of Mesa C (Karanovic and Hancock 2009).
<i>Meridiescandona sp. '2'</i>	-	X	Poor (Poor)	-	-	A, C	Known only from Mesa C buffer extent.
<i>Niphargidae sp. 'AMN007'</i>	-	X	Poor (Poor)	X	X	A, D	Singleton record only known from buffer extent
<i>Niphargidae sp. 'AMN008'</i>	-	X	Fair (Poor)	X	-	A, D	Known only from buffer extent
<i>Pilbaracandona sp. 'BOS526'</i>	-	X	Poor (Poor)	-	-	A, C	Known only from buffer extent
<b>Widespread</b>							
<i>Bogidiellidae sp. '1'</i>	-	X	Good (Good)	-	-	A, C	Widespread collections within the PSS.
<i>Diacyclops humphreysi humphreysi</i>	-	X	Good (Good)	-	-	C	Widespread collections within the PSS and subsequent sampling (Biota 2015b).
<i>Diacyclops humphreysi unispinosus</i>	-	X	Good (Fair)	-	-	C	Described from specimens on Barrow Island (Karanovic 2006b).
<i>Elaphoidella humphreysi</i>	-	X	Good (Good)	-	-	C	Widespread collections within the PSS.
<i>Halicyclops rochae</i>	-	X	Good (Good)	-	-	C	Described from the Robe Valley and North of the study area (De Laurentis et al. 1999). Widespread collections within the PSS
<i>Halosbaena tulki</i>	-	X	Good (Good)	-	-	C	Widespread coastally, Collected throughout the study area, Cape Range and Barrow Island.
<i>Haptolana yarraloola</i>	-	X	Poor (Poor)	-	-	C	Collections within the Robe Valley, also collected from PSS173 approximately 204 km south west of Mesa C
<i>Humphreyscandona fovea</i>	-	X	Good (Fair)	-	-	C	Widespread collections within the PSS
<i>Humphreyscandona woutersi</i>	-	X	Good (Good)	-	-	C	Widespread collections within the PSS
<i>Kagalana tonde</i>	-	X	Fair (Fair)	-	-	C	Widespread collections within the PSS (Bruce 2008)

Species Name	Collected From		Collection Representation (Total number sites)*	New Species	Singleton Record	SRE Sub Categories <sup>^</sup>	Notes
<i>Nedsia hurlberti</i>	-	X	Good (Good)	-	-	C	Widespread collections within the PSS and Robe Valley
<i>Nedsia</i> sp. '24'	-	X	Fair (Poor)	-	-	A, C	Widespread collections within the PSS
<i>Nedsia</i> sp. 'AMM001/029/030'	-	X	Poor (Poor)	X	-	A, D	Also recorded from Mesa H and Buckland Hills
Oribatida group 1	-	X	Good (Fair)	-	-	A, C	Widespread collections within the PSS
<i>Paracyclops chiltoni</i>	-	X	Poor (Poor)	-	-	C	Widespread collections within the PSS
<i>Paramelitidae</i> sp. '2'	-	X	Good (Good)	-	-	A, C, D	Widespread collections within the PSS
<i>Pilbarus millsii</i>	-	X	Good (Good)	-	-	C	Widespread collections within the PSS and Robe Valley
<i>Schizopera roberiverensis</i>	-	X	Good (Poor)	-	-	C	Widespread collections within the PSS
<i>Stygoridgegwayia trispinosa</i>	-	X	Good (Good)	-	-	C	Widespread collections within the PSS and subsequent sampling (Biota 2015b)

\* Within the predicted drawdown extent

\* Poor: <10 specimens/sites, Fair: 10 – 25, Good: >25 (estimated from available data).

<sup>^</sup> A. Data Deficient, B. Habitat Indicators, C. Morphology indicators, D. Molecular Evidence, E. Research and Expertise (more detail in Appendix 3)

## 6.2 Habitat Suitability

Of the 5,566.4 km<sup>2</sup> study area, 252.6 km<sup>2</sup> represents high habitat prospectivity and 1,956 km<sup>2</sup> medium prospectivity, totalling almost 39.7% of the study area (Table 6.3). Allowing for the 500 m buffer around stygofauna collection locations, an area of 75.7 km<sup>2</sup> was categorised as confirmed habitat, including 25.7 km<sup>2</sup> from high, 11.7 km<sup>2</sup> from medium, and 38.3 km<sup>2</sup> from low habitat prospectivity (Table 6.3, Figure 6.1).

Table 6.3: Overall habitat suitability of the study area.

	Habitat Prospectivity		
	High	Medium	Low
Confirmed Habitat area (km <sup>2</sup> ) (Stygofauna Recorded)	25.7	11.7	38.3
Inferred Habitat area (km <sup>2</sup> ) (No Stygofauna Recorded)	226.9	1,944.3	3,319.6
Total	252.6	1,956.0	3,357.9

A total of 8,878 specimens were recorded from the current sampling effort and from previous studies within the study area. These were spatially distributed over all of the habitat prospectivity categories, with 45.2% of specimens recorded from groundwater in low prospectivity habitat. This relatively high percentage of specimens being recorded from low prospectivity habitat may result from the assessment of confirmed habitat area being an unweighted spatial analysis, with sites with many records being weighted as of the same importance as sites with very few or single records. Another contributing factor to this bias in fauna records within low prospectivity habitat may result from the broad-scale nature of the regional surface geology mapping and its varying representation of geological units at depth below the water table.

The habitat characterisation is indicative of generally widespread stygofauna habitat across at least a third of the study area, including in areas that limits on habitat information categorise as low prospectivity, but where stygofauna do occur; suggesting additional habitat would be identified if finer resolution analysis were possible at this broader scale. This, coupled with the confirmation that at least 59 of the species recorded are categorised as widespread and occur in the wider Pilbara region (Section 6.1), indicates that there is little evidence of significant barriers to dispersal across high and medium habitat prospectivity at study area scale. Likewise, it is unlikely that there is any barrier to dispersal that would isolate the habitat within Warramboo drawdown extent, given both the lack of aquiclude in the area and the widespread distributions of most taxa recorded.

The collection of four potential SRE species currently known only from sites within the drawdown extent, and a further 11 from the buffer extent, at Warramboo is therefore likely to be an artefact of ecological sampling effects. It is unlikely that these species will truly show spatial restriction, given what is currently known about the hydrogeology of the drawdown extent and surrounding areas and the wider distributions documented for other stygofauna species known from the drawdown area.

While the Mesa C aquifer is hydrologically confined, modelling provided by Rio Tinto indicates that recharge of the aquifer may occur seasonally when the Robe River floods. This recharge is likely to carry stygofauna with it, depositing fauna within the confined aquifer, or provide for periods of hydraulic connection when animals could disperse between the Mesa C aquifer and wider groundwater systems. This model explains the presence of stygofauna within the confined aquifer, where historical sampling has yielded very few results (Biota 2004a), as well as the distribution of *Nedsia* sp. 'AMM004' at Mesa H, and *Nedsia* sp. 'AMM031' outside of the confined aquifer within the buffer extent. These species are likely associated with the alluvial geology within the Robe River and the low level of divergence between the current study area and Mesa H suggests the aquifer habitat connection inherent in this model occurs on a reasonably frequency basis, maintaining gene flow.

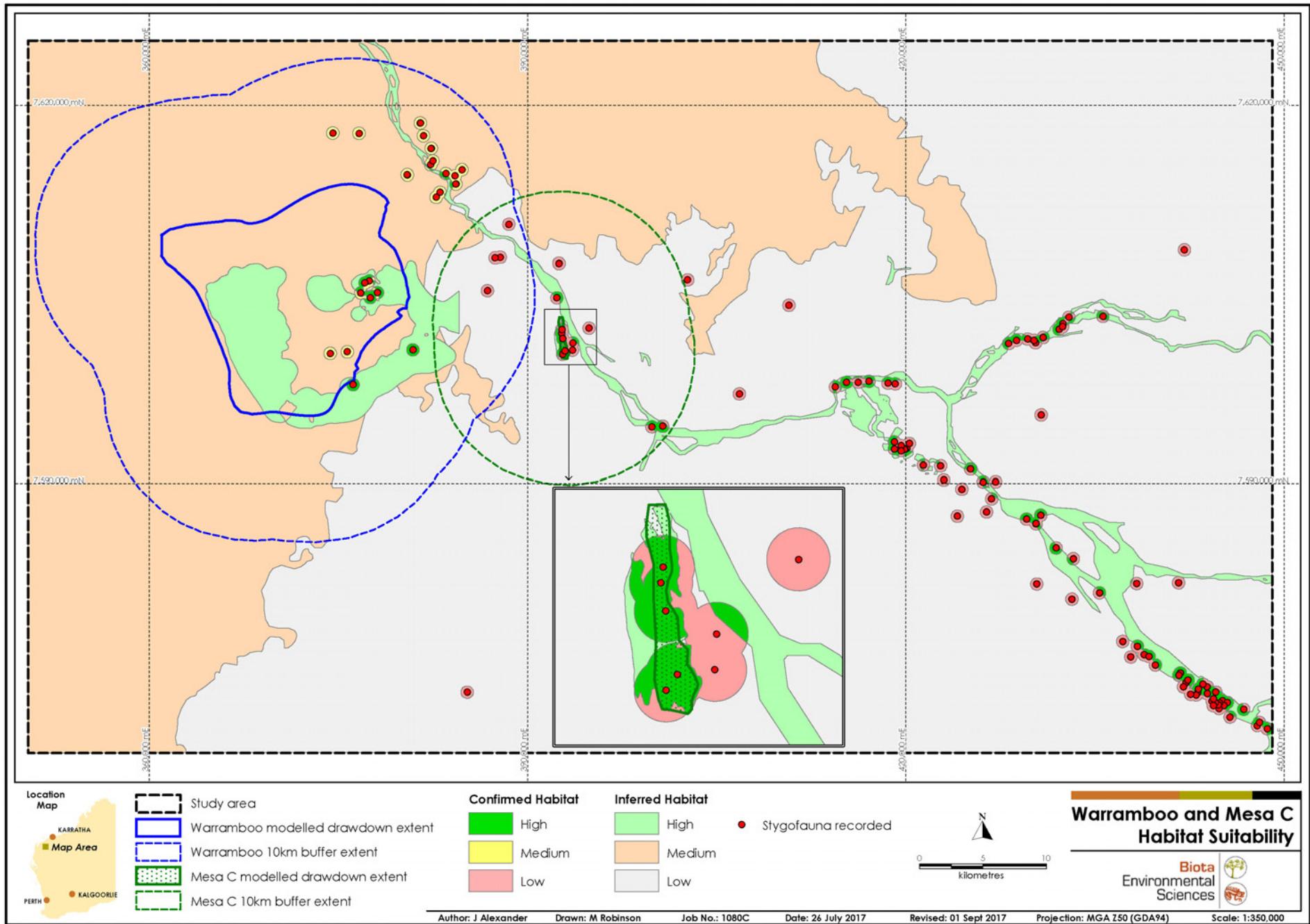


Figure 6.1: Stygofauna (current and previous records) collection location in relation to habitat suitability within the study area.

## 6.3 Conclusions

The findings from this assessment, comprising the sampling undertaken as part of the current study and the collation of records from previous studies, demonstrate that there has been comprehensive stygofauna sampling within the Robe Valley that has focused predominantly on Bungaroo, Mesa H and Warramboo. For the current study, an additional 49 sites were sampled with many of these sampled on multiple occasions.

Three species of conservation significance have been previously recorded from within the study area, all of which are from Bungaroo Valley. There are no records of any of these species from within the drawdown extents at Warramboo or Mesa C.

Overall, this study has recorded 153 distinct species from the study area, with 20 occurring within the drawdown extents at Warramboo and Mesa C, and a further 69 within the buffer extents.

At Warramboo, both sampling results and hydrogeology indicate that there is unlikely to be any physical barriers to stygofauna dispersal, with the Yarraloola conglomerate, of medium habitat prospectivity, extending almost 200 km southwest, coastally, from the study area. Likewise the alluvium and unconsolidated material associated with the Robe River (high habitat prospectivity) extends northwest from the study area to the coast as well as west from the study area. These geological units are likely to provide primary, continuous habitat for stygofauna.

The two species of amphipod recorded from the Mesa C aquifer drawdown extent have also been recorded from sites at Mesa H. It is likely this aquifer becomes seasonally connected to the Robe River regional aquifer and as such these species are likely associated with the alluvium of the river system, and are unlikely to be restricted in distribution, as evidenced by the collection of these specimens at Mesa H.

## 7.0 Glossary

Edaphobite	Deep soil inhabitant.
Endemic	Native to or confined to a certain region.
EPA	Environmental Protection Authority of Western Australia.
Epigean	Fauna from above the soil level.
Interspecific variation	Variation between species.
Intraspecific variation	Variation within species.
Karst	Soluble-rock landscape; terrain with distinctive hydrology and landforms arising from a combination of high rock solubility and well-developed secondary porosity.
Mesocaverns	Underground voids in the size range 0.1 – 20cm, especially in karst and volcanic substrates.
Pisolite	Rock composed of pisoliths.
Short-Range Endemic (SRE)	A species that has a naturally small distribution and is often characterised by having poor dispersal capabilities, confinement to disjunct habitats and low fecundity.
Species Complex	A group of closely related species currently placed within a single species name.
Stygobite / Stygofauna	Fauna inhabiting the various types of groundwater.
Troglobite / Troglofauna	Species that do not exist outside caves. They may, however, occur in the superficial underground compartment or in the upper hypogean zone.
EPA	Environmental Protection Authority of Western Australia.

This page intentionally blank.

## 8.0 References

- Bennelongia (2013). Bungaroo South: Subterranean Fauna Assessment. Unpublished report prepared for Iron Ore Holdings Ltd, Bennelongia Environmental Consultants.
- Biota (2001). Orebody 23 Stygofauna Investigations: Morphological and Molecular Variation. Unpublished report prepared for BHP Iron Ore Pty Ltd, July 2001, Biota Environmental Sciences, Western Australia.
- Biota (2004a). Mesa A and Bungaroo Creek Exploration Areas Subterranean Fauna Survey. Unpublished report prepared for Robe River Iron Mining Company, August 2004, Biota Environmental Sciences, Western Australia.
- Biota (2004b). Orebody 18, 23, 25 and Mining Area C Expansion Stygofauna Assessment Report. Unpublished report prepared for BHP Billiton Iron Ore Pty Ltd, December 2004, Biota Environmental Sciences, Western Australia.
- Biota (2006a). Mesa A and Robe Valley Mesas Troglobitic Fauna Survey. Unpublished report prepared for Robe River Iron Associates, March 2006, Biota Environmental Sciences, Western Australia.
- Biota (2006b). Mesa A / Warramboo and Yarraloola Borefield Development: Baseline Stygofauna Assessment. Unpublished report prepared for Robe River Iron Associates, January 2006, Biota Environmental Sciences, Western Australia.
- Biota (2010). Yandicoogina Subterranean Fauna Assessment Phases I - V. Unpublished report prepared for Rio Tinto Iron Ore, December 2010, Biota Environmental Sciences, Western Australia.
- Biota (2011). WPIOP Basalt Quarry Troglobitic Fauna Pilot Survey Results. Unpublished letter report prepared for API Management, 21 January 2011, Biota Environmental Sciences, Western Australia.
- Biota (2013). Bungaroo Subterranean Fauna Collections Summary; Phases 1 - 11. Unpublished report prepared for Rio Tinto, March 2013, Biota Environmental Sciences, Western Australia.
- Biota (2015a). Bungaroo Subterranean Fauna Desktop Assessment. Unpublished report prepared for Rio Tinto, June 2015, Biota Environmental Sciences, Western Australia.
- Biota (2015b). Yandi Operations Stygofauna Data Consolidation; 2003 - 2014. Unpublished report prepared for Rio Tinto, Biota Environmental Sciences.
- Biota (2016a). Bungaroo Coastal Waters Project Stygofauna Monitoring 2016. Unpublished report prepared for Rio Tinto, Biota Environmental Sciences.
- Biota (2016b). Bungaroo Coastal Waters Project Stygofauna Monitoring 2015. Unpublished report prepared for Pilbara Iron, Biota Environmental Sciences, Western Australia.
- Biota, and DC Blandford & Associates (2013). Robe Valley Troglifauna Habitat Characterisation and Reconstruction Review. Unpublished report prepared for Rio Tinto, June 2013, Biota Environmental Sciences and DC Blandford & Associates, Western Australia.
- Bradbury, J. H., and W. D. Williams (1996). Freshwater Amphipods from Barrow Island, Western Australia. *Records of the Western Australian Museum* 48:33–74.
- Bruce, N. L. (2008). New species and a new genus of Cirolanidae (Isopoda: Cymothoida: Crustacea) from groundwater in calcretes in the Pilbara, northern Western Australia. *Zootaxa* 1823:51–64.
- De Laurentiis, P., G. L. Pesce, and W. F. Humphreys (1999). Copepods from ground waters of Western Australia, IV. Cyclopids from basin and craton aquifers (Crustacea: Copepoda: Cyclopidae). *Records of the Western Australian Museum* 19(3):243–257.

DSEWPaC (2008). Approved Conservation Advice for *Ophisternon candidum* (Blind Cave Eel). EPBC Act 1999, s266B.

EPA (2007). Statement No. 756: Mesa A / Warramboo Iron Ore Project. Published on 21st November 2007, Environmental Protection Authority, Western Australia.

EPA (2016a). Statement of Environmental Principles, Factors and Objectives. Environmental Protection Authority, Western Australia.

EPA (2016b). Environmental Factor Guideline: Subterranean Fauna. Environmental Protection Authority, Western Australia.

EPA (2016c). Technical Guidance: Subterranean Fauna Survey. Environmental Protection Authority, Western Australia.

EPA (2016d). Technical Guidance - Sampling methods for subterranean fauna . Environmental Protection Authority, Western Australia.

EPA (2016e). Technical Guidance: Sampling Methods for Subterranean Fauna. Environmental Protection Authority, Western Australia.

Finston, T. L., and M. S. Johnson (2004). Geographic patterns of genetic diversity in subterranean amphipods of the Pilbara, Western Australia. *Marine and Freshwater Research* 55:619–628.

Finston, T. L., M. S. Johnson, S. M. Eberhard, J. S. Cocking, J. M. McRae, S. A. Halse, and B. Knott (2011). A new genus and two new species of groundwater paramelitid amphipods from the Pilbara, Western Australia: a combined molecular and morphological approach. *Records of the Western Australian Museum* 26:154–178.

Finston, T. L., M. S. Johnson, W. F. Humphreys, S. M. Eberhard, and S. A. Halse (2007). Cryptic speciation in two widespread subterranean amphipod genera reflects historical drainage patterns in an ancient landscape. *Molecular Ecology* 16:355–365.

Foster, R., and B. Humphreys (2011). Report on the genetic identification of a Blind Cave Eel collected near Pannawonica, Western Australia. Unpublished report prepared for Biota Environmental Sciences, 2011, Western Australian Museum.

Geological Survey of Western Australia (1968). 1:250,000 Geological Map - Yarraloola (SF50-6). Government of Western Australia Department of Mines and Petroleum.

Guzik, M. T., A. D. Austin, S. J. B. Cooper, M. S. Harvey, W. F. Humphrey, T. Bradford, S. M. Eberhard, R. A. King, R. Leys, K. A. Muirhead, and M. Tomlinson (2010). Is the Australian subterranean fauna uniquely diverse? *Invertebrate Systematics* 24:407 – 418.

Halse, S. A., M. D. Scanlon, J. S. Cocking, H. J. Barron, J. B. Richardson, and S. M. Eberhard (2014). Pilbara stygofauna: deep groundwater of an arid landscape contains globally significant radiation of biodiversity. *Records of the Western Australian Museum Supplement* 78:443–483.

Humphreys, W. F. (1991). Experimental re-establishment of pulse -driven populations in a terrestrial troglobite community.

Humphreys, W. F. (1999). Relict stygofaunas living in sea salt, karst and calcrete habitats in arid northwestern Australia contain many ancient lineages. Pages 219–227 in W. Ponder and D. Lumley, editors. *The Other 99% -The Conservation and Biodiversity of invertebrates*. Royal Zoological Society of New South Wales, Mosman.

Humphreys, W. F. (2001a). The subterranean fauna of Barrow Island, northwestern Australia, and its environment. *Memoires de Biospeologie (International Journal of Subterranean Biology)* 28:107–127.

Humphreys, W. F. (2001b). *Milyeringa veritas* (Eleotridae), a remarkably versatile cave fish from the arid tropics of northwestern Australia. *Environmental Biology of Fishes* 62:297–313.

Karanovic, I. (2006a). On the Genus *Gomphodella* (Crustacea: Ostracoda: Limnocytheridae) with Descriptions of Three New Species from Australia and Redescription of the Type Species. *Species Diversity* 11:99–135.

Karanovic, I., and P. Marmonier (2003). Three new genera and nine new species of the subfamily Candonidae (Crustacea, Ostracoda, Podocopida) from the Pilbara region (Western Australia). *Beaufortia: Bullettin Zoologgical Museum, University of Amsterdam* 53.

Karanovic, T. (2006b). Supp 70 - Records of the Western Australian Museum - Subterranean copepods (crustacea, copepoda) from the pilbara region in western australia.

Karanovic, T., and P. Hancock (2009). On the diagnostic characters of the genus *Stygonitocrella* (Copepoda, Harpacticoida), with descriptions of seven new species from Australian subterranean waters. *Zootaxa* 2324:1–85.

Larson, H. K., R. Foster, W. F. Humphreys, and M. L. Stevens (2013). A new species of the blind cave gudgeon *Milyeringa* (Pisces: Gobioidei, Eleotridae) from Barrow Island, Western Australia, with a redescription of *M. veritas* Whitley. *Zootaxa* 3616(2):135–150.

Marmonier, P., P. Vervier, J. Giber, and M. J. Dole-Olivier (1993). Biodiversity in ground waters. *Trends in Ecology & Evolution* 8:392–395.

Page, T. J., W. F. Humphreys, and J. M. Hughes (2008). Shrimps Down Under: Evolutionary Relationships of Subterranean Crustaceans from Western Australia (Decapoda: Atyidae: *Stygiocaris*). *PLoS One* 3:e1618. doi: 10.1371/journal.pone.0001618.

Rio Tinto (2010). Warramboo Bore Field Groundwater Operating Strategy; Mesa A – Warramboo Iron Ore Project. Unpublished Report Prepared for the Department of Water, Rio Tinto Iron Ore, Western Australia.

Rio Tinto (2015a). Mesa A and Warramboo Groundwater Operating Strategy. Unpublished Report Prepared for the Department of Water, Rio Tinto Iron Ore, Western Australia.

Rio Tinto (2015b). Pilbara Borefields Annual Aquifer Review 2014. Unpublished Report, Rio Tinto Iron Ore, Western Australia.

Rio Tinto (2017). Mesa C Hydrogeological Assessment - Draft. Unpublished Report Prepared Internally for Rio Tinto Use, Rio Tinto.

WAM (2017). Molecular analysis of Amphipoda from the Robe River Valley: Mesa H and Mesa B/C, Western Australia. Unpublished report prepared for Rio Tinto, Western Australian Museum.

Wilkins, H., D. C. Culver, and W. F. Humphreys (Eds.) (2000). *Ecosystems of the World* 30: Subterranean Ecosystems. Elsevier Science, Amsterdam.



# Appendix 1

## Licence to take Fauna for Scientific Purposes





# DEPARTMENT OF PARKS AND WILDLIFE



Department of  
Parks and Wildlife



Enquiries:  
Telephone:  
Facsimile:

17 DICK PERRY AVE, KENSINGTON, WESTERN AUSTRALIA  
08 9219 9000  
08 9219 8242

Correspondence:

Locked Bag 30  
Bentley Delivery Centre WA 6983

PAGE

2

NO.

SF010296

PERSON NO.

90684

## AUTHORISED PERSONS

ROY TEALE  
GARTH HUMPHREYS  
MICHAEL GREENHAM  
DANIEL JAMIEN  
TIM SACHSE  
JESSICA CAIRNES  
PENNY BROOSHOOFT  
DAVID KEIRLE  
VICKIE CARTLEDGE  
CHRIS COLE  
NICOLA WATSON  
SYLVIE SCHMIDT  
STEWART FORD  
JACINTA KING  
MICHAEL DELANEY  
ANDREW SHEPPARD  
SCOTT WERNER

AMENDED

15.12.2015

Date

OPS.

Initial

LICENSING OFFICER

(JASON)

DATE OF ISSUE 15/04/2015  
VALID FROM 08/05/2015  
DATE OF EXPIRY 30/04/2016

LICENSEE: MR J ALEXANDER  
ADDRESS BIOTA ENVIRONMENTAL SCIENCES  
PO BOX 155  
LEEDERVILLE  
WA 6903

# DEPARTMENT OF PARKS AND WILDLIFE



Department of  
Parks and Wildlife



Enquiries:  
Telephone:  
Facsimile:

17 DICK PERRY AVE, KENSINGTON, WESTERN AUSTRALIA  
08 9219 9000  
08 9219 8242

Correspondence:

Locked Bag 30  
Bentley Delivery Centre WA 6983

PAGE

1

NO.

SF010296

PERSON NO.

90684

RECEIPT NO.

AMOUNT  
\$0.00

## WILDLIFE CONSERVATION ACT 1950 REGULATION 17

### LICENCE TO TAKE FAUNA FOR SCIENTIFIC PURPOSES

THE UNDERMENTIONED PERSON MAY TAKE FAUNA FOR RESEARCH OR OTHER SCIENTIFIC PURPOSES AND WHERE AUTHORISED, KEEP IT IN CAPTIVITY, SUBJECT TO THE FOLLOWING AND ATTACHED CONDITIONS, WHICH MAY BE ADDED TO, SUSPENDED OR OTHERWISE VARIED AS CONSIDERED FIT.

DIRECTOR GENERAL

#### CONDITIONS

- 1 The licensee shall comply with the provisions of the Wildlife Conservation Act 1950, Wildlife Conservation Regulations 1970 and any notices in force under this legislation.
- 2 Unless specifically authorised in the Conditions of this Licence or otherwise in writing by the Director General, species of fauna declared as likely to become extinct, rare or otherwise in need of special protection shall not be captured or otherwise taken.
- 3 No fauna shall be taken from any Nature Reserve, National Park, Marine Park, Marine Nature Reserve, Timber Reserve or State Forest without prior written approval of the Director General. No fauna shall be taken from any other public land without the written approval of the Government Authority managing that land.
- 4 No entry or collection of fauna to be undertaken on any private property or pastoral lease without the consent in writing of the owner or occupier, or from any Aboriginal lands without the written approval of the Department of Aboriginal Affairs.
- 5 No fauna or their progeny shall be released in any area where it does not naturally occur, nor be handed over to any other person or authority unless approved by the Director General, nor shall the remains of such fauna be disposed of in such manner as to confuse the natural or present day distribution of the species.
- 6 This licence and the written permission referred to at conditions 3 & 4 must be carried by the licensee or authorised agent at all times for the purpose of proving their authority to take fauna when questioned as to their right to do so by a Wildlife Officer, any other State or Local Government employee or any member of the public.
- 7 Any interaction involving Gazetted Threatened Fauna that may be harmful and/or invasive may require approval from the Department of the Environment ph 02 6274 1111. Interaction with such species is controlled by the Commonwealth Government's "Environment Protection and Biodiversity Conservation Act 1999" and "Environment Protection and Biodiversity Conservation Regulations 2000" as well as this Department's Wildlife Conservation Act 1950 and Wildlife Conservation Regulations 1970.
- 8 No bioprospecting involving the removal of sample aquatic and terrestrial organisms (both flora and fauna) for chemical extraction and bioactivity screening is permitted to be conducted without specific written approval by the Director General.
- 9 Further conditions (numbered 1 to 9) are attached.

#### PURPOSE

SUBTERRANEAN FAUNA SURVEY OF ROBE VALLEY PROJECT 40KM EAST OF PANNAWONICA, USING REINFORCED STYGOFAUNA HAUL NETS AND TROGLOFAUNA LITTER TRAPS WITHIN DRILL HOLES. SAMPLING IN ACCORDANCE WITH EPA GUIDANCE STATEMENT NO. 54A.

# WILDLIFE CONSERVATION REGULATIONS 1970

## Regulation 17:- Licence to Take Fauna for Scientific Purposes

FURTHER CONDITIONS (OF LICENCE NUMBER SFO 10296)

1. The licensee shall take fauna only in the manner stated on the endorsed Regulation 17 licence application form and endorsed related correspondence.
2. Except in the case of approved lethal traps, the licensee shall ensure that measures are taken in the capture and handling of fauna to prevent injury or mortality resulting from that capture or handling. Where traps or other mechanical means or devices are used to capture fauna these shall be deployed so as to prevent exposure of trapped animals to ants and debilitating weather conditions and inspected at regular intervals throughout each day of their use. At the conclusion of research all markers etc and signs erected by the licensee and all traps shall be removed, all pitfalls shall be refilled or capped and the study area returned to the condition it was in prior to the research/capture program. During any break in research, cage traps should be removed and pitfalls either removed, capped or filled with sand.
3. No collecting is to be undertaken in areas where it would impinge on pre-existing scientific research programs.
4. Any form of colour marking of birds or bats shall only be undertaken in accordance with the requirements of the Australian Bird and Bat Banding Scheme.
5. Any inadvertently captured specimen of fauna which is declared as likely to become extinct, rare or otherwise in need of special protection is to be released immediately at the point of capture. Where such a specimen is injured or deceased, the licensee shall contact Department of Parks and Wildlife licensing staff at Kensington (08 9219 9831) for advice on disposal. Records are to be kept of any fauna so captured and details included in the report required under further condition 6 below.
6. Within one month of the expiration of this licence, the holder shall submit an electronic return detailing the locality, site, geocode, date and number of each species captured, sighted or vouchered during the currency of the licence, into the Department of Parks and Wildlife Fauna Survey Database (FSD). A copy of any paper, report or thesis resulting from the research shall on completion be lodged with the Director General. If a renewal of this licence is required, the licensee shall submit a written progress report for activities undertaken during this licence period prior to the expiry of this licence.
7. Not more than ten specimens of any one protected species shall be taken and removed from any location less than 20km apart. Where exceptional circumstances make it necessary to take large series in order to obtain adequate statistical data the collector will proceed with circumspection and justify their actions to the Director General in advance.
8. All holotypes and syntypes and a half share of paratypes of species or subspecies permitted to be permanently taken under this licence shall 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 shall be donated on request to the Western Australian Museum.
9. To prevent any unnecessary collecting in this State, all specimens and material collected under the authority of this license shall, on request, be loaned to the Western Australian Museum. Also, the unused portion or portions of any specimen collected under the authority of this license shall be offered for donation to the Western Australian Museum or made available to other scientific workers if so required.

# DEPARTMENT OF PARKS AND WILDLIFE



Department of  
Parks and Wildlife



Enquiries:  
Telephone:  
Facsimile:

17 DICK PERRY AVE, KENSINGTON, WESTERN AUSTRALIA  
08 9219 9000  
08 9219 8242

Correspondence:

Locked Bag 30  
Bentley Delivery Centre WA 6983

PAGE  
NO.  
PERSON NO.

2  
SF010921  
90684

## AUTHORISED PERSONS

ROY TEALE  
GARTH HUMPHREYS  
MICHAEL GREENHAM  
DANIEL JAMIEN  
TIM SACHSE  
JESSICA CAIRNES  
PENNY BROOSHOFT  
DAVID KEIRLE  
VICKIE CARTLEDGE  
CHRIS COLE  
NICOLA WATSON  
SYLVIE SCHMIDT  
STEWART FORD  
JACINTA KING  
MICHAEL DELANEY  
ANDREW SHEPPARD  
SCOTT WERNER

DATE OF ISSUE 19/07/2016  
VALID FROM 19/07/2016  
DATE OF EXPIRY 31/12/2016

LICENSING OFFICER  
(JASON)

LICENSEE: MR J ALEXANDER  
ADDRESS BIOTA ENVIRONMENTAL SCIENCES  
PO BOX 155  
LEEDERVILLE  
WA 6903

-----

# DEPARTMENT OF PARKS AND WILDLIFE



Department of  
Parks and Wildlife



Enquiries:  
Telephone:  
Facsimile:

17 DICK PERRY AVE, KENSINGTON, WESTERN AUSTRALIA  
08 9219 9000  
08 9219 8242

Correspondence:

Locked Bag 30  
Bentley Delivery Centre WA 6983

PAGE NO.	1
PERSON NO.	SF010921 90684
RECEIPT NO.	AMOUNT
	\$0.00

## WILDLIFE CONSERVATION ACT 1950 REGULATION 17 LICENCE TO TAKE FAUNA FOR SCIENTIFIC PURPOSES

THE UNDERMENTIONED PERSON MAY TAKE FAUNA FOR RESEARCH OR OTHER SCIENTIFIC PURPOSES AND WHERE AUTHORISED, KEEP IT IN CAPTIVITY, SUBJECT TO THE FOLLOWING AND ATTACHED CONDITIONS, WHICH MAY BE ADDED TO, SUSPENDED OR OTHERWISE VARIED AS CONSIDERED FIT.

DIRECTOR GENERAL

### CONDITIONS

- 1 The licensee shall comply with the provisions of the Wildlife Conservation Act 1950, Wildlife Conservation Regulations 1970 and any notices in force under this legislation.
- 2 Unless specifically authorised in the Conditions of this Licence or otherwise in writing by the Director General, species of fauna declared as likely to become extinct, rare or otherwise in need of special protection shall not be captured or otherwise taken.
- 3 No fauna shall be taken from any Nature Reserve, National Park, Marine Park, Marine Nature Reserve, Timber Reserve or State Forest without prior written approval of the Director General. No fauna shall be taken from any other public land without the written approval of the Government Authority managing that land.
- 4 No entry or collection of fauna to be undertaken on any private property or pastoral lease without the consent in writing of the owner or occupier, or from any Aboriginal lands without the written approval of the Department of Aboriginal Affairs.
- 5 No fauna or their progeny shall be released in any area where it does not naturally occur, nor be handed over to any other person or authority unless approved by the Director General, nor shall the remains of such fauna be disposed of in such manner as to confuse the natural or present day distribution of the species.
- 6 This licence and the written permission referred to at conditions 3 & 4 must be carried by the licensee or authorised agent at all times for the purpose of proving their authority to take fauna when questioned as to their right to do so by a Wildlife Officer, any other State or Local Government employee or any member of the public.
- 7 Any interaction involving Gazetted Threatened Fauna that may be harmful and/or invasive may require approval from the Department of the Environment ph 02 6274 1111. Interaction with such species is controlled by the Commonwealth Government's "Environment Protection and Biodiversity Conservation Act 1999" and "Environment Protection and Biodiversity Conservation Regulations 2000" as well as this Department's Wildlife Conservation Act 1950 and Wildlife Conservation Regulations 1970.
- 8 No bioprospecting involving the removal of sample aquatic and terrestrial organisms (both flora and fauna) for chemical extraction and bioactivity screening is permitted to be conducted without specific written approval by the Director General.
- 9 Further conditions (numbered 1 to 9) are attached.

### PURPOSE

SUBTERRANEAN FAUNA SURVEY OF ROBE VALLEY PROJECT 40KM EAST OF PANNAWONICA, USING REINFORCED STYGOFAUNA HAUL NETS AND TROGLOFAUNA LITTER TRAPS WITHIN DRILL HOLES.  
SAMPLING IN ACCORDANCE WITH EPA GUIDANCE STATEMENT NO. 54A.

# WILDLIFE CONSERVATION REGULATIONS 1970

## Regulation 17:- Licence to Take Fauna for Scientific Purposes

FURTHER CONDITIONS (OF LICENCE NUMBER SF 010921)

1. The licensee shall take fauna only in the manner stated on the endorsed Regulation 17 licence application form and endorsed related correspondence.
2. Except in the case of approved lethal traps, the licensee shall ensure that measures are taken in the capture and handling of fauna to prevent injury or mortality resulting from that capture or handling. Where traps or other mechanical means or devices are used to capture fauna these shall be deployed so as to prevent exposure of trapped animals to ants and debilitating weather conditions and inspected at regular intervals throughout each day of their use. At the conclusion of research all markers etc and signs erected by the licensee and all traps shall be removed, all pitfalls shall be refilled or capped and the study area returned to the condition it was in prior to the research/capture program. During any break in research, cage traps should be removed and pitfalls either removed, capped or filled with sand.
3. No collecting is to be undertaken in areas where it would impinge on pre-existing scientific research programs.
4. Any form of colour marking of birds or bats shall only be undertaken in accordance with the requirements of the Australian Bird and Bat Banding Scheme.
5. Any inadvertently captured specimen of fauna which is declared as likely to become extinct, rare or otherwise in need of special protection is to be released immediately at the point of capture. Where such a specimen is injured or deceased, the licensee shall contact Department of Parks and Wildlife licensing staff at Kensington (08 9219 9831) for advice on disposal. Records are to be kept of any fauna so captured and details included in the report required under further condition 6 below.
6. Within one month of the expiration of this licence, the holder shall submit an electronic return detailing the locality, site, geocode, date and number of each species captured, sighted or voucherised during the currency of the licence, into the Department of Parks and Wildlife Fauna Survey Database (FSD). A copy of any paper, report or thesis resulting from the research shall on completion be lodged with the Director General. If a renewal of this licence is required, the licensee shall submit a written progress report for activities undertaken during this licence period prior to the expiry of this licence.
7. Not more than ten specimens of any one protected species shall be taken and removed from any location less than 20km apart. Where exceptional circumstances make it necessary to take large series in order to obtain adequate statistical data the collector will proceed with circumspection and justify their actions to the Director General in advance.
8. All holotypes and syntypes and a half share of paratypes of species or subspecies permitted to be permanently taken under this licence shall 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 shall be donated on request to the Western Australian Museum.
9. To prevent any unnecessary collecting in this State, all specimens and material collected under the authority of this license shall, on request, be loaned to the Western Australian Museum. Also, the unused portion or portions of any specimen collected under the authority of this license shall be offered for donation to the Western Australian Museum or made available to other scientific workers if so required.

# DEPARTMENT OF PARKS AND WILDLIFE



Department of  
Parks and Wildlife



Enquiries: 17 DICK PERRY AVE, KENSINGTON, WESTERN AUSTRALIA  
Telephone: 08 9219 9000  
Facsimile: 08 9219 8242  
Web Site: <https://wildlifelicensing.dpaw.wa.gov.au/>  
Correspondence: Locked Bag 30  
Bentley Delivery Centre WA 6983

PAGE 1  
NO. 08-000238-1

## Wildlife Conservation Act 1950

### REGULATION 17

#### Regulation 17 – Licence to take fauna for scientific purposes (Regulation 17 - Standard)

**The undermentioned person may take fauna for research or other scientific purposes and where authorised, keep it in captivity, subject to the following and attached conditions, which may be added to, suspended or otherwise varied as considered fit.**

**Director General**

#### Conditions

- 1 The licensee shall comply with the provisions of the Wildlife Conservation Act 1950, Wildlife Conservation Regulations 1970 and any Notices in force under this legislation.
- 2 The licensee shall take fauna only in the manner stated on the endorsed Regulation 17 licence application form and endorsed related correspondence.
- 3 Unless specifically authorised in the conditions of this Licence or otherwise in writing by the Director General, species of fauna declared as likely to become extinct, rare or otherwise in need of special protection shall not be taken.
- 4 Any by-catch of fauna, which is declared to be rare, likely to become extinct, or otherwise in need of special protection shall be released immediately at the point of capture. Where such fauna taken under this licence is injured or deceased, the licensee shall contact the Department's Wildlife Licensing Section for advice on disposal. Records must be kept of any such fauna so captured and details are to be included in the report required under further condition below.
- 5 Any interaction involving Gazetted Threatened Fauna that may be harmful to the fauna and/or invasive may require approval from the Commonwealth Department of the Environment ph 02 6274 1111. 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 Wildlife Conservation Act 1950 and Wildlife Conservation Regulations 1970.
- 6 No fauna shall be taken in areas where it would impinge on pre-existing scientific research programs.
- 7 Except in the case of approved lethal traps, the licensee shall ensure that measures are taken in the capture and handling of fauna to prevent injury or mortality resulting from that capture or handling. Where traps or other mechanical means or devices are used to capture fauna these shall be deployed so as to prevent exposure of trapped animals to ants and debilitating weather conditions and inspected at regular intervals throughout each day of their use. At the conclusion of research all markers used, and signs and structures erected by the licensee shall be removed and the environment returned to its original condition.
- 8 Not more than ten specimens of any one protected species of fauna shall be taken and removed 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.
- 9 The licensee shall not release any fauna or their progeny in any area where it does not naturally occur, nor hand such fauna over to any other person or authority unless approved by the Director General, nor dispose of the remains of such fauna in any manner likely to confuse the natural or present day distribution of the species.
- 10 Bioprospecting involving the removal of sample aquatic and terrestrial organisms for chemical extraction and bioactivity screening shall not be conducted without specific written approval by the Director General.
- 11 No fauna shall be taken from any CALM land, as defined in the Conservation and Land Management Regulations 2002, without prior written approval of the Director General. No fauna shall be taken from any public land without the prior written approval of the Government Authority managing that land.
- 12 The licensee shall not enter upon any private property or pastoral lease for the purposes of this licence, nor take any fauna from any private land or pastoral lease without the prior consent in writing of the owner or occupier. Similarly, in the case of Aboriginal lands, the licensee must not enter upon or take fauna from such lands without the written approval of the Department of Aboriginal Affairs and/or the relevant native title holders or applicants.
- 13 Copies of this licence and any written approval or consent required by conditions of this licence must be carried by the licensee and any person/s authorised under the licence at all times when conducting activities relevant to the licence

# DEPARTMENT OF PARKS AND WILDLIFE



Department of  
Parks and Wildlife



Enquiries: 17 DICK PERRY AVE, KENSINGTON, WESTERN AUSTRALIA  
Telephone: 08 9219 9000  
Facsimile: 08 9219 8242  
Web Site: <https://wildlifelicensing.dpaw.wa.gov.au/>  
Correspondance: Locked Bag 30  
Bentley Delivery Centre WA 6983

PAGE 2  
NO. 08-000238-1

and must be presented to an authorised officer of the Department upon request.

- 14 All holotypes and syntypes and a half share of paratypes of species or subspecies permitted to be permanently taken under this licence shall 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 shall upon request be donated to the Western Australian Museum.
- 15 To prevent any unnecessary collecting in this State, all specimens and material taken and retained under the authority of this license shall, upon request, be loaned to the Western Australian Museum. Any unused portion or portions of any specimen collected under the authority of this license shall be offered to the Western Australian Museum for inclusion in its collection or made available to other scientific workers if so required.
- 16 Within one month of the expiration of this licence, the holder shall submit an electronic return into the department's Wildlife Licensing System, detailing the locality, site, geocode, date and number of each species of fauna captured, sighted or vouchered during the currency of the licence. A copy of any paper, report or thesis resulting from the research shall upon completion be lodged with the Director General.

## Purpose

Troglofauna and Stygofauna survey for environmental impact assessment via plankton net hauls, PVC leaf-litter traps and net haul scrapings in accordance with EPA guidance statement 54a

## Locations

Warramboo, Mesa A, Mesa C, Mesa K

## Authorised Person

Surname	Given name(s)
Alexander	Jason
Watson	Nicola
King	Jacinta
Teale	Roy
Kamien	Daniel
Schmidt	Sylvie
Humphreys	Garth
Werner	Scott
Keirle	David
Ford	Stewart
Greenham	Michael
Adam	Cassie

# DEPARTMENT OF PARKS AND WILDLIFE



Department of  
Parks and Wildlife



Enquiries: 17 DICK PERRY AVE, KENSINGTON, WESTERN AUSTRALIA  
Telephone: 08 9219 9000  
Facsimile: 08 9219 8242  
Web Site: <https://wildlifelicensing.dpaw.wa.gov.au/>  
Correspondance: Locked Bag 30  
Bentley Delivery Centre WA 6983

PAGE 3  
NO. 08-000238-1

**Date of Issue** 21/02/2017  
**Valid From** 21/02/2017  
**Date of Expiry** 20/02/2018

**Licensee:** Ms Penny Brooshoof  
**Address** Biota Environmental Sciences  
PO Box 155  
Leederville WA 6903  
Australia

Issued by a Wildlife Licensing Officer of the Department of Parks and Wildlife under delegation from the Minister for Environment pursuant to section 133(1) of the Conservation and Land Management Act 1984.



## Appendix 2

### Molecular Reports







# Helix

## Molecular Solutions

School of Animal Biology The University of Western Australia Hackett Entrance No. 4 Hackett Drive Crawley WA 6009	PO Box 155 Leederville WA 6903
t. (08) 6488 4509 f. (08) 6488 1029 abn. 32 133 230 243	w. <a href="http://www.helixsolutions.com.au">www.helixsolutions.com.au</a>

6 January, 2015

Jason Alexander  
Biota Environmental Sciences  
Level 1, 228 Carr Place  
Leederville, WA 6007

Via email

**Re. Report on the molecular systematics of subfauna from the Robe River Valley**

Dear Jason,

Following is a summary of the results of the subfauna study we have completed on nine taxonomic groups from the Robe River Valley. Fifty-five distinct genetic lineages were detected among the seven groups for which sequences were obtained. The 55 lineages likely represent between 51 and 54 species, only five of which have been detected previously in the Pilbara. A further species matched a Genbank specimen of Coleoptera which does not appear to have been recorded in Australia, although the family to which it belongs is well-represented.

Thanks once again for collaborating on this project with Helix. We hope we can continue to provide you with useful information, and feel free to contact us if you have any questions or would like to discuss the results in detail.

Sincerely,

Dr. Terrie Finston, Yvette Hitchen and Dr. Oliver Berry  
Helix Molecular Solutions

## Background and Objective

Two hundred and thirty specimens of subfauna (troglofauna and stygofauna) belonging to nine taxonomic groups (Amphipoda, Chilopoda, Coleoptera, Diplopoda, Diplura, Isopoda, Pseudoscorpiones, Schizomida, Thysanura) were collected from Robe River Valley and sequenced for variation at the mitochondrial COXI gene. The molecular data were assessed in order to determine the number of species present in each group and compare the results to those obtained during previous surveys that have been undertaken for the these groups elsewhere in the Pilbara.

## Executive summary

- Two hundred and thirty specimens from the Robe River Valley belonging to nine taxonomic groups were sequenced for variation at the COI gene.
- Fifty-five lineages were detected among the seven groups for which sequences were obtained.
- The 55 lineages likely represent between 51 and 54 species.
- Five of the species have been detected previously in the Pilbara, whereas the remainder appear to be new, based on the material available for comparison.

## Methods

Two hundred and thirty-eight specimens of subfauna collected from the Robe River Valley area were sequenced for variation at the mitochondrial cytochrome oxidase subunit I gene (COXI) using multiple pairs of primers (LCO1/HCO2, LCO1-long/HCO2-long, NemF1/NemR1 and LCO1/CIN2341).

Sequences were edited using GENEIOUS software (Drummond et al. 2011). Alignment was performed with CLUSTAL W (Thompson et al. 1994) using default parameters. Genetic distances between unique genetic sequences (haplotypes) were measured using uncorrected p-distances (total percentage of nucleotide differences between sequences).

MODELTEST software (Posada and Crandall, 1998) was used to determine the model of sequence evolution that best fitted the data for each taxonomic group. Bayesian analysis was used to construct the phylogenetic trees, incorporating the model as identified in MODELTEST for each taxonomic group. The phylogeny, branch lengths and posterior probabilities were obtained by running two trees simultaneously, each running four simultaneous MCMC chains. The number of cycles needed was determined by the standard deviation of the split frequencies of the two trees. The analysis was paused after every  $1 \times 10^6$  generations and when the standard deviation fell below 0.01, the analysis was stopped. A majority rule consensus tree was constructed after discarding the “burn-in” trees in both analyses. The burn-in value was determined by plotting the posterior probabilities obtained after every generation and identifying the point at which the values reach stationarity (= the asymptote). Trees produced prior to stationarity were discarded.

For the purposes of this report, lineages were defined as haplotypes or groups of haplotypes differing from other such groups by >3% sequence divergence. This cut-off was selected based on bar-coding data, which indicates that intra-specific variation rarely exceeds 3% (Hebert et al., 2003b).

## Results

### Schizomids

#### Preliminary analysis - Reference sequences and outgroups

Ninety-one schizomids were sequenced from the Robe River Valley (Table 1). In order to reduce analysis time and to simplify the presentation of results, a preliminary neighbour-joining (NJ) analysis was conducted with the 91 Robe River Valley sequences to identify the number of genetic lineages present. A representative from each lineage was analysed with 373 reference sequences of schizomids from previous surveys in the Pilbara to compile a manageable and relevant reference data set. The reference sequences were selected based on the criteria that they showed  $\leq 15\%$  sequence divergence from at least one of the Robe River Valley lineages.

Ten distinct genetic lineages were identified (Figure 1) and a representative from each was analysed in a model-based phylogenetic analysis with 26 reference specimens. Two representatives were included from lineage 4 (lineage 4 and 4a) to more fully represent the genetic variation within the lineage. A specimen of schizomid from the family Hubbardiidae, *Brignolozomus woodwardi* (GenBank accession # EU272675) was used as an outgroup.

#### *Phylogenetic analysis*

The phylogenetic analysis, which included the ten Robe River Valley lineages, in addition to 26 reference specimens of schizomids, placed the Robe River Valley specimens in ten distinct lineages, two of which (lineages 8 and 1) also contained reference specimens from a previous survey at the Robe River Valley (*Draculoides mesozeirus* and *P. bythius*). A third Robe Valley lineage (lineage 3) formed a close relationship with *Paradraculoides* sp. whereas the remaining seven lineages were genetically distinct from the reference specimens as evidenced by long branch lengths (Figure 2). Lineages 1 -4 formed a well-supported clade with five reference specimens of *Paradraculoides* and lineages 7 – 9 formed a well-supported clade with the reference specimen of *Draculoides mesozeirus* (Figure 2). Lineage 10 formed a well-supported clade with specimens identified as *Draculoides* from the Pilbara, although no Genbank voucher specimens were contained in the clade (Figure 2). Lineage 5 was highly distinct, and was placed outside all of the clades containing *Draculoides* and *Paradraculoides* specimens (Figure 2).

#### *Differentiation within and between lineages*

Lineage 4 and 4a differed from one another by an average of 3.1% sequence divergence (Table 2). Excluding the divergence within lineage 4, the ten lineages of schizomids detected at the Robe River Valley differed from one another by between 5.8 and 18.0% mean sequence divergence (Table 2). Individuals within each of the ten lineages differed from one another by between 0.1 and 1.3% mean sequence divergence (Table 3).

Two of the ten lineages (8 and 1) differed from the closest reference lineage (*D. mesozeirus* and *P. bythius*, respectively), collected during previous surveys at the Robe River Valley by <1% sequence divergence (Table 4). Lineage 3 differed from the closest reference lineage (*Paradraculoides* sp.) by 3.9% (Table 4). The remaining lineages differed from the nearest reference specimens by >7% (Table 4).

#### *Distribution of lineages*

Two lineages (1 and 4/4a) were detected in multiple deposits (Table 5). Lineage 1 was detected at Mesa B and C, and lineage 4/4a was detected at Mesas L, M and N, and Highway and Tod bore (Table 5). Two deposits (Mesa B and Highway and Tod bore) contained multiple lineages. Mesa B contained lineages 1 and 5, and Highway and Tod bore contained lineages 3 and 4 (Table 5).

### Amphipoda

#### *Preliminary analysis - Reference sequences and outgroups*

Forty-seven specimens of amphipods from seven sites were sequenced from Robe Valley (Table 6). In order to reduce analysis time and to simplify the presentation of results, a preliminary neighbour-joining (NJ) analysis was conducted on the 25 Robe Valley amphipods for which sequences were obtained, and haplotypes were selected from each genetic lineage to include in a model-based phylogenetic analysis. Two sequences of the cladoceran genus *Daphnia* were used as outgroups for both analyses as follows: *Daphnia pulex* (Genbank accession number J150976) and *Daphnia pulicaria* (Genbank accession number JN233925).

The neighbour-joining analysis placed the 25 specimens of amphipods for which sequences were obtained into eight lineages (Figure 3). Comparisons to the GenBank sequence database indicated that six of the eight lineages (1 – 6) were most similar to sequences of Melitidae, whereas two lineages (7, 8) were most similar to sequences of Niphargidae. The Melitidae lineages contained between one and six specimens, and the putative Niphargidae lineages contained between one and five specimens (Figure 3).

For the Melitidae, 20 reference sequences were included, two GenBank vouchers of Melitidae, *Norcapensis mandibularis* (Genbank accession #JQ608487) and *Nedsia* sp. (Genbank

accession # EU304458) and 18 specimens of Melitidae detected in previous surveys of the Robe River, Cape Range, Barrow Island and Ashburton River drainage basins.

For the Niphargidae, two reference sequences were included in the phylogenetic analysis, , *Niphargus fontanus* (Genbank accession #KC315635) and *Niphargus glenniei* (Genbank accession # KC315646) as well as 19 specimens from previous surveys of the Central Pilbara, Barrow Island, Lower Shaw River, Fortescue River, and Marillana Creek.

#### *Phylogenetic analysis*

The phylogenetic analysis, revealed the presence of two distinct, well-supported clades, one containing lineages 1-6 and reference specimens of Melitidae and one containing lineages 7 and 8 and reference specimens of Niphargidae (Figure 4). Two of the two Robe Valley Melitidae lineages contained closely related reference specimens. Lineages 1 (IV126) and 2 (IV92) formed well-supported clades with reference specimens of *Nedsia* from a previous survey in the Robe River Valley, rr3a and nr5mi well, respectively (Figure 4). Further, lineage 5 formed a well-supported clade with specimens of *Nedsia* from Barrow Island and the Cape Range peninsula, and lineages 7 and 8 formed a well-supported clade with each other and the two *Niphargus* reference sequences (Figure 4).

#### *Differentiation within and between lineages*

The six lineages of Melitidae detected at Robe Valley differed from one another by between 6.7 and 15.6% mean sequence divergence and the two lineages of Niphargidae differed by 15.1% sequence divergence (Table 7). Differentiation within the six melitid lineages averaged between 0.0 and 1.8% sequence divergence and differentiation within Niphargidae lineage 8 averaged 0.5% sequence divergence (Table 8).

Robe Valley Melitidae lineage 1 differed from the closest reference lineage (rr3a-2b) by 2.7% and Melitidae lineage 2 differed from the closest reference lineage (nr5miwell-d) by 0.2% (Table 9). The remaining lineages of Melitidae differed from the nearest reference lineages by between 6.8 and 10.3% sequence divergence (Table 9). The two lineages of Niphargidae from the Robe Valley differed from the reference lineages of *Niphargus* by between 19.0 and 21.3% sequence divergence (Table 9).

#### *Distribution of lineages*

Three of the eight lineages were detected at multiple sites (Table 10), Similarly, three of the six sites contained multiple lineages- lineages 1, 2 and 8 were detected at Budgie, lineages 4, 7 and 8 were detected at Daves and lineages 3 and 5 were detected at MB13WARR (Table 10).

### Chilopoda

Five specimens of Chilopoda from three deposits were sequenced (Table 11). Sequences were obtained from four specimens and these were analysed with six Genbank vouchers from four families of Chilopoda, Cryptopidae, Henicopidae, Geophilidae and Mecistocephalidae (in the superfamily Geophilomorpha) as follows: *Scolopocryptops sexspinosis* (Genbank accession # AY288745), *Paralamyctes monteithi* (Genbank accession # AF334321), *Gnathoribautia bonensis* (Genbank accession # KF569297), *Geophilus flavus* (Genbank accession # JN306685), *Stenotaenia linearis* (Genbank accession # KR736251), and *Mecistocephalus multidentatus* (Genbank accession # AB610774) as well as 17 reference specimens of Chilopoda from nine sites in the Pilbara. Two specimens of Onychophora, *Metaperipatus inae* (Genbank accession # HQ453464) and *Opisthopatus cinctipes* (Genbank accession #NC014273) were used as outgroups.

#### *Phylogenetic analysis*

The phylogenetic analysis, which included the four specimens from the Robe Valley in addition to 23 reference specimens, placed the Robe Valley specimens in two genetically distinct clades (Figure 5). Three of the specimens (IV139- IV141) formed a well-supported lineage, which was placed in a well-supported clade with Genbank specimens of Geophilomorpha (Geophilidae and Mecistocephalidae; Figure 5). The fourth specimen (IV143) was placed in a well-supported

clade containing reference specimens from the Pilbara assigned to the genus *Cryptops* (Figure 5).

#### Differentiation within and between lineages

Robe Valley Chilopoda lineage 1 (specimens IV139 – IV141) differed from one another by between 0.0 and 0.3% sequence divergence and from lineage 2 (IV143) by 22.8 – 22.9% sequence divergence (Table 12). The Robe Valley specimens differed from the reference specimens by between 18.0 and 28.1% sequence divergence (Table 12).

#### Distribution of lineages

The Robe Valley Chilopoda lineage 1 was detected at deposit 2403A and lineage 2 was detected at Highway/Tod bore (Table 13).

#### Coleoptera

Eleven specimens of Coleoptera from five drillholes at four sites were sequenced from the Robe Valley (Table 14). The nine specimens for which sequences were obtained were analysed with six Genbank voucher sequences of Coleoptera, selected on their similarity to the Robe Valley specimens: *Stricticollis tobias* (Anthicidae; Genbank accession # KJ962132), *Necrobia violacea* (Cleridae; Genbank accession #KJ961916), *Pterostichus mutus* (Carabidae; Genbank accession #EU710801), *Harpalus disrepans* (Carabidae; HM180603), *Trigonopterus* sp (Curculionidae; Genbank accession #HE615891), *Echinodera ibleiensis* (Curculionidae, Genbank accession #GU213687) as well as 14 reference specimens of Coleoptera from six sites in the Pilbara. Two specimens of Hemiptera (*Nisia carolinensis* Genbank accession #LC015451) and *Lycorma delicatula* (Genbank accession #EU909203) were used as outgroups.

#### Phylogenetic analysis

The phylogenetic analysis, which included the nine specimens from the Robe Valley for which sequences were obtained in addition to 20 reference specimens, placed the Robe Valley specimens in six genetically distinct lineages (Figure 9). The lineages contained between one and four specimens (Figure 6). One of the Robe Valley lineages contained a closely related reference specimen. Lineage 3 (IV153) contained the reference specimen of *Stricticollis tobias* from the family Anthicidae (Figure 6). The remaining lineages did not show close relationships with other reference specimens, however, most of them were placed in well-supported clades containing reference specimens, allowing some tentative taxonomic assignments. Lineage 1 (IV151) formed a well-supported clade with specimens of Carabidae from Genbank and the Pilbara, and lineages 4 and 5 (IV150 and IV152, respectively) formed a well-supported clade with each other and the Genbank and reference sequences of Curculionidae (Figure 6). Lineage 6 formed a well-supported clade containing Genbank specimens of Curculionidae as well as Pilbara specimens of Curculionidae (Figure 9). The remaining lineage was less well resolved. Lineage 2 formed a well-supported clade with Genbank reference specimens of both Anthicidae and Cleridae (Figure 6).

#### Differentiation within and between lineages

The four specimens within lineage 2 were genetically identical (Table 15). The six Robe Valley lineages differed from one another by between 3.2 and 27.1% sequence divergence (Table 15). The Robe Valley lineages differed from the reference specimens by between 0.9 and 31.0% sequence divergence (Table 15).

#### Distribution of lineages

The Robe Valley Coleoptera lineages were each detected in single deposits (Table 16). Similarly, each deposit contained a single lineage, except Highway/Tod which contained three lineages: 1, 3 and 5 (Table 16).

#### Diplopoda

### Reference specimens and outgroups

Eleven specimens of Diplopoda assigned to the Polydesmida on the basis of morphology, were sequenced (Table 17). Six specimens yielded a DNA sequence, however, the DNA appeared to be contaminated with DNA from flies (muscomorpha).

### Diplura

#### Reference specimens and outgroups

Seven specimens of Diplura from six drillholes at three deposits were sequenced (Table 18). The five specimens for which sequences were obtained were analysed with 20 specimens of Diplura from nine sites in the Pilbara belonging to four families: Anajapygidae, Japygidae, Parajapygidae and Projapygidae, as well as four Genbank voucher specimens, Diplura sp. (Genbank accession #HQ943342), *Campodea tillyardi* (Genbank accession # AF370844) and *Lepiodocampa weberi* (Genbank accession #HQ882832) from the family Campodeidae and *Japyx solifugus* (Genbank accession #AY771989) from the family Japygidae. The planthopper *Lycorma delicatula* (Genbank accession # FJ456942) and a specimen of Fulgoridae (Hemiptera sp.; Genbank accession #GU671563) were used as outgroups.

#### Phylogenetic analysis

The phylogenetic analysis, which included the five specimens of Diplura from Robe Valley in addition to 24 reference specimens, placed the Robe Valley specimens in four distinct lineages (Figure 7). The Robe Valley specimens showed no close relationship to any of the reference specimens, however, one (lineage 4) was placed in a well-supported clade containing the Pilbara specimens of Parajapygidae and three (lineages 1, 2 and 3) were placed in a well-supported clade containing the Genbank reference specimens of Campodeidae (Figure 7).

#### Differentiation within and between lineages

The two specimens from the Robe Valley in lineage 3 differed from one another by 0.6% sequence divergence (Table 19). The Robe Valley lineages of putative Campodeidae differed from one another by between 4.7 and 15.3% sequence divergence and from the nearest reference specimen (*Campodea tillyardi*) by 21.4 to 22.2% sequence divergence (Table 19). The Robe Valley specimen of Parajapygidae differed from the nearest reference specimen (BX29 from Murrays Hill) by 17.5% sequence divergence (Table 19).

#### Distribution of lineages

The Robe Valley Diplura lineages were each detected in single deposits (Table 20). Mesa C contained a single lineage (lineage 4), however Mesa B contained three lineages: 1, 2 and 3 (Table 20). Two lineages, 1 and 2, were found in the same drillhole at Mesa B (Table 20).

### Isopoda

#### Preliminary analysis, reference specimens and outgroups

Twenty-seven specimens of Isopoda were sequenced from 17 drillholes at six deposits at Robe Valley (Table 21). Fifteen specimens yielded a DNA sequence. In order to reduce analysis time and to simplify the presentation of results, a preliminary neighbour-joining (NJ) analysis was conducted on the 15 Robe Valley isopods for which sequences were obtained, and haplotypes were selected from each genetic lineage to include in a model-based phylogenetic analysis. Ten distinct genetic lineages were detected in the NJ analysis (Figure 8), and the ten representatives were analysed in a model-based phylogenetic analysis with 35 reference specimens of both aquatic and terrestrial Isopoda from Genbank and 14 sites in the Pilbara. While the specimens were collected from troglofauna traps, a search of similar sequences on Genbank and in the Helix database indicated the specimens were most closely matched with *Haloniscus*, *Burmoniscus* and *Armadillidium*, the former of which is an aquatic genus. It should be noted however, that *Haloniscus* is considered to be a terrestrial isopod living in aquatic habitats (Bayley and Ellis, 1969). Hence we included Genbank voucher specimens of both aquatic and terrestrial isopods: *Pygolabis* sp. 1 (Genbank accession # EU107646) and *Pygolabis*

sp. 4 (Genbank accession #EU107664), *Haloniscus* sp. 10 (Genbank accession #EU364592), *Halonsicus* sp. 12 (Genbank accession #EU364601), *Halonsicus* sp. 21 (Genbank accession #EU364622) *Laevophiloscia yalgoorensis* (Genbank accession #EU364629), *Armadillidium nasatum* (Genbank accession #FN824099) and *Burmoniscus* sp. (Genbank accession #AB626254). Two specimens of the shrimp *Stygiocaris*, *S. stylifera* (Genbank accession #EU123818) and *S. lancifera* (Genbank accession #EU123826) were used as outgroups.

#### *Phylogenetic analysis*

The phylogenetic analysis, which included the ten representatives from Robe Valley in addition to 35 reference specimens, placed the Robe Valley specimens in ten distinct lineages (Figure 9). One of the lineages (lineage 9a; IV181) also contained a reference specimen from Mesa A (Figure 9). Lineage 9a in turn, formed a well-supported clade with lineage 8 and 9b (Figure 9). The remaining lineages did not show close relationships with any of the reference specimens, however lineages 1 and 2 formed a well-supported clade with one another and with two lineages from Buckland Hills and Red Hill (Figure 9). Lineages 3 and 4 formed a poorly supported clade with the clade containing lineages 1 and 2 (Figure 9). Lineages 5, 6, and 7 formed a well-supported clade with specimens of *Troglarmadillo* from the Pilbara (Figure 9).

#### *Differentiation within and between lineages*

The Robe Valley lineages of Isopoda differed from one another by a mean of 3.7 to 25.9% sequence divergence (Table 22). Differentiation within lineages ranged from a mean of 0.1 to 2.5% sequence divergence (Table 23). The Robe valley lineages differed from the reference specimens by between 1.2 and 30.1% sequence divergence (Table 24). In particular, lineages 9a and 9b differed from IE45 (a Mesa A reference specimen) by 1.2 to 3.8% sequence divergence (Table 24). The remaining Robe Valley lineages differed from the reference lineages by >12% (Table 24).

#### *Distribution of lineages*

The Robe Valley Isopoda lineages were each detected in single deposits (Table 24). Mesa B contained three lineages: 4, 5 and 8, and Highway/Tod bore contained four lineages: 6, 7, 9a and 9b (Table 25). One drillhole, TOBRC0020 at Highway/Tod bore contained two lineages, 6 and 7 (Table 25).

### Pseudoscorpions

#### *Reference sequences and outgroups*

Twenty-six pseudoscorpions were sequenced from 16 drillholes at seven deposits at Robe Valley (Table 26). In order to reduce analysis time and to simplify the presentation of results, a preliminary neighbour-joining (NJ) analysis was conducted on the 18 Robe Valley pseudoscorpions for which sequences were obtained, and haplotypes were selected from each genetic lineage to include in a model-based phylogenetic analysis. Fifteen distinct genetic lineages were detected in the NJ analysis (Figure 10), and the 15 representatives were analysed in a model-based phylogenetic analysis with selected reference specimens. A search of similar sequences on Genbank and in the Helix database indicated that four of the lineages (9 – 12) most closely matched the family Chthoniidae and 11 of the lineages most closely matched Helix database specimens of Hyiidae and a Genbank specimen of Atemnidae. Based on those results, GenBank voucher sequences were included as reference sequences of Hyiidae (one specimen) and Atemnidae (one specimen) as follows: *Indohya* sp JM 2008 (Genbank accession # EU559564) and *Paratemnoides sumatrana* (GenBank accession # JN018204). In addition, as local references, seven specimens of Hyiidae from seven sites in the Pilbara and 22 specimens of Chthoniidae from 11 sites were included in the analysis. Sequences of the scorpion *Pandinus imperator* (Genbank accession # AY1565821) and harvestman spider *Siro rubens* (Genbank accession # DQ5131111) were used as outgroups.

#### *Phylogenetic analyses*

Two phylogenetic analyses were conducted, one for the Chthoniidae and one for the Hyiidae/Atemnidae. The phylogenetic analysis of the Chthoniidae, which included the four Chthoniidae lineages from Robe Valley, in addition to 25 reference specimens, placed the

Robe Valley specimens in four distinct genetic lineages (Figure 11). The Robe Valley Chthoniidae lineages did not show close relationships to any of the reference specimens, however lineages 9 and 10 formed a well-supported clade with one another and with six specimens of Chthoniidae from the Red Hill and Ophthalmia (Figure 11). Similarly, lineages 11 and 12 formed a well-supported clade with one another and with a specimen of Chthoniidae from Red Hill (Figure 11).

The phylogenetic analysis of the Hyiidae and Atemnidae, which included the 11 lineages from Robe Valley, in addition to nine reference specimens, placed the Robe Valley specimens in 11 distinct genetic lineages (Figure 12). Lineages 1 – 8 were placed in a clade containing the Pilbara and Genbank reference specimens of Hyiidae (Figure 12). The Robe Valley Hyiidae lineages did not show close relationships to any of the reference specimens, however lineages 3 and 4 formed a well-supported clade with one another and with two specimens of Hyiidae from the Central Pilbara and Hardey River (Figure 12). Similarly, lineages 6, 7 and 8 formed a well-supported clade with one another and with a specimen of Hyiidae from Buckland Hills (Figure 12). The remaining Hyiidae lineages were poorly resolved (Figure 12). Lineages 13 – 15 formed a well-supported clade with one another and with the Genbank specimen of Atemnidae (Figure 12).

#### *Differentiation within and between lineages*

The fifteen lineages of pseudoscorpions from the Robe Valley differed from one another by between a mean of 3.8 and 29.5% sequence divergence (Table 27). Variation within lineages ranged from between a mean of 0.1 and 1.2% sequence divergence (Table 28). The four lineages of Chthoniidae from the Robe Valley differed from one another by between a mean of 10.5 and 22.6% sequence divergence (Table 27), and from the reference specimens of Chthoniidae by between 14.4 and 29.6% sequence divergence (Table 29). The eight lineages of Hyiidae from the Robe Valley differed from one another by between a mean of 3.8 and 26.5% sequence divergence (Table 27), and from the reference specimens of Hyiidae by between 11.3 and 34.9% sequence divergence (Table 30). The three lineages of Atemnidae differed from one another by between a mean of 7.6 and 14.6% sequence divergence (Table 27) and from the reference specimens of Atemnidae by between 18.0 and 19.8% sequence divergence (Table 30).

#### *Distribution of lineages*

The Robe Valley pseudoscorpion lineages were each detected in single deposits (Table 31). Only two of the 15 lineages were detected in more than one bore – Chthoniidae lineage 11 and Atemnidae lineage 15 were both detected in two bores (Table 31). Deposits Mesa B, 2402D and 2403A each contained three lineages and Highway/Tod bore and 2402E each contained two lineages, whereas two deposits, Mesa L and 2401A contained single lineages (Table 31).

### Thysanura

#### *Reference specimens and outgroups*

Four specimens of Thysanura were sequenced from three bores at two deposits (Table 32). None of the specimens yielded a DNA sequence.

### **Conclusions**

COXI is widely considered to show suitable variation to distinguish species (Hebert et al., 2003a). In a comparison of COXI sequences for over 13,000 pairs of taxa, Hebert et al (2003b) found a mean of 11.1% sequence divergence between distinct species. Nearly 80% of the comparisons showed that species pairs differed from one another by greater than 8% sequence divergence.

### Schizomida

Previous analyses of genetic variation between morphologically distinct species of Schizomida can be used as a genetic 'yardstick' to interpret the current data set. The five described species of *Paradraculoides* (Harvey et al, 2008) differ from one another by between 8.4 to 12.1% sequence divergence (uncorrected p-distances; calculated by us from the Harvey et al., 2008

data). Similarly, the four described species of *Draculoides* differ from one another by between 4.5 to 13.7% sequence divergence (uncorrected p-distances calculated by us from Harvey et al., 2008).

Ten genetically distinct lineages of schizomids were detected at the Robe River Valley. The ten lineages differed from one another by >approximately 6% sequence divergence, thus each is likely to represent a distinct species. Variation within lineage 4 (between lineages 4 and 4a) is slightly higher than would be expected within a single species, and this is likely due to geographic separation between Mesa L, where lineage 4a was detected, and Highway and Tod bore and Mesas M and N, where lineage 4 was detected. Thus lineages 4 and 4a may represent incipient species, or a single species showing differentiation due to limited sampling or the poor dispersal ability of the group. We suggest the latter conclusion of a single species is more likely, however, sampling additional specimens from intermediate areas may help resolve this.

Two of the lineages, 1 and 8, corresponded to previously described species, *P. bythius* and *D. mesozeirus*, respectively. A third lineage (3) may correspond to a third described species, *Paradraculoides* sp. OFB 2008, although the genetic distance between the specimens from the present study and the reference specimen was somewhat higher than is generally observed between individuals of the same species. Thus lineage 3 and *Paradraculoides* sp. may represent incipient species, or a single species showing differentiation due to limited sampling or the poor dispersal ability of the group. Morphological evidence or sampling additional specimens from intermediate areas may help resolve this relationship. The remaining seven lineages appear to be new, based on the material available for comparison. Lineages 1 – 4 are likely to belong to the genus *Paradraculoides* and lineages 7 – 9 are likely to belong to the genus *Draculoides*. Lineage 10 may also belong to the genus *Draculoides*, although more voucher sequences are needed for this genus.

#### Amphipoda

Eight genetically distinct lineages of amphipods were detected at the Robe River Valley. The eight lineages differed from one another by > 6% sequence divergence, thus each is likely to represent a distinct species. Six of the species are Melitidae, and two show the greatest similarity to sequences of Niphargidae. Lineages 1-5 were placed in the large clade containing reference specimens of *Nedsia* and thus are all likely to belong to that genus. Lineage 6 was placed outside the *Nedsia* clade and may represent a different genus of Melitidae. Two of the *Nedsia* species have been detected previously in the Robe Valley (lineages 1 and 2), based on their high genetic similarity to reference sequences (<3% sequence divergence). In contrast, the remaining four Melitidae lineages and the two Niphargidae lineages differed from the nearest reference lineages by >7% sequence divergence and thus appear to be new, based on the material available for comparison.

#### Chilopoda

Two genetically distinct lineages of Chilopoda were detected at the Robe River Valley. The two lineages differed from one another by > 20% sequence divergence, thus each is likely to represent a distinct species. Neither showed close genetic relationships to reference specimens, differing from the references by >18.0% sequence divergence, thus both species are likely to be new, based on the material available for comparison. Lineage 1 was placed with the Geophilomorpha, and lineage 2 was placed with specimens of the genus *Cryptops*.

#### Coleoptera

Six genetically distinct lineages of Coleoptera were detected at Robe Valley. Two of the lineages, 4 and 5, differed from one another by 3.2% sequence divergence. As they were detected at different deposits, it is likely that they represent a single species, which shows genetic differentiation due to the geographic distance between deposits. The remaining lineages differ from one another by  $\geq$  19% sequence divergence, thus each is likely to represent a distinct species. With one exception, the lineages detected at Robe Valley differ from the reference lineages by >10% sequence divergence, thus each is likely to represent a new species, which has so far not been detected, based on the material available for comparison. Only lineage 3 showed a close relationship to a reference specimen. Lineage 3 showed <1% sequence divergence from the Genbank specimen of *Stricticollis tobias* in the family Anthicidae

and the subfamily Anthicinae. While we could find no record of this species in Australia, the subfamily is well-represented, with 18 genera recorded from Australia (Australian Faunal Directory).

#### Diplopoda

None of the Diplopoda specimens yielded a useable DNA sequence.

#### Diplura

Four distinct genetic lineages of Diplura were detected at Robe Valley. The four lineages differed from one another by a mean of >5%, thus each is likely to represent a distinct species. While the genetic distance between lineages 2 and 3 is moderately low (mean=5%), both lineages were detected at Mesa B, although in different drillholes, indicating there are barriers to gene flow between the two lineages over short geographic distances, supporting the notion that they are separate species. Sampling of intermediate sites may help resolve the relationship between lineages 2 and 3. All four lineages differ from the reference specimens by >20% and thus appear to be new, based on the material available for comparison. Three of the lineages (1 – 3) may belong to the Dipluran family Campodeidae, which is represented in Australia by four genera, and one lineage (4) likely belongs to the Parajapygidae family.

#### Isopoda

Ten distinct genetic lineages of Isopoda were detected at Robe Valley. Two of the lineages, 9a and 9b differed from one another by a mean of 3.7%, which, while low, is higher than is typically observed between members of the same species. Both lineages were detected at the Highway/Tod bore deposit, although in different drillholes, indicating there are barriers to gene flow between the two lineages over short geographic distances, re-enforcing the notion of separate species. Sampling of intermediate sites may help resolve the relationship between lineages 9a and 9b. One of the lineages, 9b, was detected previously at Mesa A. The remaining lineages differ from the reference specimens by >12% and thus appear to be new, based on the material available for comparison. Three of the lineages (5 - 7) may belong to the genus *Troglarmadillo*, as they were placed in a large clade containing reference specimens of that genus, whereas the remaining lineages could not be given taxonomic assignments, owing to their distant relationships to reference taxa.

#### Pseudoscorpiones

Fifteen distinct genetic lineages of pseudoscorpions were detected at Robe Valley, four Chthoniidae, eight Hyiidae and three putative Atemnidae. The four lineages of Chthoniidae differed from one another by >10% sequence divergence, thus each is likely to represent a distinct species. Further, the four Chthoniidae lineages from Robe Valley differed from the reference specimens by >14%, indicating that the four are likely to be new species that have so far not been detected in the Pilbara, based on the material available for comparison.

The three putative lineages of Atemnidae differed from one another by >7% sequence divergence, thus each is likely to represent a distinct species. There are currently no DNA sequences of Atemnidae from other sites in the Pilbara available for comparison, thus we assign it tentatively to this family, and no conclusions can be reached regarding the broader distributions of these species. However, a new species of *Anatemnus* was recently described from the Pilbara, and four other species in the family are known from Australia (Alexander et al., 2014).

With two exceptions, the eight lineages of Hyiidae differed from one another by >13% sequence divergence. Two of the lineages, 3 and 4, differed from one another by a mean of 3.8%, which, while low, is higher than is typically observed between members of the same species. The two lineages were detected at different deposits, 2402D and 2402E, thus the observed genetic differentiation may reflect the poor dispersal abilities of this group. Sampling of intermediate sites may help resolve the relationship between lineages 3 and 4. In contrast, lineages 1 and 2 differed by approximately 5% sequence divergence, but both were detected at Mesa B, indicating that there are barriers to gene flow, over a relatively short geographic distance, and supporting the notion that the two should be considered separate species. However, sampling of intermediate sites may help resolve the relationship between the two lineages. The eight

lineages differ from the reference specimens by >13% and thus appear to be new, based on the material available for comparison.

#### Summary

Fifty-five lineages from seven taxonomic groups were detected at Robe Valley, as shown below. The 55 lineages likely represent 51 - 54 species. Five of the species have been detected previously in the Pilbara, and one matched a Genbank sequence of a species apparently not recorded from Australia, although the family to which it belongs is well-represented. The remaining species at Robe Valley are likely to be new, based on the material available for comparison.

The failure rate was somewhat higher than usual with this project. In addition to our inability to produce amplification products from some specimens (e.g. Thysanura), of those that did amplify, some sequences were contaminated with foreign DNA - flies, even human. This happens when there isn't enough target DNA to out-amplify contaminants.

#### Schizomida

Ten lineages were detected at Robe Valley, likely corresponding to ten species. Two of the species have been detected previously in the Pilbara (*P. bythius* and *D. mesozeirus*), and a third shows moderate genetic similarity to *Paradraculoides* sp. OFB 2008 and requires further investigation, while the remaining seven appear to be new, based on the material available for comparison.

#### Amphipoda

Eight lineages were detected at Robe Valley, likely corresponding to eight species. Two of the species have been detected previously in the Pilbara (undescribed Melitidae, possibly *Nedsia*), while the remaining six appear to be new, based on the material available for comparison.

#### Chilopoda

Two lineages were detected at Robe Valley, likely corresponding to two species. Neither of the species has been detected previously in the Pilbara, based on the material available for comparison.

#### Coleoptera

Six lineages were detected at Robe Valley, likely corresponding to five species. One of the species matched a Genbank sequence of a species apparently not recorded from Australia (*Stricticollis tobias* from the family Anthicidae), although the family is well-represented in Australia. The remaining four species are likely to be new, based on the material available for comparison.

#### Diplopoda

No clean sequences were obtained from the specimens of Polydesmida.

#### Diplura

Four lineages were detected at Robe Valley, likely corresponding to four species. None of the species have been detected previously in the Pilbara, based on the material available for comparison.

#### Isopoda

Ten lineages were detected at Robe Valley, likely corresponding to nine or ten species. One of the species has been detected previously at Mesa A, whereas the remainder appear to be new, based on the material available for comparison.

#### Pseudoscorpiones

Fifteen lineages were detected at Robe Valley, likely corresponding to 13 - 15 species. None of the species have been detected previously in the Pilbara, based on the material available for comparison.

#### Thysanura

No sequences were obtained from the specimens of Thysanura.

## References

- Alexander, J. B. , Burger M. A.A., and Harvey, M.S. (2014). A new species of troglobitic *Anatemnus* (Pseudoscorpiones: Atemnidae) from the Pilbara bioregion of Australia. Records of the Western Australian Museum 29: 141 – 148.
- Australian Faunal Directory. <http://www.environment.gov.au/biodiversity/abrs/online-resources/>. Accessed 27 Dec., 2015.
- Bayly, I. A.E, Ellis p. (1969). *Haloniscus searlei* chilton: An aquatic “terrestrial” isopod with remarkable powers of osmotic regulation. Comparative Biochemistry and Physiology 31: 523-528
- Drummond AJ, Ashton B, Buxton S, Cheung M, Cooper A, Duran C, Field M, Heled J, Kearse M, Markowitz S, Moir R, Stones-Havas S, Sturrock S, Thierer T, Wilson A (2011) Geneious v5.4, <http://www.geneious.com/>
- Harvey, M. S., Berry, O. Edward, K. L., Humphreys, G. (2008) Molecular and morphological systematics of hypogean schizomids (Schizomida: Hubbardiidae) in semiarid Australia. Invertebrate Systematics 22: 167-194.
- Hebert, P.D.N., Cywinska, A., Ball, S.L., deWaard J.R. (2003a). Biological identifications through DNA barcodes. Proceedings of the Royal Society of London B 270: 313-321.
- Hebert, P.D.N., Ratnasingham, S., deWaard J.R. (2003b). Barcoding animal life: cytochrome c oxidase subunit 1 divergences among closely related species. Proceedings of the Royal Society of London B (supplement) 270: S96-S99.
- Helix Molecular Solutions (2015). Report on the molecular systematics of Schizomida from The Robe River Valley. Prepared for Biota Environmental Sciences, 5 February.
- Posada, D., Crandall, K.A. (1998). MODELTEST: testing the model of DNA substitution. Bioinformatics 14: 817-818.
- Thompson, J., Higgins, D., and Gibson, T. (1994). CLUSTAL W: improving the sensitivity of progressive multiple sequence alignment through sequence weighting, position-specific gap penalties and weight matrix choice. Nucleic Acids Research 22: 4673–4680. doi:10.1093/nar/ 22.22.4673

Table 1. Specimens of Schizomida used in the present study and the lineage to which they were assigned, based on variation at the COXI gene. nd=no data.

Phase	Tracking Number	Cap #	Helix ID	Lineage
P1	2402eUnk03-20150809-T1-01	343	IV01	Lin 8= D. mesozeirus
P1	2402EUNK05T3-01	672	IV02	Lin 8= D. mesozeirus
P1	2402eUnk08-20150809-T1-01	299	IV03	Lin 8= D. mesozeirus
P1	2402eUNK09-T3-01	651	IV04	Lin 8= D. mesozeirus
P1	2402eUnk11-20150809-T2-01	293	IV05	Lin 8= D. mesozeirus
P1	2402EUNK13T2-01	692	IV06	Lin 8= D. mesozeirus
		STYGO CAP 11		
P1	Budgie20150604-06		IV07	Lin 2
P1	DD11MEB001T3-02	683	IV08	Lin 1= P. bythius
P1	DD14MEL0001-t2-01	759	IV09	Lin 4a
P1	DD14MEM0001T2-03	525	IV10	Lin 4
P1	DD14MEN0001-20150808-T2-02	580	IV11	Lin 4
P1	DD14MRR0004-t2-01	782	IV12	Lin 7
P1	DD14MRR0005-T1-01	604	IV13	Lin 7
P1	DD14MRR0005-T1-01		IV14	Lin 7
P1	DD14MRR0005-T2-03	775	IV15	Lin 7
P1	DD14MRR007-20150808-T2-01	439	IV16	Lin 6
P1	DD14MRR007-20150808-T1-02	446	IV17	Lin 6
P1	DD14MRR0008-20150808-T3-01	494	IV18	Lin 6
P1	DD14MRR009-20150808-T2-02	572	IV19	Lin 6
P1	M2ERC0039-20150809-T1-01	386	IV20	Lin 8= D. mesozeirus
P1	M2ERC0039-20150809-T1-01		IV21	Lin 8= D. mesozeirus
P1	M2ERC027-t2-01	761	IV22	Lin 8= D. mesozeirus
P1	M2ERC027-t2-01		IV23	Lin 8= D. mesozeirus
P1	M2ERC049-t2-01	752	IV24	Lin 8= D. mesozeirus
P1	M2ERC053-t1-01	772	IV25	Lin 8= D. mesozeirus
P1	M2ERC053-t1-01		IV26	Lin 8= D. mesozeirus
P1	M2ERC0053-T2-02	777	IV27	Lin 8= D. mesozeirus
P1	M2ERC0053-T2-02		IV28	Lin 8= D. mesozeirus
P1	MEARC3790.20150606-01	3	IV29	Lin 3
P1	MEARC3790.20150606-01		IV30	Lin 3
P1	MEARC3790.20150606-01		IV31	Lin 3
P1	MEARC3790.20150606-01		IV32	Lin 3
P1	MEARC3790-20150807-T1-01	409	IV33	Lin 3
P1	MEARC3811-20150807-T1-01	389	IV34	Lin 3
P1	MEARC4273-t1-01	756	IV35	Lin 4
P1	MEARC4400-t1-02	766	IV36	Lin 3
P1	MEBRC0027T2-01	673	IV37	Lin 1= P. bythius
P1	MEBRC0027T2-01		IV38	Lin 1= P. bythius
P1	MEBRC0027T3-01	675	IV39	Lin 1= P. bythius
P1	MELUnk02-t2-01	757	IV40	Lin 4
P1	MELUnk02-t2-01		IV41	Lin 4
P1	MELUNK03-t1-01	758	IV42	Lin 4

P1	MELUNK06-201508-T2-01	366	IV43	Lin 4
P1	MELUNK06-20150809-T1-01	372	IV44	Lin 4
P1	MELUNK07-20150809-T2-02	469	IV45	Lin 4
P1	MELUNK09T1-01	693	IV46	Lin 4
P1	Melunk10-t1-01	789	IV47	Lin 4
P1	Melunk10-t1-01		IV48	Lin 4
P1	RC13MEN0005-20150808-T1-01	472	IV49	Lin 4
P1	RC13MEN0005-20150808-T1-01		IV50	Lin 4
P1	RC13MRR0014-t1-01	788	IV51	Lin 9
P1	RC13MRR0026-t2-01	780	IV52	Lin 7
P1	RC13MRR0051T2-01	688	IV53	Lin 9
P1	RC13MRR0051T2-01		IV54	Lin 9
P1	RC13MRR0077-T1-02	717	IV55	Lin 9
P1	RC14MEB0071-01	751	IV56	Lin 1= <i>P. bythius</i>
P1	RC14MEB0081-t2-01	771	IV57	Lin 1= <i>P. bythius</i>
P1	RC14MEB0081-t2-01		IV58	Lin 1= <i>P. bythius</i>
P2	2402EUNK05-20151002-T1-01	423	IV59	Lin 8= <i>D. mesozeirus</i>
P2	2402EUNK11-20151002-T2-01	302	IV60	Lin 8= <i>D. mesozeirus</i>
P2	DD14MEC0002-20150929-T3-03	508	IV61	Lin 1= <i>P. bythius</i>
P2	DD14MEC0002-20150929-T3-03		IV62	Lin 1= <i>P. bythius</i>
P2	DD14MEL0002-20151001-T2-01	646	IV63	Lin 4
P2	DD14MEL0002-20151001-T2-01		IV64	Lin 4
P2	DD14MEL0002-20151001-T2-01		IV65	Lin 4
P2	DD14MEM0001-20151001-T1-01	601	IV66	Lin 4
P2	DD14MEM0002-20151001-T2-01	611	IV67	Lin 4
P2	DD14MEM0003-20151001-T1-01	541	IV68	Lin 4
P2	DD14MRR0008-20151002-T3-01	449	IV69	Lin 6
P2	DD14MRR0009-20151002-T2-01	432	IV70	Lin 6
P2	DD14MRR0009-20151002-T3-03	439	IV71	Lin 6
P2	M2ERC0057-20151002-T2-01	407	IV72	Lin 8= <i>D. mesozeirus</i>
P2	MEARC3790-20150930-T1-01	486	IV73	Lin 3
P2	MELUNK02-20151001-T1-01	624	IV74	Lin 4
P2	MELUNK02-20151001-T1-01		IV75	Lin 4
P2	MELUNK11-20151001-T2-01	653	IV76	Lin 4
P2	RC13MRR0026-20151002-T2-02	395	IV77	Lin 7
P2	RC14MEB0029-20151001-T1-02	133	IV78	Lin 1
P2	RC14MEB0060-20151001-T2-01	203	IV79	Lin 5
P2	RC14MEB0150-20151001-T2-01	38	IV80	Lin 1= <i>P. bythius</i>
P2	RC14MRR0017-20151002-T2-01	380	IV81	Lin 10
P2	TOBRC0023-20151001-T1-01	31	IV82	Lin 3
P1	DD11MEC0003T2-01	685	IV83	Lin 1= <i>P. bythius</i>
P1	DD11MEC0003T2-01		IV84	Lin 1= <i>P. bythius</i>
P1	DD11MEC0003T3-01	686	IV85	Lin 1= <i>P. bythius</i>
P1	DD11MEC0003T3-01		IV86	Lin 1= <i>P. bythius</i>
P1	DD14MEC001-20150810-T1-01	559	IV87	Lin 1= <i>P. bythius</i>

P1	MERC0114-T3-01	600	IV88	Lin 1= P. bythius
P1	MERC0114-T2-04	604		
P1	Nonumber-t1-01	792	IV89	Lin 4
P1	Nonumber-t1-01		IV90	Lin 4
P1	Nonumber-t2-01	793	IV91	Lin 4

Table 2. Mean genetic distance (below diagonal) and standard error (above diagonal, in blue) between lineages of Schizomida detected in the NJ analysis as shown in Figure 1.

lineage	1	2	3	4	4a	5	6	7	8	9	10
lin 1		0.007	0.008	0.010	0.009	0.012	0.013	0.013	0.011	0.012	0.010
lin 2	0.065		0.007	0.009	0.008	0.012	0.013	0.013	0.012	0.013	0.011
lin 3	0.080	0.058		0.009	0.010	0.011	0.013	0.013	0.012	0.011	0.010
lin 4	0.105	0.104	0.096		0.005	0.011	0.013	0.012	0.012	0.012	0.011
Lin 4a	0.113	0.097	0.099	0.031		0.011	0.013	0.012	0.012	0.013	0.011
lin 5	0.158	0.144	0.140	0.149	0.150		0.015	0.013	0.011	0.013	0.012
lin 6	0.161	0.149	0.141	0.147	0.151	0.169		0.010	0.012	0.012	0.011
lin 7	0.161	0.153	0.157	0.141	0.144	0.170	0.087		0.009	0.011	0.011
lin 8	0.155	0.141	0.142	0.131	0.135	0.157	0.081	0.065		0.012	0.010
lin 9	0.159	0.147	0.139	0.130	0.136	0.180	0.123	0.122	0.117		0.011
lin 10	0.150	0.143	0.139	0.148	0.151	0.172	0.145	0.155	0.148	0.167	

Table 3. Mean distance (D) and standard error (s.e.) within lineages of Schizomida detected in the NJ analysis as shown in Figure 1 and the number (N) of individuals assigned to that lineage. n/c = not calculated, for groups where n=1. Rep=individual selected to represent the lineage in the model-based analysis.

Lineage	D	s.e.	N	rep
lin 1	0.007	0.002	18	IV61
lin 2	n/c	n/c	1	IV07
lin 3	0.011	0.002	9	IV82
lin 4	0.008	0.001	26	IV76
lin 4a	n/c	n/c	1	IV09
lin 5	n/c	n/c	1	IV79
lin 6	0.001	0.001	7	IV17
lin 7	0.002	0.001	6	IV14
lin 8	0.005	0.001	18	IV27
lin 9	0.013	0.004	4	IV55
lin 10	n/c	n/c	1	IV81

Table 4. (attached). Genetic distances (below diagonal) and standard error (above diagonal, in blue) between specimens of Schizomida detected at Robe Valley and the reference lineages as shown in Figure 2.

Table 5. Distribution of the eight Schizomida lineages detected in the present study.

Lineage	drillholes	deposits
1	DD11MEB001, DD11MEC0003, DD14MEC001, DD14MEC002, MEBRC0027, MERC0114, RC14MEB0029, RC14MEB0071, RC14MEB0081, RC14MEB0150	Mesa B, Mesa C
2	Budgie20150604	Waramboo
3	MEARC3790, MEARC3811, MEARC4400, TOBRC0023,	Highway and Tod bore
4	DD14MEL0002, DD14MEM0001, DD14MEM0002, DD14MEM0003, DD14MEN0001, MEARC4273, MELUNK02, MELUNK03, MELUNK06, MELUNK07, MELUNK09, MELUNK10, MELUNK11, nonumber, RC13MEN0005	Mesa L, Mesa M, Mesa N, Highway and Tod bore
4a	DD14MEL0001	Mesa L
5	RC14MEB0060	Mesa B
6	DD14MRR007, DD14MRR008, DD14MRR009	2402D
7	DD14MRR004, DD14MRR005, DD14MRR0026,	2402A
8	M2ERC0027, M2ERC0039, M2ERC0049, M2ERC0053, M2ERC0057, 2402EUNK03, 2402EUNK05, 2402EUNK08, 2402EUNK09, 2402EUNK11, 2402EUNK13	2402E
9	RC13MRR0014, RC13MRR0051	2403D
10	RC14MRR0017	2401A

Table 6. Specimens of Amphipoda used in the present study and the lineage to which they were assigned, based on variation at the COXI gene. nd=no data

Phase	Tracking number	Cap no.	Helix ID	Lineage
P1	Budgie.20150604-02	7	IV92	Lineage 2
P1	Budgie.20150604-02		IV93	Lineage 1
P1	Budgie.20150604-02		IV94	Lineage 8
P1	Budgie.20150604-02		IV95	Lineage 8
P1	Budgie.20150604-02		IV96	nd
P1	Camp-20150604-02	15	IV97	nd
P1	Camp-20150604-02		IV98	nd
P1	Daisy-20150604-02	13	IV99	nd
P1	Daves-20150604-01	1	IV100	Lineage 8
P1	Daves-20150604-01		IV101	nd
P1	Daves-20150604-01		IV102	nd
P1	Daves-20150604-01		IV103	nd
P1	Daves-20150604-01		IV104	Lineage 8
P1	MB13WARR001-20150605-01	20	IV105	Lineage 5
P1	MB13WARR001-20150605-01		IV106	Lineage 5
P1	MB13WARR001-20150605-01		IV107	Lineage 5
P1	MB13WARR001-20150605-01		IV108	Lineage 5
P1	MB13WARR001-20150605-01		IV109	Lineage 5

P1	MB13WARR010.20150606-01	18	IV110	nd
P1	MB13WARR010.20150606-01		IV111	Lineage 3
P1	MB13WARR010.20150606-01		IV112	Lineage 3
P1	MB13WARR010.20150606-01		IV113	nd
P1	MB13WARR010.20150606-01		IV114	Lineage 3
P1	TOBRC009-20150605-01	19	IV115	nd
P1	TOBRC009-20150605-01		IV116	nd
P1	TOBRC009-20150605-01		IV117	nd
P1	TOBRC009-20150605-01		IV118	nd
P1	TOBRC009-20150605-01		IV119	nd
P1	Budgie-20150930-01	7	IV120	Lineage 1
P1	Budgie-20150930-01		IV121	Lineage 1
P1	Budgie-20150930-01		IV122	nd
P1	Budgie-20150930-01		IV123	Lineage 1
P1	Budgie-20150930-01		IV124	nd
P2	Camp-20150930-02	14	IV125	Lineage 1
P2	Camp-20150930-02		IV126	Lineage 1
P2	Daisy-201509-02	12	IV127	Lineage 2
P2	DAVES-20150930-04	4	IV128	Lineage 4
P2	DAVES-20150930-04		IV129	Lineage 7
P2	DAVES-20150930-04		IV130	Lineage 8
P2	DAVES-20150930-04		IV131	nd
P2	DAVES-20150930-04		IV132	Lineage 4
P2	RC13MEA0279-20150930-02	17	IV133	nd
P2	TOBRC0099-20150930-01	18	IV134	Lineage 6
P2	TOBRC0099-20150930-01		IV135	nd
P2	TOBRC0099-20150930-01		IV136	nd
P2	TOBRC0099-20150930-01		IV137	nd
P2	TOBRC0099-20150930-01		IV138	nd

Table 7. Mean genetic distance (below diagonal) and standard error (above diagonal, in blue) between lineages of Amphipoda detected in the NJ analysis as shown in Figure 3.

Lineage	lin 1	lin 2	lin 3	lin 4	lin 5	lin 6	lin 7	lin 8
lin 1		0.009	0.010	0.013	0.013	0.012	0.016	0.017
lin 2	0.067		0.009	0.013	0.011	0.013	0.016	0.018
lin 3	0.086	0.075		0.012	0.012	0.013	0.015	0.016
lin 4	0.099	0.107	0.107		0.011	0.012	0.017	0.017
lin 5	0.137	0.138	0.147	0.143		0.013	0.016	0.017
lin 6	0.145	0.145	0.148	0.149	0.156		0.017	0.017
lin 7	0.286	0.281	0.279	0.289	0.290	0.264		0.012
lin 8	0.304	0.300	0.298	0.321	0.300	0.298	0.151	

Table 8. Mean distance (D) and standard error (s.e.) within lineages of Amphipoda detected in the NJ analysis as shown in Figure 3 and the number (N) of individuals assigned to that lineage. n/c = not calculated, for groups where n=1. Rep=individual selected to represent the lineage in the model-based analysis.

Lineage	D	s.e.	N	rep
lin 1	0.011	0.003	6	IV126
lin 2	0.001	0.001	2	IV92
lin 3	0.001	0.001	3	IV111
lin 4	0.000	0.000	2	IV128
lin 5	0.018	0.003	5	IV108
lin 6	n/c	n/c	1	IV134
lin 7	n/c	n/c	1	IV129
lin 8	0.005	0.002	5	IV100

Table 9 (attached). Genetic distances (below diagonal) and standard error (above diagonal, in blue) between specimens of Amphipoda detected at Robe Valley and the reference lineages as shown in Figure 4.

Table 10. Distribution of the eight Amphipoda lineages detected in the present study.

Lineage	drillholes	deposits
1	Budgie, Camp	Waramboo
2	Budgie, Daisy	Waramboo
3	MB13WARR010	Waramboo
4	Daves	Waramboo
5	MB13WARR001	Waramboo
6	TOBRC009	Highway and Tod bore
7	Daves	Waramboo
8	Budgie, Daves	Waramboo

Table 11. Specimens of Chilopoda used in the present study and the lineage to which they were assigned, based on variation at the COXI gene. nd=no data.

Phase	Tracking number	Cap no.	Helix ID	Lineage
P1	DD14MRR0004T1-01	694	IV139	Lineage 1
P1	DD14MRR0004T1-01	694	IV140	Lineage 1
P1	DD14MRR0005-T1-04	607	IV141	Lineage 1
P2	DD14MEL0001-20151001-T1-01	632	IV142	nd
P2	MEARC4383-20151001-T2-01	217	IV143	Lineage 2

Table 12 (attached). Genetic distances (below diagonal) and standard error (above diagonal, in blue) between specimens of Chilopoda detected at Robe Valley and the reference lineages as shown in Figure 5.

Table 13. Distribution of the two Chilopoda lineages detected in the present study.

Lineage	drillholes	deposits
1	DD14MRR0004, DD14MRR0005	2304A
2	MEARC4383	Highway/Tod bore

Table 14. Specimens of Coleoptera used in the present study and the lineage to which they were assigned, based on variation at the COXI gene.

Phase	Drillhole	Cap no.	Helix ID	Lineage
P1	DD14MRR0004T1-03	696	IV144	Lineage 2
P1	DD14MRR0004T1-03		IV145	Lineage 2

P1	DD14MRR0004T1-03		IV146	Lineage 2
P1	DD14MRR0004T1-03		IV147	Lineage 2
P1	DD14MRR009-20150808-T3-01	562	IV148	Lineage 6
P1	RC14MEB0068-20150807-T1-02	424	IV149	nd
P2	RC14MEB0060-20151001-T2-02	204	IV150	Lineage 4
P1	MEARC3814-20150807-T1-02	379	IV151	Lineage 1
P1	MEARC4400-t1-01	765	IV152	Lineage 5
P1	MEARC4400-t1-01		IV153	Lineage 3

Table 15 (attached). Genetic distances (below diagonal) and standard error (above diagonal, in blue) between specimens of Coleoptera detected at Robe Valley and the reference lineages as shown in Figure 6.

Table 16. Distribution of the six Coleoptera lineages detected in the present study.

Lineage	drillholes	deposits
1	MEARC3814	Highway/Tod bore
2	DD14MRR0004	2403A
3	MEARC4400	Highway/Tod bore
4	RC14MEB0060	Mesa B
5	MEARC4400	Highway/Tod bore
6	DD14MRR0009	2402D

Table 17. Specimens of Polydesmida (Diplopoda) used in the present study and the lineage to which they were assigned, based on variation at the COXI gene. nd=no data.

Phase	Tracking number	Cap no.	Helix ID	Lineage
P1	MEARC2401-20150807-T2-02	400	IV190	nd
P1	MEARC3500T2-02	691	IV191	nd
P1	RC13MEA0279-20150807-T1-01	382	IV192	nd
P1	RC13MEA0279-20150807-T1-01	382	IV193	nd
P1	RC13MEA0279-20150807-T1-01	382	IV194	nd
P2	DD14MEB0005-20151001-T2-02	81	IV195	nd
P2	DD14MEB0005-20151001-T3-01	84	IV196	nd
P2	DD14MEB0005-20151001-T3-01	84	IV197	nd
P2	DD14MEB0005-20151001-T3-01	84	IV198	nd
P2	MEARC3500-20150930-T1-02	267	IV199	nd
P2	MEARC3500-20150930-T1-02	267	IV200	nd

Table 18. Specimens of Diplura used in the present study and the lineage to which they were assigned, based on variation at the COXI gene. nd=no data.

Phase	Tracking number	Cap no.	Helix ID	Lineage
P1	DD11MEB001T1-01	679	IV154	Lineage 1
P1	DD11MEB001T1-01		IV155	Lineage 2
P1	DD11MEC0005-02	7	IV156	Lineage 4
P2	DD14MEB0005-20151001-T3-02	85	IV157	Lineage 3
P2	MEARC5017-20151001-T2-01	65	IV158	nd
P2	RC14MEB0101-20151001-T2-01	93	IV159	Lineage 3
P1	MEARC3790-20150807-T2-03	414	IV160	nd

Table 19 (attached). Genetic distances (below diagonal) and standard error (above diagonal, in blue) between specimens of Diplura detected at Robe Valley and the reference lineages as shown in Figure 7.

Table 20. Distribution of the four Diplura lineages detected in the present study.

Lineage	drillholes	deposits
1	DD11MEB001	Mesa B
2	DD11MEB001	Mesa B
3	DD14MEB0005, RC14MEB0101	Mesa B
4	DD11MEC0005	Mesa C

Table 21. Specimens of Isopoda used in the present study and the lineage to which they were assigned, based on variation at the COXI gene. nd=no data.

Phase	Tracking number	Cap no.	Helix ID	Lineage
P1	M2ERC027-t2-02	762	IV163	Lineage 1
P1	M2ERC029-t2-01	769	IV164	nd
P1	M2ERC053-T2-01	776	IV165	Lineage 1
P1	M2ERC053-T2-01		IV166	nd
P1	M2ERC053-T2-01		IV167	Lineage 1
P1	M2ERC053-T2-01		IV168	nd
P1	RC13MRR0026-t2-02	781	IV169	nd
P2	M2ERC0057-20151002-T2-03	409	IV170	nd
P2	MEARC4923-20150930-T1-01	343	IV171	Lineage 9a
P2	MELUNK02-20151001-T1-03	626	IV172	Lineage 3
P2	MELUNK02-20151001-T2-02	629	IV173	Lineage 3
P2	MELUNK02-20151001-T2-02		IV174	Lineage 3
P2	RC13MRR0014-20151002-T1-01	548	IV175	Lineage 2
P2	RC14MEB0060-20151001-T2-03	205	IV176	Lineage 5
P2	RC14MEB0088-20151001-T3-01	576	IV177	Lineage 8
P2	RC14MEB0101-20151001-T1-01	89	IV178	Lineage 4
P2	TOBRC0020-20151001-T2-02	13	IV179	Lineage 7
P2	TOBRC0020-20151001-T2-02		IV180	nd
P1	MEARC2401-20150807-T2-03	401	IV181	Lineage 9b
P1	MEARC3811-20150807-T1-04	392	IV182	nd
P1	MEARC4795-20150807-T1-03	269	IV183	nd
P1	MEARC4795-20150807-T2-02	273	IV184	nd
P1	MEARC4795-20150807-T2-02		IV185	nd
P1	MEARC4795-20150807-T2-02		IV186	nd
P1	MEARC4795-20150807-T2-02		IV187	nd
P1	MEARC5053T3-03	541	IV188	Lineage 9b
P1	TOBRC0020-t1-01	784	IV189	Lineage 6

Table 22. Mean genetic distance (below diagonal) and standard error (above diagonal, in blue) between lineages of Isopoda detected in the NJ analysis as shown in Figure 8.

Lineage	1	2	3	4	5	6	7	8	9a	9b
1		0.011	0.016	0.017	0.016	0.016	0.016	0.016	0.016	0.014
2	0.070		0.016	0.015	0.018	0.016	0.017	0.015	0.016	0.014
3	0.201	0.191		0.017	0.017	0.016	0.015	0.015	0.015	0.015
4	0.189	0.191	0.194		0.017	0.016	0.015	0.017	0.015	0.015
5	0.244	0.242	0.259	0.224		0.010	0.010	0.016	0.017	0.017
6	0.239	0.236	0.242	0.235	0.076		0.009	0.016	0.016	0.015
7	0.238	0.232	0.238	0.227	0.082	0.067		0.016	0.017	0.016
8	0.228	0.220	0.226	0.238	0.218	0.211	0.207		0.014	0.014
9a	0.227	0.224	0.238	0.201	0.231	0.216	0.201	0.166		0.006
9b	0.231	0.225	0.230	0.204	0.223	0.207	0.204	0.167	0.037	

Table 23. Mean distance (D) and standard error (s.e.) within lineages of Isopoda detected in the NJ analysis as shown in Figure 8 and the number (N) of individuals assigned to that lineage. n/c = not calculated, for groups where n=1. Rep=individual selected to represent the lineage in the model-based analysis.

Lineage	D	s.e.	N	Rep
1	0.002	0.001	3	IV167
2	n/c	n/c	1	IV175
3	0.001	0.001	3	IV172
4	n/c	n/c	1	IV178
5	n/c	n/c	1	IV176
6	n/c	n/c	1	IV189
7	n/c	n/c	1	IV179
8	n/c	n/c	1	IV177
9a	n/c	n/c	1	IV171
9b	0.025	0.006	2	IV181

Table 24 (attached). Genetic distances (below diagonal) and standard error (above diagonal, in blue) between specimens of Isopoda detected at Robe Valley and the reference lineages as shown in Figure 9.

Table 25. Distribution of the ten Isopoda lineages detected in the present study.

Lineage	drillholes	deposits
1	M2ERC027	2402E
2	RC13MRR0014	2403A,B,D
3	MELUNK02	Mesa L
4	RC14MEB0101	Mesa B
5	RC14MEB0060	Mesa B
6	TOBRC0020	Highway/Tod bore
7	TOBRC0020	Highway/Tod bore
8	RC14MEB0088	Mesa B
9a	MEARC4923	Highway/Tod bore
9b	MEARC2401, MEARC5053	Highway/Tod bore

Table 26. Specimens of Pseudoscorpiones used in the present study and the lineage to which they were assigned, based on variation at the COXI gene. nd=no data.

Phase	Tracking number	Cap. No.	Helix ID	Lineage
P1	DD14MEB0002-20150607-01sc	5	IV201	Hyiidae 1
P1	DD14MRR0004T1-04	697	IV202	Hyiidae 5
P1	DD14MRR0004T1-04		IV203	Chthoniidae 11
P1	DD14MRR0005-T1-05	608	IV204	Chthoniidae 11
P1	DD14MRR0005-T2-01	773	IV205	Atemnidae? 13
P1	DD14MRR0008-20150808-T1-02	484	IV206	Hyiidae 3
P1	DD14MRR0008-20150808-T2-03	491	IV207	Atemnidae? 15
P1	M2ERC027-t2-03	763	IV208	Atemnidae? 14
P1	M2ERC027-t2-03		IV209	Hyiidae 4
P1	MEARC3814-20150606-02sc	2	IV210	Chthoniidae 12
P1	RC13MEA0279-20150807-T1-02	383	IV211	Hyiidae 6
P2	DD14MEL0001-20151001-T2-02	637	IV212	Chthoniidae 9
P2	DD14MRR0009-20151002-T2-02	433	IV213	Hyiidae 7
P2	DD14MRR0009-20151002-T3-01	437	IV214	Atemnidae? 15
P2	MEARC3814-20150930-T1-01	279	IV215	Chthoniidae 12
P2	RC14MEB0010-20151001-T3-01	122	IV216	nd
P2	RC14MEB0029-20151001-T1-01	132	IV217	Hyiidae 2
P2	RC14MEB0060-20151001-T3-02	209	IV218	Hyiidae 8
P2	RC14MEB0101-20151001-T1-02	90	IV219	nd
P2	RC14MEB0115-20151001-T1-01	101	IV220	nd
P2	RC14MEB0115-20151001-T1-01		IV221	nd
P2	RC14MEB0123-20151001-T2-01	310	IV222	nd
P2	RC14MEB0123-20151001-T2-01		IV223	nd
P2	RC14MEB0123-20151001-T3-01	313	IV224	nd
P2	RC14MEB0123-20151001-T3-01		IV225	nd
P2	RC14MRR0020-20151002-T2-01	369	IV226	Chthoniidae 10

Table 27. Mean genetic distance (below diagonal) and standard error (above diagonal, in blue) between lineages of Pseudoscorpiones detected in the NJ analysis as shown in Figure 10. Distances between lineages within each family are highlighted in yellow.

Lineage	Hysiidae								Chthoniidae				Atemnidae		
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
1		0.008	0.015	0.015	0.017	0.016	0.016	0.016	0.018	0.018	0.016	0.018	0.016	0.015	0.014
2	0.051		0.016	0.016	0.017	0.016	0.015	0.016	0.019	0.020	0.016	0.017	0.017	0.015	0.015
3	0.221	0.227		0.007	0.016	0.015	0.017	0.016	0.017	0.017	0.017	0.016	0.017	0.016	0.017
4	0.211	0.218	0.038		0.017	0.015	0.017	0.016	0.017	0.017	0.017	0.016	0.017	0.016	0.017
5	0.265	0.262	0.265	0.262		0.015	0.016	0.016	0.016	0.015	0.017	0.016	0.015	0.014	0.015
6	0.232	0.227	0.251	0.245	0.240		0.012	0.013	0.016	0.017	0.016	0.015	0.015	0.013	0.014
7	0.254	0.254	0.264	0.249	0.240	0.133		0.012	0.015	0.016	0.015	0.014	0.015	0.016	0.015
8	0.251	0.245	0.272	0.258	0.244	0.150	0.133		0.015	0.016	0.015	0.015	0.014	0.013	0.013
9	0.275	0.274	0.284	0.287	0.268	0.255	0.257	0.263		0.012	0.015	0.016	0.016	0.016	0.016
10	0.265	0.265	0.283	0.286	0.266	0.258	0.252	0.257	0.105		0.015	0.016	0.019	0.017	0.017
11	0.264	0.274	0.277	0.272	0.274	0.277	0.254	0.267	0.194	0.204		0.014	0.016	0.014	0.015
12	0.274	0.278	0.257	0.251	0.283	0.265	0.247	0.266	0.210	0.226	0.165		0.016	0.014	0.014
13	0.290	0.295	0.293	0.283	0.280	0.284	0.288	0.285	0.288	0.286	0.291	0.286		0.013	0.012
14	0.258	0.267	0.273	0.261	0.274	0.257	0.254	0.251	0.281	0.271	0.264	0.266	0.119		0.009
15	0.273	0.286	0.299	0.282	0.292	0.273	0.263	0.275	0.288	0.294	0.282	0.285	0.146	0.076	

Table 28. Mean distance (D) and standard error (s.e.) within lineages of Pseudoscorpiones detected in the NJ analysis as shown in Figure 10 and the number (N) of individuals assigned to that lineage. n/c = not calculated, for groups where n=1. Rep=individual selected to represent the lineage in the model-based analysis.

Lineage	D	s.e.	N	Ref
1	n/c	n/c	1	IV201
2	n/c	n/c	1	IV217
3	n/c	n/c	1	IV206
4	n/c	n/c	1	IV209
5	n/c	n/c	1	IV202
6	n/c	n/c	1	IV211
7	n/c	n/c	1	IV213
8	n/c	n/c	1	IV219
9	n/c	n/c	1	IV212
10	n/c	n/c	1	IV226
11	0.001	0.001	2	IV203
12	0.001	0.001	2	IV210
13	n/c	n/c	1	IV205
14	n/c	n/c	1	IV208
15	0.012	0.004	2	IV207

Table 29 (attached). Genetic distances (below diagonal) and standard error (above diagonal, in blue) between specimens of Chthoniidae (Pseudoscorpiones) detected at Robe Valley and the reference lineages as shown in Figure 11.

Table 30 (attached). Genetic distances (below diagonal) and standard error (above diagonal, in blue) between specimens of Hyiidae and Atemnidae (Pseudoscorpiones) detected at Robe Valley and the reference lineages as shown in Figure 12.

Table 31. Distribution of the 15 Pseudoscorpiones lineages detected in the present study.

Lineage	drillholes	deposits
Hyiidae		
1	DD14MEB0002	Mesa B
2	RC14MEB0029	Mesa B
3	DD14MRR0008	2402D
4	M2ERC027	2402E
5	DD14MRR0004	2403A
6	RC13MEA0279	Highway/Tod bore
7	DD14MRR0009	2402D
8	RC14MEB0101	Mesa B
Chthoniidae		
9	DD14MEL0001	Mesa L
10	RC14MRR020	2401A
11	DD14MRR0004, DD14MRR0005	2403A
12	MEARC3814	Highway/Tod bore
Atemnidae		
13	DD14MRR0005	2403A
14	M2ERC027	2402E
15	DD14MRR0008, DD14MRR0009	2402D

Table 32. Specimens of Thysanura used in the present study and the lineage to which they were assigned, based on variation at the COXI gene. nd=no data.

Phase	Tracking number	Cap. No.	Helix ID	Lineage
P2	MEARC4383-20151001-T1-01	213	IV227	nd
P2	RC14MEB0060-20151001-T3-01	208	IV228	nd
P2	RC14MEB0060-20151001-T3-01		IV229	nd
P1	MEARC3814-20150606-01sc	1	IV230	nd

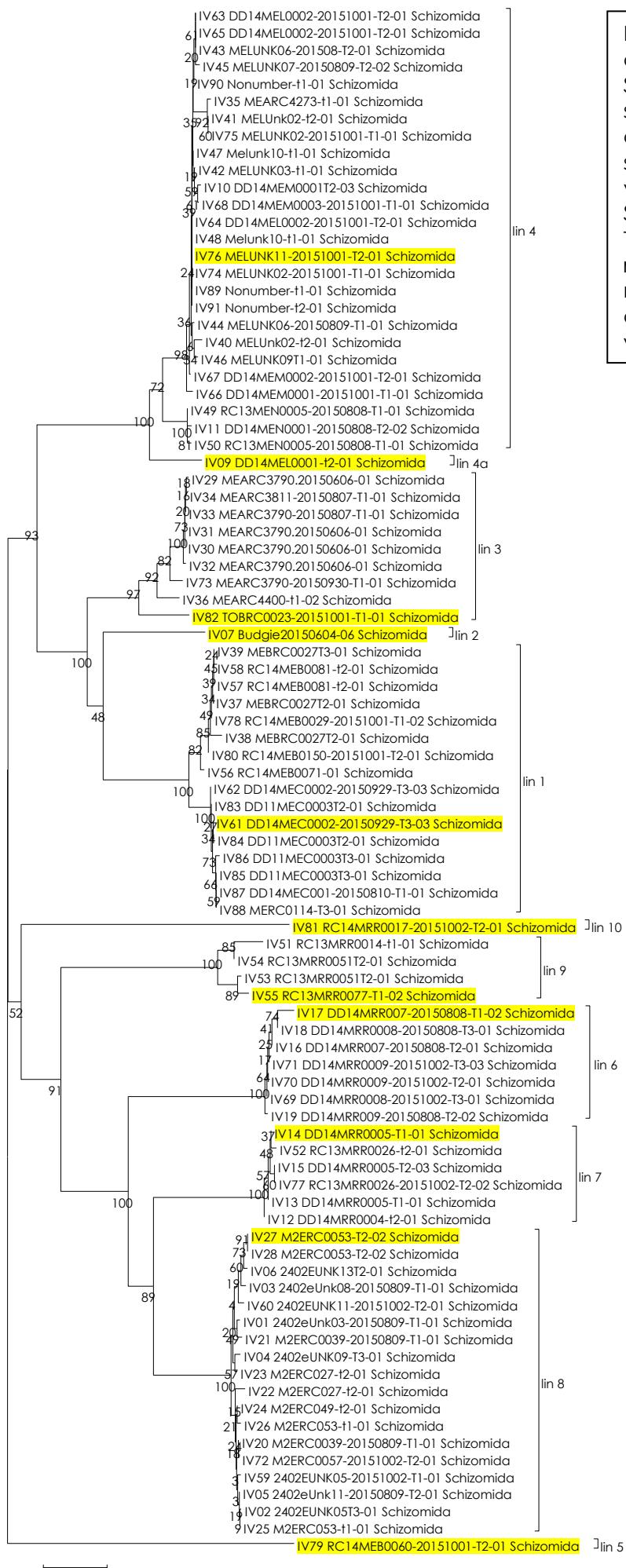


Figure 1. Neighbour-joining analysis of specimens of Schizomida from the present study. Numbers on major nodes correspond to bootstrap support over 100 iterations; values <50% are not shown. Scale bar= genetic distance. The specimens used to represent each lineage in the model-based phylogenetic analysis are highlighted in yellow.

0.02

Figure 2. Bayesian analysis of COXI haplotypes of Schizomida from the present study and reference specimens from previous surveys in the Pilbara. Numbers on major nodes correspond to posterior probabilities; values <50% are not shown. Specimens from the present study are highlighted in yellow; GenBank voucher specimens highlighted in turquoise. Scale bar= number of substitutions per site.

EU272675 Brignolozomus woodwardi SzA

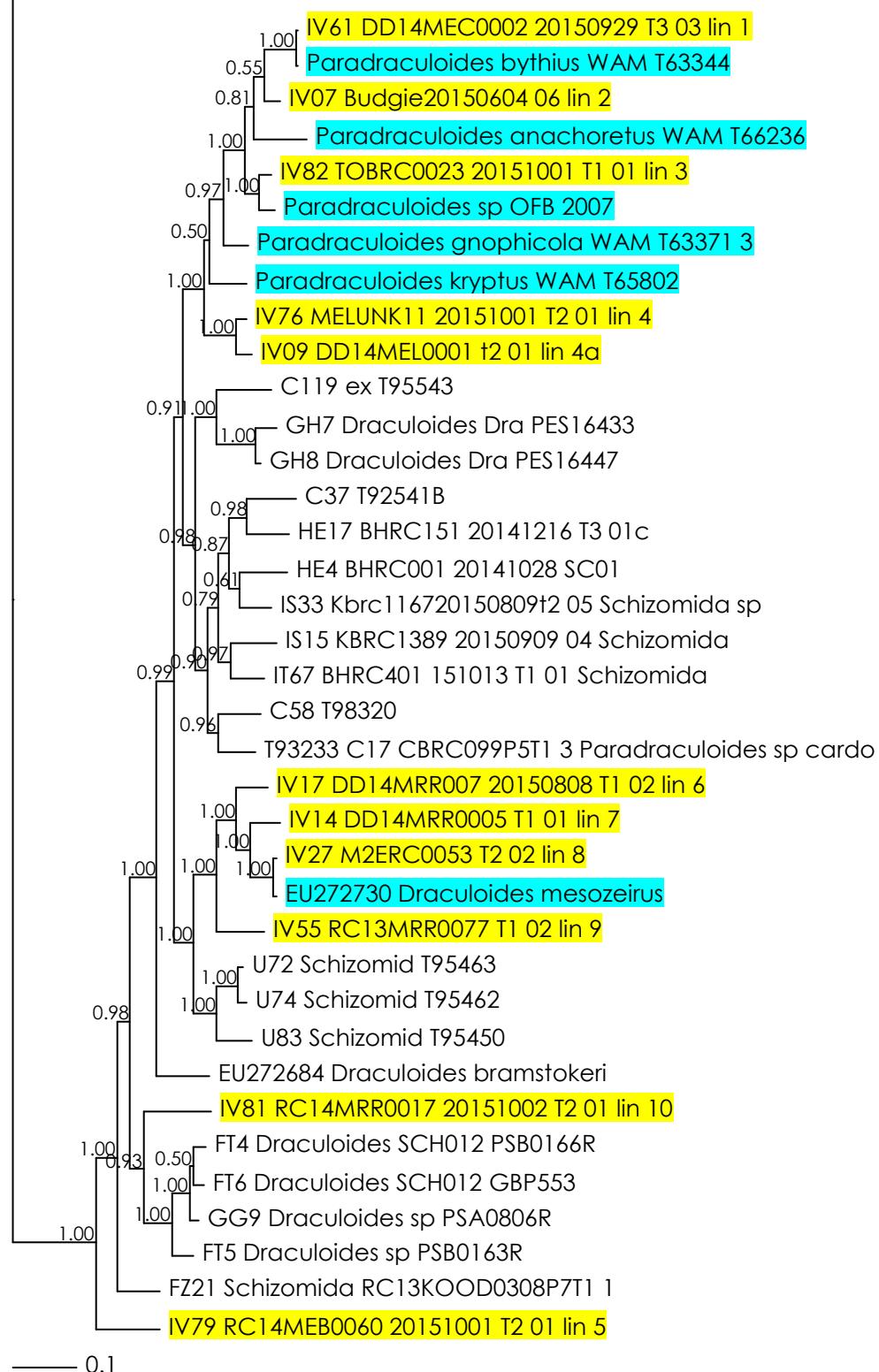


Figure 3. Neighbour-joining analysis of specimens of Amphipoda from the present study. Numbers on major nodes correspond to bootstrap support over 100 iterations; values <50% are not shown. Scale bar= genetic distance. The specimens used to represent each lineage in the model-based phylogenetic analysis are highlighted in yellow.

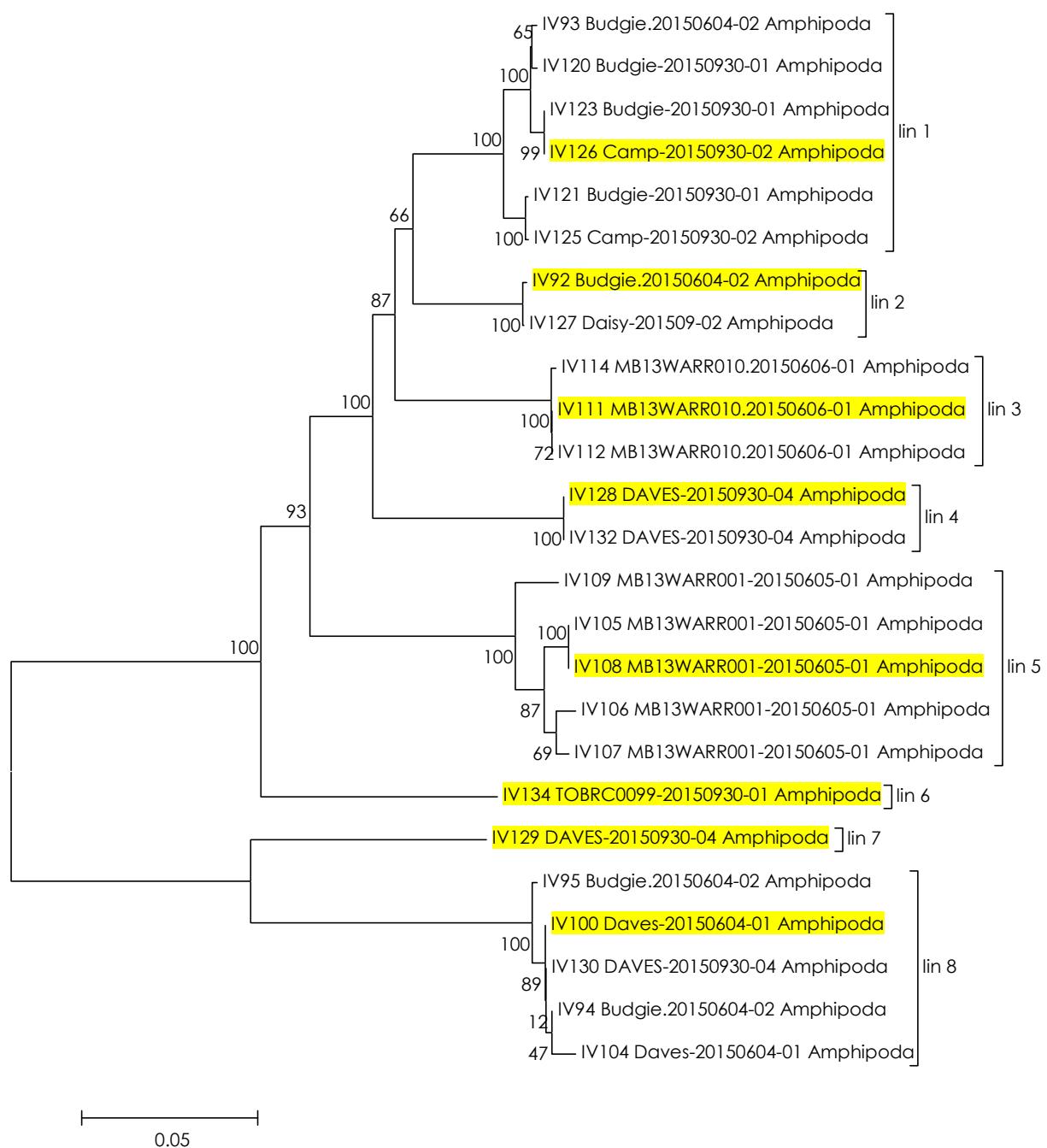


Figure 4. Bayesian analysis of COXI haplotypes of Amphipoda from the present study and reference specimens from previous surveys in the Pilbara. Numbers on major nodes correspond to posterior probabilities; values <50% are not shown. Specimens from the present study are highlighted in yellow; GenBank voucher specimens highlighted in turquoise. Scale bar= number of substitutions per site.

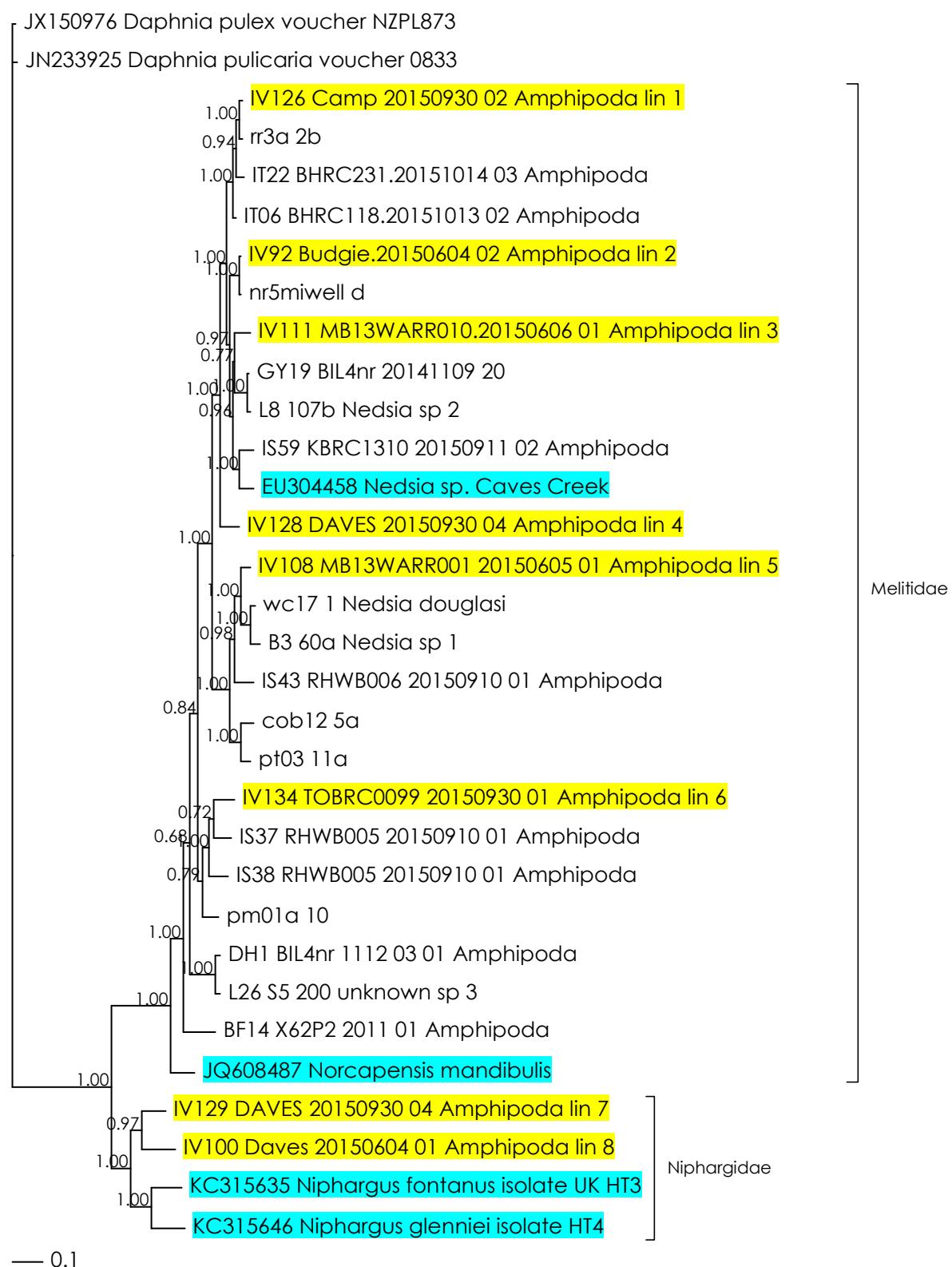


Figure 5. Bayesian analysis of COXI haplotypes of Chilopoda from the present study and reference specimens from previous surveys in the Pilbara. Numbers on major nodes correspond to posterior probabilities; values <50% are not shown. Specimens from the present study are highlighted in yellow; GenBank voucher specimens highlighted in turquoise. Scale bar= number of substitutions per site.

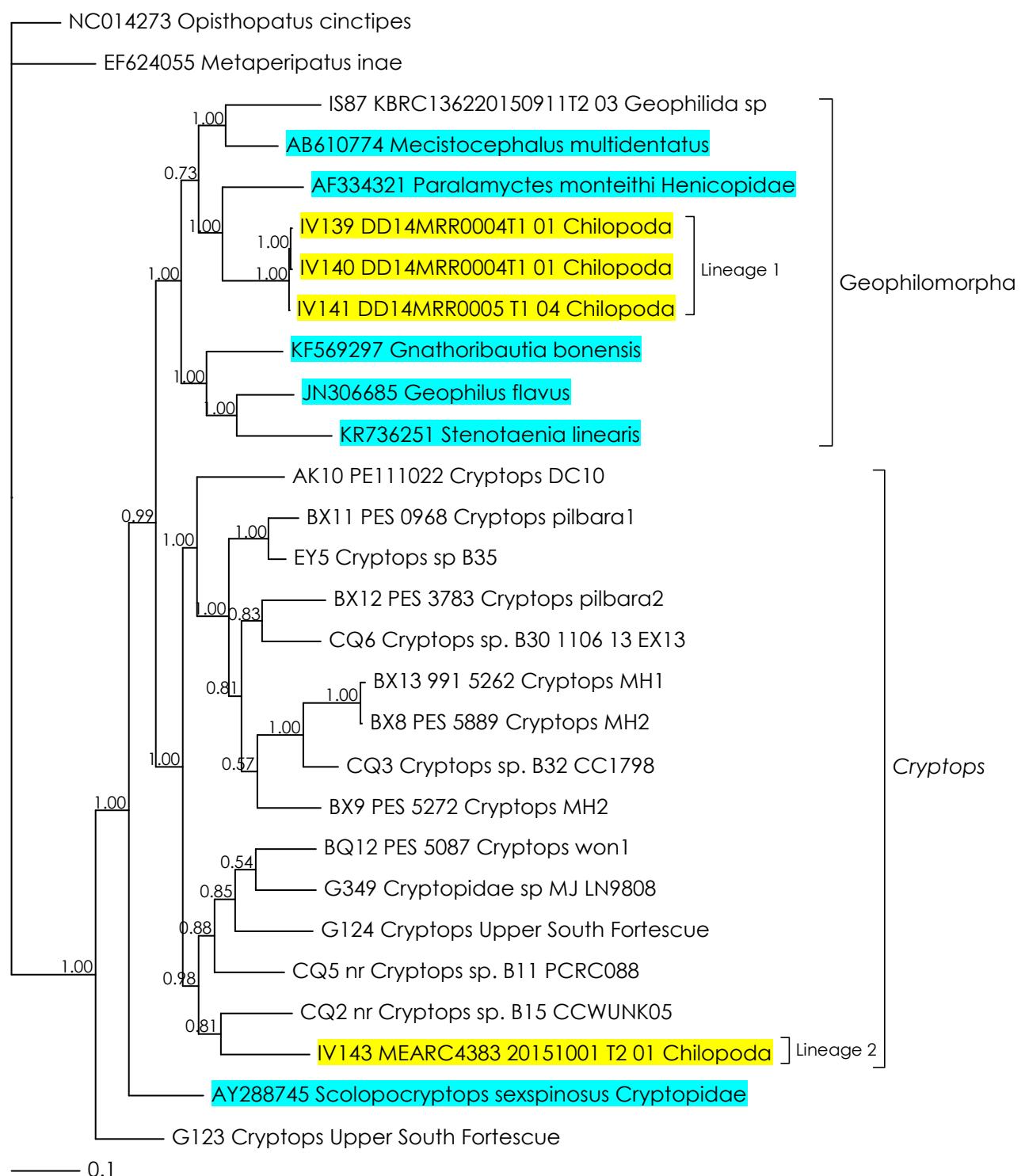


Figure 6. Bayesian analysis of COXI haplotypes of Coleoptera from the present study and reference specimens from previous surveys in the Pilbara. Numbers on major nodes correspond to posterior probabilities; values <50% are not shown. Specimens from the present study are highlighted in yellow; GenBank voucher specimens highlighted in turquoise. Scale bar= number of substitutions per site.

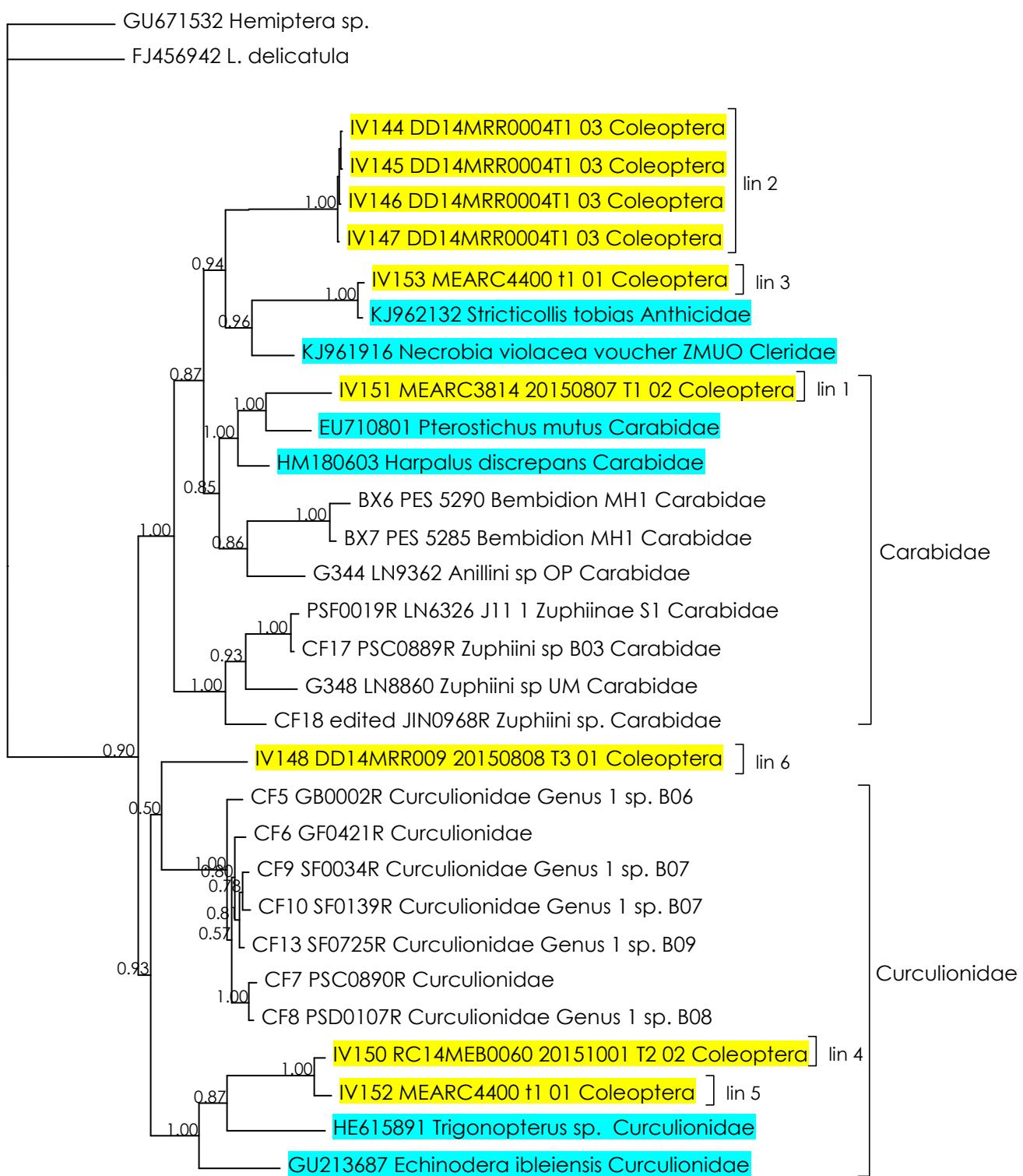


Figure 7. Bayesian analysis of COXI haplotypes of Diplura from the present study and reference specimens from previous surveys in the Pilbara. Numbers on major nodes correspond to posterior probabilities; values <50% are not shown. Specimens from the present study are highlighted in yellow; GenBank voucher specimens highlighted in turquoise. Scale bar= number of substitutions per site.

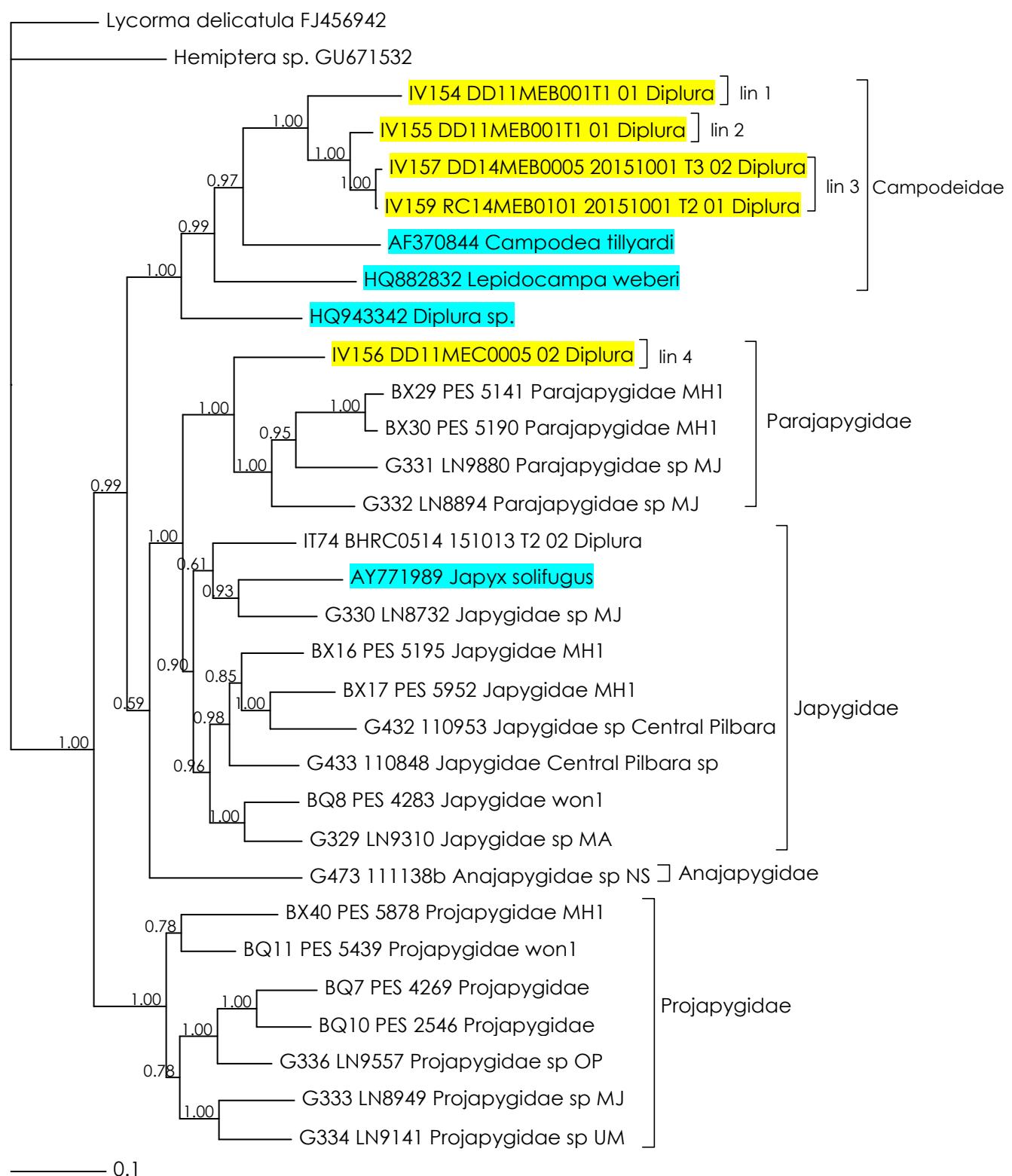


Figure 8. Neighbour-joining analysis of specimens of Isopoda from the present study. Numbers on major nodes correspond to bootstrap support over 100 iterations; values <50% are not shown. Scale bar= genetic distance. The specimens used to represent each lineage in the model-based phylogenetic analysis are highlighted in yellow.

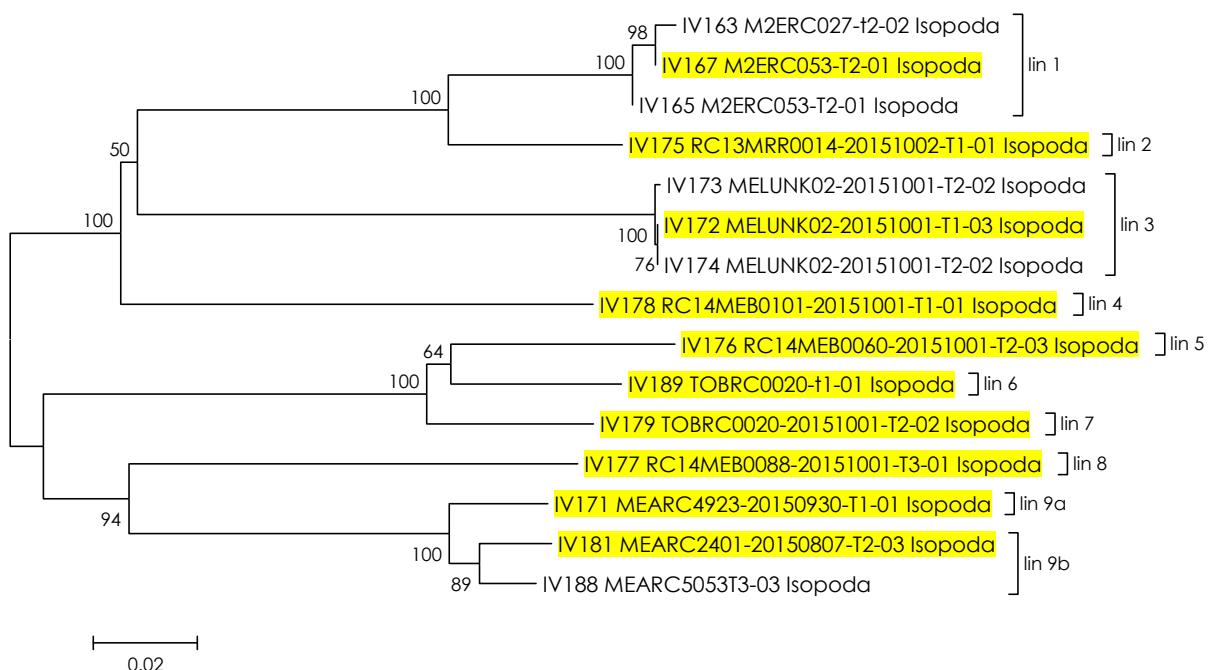


Figure 9. Bayesian analysis of COXI haplotypes of Isopoda from the present study and reference specimens from previous surveys in the Pilbara. Numbers on major nodes correspond to posterior probabilities; values <50% are not shown. Specimens from the present study are highlighted in yellow; GenBank voucher specimens highlighted in turquoise. Scale bar= number of substitutions per site.

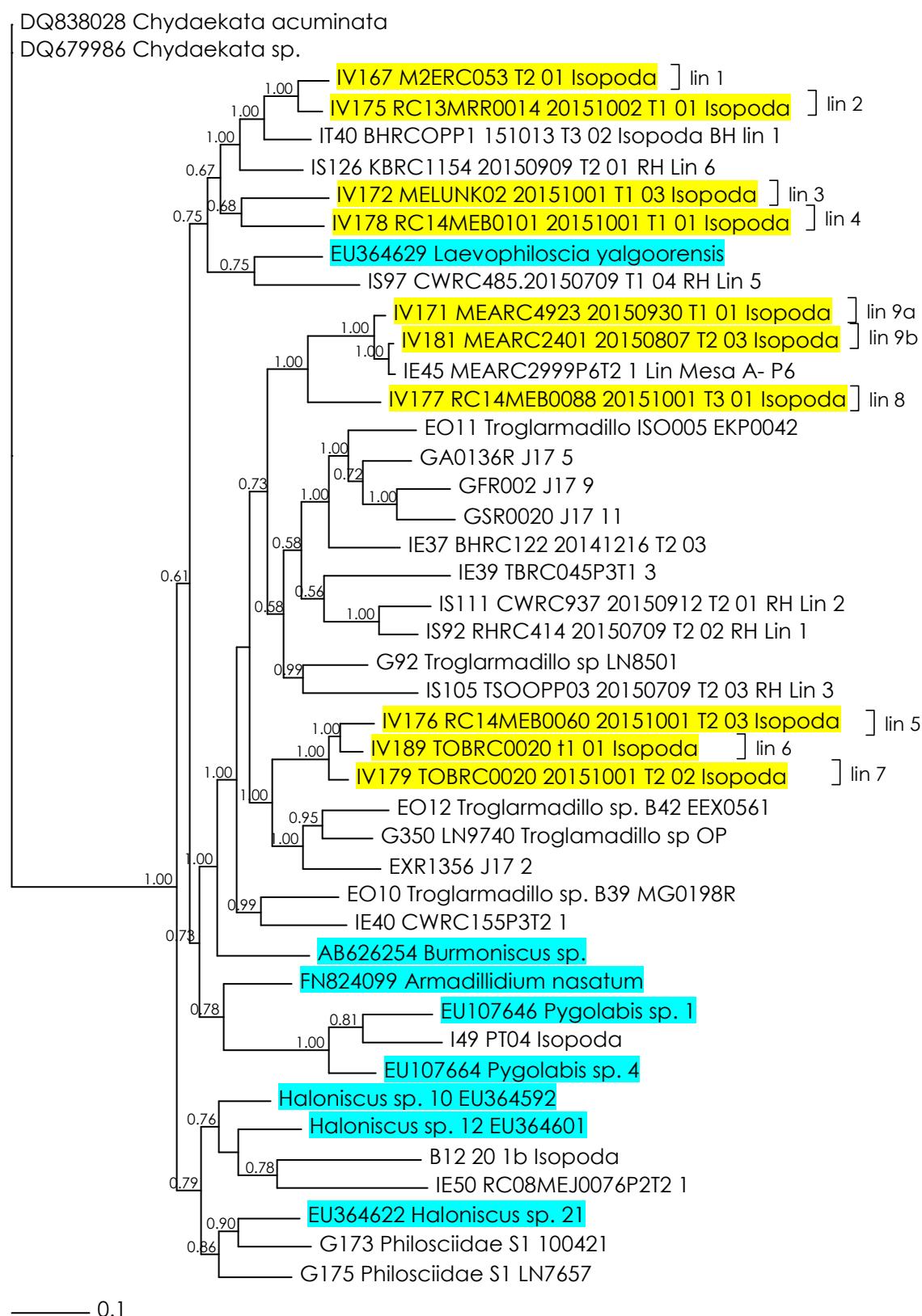


Figure 10. Neighbour-joining analysis of specimens of Pseudoscorpiones from the present study. Numbers on major nodes correspond to bootstrap support over 100 iterations; values <50% are not shown. Scale bar= genetic distance. The specimens used to represent each lineage in the model-based phylogenetic analysis are highlighted in yellow.

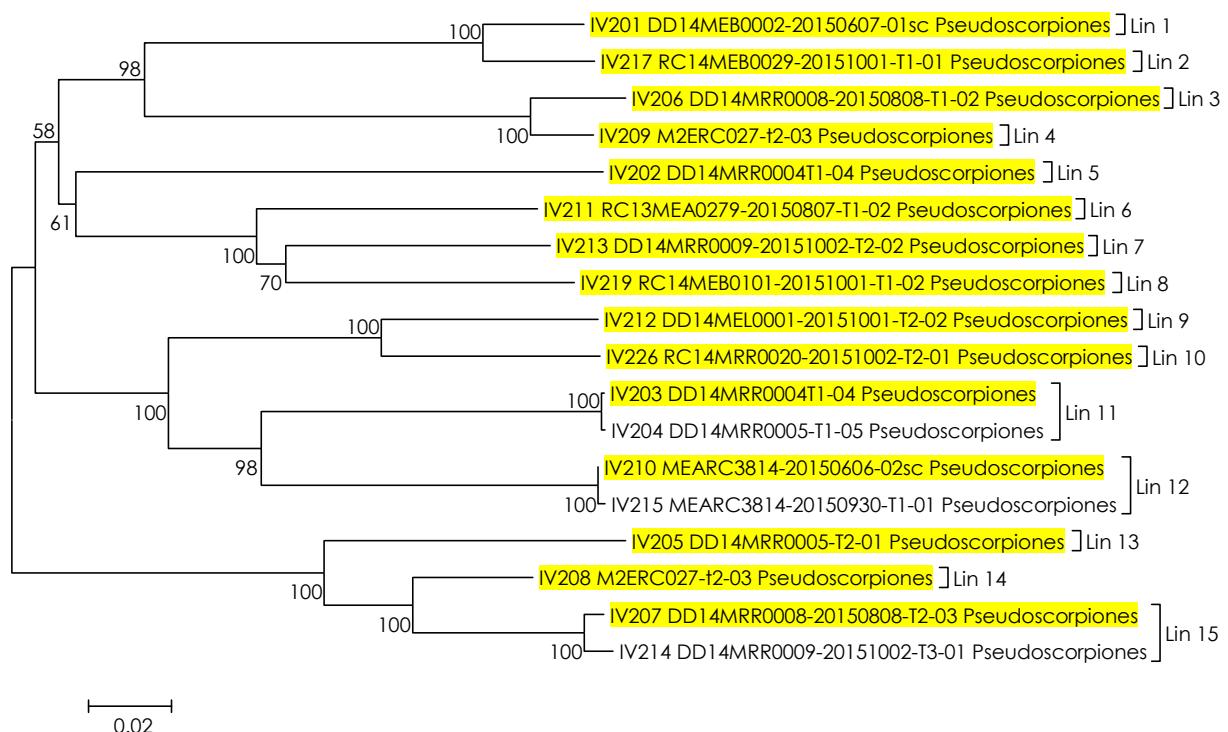


Figure 11. Bayesian analysis of COXI haplotypes of Chthoniidae (Pseudoscorpiones) from the present study and reference specimens from previous surveys in the Pilbara. Numbers on major nodes correspond to posterior probabilities; values <50% are not shown. Specimens from the present study are highlighted in yellow; GenBank voucher specimens highlighted in turquoise. Scale bar= number of substitutions per site.

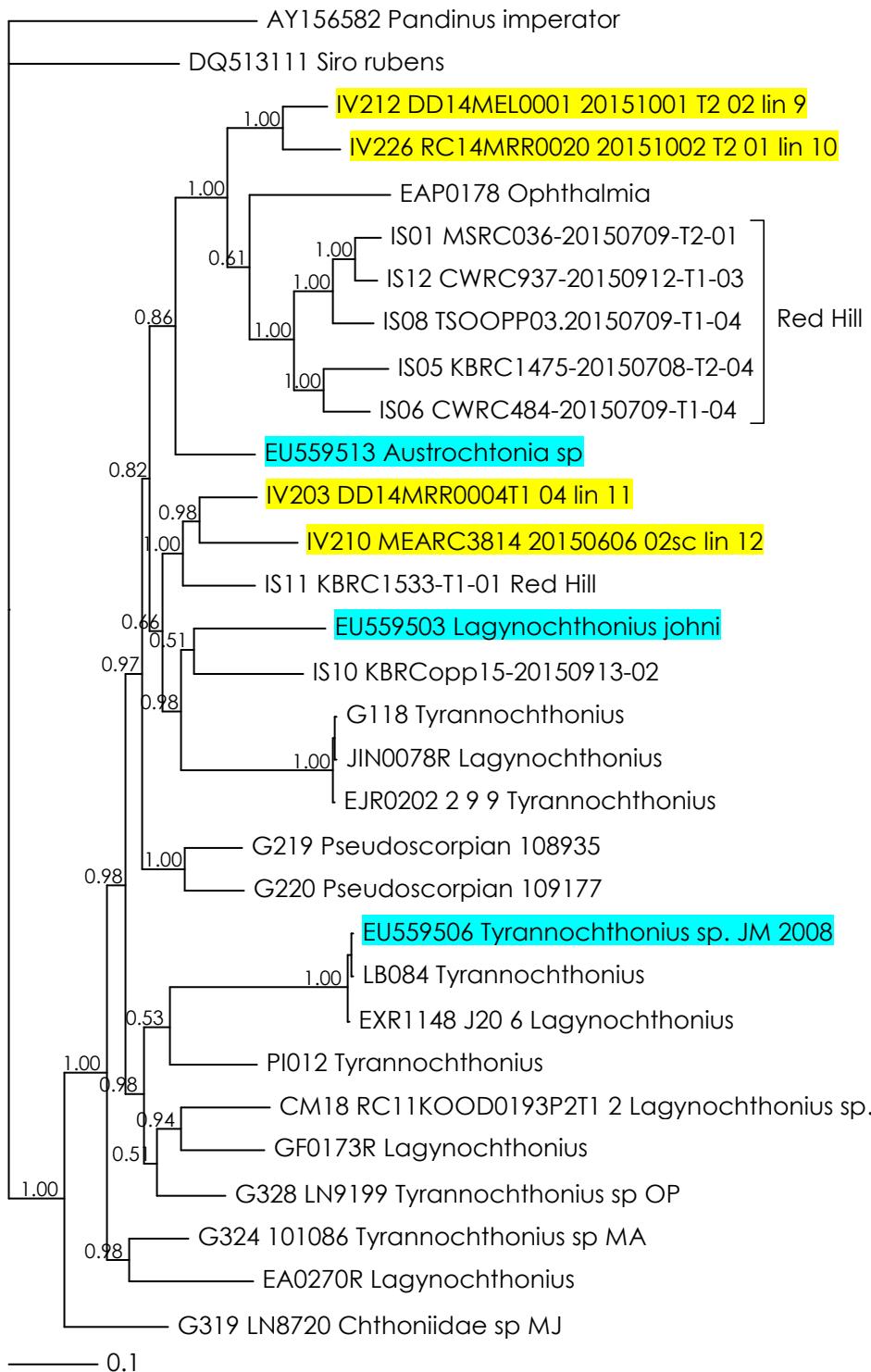


Figure 12. Bayesian analysis of COXI haplotypes of Hyiidae (Pseudoscorpiones) from the present study and reference specimens from previous surveys in the Pilbara. Numbers on major nodes correspond to posterior probabilities; values <50% are not shown. Specimens from the present study are highlighted in yellow; GenBank voucher specimens highlighted in turquoise. Scale bar= number of substitutions per site.

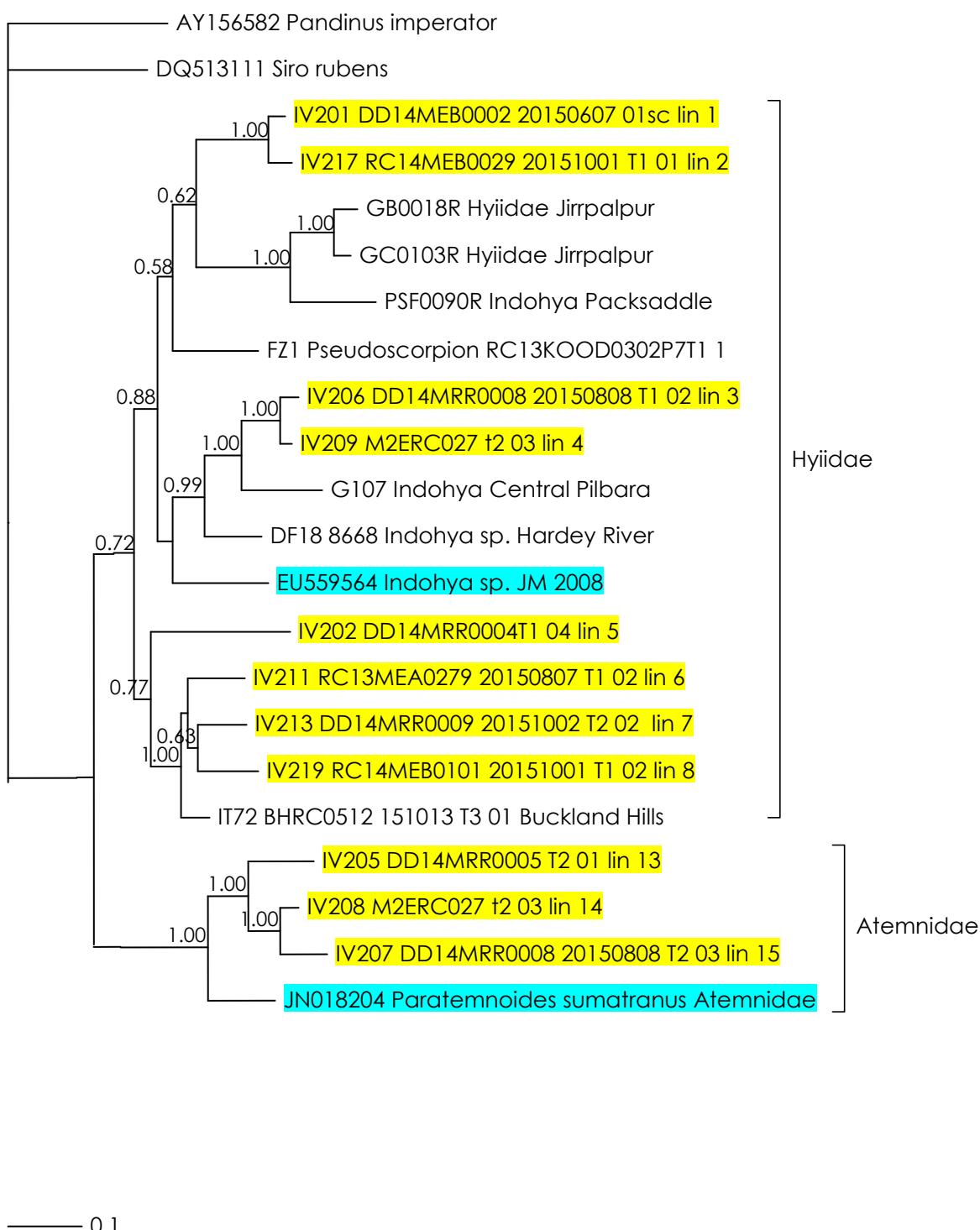


Table 4. Estimates of Evolutionary Divergence between Sequences

Specimen ID	IV55	IV81	IV07	IV09	IV14	IV17	IV27	IV61	IV76	IV79	Dbram	Dmes	Pan	Pbyt	Pgno	Pkry	Psp	C119	C37	C58	FT4	FT5	FT6	FZ21	GG9	GH7	GH8	HE17	HE4	IS15	IS33	IT67	C17	U72_Shizomid_T95463	U74_Shizomid_T95462	U83_Shizomid_T95450
IV55_RC13MRR0077-T1-02_Schizomida		<b>0.015</b>	<b>0.014</b>	<b>0.013</b>	<b>0.012</b>	<b>0.014</b>	<b>0.012</b>	<b>0.016</b>	<b>0.014</b>	<b>0.014</b>	<b>0.013</b>	<b>0.015</b>	<b>0.017</b>	<b>0.013</b>	<b>0.015</b>	<b>0.015</b>	<b>0.016</b>	<b>0.014</b>	<b>0.014</b>	<b>0.015</b>	<b>0.016</b>	<b>0.016</b>	<b>0.014</b>	<b>0.015</b>	<b>0.016</b>	<b>0.014</b>	<b>0.015</b>	<b>0.015</b>	<b>0.015</b>	<b>0.015</b>	<b>0.015</b>					
IV81_RC14MRR0017-20151002-T2-01_Schizomida	0.172		<b>0.014</b>	<b>0.014</b>	<b>0.014</b>	<b>0.016</b>	<b>0.014</b>	<b>0.014</b>	<b>0.014</b>	<b>0.013</b>	<b>0.013</b>	<b>0.014</b>	<b>0.014</b>	<b>0.015</b>	<b>0.015</b>	<b>0.014</b>	<b>0.015</b>	<b>0.014</b>	<b>0.014</b>	<b>0.015</b>	<b>0.016</b>	<b>0.016</b>	<b>0.015</b>	<b>0.015</b>	<b>0.016</b>	<b>0.014</b>	<b>0.013</b>	<b>0.013</b>	<b>0.016</b>	<b>0.014</b>	<b>0.014</b>	<b>0.014</b>				
IV07_Budgie20150604-06_Schizomida	0.152	0.153		<b>0.011</b>	<b>0.016</b>	<b>0.014</b>	<b>0.015</b>	<b>0.011</b>	<b>0.012</b>	<b>0.013</b>	<b>0.014</b>	<b>0.014</b>	<b>0.011</b>	<b>0.011</b>	<b>0.013</b>	<b>0.010</b>	<b>0.014</b>	<b>0.013</b>	<b>0.014</b>	<b>0.014</b>	<b>0.015</b>	<b>0.014</b>	<b>0.014</b>	<b>0.015</b>	<b>0.014</b>	<b>0.014</b>	<b>0.012</b>	<b>0.012</b>	<b>0.012</b>	<b>0.014</b>	<b>0.013</b>	<b>0.013</b>	<b>0.014</b>	<b>0.013</b>		
IV09_DD14MEL0001-t2-01_Schizomida	0.131	0.167	0.108		<b>0.015</b>	<b>0.015</b>	<b>0.014</b>	<b>0.012</b>	<b>0.006</b>	<b>0.014</b>	<b>0.014</b>	<b>0.012</b>	<b>0.013</b>	<b>0.011</b>	<b>0.012</b>	<b>0.010</b>	<b>0.014</b>	<b>0.012</b>	<b>0.013</b>	<b>0.013</b>	<b>0.012</b>	<b>0.013</b>	<b>0.012</b>	<b>0.013</b>	<b>0.012</b>	<b>0.014</b>	<b>0.011</b>	<b>0.013</b>	<b>0.014</b>	<b>0.014</b>	<b>0.013</b>	<b>0.013</b>	<b>0.013</b>			
IV14_DD14MRR0005-T1-01_Schizomida	0.123	0.172	0.166	0.153		<b>0.011</b>	<b>0.009</b>	<b>0.015</b>	<b>0.015</b>	<b>0.014</b>	<b>0.016</b>	<b>0.009</b>	<b>0.015</b>	<b>0.016</b>	<b>0.015</b>	<b>0.016</b>	<b>0.017</b>	<b>0.015</b>	<b>0.013</b>	<b>0.014</b>	<b>0.014</b>	<b>0.016</b>	<b>0.014</b>	<b>0.015</b>	<b>0.016</b>	<b>0.013</b>	<b>0.013</b>	<b>0.014</b>	<b>0.015</b>	<b>0.014</b>	<b>0.014</b>	<b>0.014</b>	<b>0.014</b>			
IV17_DD14MRR007-20150808-T1-02_Schizomida	0.122	0.150	0.156	0.158	0.091		<b>0.011</b>	<b>0.016</b>	<b>0.014</b>	<b>0.013</b>	<b>0.014</b>	<b>0.011</b>	<b>0.014</b>	<b>0.016</b>	<b>0.014</b>	<b>0.016</b>	<b>0.016</b>	<b>0.014</b>	<b>0.015</b>	<b>0.012</b>	<b>0.013</b>	<b>0.013</b>	<b>0.014</b>	<b>0.015</b>	<b>0.014</b>	<b>0.013</b>	<b>0.014</b>	<b>0.013</b>	<b>0.013</b>	<b>0.014</b>	<b>0.014</b>	<b>0.014</b>	<b>0.014</b>			
IV27_M2ERC0053-T2-02_Schizomida	0.119	0.161	0.152	0.147	0.072	0.086		<b>0.015</b>	<b>0.013</b>	<b>0.013</b>	<b>0.013</b>	<b>0.004</b>	<b>0.014</b>	<b>0.015</b>	<b>0.014</b>	<b>0.016</b>	<b>0.016</b>	<b>0.014</b>	<b>0.013</b>	<b>0.014</b>	<b>0.013</b>	<b>0.014</b>	<b>0.015</b>	<b>0.014</b>	<b>0.014</b>	<b>0.014</b>	<b>0.012</b>	<b>0.013</b>	<b>0.015</b>	<b>0.013</b>	<b>0.012</b>	<b>0.012</b>	<b>0.013</b>	<b>0.013</b>		
IV61_DD14MEC0002-20150929-T3-03_Schizomida	0.163	0.156	0.069	0.117	0.172	0.166	0.167		<b>0.012</b>	<b>0.015</b>	<b>0.015</b>	<b>0.013</b>	<b>0.002</b>	<b>0.013</b>	<b>0.011</b>	<b>0.014</b>	<b>0.011</b>	<b>0.013</b>	<b>0.015</b>	<b>0.014</b>	<b>0.014</b>	<b>0.013</b>	<b>0.013</b>	<b>0.012</b>	<b>0.012</b>	<b>0.013</b>	<b>0.015</b>	<b>0.014</b>	<b>0.012</b>	<b>0.012</b>	<b>0.013</b>	<b>0.015</b>	<b>0.014</b>	<b>0.012</b>		
IV76_MELUNK11-20151001-T2-01_Schizomida	0.128	0.160	0.111	0.034	0.146	0.152	0.139	0.102		<b>0.013</b>	<b>0.014</b>	<b>0.013</b>	<b>0.012</b>	<b>0.011</b>	<b>0.011</b>	<b>0.014</b>	<b>0.012</b>	<b>0.013</b>	<b>0.013</b>	<b>0.012</b>	<b>0.013</b>	<b>0.013</b>	<b>0.012</b>	<b>0.013</b>	<b>0.013</b>	<b>0.011</b>	<b>0.013</b>	<b>0.010</b>	<b>0.014</b>	<b>0.014</b>	<b>0.013</b>	<b>0.012</b>				
IV79_RC14MEB0060-20151001-T2-01_Schizomida	0.183	0.181	0.156	0.166	0.178	0.172	0.159	0.161	0.160		<b>0.015</b>	<b>0.014</b>	<b>0.015</b>	<b>0.016</b>	<b>0.015</b>	<b>0.015</b>	<b>0.014</b>	<b>0.015</b>	<b>0.016</b>	<b>0.014</b>	<b>0.014</b>	<b>0.012</b>	<b>0.014</b>	<b>0.015</b>	<b>0.013</b>	<b>0.013</b>	<b>0.014</b>	<b>0.014</b>	<b>0.014</b>	<b>0.013</b>	<b>0.013</b>	<b>0.014</b>	<b>0.013</b>			
EU272684_Draculoides_bramstokeri	0.152	0.165	0.148	0.135	0.148	0.146	0.144	0.152	0.132	0.155		<b>0.013</b>	<b>0.014</b>	<b>0.015</b>	<b>0.013</b>	<b>0.014</b>	<b>0.012</b>	<b>0.015</b>	<b>0.014</b>	<b>0.012</b>	<b>0.013</b>	<b>0.012</b>	<b>0.013</b>	<b>0.014</b>	<b>0.013</b>	<b>0.014</b>	<b>0.012</b>	<b>0.013</b>	<b>0.012</b>	<b>0.013</b>	<b>0.012</b>	<b>0.013</b>	<b>0.012</b>			
EU272730_Draculoides_mesozeirus_SzJ	0.120	0.162	0.149	0.141	0.073	0.089	0.006	0.165	0.136	0.157	0.141		<b>0.014</b>	<b>0.015</b>	<b>0.013</b>	<b>0.016</b>	<b>0.015</b>	<b>0.014</b>	<b>0.015</b>	<b>0.013</b>	<b>0.014</b>	<b>0.013</b>	<b>0.015</b>	<b>0.014</b>	<b>0.015</b>	<b>0.015</b>	<b>0.013</b>	<b>0.013</b>	<b>0.015</b>	<b>0.015</b>	<b>0.013</b>	<b>0.013</b>	<b>0.011</b>			
Panachoretus_WAM_T66236_Padraculoides	0.166	0.160	0.085	0.121	0.165	0.155	0.152	0.113	0.124	0.169	0.147	0.151		<b>0.013</b>	<b>0.012</b>	<b>0.013</b>	<b>0.015</b>	<b>0.015</b>	<b>0.012</b>	<b>0.014</b>	<b>0.015</b>	<b>0.015</b>	<b>0.017</b>	<b>0.015</b>	<b>0.016</b>	<b>0.015</b>	<b>0.016</b>	<b>0.015</b>	<b>0.016</b>	<b>0.012</b>	<b>0.014</b>	<b>0.014</b>	<b>0.012</b>	<b>0.013</b>	<b>0.012</b>	
Pbythius_WAM_T63344_Padraculoides_byth	0.166	0.161	0.069	0.119	0.171	0.169	0.168	0.002	0.103	0.165	0.156	0.164	0.111		<b>0.013</b>	<b>0.013</b>	<b>0.011</b>	<b>0.014</b>	<b>0.012</b>	<b>0.014</b>	<b>0.016</b>	<b>0.015</b>	<b>0.014</b>	<b>0.014</b>	<b>0.014</b>	<b>0.013</b>	<b>0.012</b>	<b>0.012</b>	<b>0.014</b>	<b>0.014</b>	<b>0.013</b>	<b>0.013</b>	<b>0.013</b>			
Pgnophicola_WAM_T63371_3_Padraculoides	0.131	0.150	0.087	0.095	0.161	0.135	0.148	0.100	0.090	0.174	0.137	0.144	0.121	0.102		<b>0.012</b>	<b>0.009</b>	<b>0.014</b>	<b>0.011</b>	<b>0.013</b>	<b>0.015</b>	<b>0.013</b>	<b>0.016</b>	<b>0.015</b>	<b>0.016</b>	<b>0.013</b>	<b>0.013</b>	<b>0.012</b>	<b>0.013</b>	<b>0.011</b>	<b>0.014</b>	<b>0.013</b>	<b>0.013</b>	<b>0.014</b>	<b>0.014</b>	
Pkryptus_WAM_T65802_Padraculoid																																				

**Table 9. Estimates of Evolutionary Divergence between Sequences**

Lineage	IV126	IV92	IV111	IV128	IV108	IV134	IV129	IV100	Nfon	Ngle	IT06	IT22	IS37	IS38	IS43	IS59	GY19	DH1	L8 107b	Nman	Ndou	B3 60a	L26	BF14	sge1m4 2	pm01a	cob12	pt03	rr3a	nr5miwell
IV126 Camp-20150930-02 lin 1		0.011	0.011	0.013	0.013	0.014	0.018	0.019	0.020	0.021	0.008	0.010	0.014	0.013	0.014	0.012	0.011	0.016	0.013	0.016	0.017	0.015	0.017	0.013	0.016	0.016	0.008	0.014		
IV92 Budgie-20150604-02 lin 2	0.074		0.010	0.014	0.013	0.014	0.017	0.019	0.020	0.020	0.010	0.013	0.014	0.014	0.013	0.009	0.011	0.016	0.013	0.015	0.017	0.014	0.017	0.014	0.014	0.015	0.014	0.016	0.012	0.002
IV111 MB13WARR01.20150606-01 lin 3	0.088	0.077		0.012	0.014	0.014	0.017	0.018	0.019	0.020	0.012	0.013	0.015	0.014	0.014	0.011	0.010	0.016	0.012	0.015	0.015	0.014	0.017	0.015	0.015	0.017	0.013	0.013		
IV128 DAVES-20150930-04 lin 4	0.101	0.110	0.109		0.014	0.015	0.019	0.020	0.020	0.021	0.011	0.015	0.014	0.015	0.014	0.012	0.013	0.016	0.015	0.017	0.017	0.016	0.018	0.016	0.013	0.016	0.017	0.017	0.014	0.016
IV108 MB13WARR001-20150605-01 lin 5	0.139	0.137	0.147	0.142		0.015	0.018	0.019	0.021	0.021	0.013	0.017	0.013	0.015	0.012	0.014	0.016	0.017	0.016	0.014	0.011	0.011	0.018	0.013	0.016	0.017	0.014	0.013	0.015	0.015
IV134 TOBRC0099-20150930-01 lin 6	0.148	0.147	0.151	0.150	0.158		0.016	0.017	0.018	0.020	0.014	0.015	0.012	0.013	0.016	0.015	0.015	0.017	0.016	0.017	0.017	0.017	0.017	0.015	0.016	0.014	0.015	0.017	0.016	0.016
IV129 DAVES-20150930-04 lin 7	0.302	0.292	0.291	0.303	0.295	0.273		0.013	0.015	0.015	0.018	0.022	0.015	0.016	0.017	0.018	0.018	0.018	0.018	0.021	0.022	0.019	0.019	0.017	0.022	0.020	0.021	0.021	0.020	0.020
IV100 Daves-20150604-01 lin 8	0.322	0.314	0.312	0.341	0.308	0.309	0.155		0.015	0.017	0.020	0.024	0.017	0.018	0.019	0.019	0.019	0.018	0.020	0.020	0.022	0.019	0.018	0.021	0.020	0.021	0.022	0.021	0.022	
KC315635 Niphargus fontanus	0.319	0.314	0.309	0.326	0.322	0.308	0.190	0.205		0.014	0.019	0.026	0.019	0.018	0.020	0.019	0.019	0.021	0.020	0.024	0.020	0.019	0.018	0.023	0.022	0.023	0.023	0.023		
KC315646 Niphargus glenniei	0.330	0.322	0.315	0.330	0.326	0.328	0.190	0.213	0.167		0.020	0.026	0.020	0.020	0.021	0.022	0.021	0.020	0.019	0.022	0.019	0.020	0.022	0.021	0.023	0.022	0.023			
IT06 BHRC118.20151013-02	0.034	0.060	0.077	0.097	0.135	0.148	0.306	0.330	0.324	0.333		0.010	0.013	0.012	0.013	0.011	0.011	0.016	0.013	0.015	0.015	0.013	0.016	0.015	0.015	0.016	0.010	0.012		
IT22 BHRC231.20151014-03	0.047	0.074	0.079	0.108	0.140	0.145	0.322	0.348	0.348	0.338	0.045		0.017	0.018	0.016	0.015	0.014	0.021	0.014	0.018	0.017	0.016	0.021	0.018	0.016	0.017	0.017	0.011	0.014	
IS37 RHWB005 20150910 01	0.155	0.155	0.155	0.153	0.161	0.103	0.273	0.306	0.326	0.326	0.151	0.164		0.014	0.013	0.014	0.014	0.016	0.015	0.018	0.016	0.015	0.017	0.016	0.017	0.013	0.016	0.017	0.016	
IS38 RHWB005 20150910 01	0.166	0.151	0.162	0.166	0.172	0.114	0.269	0.311	0.326	0.326	0.159	0.177	0.110		0.016	0.013	0.014	0.015	0.015	0.017	0.017	0.015	0.015	0.016	0.013	0.018	0.019	0.015	0.015	
IS43 RHWB006 20150910 01	0.144	0.136	0.144	0.147	0.099	0.186	0.297	0.311	0.325	0.331	0.134	0.129	0.158	0.188		0.014	0.014	0.017	0.015	0.017	0.013	0.011	0.020	0.015	0.015	0.018	0.016	0.015	0.015	0.016
IS59 KBRC1310 20150911 02	0.104	0.084	0.093	0.107	0.153	0.175	0.292	0.322	0.326	0.330	0.101	0.103	0.169	0.169	0.148		0.011	0.014	0.013	0.015	0.017	0.015	0.016	0.015	0.012	0.015	0.016	0.017	0.013	0.012
GY19 BIL4nr-20141109-20	0.078	0.077	0.081	0.110	0.145	0.160	0.270	0.305	0.318	0.316	0.072	0.080	0.149	0.145	0.134	0.101		0.015	0.005	0.016	0.017	0.015	0.016	0.015	0.013	0.017	0.017	0.013	0.014	
DH1 BIL4nr-1112-03-01	0.166	0.169	0.167	0.155	0.188	0.151	0.291	0.309	0.317	0.319	0.163	0.179	0.137	0.151	0.196	0.175	0.155		0.017	0.016	0.018	0.017	0.007	0.016	0.018	0.017	0.018	0.019		
L8 107b Nedisia sp 2	0.082	0.086	0.086	0.124	0.143	0.163	0.283	0.323	0.324	0.317	0.077	0.076	0.151	0.152	0.138	0.111	0.016	0.170		0.016	0.017	0.015	0.017	0.016	0.014	0.017	0.017	0.013	0.015	
Norcapensis mandibulitis	0.168	0.159	0.152	0.176	0.182	0.168	0.294	0.292	0.315	0.294	0.165	0.168	0.171	0.168	0.197	0.173	0.165	0.170	0.163		0.016	0.016	0.017	0.016	0.018	0.018	0.017	0.016	0.017	
wc17 1 Nedisia douglasi	0.149	0.149	0.142	0.140	0.068	0.153	0.297	0.310	0.323	0.312	0.136	0.142	0.161	0.178	0.096	0.159	0.144	0.185	0.142	0.166		0.008	0.019	0.015	0.015	0.017	0.014	0.012	0.017	0.017
B3 60a Nedisia sp 1	0.152	0.154	0.151	0.145	0.081	0.156	0.320	0.330	0.337	0.337	0.139	0.152	0.170	0.173	0.114	0.164	0.158	0.197	0.154	0.180	0.038		0.018	0.014	0.015	0.017	0.013	0.012	0.016	0.016
L26 S5-200 unknown sp 3	0.175	0.171	0.175	0.168	0.189	0.152	0.289	0.311	0.315	0.317																				

**Table 12. Estimates of Evolutionary Divergence between Sequences**

Specimen ID	IV139	IV140	IV141	IV143	IS87	Mmult	Gbon	Gflav	Slin	Ssex	Pmon	AK10	BQ12	BX11	BX12	BX13	BX8	BX9	CQ2	CO3	CO5	CQ6	EY5	G123	G349	
IV139_DD14MRR0004T1-01_Chilopoda		0.000	0.002	0.017	0.019	0.018	0.019	0.017	0.019	0.018	0.019	0.021	0.020	0.018	0.020	0.020	0.020	0.019	0.021	0.017	0.019	0.017	0.020	0.019	0.019	0.019
IV140_DD14MRR0004T1-01_Chilopoda	0.000		0.002	0.017	0.019	0.018	0.019	0.017	0.019	0.018	0.019	0.021	0.020	0.018	0.020	0.020	0.020	0.019	0.021	0.017	0.019	0.017	0.020	0.019	0.019	0.019
IV141_DD14MRR0005-T1-04_Chilopoda	0.003	0.003		0.017	0.018	0.018	0.019	0.017	0.019	0.018	0.019	0.021	0.020	0.017	0.020	0.020	0.020	0.018	0.021	0.017	0.018	0.017	0.019	0.019	0.019	0.019
IV143_MEARC4383-20151001-T2-01_Chilopoda	0.229	0.229	0.228		0.017	0.018	0.020	0.018	0.019	0.017	0.018	0.017	0.018	0.017	0.019	0.019	0.017	0.017	0.017	0.017	0.015	0.017	0.018	0.019	0.016	0.018
IS87_KBRC136220150911T2_03_Geophilida_sp	0.227	0.227	0.225	0.219		0.014	0.018	0.018	0.018	0.016	0.019	0.018	0.017	0.017	0.017	0.019	0.019	0.018	0.016	0.017	0.018	0.017	0.017	0.017	0.017	0.017
AB610774_Mecistocephalus_multidentatus	0.191	0.191	0.190	0.229	0.188		0.020	0.016	0.017	0.017	0.017	0.018	0.018	0.019	0.018	0.021	0.021	0.019	0.017	0.019	0.020	0.017	0.021	0.018	0.018	0.019
KF569297_Gnathoribautia_bonensis	0.206	0.206	0.206	0.235	0.239	0.202		0.020	0.020	0.019	0.018	0.018	0.017	0.019	0.021	0.021	0.021	0.022	0.022	0.021	0.021	0.022	0.022	0.020	0.020	0.019
JN306685_Geophilus_flavus	0.223	0.223	0.220	0.281	0.231	0.217	0.194		0.016	0.018	0.020	0.019	0.019	0.019	0.020	0.020	0.020	0.021	0.018	0.019	0.019	0.019	0.019	0.018	0.018	
KR736251_Stenotaenia_linearis	0.245	0.245	0.243	0.271	0.264	0.240	0.216	0.196		0.021	0.018	0.020	0.019	0.021	0.020	0.020	0.020	0.020	0.018	0.018	0.020	0.018	0.022	0.019	0.018	
AY288745_Scolopocryptops_sexspinosus_Cryptopidae	0.221	0.221	0.220	0.218	0.220	0.223	0.225	0.235	0.244		0.017	0.018	0.018	0.016	0.019	0.020	0.021	0.019	0.018	0.019	0.019	0.017	0.017	0.019	0.019	0.017
AF334321_Paralamyctes_monteithi_Henicopidae	0.191	0.191	0.189	0.210	0.232	0.198	0.205	0.254	0.242	0.206		0.018	0.019	0.019	0.018	0.020	0.019	0.020	0.019	0.017	0.019	0.020	0.020	0.019	0.018	
AK10_PE111022_Cryptop_DC10	0.252	0.252	0.251	0.211	0.239	0.250	0.229	0.245	0.272	0.218	0.213		0.017	0.018	0.018	0.018	0.018	0.019	0.017	0.018	0.017	0.016	0.019	0.019	0.018	
BQ12_PES_5087_Cryptops_won1	0.232	0.232	0.232	0.215	0.225	0.226	0.227	0.237	0.262	0.190	0.213	0.198		0.019	0.019	0.020	0.019	0.019	0.018	0.017	0.020	0.019	0.022	0.020	0.017	0.015
BX11_PES-0968_Cryptops_pilbara1	0.250	0.250	0.246	0.227	0.230	0.240	0.241	0.243	0.268	0.214	0.224	0.194	0.213		0.017	0.019	0.019	0.018	0.017	0.018	0.018	0.016	0.010	0.019	0.018	
BX12_PES-3783_Cryptops_pilbara2	0.234	0.234	0.233	0.209	0.231	0.229	0.249	0.260	0.260	0.240	0.247	0.219	0.233	0.169		0.017	0.017	0.018	0.016	0.016	0.017	0.015	0.018	0.018	0.017	0.018
BX13_991-5262_Cryptops_MH1	0.237	0.237	0.237	0.230	0.248	0.246	0.260	0.271	0.271	0.239	0.251	0.218	0.236	0.201	0.184		0.003	0.017	0.017	0.015	0.018	0.018	0.023	0.019	0.019	0.019
BX8_PES-5889_Cryptops_MH2	0.239	0.239	0.239	0.225	0.248	0.248	0.262	0.272	0.272	0.244	0.253	0.215	0.233	0.201	0.181	0.006		0.017	0.017	0.014	0.018	0.018	0.023	0.018	0.019	0.019
BX9_PES-5272_Cryptops_MH2	0.232	0.232	0.229	0.204	0.231	0.247	0.255	0.271	0.266	0.213	0.215	0.208	0.218	0.173	0.186	0.175	0.175		0.018	0.019	0.019	0.018	0.018	0.020	0.019	
CQ2_nr_Cryptops_sp_B15_CCWUNK05	0.246	0.246	0.246	0.198	0.225	0.228	0.238	0.240	0.283	0.230	0.249	0.207	0.192	0.210	0.194	0.228	0.222	0.228		0.015	0.018	0.015	0.018	0.017	0.018	0.016
CQ3_Cryptops_sp_B32_CC1798	0.227	0.227	0.227	0.220	0.229	0.229	0.246	0.246	0.254	0.220	0.239	0.211	0.198	0.193	0.174	0.127	0.124	0.171	0.197		0.017	0.016	0.020	0.019	0.019	0.016
CQ5_nr_Cryptops_sp_B11_PCRC088	0.236	0.236	0.233	0.180	0.225	0.236	0.233	0.257	0.272	0.220	0.191	0.204	0.194	0.209	0.218	0.220	0.225	0.229	0.185	0.205		0.016	0.021	0.018	0.017	0.016
CQ6_Cryptops_sp_B30_1106_13_EX13	0.227	0.227	0.228	0.220	0.244	0.246	0.255	0.264	0.271	0.211	0.227	0.193	0.220	0.178	0.153	0.178	0.175	0.167	0.204	0.164	0.205		0.019	0.017	0.018	0.018
EY5_Cryptops_sp_B35	0.241	0.241	0.238	0.202	0.229	0.241	0.249	0.236	0.268	0.217	0.230	0.197	0.225	0.062	0.157	0.213	0.210	0.150	0.208	0.180	0.218	0.176		0.021	0.021	0.019
G123_Cryptops_Upper_South_Fortescue	0.235	0.235	0.232	0.234	0.239	0.246	0.223	0.243	0.267	0.207	0.216	0.222	0.237	0.242	0.236	0.257	0.254	0.250	0.236	0.248	0.230	0.213	0.261		0.019	0.017
G124_Cryptops_Upper_South_Fortescue	0.242	0.242	0.241	0.204	0.236	0.236	0.232	0.265	0.271	0.216	0.214	0.220	0.170	0.227	0.236	0.228	0.231	0.225	0.209	0.220	0.182	0.221	0.225	0.241		0.016
G349_Cryptopidae_sp_MJ_LN9808	0.240	0.240	0.240	0.211	0.219	0.243	0.224	0.245	0.280	0.211	0.210	0.203	0.158	0.220												

Table 15. Estimates of Evolutionary Divergence between Sequences

Specimen ID	IV144	IV145	IV146	IV147	IV148	IV150	IV151	IV152	IV153	FH1	J11-1	BX6	BX7	G344	G348	CF5	CF6	CF7	CF8	CF9	CF10	CF13	CF17	CF18+Y1:Y31edited_JIN0968R_Zuphiini_sp_Carabidae	Nvio	Pmut	Hdis	Stob	Etbl	Tsp	Kalm	
IV144_DD14MRR0004T1-03_Coleoptera	0.000	0.000	0.000	0.016	0.015	0.015	0.016	0.016	0.017	0.018	0.020	0.020	0.019	0.018	0.016	0.016	0.016	0.016	0.016	0.016	0.016	0.016	0.016	0.016	0.016	0.016	0.016	0.016	0.016	0.016		
IV145_DD14MRR0004T1-03_Coleoptera	0.000		0.000	0.016	0.015	0.015	0.016	0.016	0.017	0.018	0.020	0.020	0.019	0.018	0.016	0.016	0.016	0.016	0.016	0.016	0.016	0.016	0.016	0.016	0.016	0.016	0.016	0.016	0.016	0.016		
IV146_DD14MRR0004T1-03_Coleoptera	0.000	0.000		0.016	0.015	0.015	0.016	0.016	0.017	0.018	0.020	0.020	0.019	0.018	0.016	0.016	0.016	0.016	0.016	0.016	0.016	0.016	0.016	0.016	0.016	0.016	0.016	0.016	0.016	0.016		
IV147_DD14MRR0004T1-03_Coleoptera	0.000	0.000	0.000	0.016	0.015	0.015	0.016	0.016	0.017	0.018	0.020	0.020	0.019	0.018	0.016	0.016	0.016	0.016	0.016	0.016	0.016	0.016	0.016	0.016	0.016	0.016	0.016	0.016	0.016	0.016		
IV148_DD14MRR009-20150808-T3-01_Coleoptera	0.240	0.240	0.240	0.240		0.016	0.017	0.016	0.015	0.015	0.019	0.021	0.021	0.020	0.019	0.013	0.014	0.014	0.014	0.015	0.015	0.015	0.015	0.018	0.015	0.015	0.017	0.016	0.016	0.017	0.015	
IV150_RC14MEB060-20151001-T2-02_Coleoptera	0.258	0.258	0.258	0.258	0.190		0.015	0.007	0.014	0.016	0.018	0.019	0.020	0.018	0.020	0.015	0.015	0.015	0.015	0.016	0.016	0.016	0.016	0.017	0.016	0.016	0.018	0.015	0.016	0.014	0.015	
IV151_MEARC3814-20150807-T1-02_Coleoptera	0.198	0.198	0.198	0.198	0.205	0.234		0.017	0.015	0.018	0.017	0.015	0.016	0.016	0.020	0.015	0.014	0.014	0.015	0.015	0.015	0.016	0.016	0.016	0.015	0.016	0.016	0.018	0.016	0.014	0.015	
IV152_MEARC4400-t1-01_Coleoptera	0.271	0.271	0.271	0.271	0.190	0.032	0.234		0.015	0.016	0.019	0.019	0.021	0.019	0.020	0.015	0.014	0.015	0.015	0.015	0.015	0.015	0.017	0.017	0.017	0.017	0.017	0.018	0.016	0.017	0.016	0.015
IV153_MEARC4400-t1-01_Coleoptera	0.211	0.211	0.211	0.211	0.215	0.239	0.198	0.236		0.016	0.015	0.020	0.018	0.019	0.018	0.017	0.017	0.017	0.017	0.016	0.017	0.017	0.014	0.012	0.015	0.016	0.015	0.003	0.015	0.015	0.016	
FH1_Curculionidae_Genus2_B15_EW0540	0.236	0.236	0.236	0.236	0.202	0.231	0.225	0.234	0.234		0.017	0.019	0.019	0.020	0.020	0.014	0.014	0.014	0.014	0.013	0.013	0.015	0.014	0.017	0.018	0.018	0.016	0.015	0.014	0.015	0.015	
PSF0019R_LN6326_J11-1_Zuphiinae_S1_Carabidae	0.216	0.216	0.216	0.216	0.249	0.268	0.197	0.274	0.232	0.211		0.023	0.021	0.021	0.017	0.017	0.016	0.017	0.016	0.016	0.017	0.004	0.013	0.016	0.017	0.015	0.016	0.018	0.017	0.019		
BX6_PES-5290_Bembidion_MH1_CaK_Carabidae	0.222	0.222	0.222	0.222	0.243	0.300	0.197	0.310	0.222	0.262	0.202		0.008	0.018	0.017	0.018	0.019	0.018	0.018	0.019	0.019	0.020	0.019	0.017	0.017	0.016	0.015	0.019	0.020	0.018		
BX7_PES-5285_Bembidion_MH1_CaK_Carabidae	0.225	0.225	0.225	0.225	0.239	0.296	0.186	0.303	0.216	0.255	0.190	0.031		0.017	0.016	0.019	0.020	0.018	0.018	0.019	0.019	0.020	0.018	0.017	0.017	0.017	0.015	0.018	0.020	0.021	0.020	
G344_LN9362_Anillini_sp_OP_Carabidae	0.211	0.211	0.211	0.211	0.217	0.274	0.164	0.269	0.211	0.247	0.196	0.160	0.152		0.017	0.018	0.018	0.019	0.019	0.019	0.019	0.018	0.017	0.017	0.014	0.013	0.019	0.021	0.020	0.019		
G348_LN8860_Zuphiini_sp_UM_Carabidae	0.236	0.236	0.236	0.236	0.261	0.287	0.202	0.280	0.216	0.224	0.116	0.198	0.180	0.189		0.019	0.020	0.020	0.020	0.019	0.019	0.020	0.014	0.014	0.018	0.020	0.017	0.018	0.021	0.023	0.022	
CF5_GB0002R_Curculionidae_Genus_1_sp_B06	0.220	0.220	0.220	0.220	0.173	0.224	0.204	0.228	0.214	0.199	0.231	0.217	0.219	0.234	0.228		0.007	0.008	0.008	0.006	0.007	0.007	0.015	0.014	0.016	0.015	0.014	0.017	0.017	0.016	0.014	
CF6_GF0421R_Curculionidae_Genus_1_sp_B02	0.217	0.217	0.217	0.217	0.180	0.217	0.196	0.218	0.214	0.197	0.230	0.226	0.223	0.242	0.228		0.007	0.006	0.006	0.006	0.005	0.015	0.015	0.016	0.015	0.015	0.017	0.017	0.016	0.013		
CF7_PSC0890R_Curculionidae_Genus_1_sp_B02	0.223	0.223	0.223	0.223	0.177	0.215	0.193	0.223	0.206	0.200	0.233	0.228	0.217	0.230	0.233		0.046	0.045	0.004	0.007	0.008	0.007	0.015	0.016	0.015	0.016	0.014	0.018	0.016	0.015	0.013	
CF8_PSD0107R_Curculionidae_Genus_1_sp_B08	0.220	0.220	0.220	0.220	0.177	0.217	0.201	0.224	0.209	0.199	0.236	0.235	0.223	0.234	0.239		0.042	0.038	0.013	0.007	0.007	0.006	0.015	0.015	0.016	0.015	0.014	0.018	0.016	0.013	0.013	
CF9_SF0034R_Curculionidae_Genus_1_sp_B07	0.215	0.215	0.215	0.215	0.167	0.209	0.190	0.214	0.208	0.188	0.224	0.223	0.221	0.238	0.226		0.029	0.024	0.041	0.039	0.004	0.004	0.015	0.015	0.016	0.014	0.015	0.017	0.017	0.015		
CF10_SF0139R_Curculionidae_Genus_1_sp_B07	0.214	0.214	0.214	0.214	0.176	0.220	0.192	0.221	0.209	0.188	0.219	0.228	0.221	0.240	0.226		0.038	0.024	0.039	0.035	0.014		0.004	0.015	0.015	0.017	0.015	0.017	0.018	0.015</		

**Table 19. Estimates of Evolutionary Divergence between Sequences**

Specimen ID	IV154_DD11MEB001T1-01_Diplura	IV155_DD11MEB001T1-01_Diplura	IV156_DD11MEC0005-02_Diplura	IV157_DD14MEB0005-20151001-T3-02_Diplura	IV159_RC14MEB0101-20151001-T2-01_Diplura	Dsp	Jsol	Ctil	Lweb	BX29	BX30	BX40	BX16	BX17	G473	BQ7	BQ10	G333	G334	G336	BQ11	BQ8	G432	G433	G329	G330	G331	G332	IT74				
IV154_DD11MEB001T1-01_Diplura		0.014	0.016	0.013	0.013																												
IV155_DD11MEB001T1-01_Diplura	0.144		0.015	0.009	0.008	0.015	0.016	0.016	0.017	0.016	0.017	0.016	0.013	0.015	0.015	0.017	0.017	0.018	0.017	0.017	0.018	0.014	0.016	0.015	0.015	0.016	0.014	0.014					
IV156_DD11MEC0005-02_Diplura	0.261	0.256		0.014	0.015	0.016	0.013	0.018	0.016	0.012	0.014	0.016	0.013	0.016	0.017	0.015	0.015	0.018	0.018	0.015	0.017	0.015	0.013	0.015	0.015	0.013	0.013	0.014					
IV157_DD14MEB0005-20151001-T3-02_Diplura	0.153	0.054	0.243		0.003	0.014	0.015	0.016	0.017	0.016	0.017	0.015	0.013	0.014	0.015	0.016	0.016	0.017	0.016	0.015	0.016	0.014	0.017	0.016	0.016	0.014	0.016	0.014					
IV159_RC14MEB0101-20151001-T2-01_Diplura	0.153	0.047	0.241	0.006		0.014	0.015	0.016	0.017	0.016	0.017	0.015	0.013	0.014	0.015	0.016	0.016	0.017	0.016	0.015	0.016	0.014	0.017	0.015	0.016	0.014	0.016	0.014					
Diplura_sp_HQ943342_DA	0.249	0.227	0.263	0.223	0.222		0.014	0.014	0.015	0.018	0.017	0.015	0.015	0.015	0.016	0.015	0.017	0.017	0.016	0.016	0.015	0.016	0.015	0.015	0.017	0.016	0.014						
Japyx_solidifugus_AY771989_DC	0.257	0.254	0.207	0.239	0.242	0.243		0.017	0.017	0.013	0.013	0.016	0.015	0.016	0.017	0.017	0.019	0.016	0.017	0.016	0.018	0.014	0.015	0.015	0.013	0.014	0.014	0.016					
AF370844_Campodea_tillyardi	0.219	0.222	0.281	0.216	0.214	0.214	0.260		0.017	0.016	0.016	0.018	0.017	0.017	0.017	0.017	0.017	0.018	0.019	0.018	0.018	0.015	0.017	0.016	0.017	0.019	0.017	0.018					
HO882832_Lepidocampa_weberi	0.253	0.211	0.263	0.213	0.215	0.233	0.250	0.233		0.016	0.017	0.016	0.014	0.015	0.015	0.016	0.015	0.019	0.017	0.014	0.016	0.017	0.018	0.016	0.016	0.018	0.016	0.017	0.018				
BX29_PES-5141_Projapygidae_MH1_DS	0.273	0.270	0.175	0.258	0.258	0.263	0.222	0.278	0.247		0.007	0.016	0.016	0.014	0.016	0.016	0.013	0.018	0.017	0.015	0.017	0.014	0.013	0.014	0.015	0.014	0.012	0.015	0.016				
BX30_PES-5190_Projapygidae_MH1_DS	0.276	0.268	0.178	0.255	0.255	0.267	0.226	0.274	0.244	0.030		0.016	0.016	0.015	0.017	0.017	0.015	0.019	0.017	0.016	0.018	0.015	0.013	0.014	0.014	0.013	0.011	0.014	0.017				
BX40_PES-5878_Projapygidae_MH1_DT	0.283	0.295	0.274	0.281	0.278	0.275	0.257	0.287	0.289	0.270	0.280		0.016	0.016	0.012	0.013	0.014	0.014	0.012	0.013	0.015	0.016	0.015	0.016	0.016	0.015	0.016	0.017	0.018				
BX16_PES-5195_Japygidae_MH1_DQ	0.229	0.215	0.203	0.210	0.210	0.220	0.179	0.249	0.204	0.213	0.219	0.235		0.011	0.016	0.013	0.015	0.018	0.017	0.015	0.016	0.011	0.013	0.013	0.013	0.015	0.014	0.015	0.014	0.014			
BX17_PES-5952_Japygidae_MH1_DR	0.252	0.237	0.204	0.223	0.224	0.248	0.200	0.267	0.213	0.204	0.208	0.262	0.130		0.016	0.014	0.015	0.017	0.017	0.015	0.016	0.013	0.015	0.013	0.014	0.014	0.015	0.016	0.013	0.013			
G473_111138b_Anajapygidae_sp_NS_DB	0.226	0.251	0.242	0.248	0.247	0.245	0.236	0.252	0.257	0.244	0.253	0.253	0.215	0.232		0.016	0.017	0.018	0.017	0.017	0.018	0.018	0.016	0.017	0.018	0.014	0.014	0.017	0.016	0.017	0.017		
BQ7_PES_4269_Projapygidae_DK	0.285	0.267	0.246	0.253	0.251	0.287	0.278	0.282	0.285	0.251	0.256	0.168	0.235	0.234	0.258		0.010	0.014	0.014	0.012	0.013	0.016	0.016	0.017	0.017	0.016	0.017	0.017	0.016	0.017	0.017		
BQ10_PES_2546_Projapygidae_DL	0.292	0.285	0.245	0.262	0.264	0.283	0.265	0.280	0.286	0.246	0.251	0.168	0.246	0.248	0.258	0.113		0.014	0.015	0.011	0.014	0.015	0.015	0.016	0.017	0.015	0.016	0.017	0.015	0.016	0.017	0.017	
G333_LN8949_Projapygidae_sp_MJ_DN	0.290	0.298	0.270	0.281	0.284	0.278	0.251	0.283	0.283	0.265	0.264	0.187	0.248	0.241	0.267	0.170	0.187		0.013	0.013	0.014	0.018	0.017	0.019	0.016	0.016	0.017	0.018	0.017				
G334_LN9141_Projapygidae_sp UM DO	0.287	0.297	0.262	0.283	0.280	0.269	0.254	0.275	0.269	0.270	0.274	0.168	0.246	0.258	0.276	0.183	0.181	0.141		0.012	0.014	0.016	0.017	0.018	0.017	0.017	0.017	0.017	0.017				
G336_LN9557_Projapygidae_sp_OP_DM	0.271	0.289	0.251	0.265	0.265	0.254	0.246	0.278	0.277	0.242	0.254	0.168	0.236	0.243	0.255	0.143	0.134	0.160	0.145		0.012	0.014	0.016	0.015	0.014	0.015	0.016	0.017	0.017				
BQ11_PES_5439_Projapygidae_won1_DP	0.271	0.300	0.249	0.286	0.281	0.255	0.233	0.246	0.268	0.257	0.270	0.143	0.220	0.238	0.242	0.156	0.162	0.156	0.152	0.146		0.016	0.016	0.016	0.017	0.016	0.018	0.017	0.018	0.017			
BQ8_PES_4283_Japygidae_won1_DE	0.248	0.233	0.185	0.226	0.224	0.216	0.185	0.251	0.230	0.210	0.217	0.252	0.138	0.147	0.215	0.247	0.252	0.255	0.242	0.242	0.233		0.015	0.013	0.011	0.015	0.015	0.016	0.014	0.016			
G432_110953																																	

**Table 24. Estimates of Evolutionary Divergence between Sequences**

Specimen ID	V167	V171	V172	V175	V176	V177	V178	V179	V181	V189	Anas	Bsp	Hsp10	Hsp12	Hsp21	Lyal	Psp1	Psp4	B12	EO10	EO11	EO12	J17-2	G173	G175	G350	G92	J17-5	J17-9	J17-11	J17-149	E37	E39	E40	E45	E50	IS105	IS111	IS126	IS92	IS97	T40		
IV167_M2ERC053-T2-01_Isopoda		0.016	0.016	0.009	0.016	0.016	0.016	0.015	0.016	0.015	0.017	0.016	0.014	0.015	0.014	0.015	0.017	0.016	0.016	0.018	0.018	0.013	0.015	0.016	0.017	0.017	0.016	0.015	0.020	0.018	0.017	0.020	0.013	0.018	0.024	0.013								
IV171_MEARC4923-20150930-T1-01_Isopoda	0.225		0.014	0.014	0.016	0.014	0.016	0.015	0.007	0.015	0.015	0.016	0.015	0.015	0.014	0.016	0.016	0.018	0.017	0.015	0.013	0.014	0.013	0.014	0.015	0.015	0.016	0.021	0.014	0.025	0.014	0.010	0.021	0.017	0.015	0.015	0.024	0.015						
IV172_MELUNK02-20151001-T1-03_Isopoda	0.203	0.238		0.015	0.017	0.015	0.016	0.015	0.015	0.015	0.016	0.016	0.018	0.015	0.018	0.018	0.016	0.015	0.014	0.016	0.014	0.014	0.014	0.016	0.017	0.017	0.016	0.014	0.019	0.015	0.022	0.015	0.018	0.016	0.016	0.021	0.015							
IV175_RC13MRR0014-20151002-T1-01_Isopoda	0.070	0.224	0.191		0.016	0.015	0.015	0.016	0.014	0.014	0.016	0.015	0.014	0.016	0.015	0.015	0.016	0.017	0.017	0.015	0.014	0.016	0.018	0.013	0.016	0.017	0.017	0.016	0.014	0.019	0.015	0.022	0.015	0.018	0.016	0.019	0.013	0.017	0.021	0.012				
IV176_RC14MEB0060-20151001-T2-03_Isopoda	0.240	0.231	0.259	0.242		0.017	0.017	0.011	0.016	0.016	0.015	0.016	0.017	0.019	0.020	0.016	0.016	0.015	0.014	0.017	0.016	0.015	0.014	0.016	0.017	0.017	0.018	0.015	0.023	0.015	0.020	0.021	0.015	0.021	0.016	0.022	0.014	0.016	0.024	0.014				
IV177_RC14MEB0088-20151001-T3-01_Isopoda	0.227	0.166	0.226	0.220	0.218		0.017	0.016	0.015	0.017	0.014	0.016	0.014	0.015	0.016	0.017	0.017	0.016	0.014	0.014	0.014	0.016	0.016	0.015	0.015	0.020	0.016	0.023	0.014	0.019	0.019	0.018	0.020	0.017	0.017	0.024	0.016	0.016	0.022	0.014				
IV178_RC14MEB0101-20151001-T1-01_Isopoda	0.189	0.201	0.194	0.191	0.224	0.238		0.017	0.016	0.015	0.016	0.017	0.014	0.016	0.019	0.018	0.016	0.017	0.016	0.016	0.016	0.017	0.017	0.017	0.023	0.015	0.021	0.015	0.019	0.021	0.017	0.018	0.015	0.017	0.022	0.014	0.016	0.022	0.014					
IV179_TOBRC0020-20151001-T2-02_Isopoda	0.240	0.201	0.238	0.232	0.082	0.207	0.227		0.015	0.010	0.014	0.016	0.015	0.013	0.016	0.016	0.018	0.018	0.017	0.016	0.015	0.015	0.014	0.015	0.017	0.017	0.019	0.014	0.023	0.015	0.020	0.020	0.015	0.019	0.015	0.022	0.016	0.016	0.022	0.016				
IV181_MEARC2401-20150807-T2-03_Isopoda	0.230	0.038	0.230	0.224	0.228	0.169	0.207	0.207		0.015	0.016	0.016	0.015	0.015	0.016	0.017	0.018	0.017	0.014	0.015	0.016	0.014	0.015	0.015	0.016	0.015	0.016	0.019	0.016	0.024	0.015	0.006	0.022	0.017	0.018	0.016	0.017	0.024	0.016					
IV189_TOBRC0020-t1-01_Isopoda	0.241	0.216	0.242	0.236	0.076	0.211	0.235	0.067	0.207		0.014	0.016	0.014	0.015	0.016	0.020	0.017	0.016	0.014	0.015	0.015	0.014	0.014	0.015	0.015	0.016	0.014	0.017	0.016	0.020	0.018	0.016	0.020	0.014	0.015	0.022	0.014							
FN824099_Armadillidium_nasatum	0.203	0.215	0.195	0.206	0.223	0.219	0.189	0.212	0.212	0.212		0.015	0.016	0.015	0.016	0.014	0.017	0.016	0.016	0.016	0.016	0.015	0.016	0.016	0.016	0.018	0.017	0.020	0.015	0.023	0.016	0.020	0.017	0.016	0.020	0.015	0.016	0.022	0.015					
AB626254_Burmoniscus_sp.	0.222	0.210	0.244	0.210	0.229	0.206	0.207	0.209	0.216	0.219	0.206		0.015	0.016	0.015	0.016	0.019	0.019	0.016	0.016	0.016	0.016	0.016	0.017	0.016	0.017	0.017	0.017	0.021	0.015	0.020	0.017	0.017	0.020	0.017	0.018	0.022	0.016	0.016	0.022	0.014			
Haloniscus_sp._10_EU364592	0.193	0.230	0.197	0.194	0.232	0.219	0.196	0.227	0.228	0.230	0.182	0.205		0.013	0.013	0.016	0.017	0.017	0.016	0.017	0.015	0.015	0.016	0.017	0.018	0.019	0.017	0.021	0.017	0.018	0.018	0.019	0.015	0.016	0.023	0.014	0.016	0.022	0.014					
Haloniscus_sp._12_EU364601	0.206	0.233	0.230	0.223	0.227	0.231	0.208	0.220	0.231	0.222	0.197	0.220	0.149		0.014	0.014	0.017	0.016	0.016	0.015	0.014	0.015	0.015	0.016	0.017	0.017	0.016	0.015	0.015	0.023	0.016	0.019	0.019	0.016	0.021	0.016	0.015	0.022	0.017	0.016	0.022	0.017		
EU364622_Haloniscus_sp._21	0.186	0.202	0.213	0.190	0.225	0.217	0.191	0.213	0.208	0.211	0.204	0.222	0.147	0.168		0.013	0.013	0.016	0.017	0.015	0.016	0.013	0.013	0.015	0.015	0.016	0.013	0.019	0.015	0.020	0.016	0.018	0.016	0.020	0.014	0.016	0.022	0.015	0.016	0.022	0.015			
EU364629_Laevophiloscia_yalgoorensis	0.193	0.250	0.202	0.197	0.235	0.246	0.212	0.241	0.246	0.239	0.210	0.230	0.207	0.223	0.221		0.017	0.016	0.015	0.017	0.013	0.017	0.016	0.015	0.015	0.015	0.015	0.015	0.015	0.015	0.020	0.015	0.022	0.016	0.018	0.017	0.022	0.014	0.019	0.019	0.014	0.016	0.022	0.014
EU107646_Pygolabis_sp._1	0.248	0.259	0.264	0.239	0.282	0.250	0.253	0.255																																				

**Table 29. Estimates of Evolutionary Divergence between Sequences**

Specimen ID	IV212	IV226	IV203	IV210	Aussp	Tyrsp	Lagjo	CM18	G319	G324	G328	G219	G220	G118	J20-6	P1012	EA0270R	LB084	EAP0178	GF0173R	JIN0078R	EJR0202	IS01	IS05	IS06	IS08	IS10	IS11	IS12	
IV212_DD14MEL0001-20151001-T2-02_lin_9		0.015	0.018	0.019	0.019	0.022	0.022	0.019	0.023	0.019	0.019	0.019	0.021	0.024	0.024	0.020	0.025	0.022	0.022	0.024	0.024	0.018	0.020	0.018	0.019	0.021	0.017	0.020		
IV226_RC14MRR0020-20151002-T2-01_lin_10	0.111		0.018	0.019	0.019	0.021	0.021	0.018	0.021	0.021	0.018	0.020	0.023	0.022	0.021	0.022	0.024	0.021	0.020	0.020	0.022	0.023	0.018	0.020	0.019	0.019	0.020	0.016	0.019	
IV203_DD14MRR0004T1-04_lin_11	0.204	0.207		0.017	0.018	0.021	0.017	0.016	0.020	0.017	0.019	0.016	0.017	0.022	0.021	0.020	0.022	0.022	0.023	0.020	0.022	0.021	0.019	0.018	0.017	0.017	0.018	0.015	0.019	
IV210_MEARC3814-20150606-02sc_lin_12	0.218	0.238	0.156		0.019	0.023	0.022	0.019	0.020	0.019	0.018	0.019	0.020	0.020	0.022	0.022	0.024	0.023	0.021	0.021	0.020	0.020	0.016	0.016	0.017	0.019	0.019	0.019	0.019	
EU559513_Austrochtonia_sp	0.196	0.207	0.166	0.189		0.023	0.019	0.018	0.019	0.017	0.020	0.019	0.020	0.023	0.024	0.022	0.025	0.023	0.023	0.023	0.020	0.019	0.020	0.021	0.020	0.018	0.021	0.021	0.021	0.021
EU559506_Tyrannochthonius_sp._JM-2008	0.296	0.293	0.283	0.278	0.261		0.023	0.020	0.021	0.020	0.021	0.021	0.021	0.022	0.022	0.021	0.000	0.022	0.021	0.000	0.024	0.021	0.022	0.022	0.023	0.023	0.024	0.024	0.021	0.023
EU559503_Lagynochthonius_johni	0.231	0.226	0.215	0.233	0.203	0.276		0.021	0.020	0.020	0.020	0.022	0.020	0.024	0.023	0.020	0.024	0.023	0.025	0.022	0.024	0.023	0.022	0.021	0.021	0.020	0.020	0.019	0.021	0.021
CM18_RC11KOOD0193P2T1-2_Lagynochthonius_sp.	0.216	0.216	0.182	0.216	0.203	0.254	0.226		0.019	0.017	0.018	0.017	0.019	0.022	0.021	0.024	0.024	0.020	0.026	0.018	0.022	0.021	0.019	0.018	0.018	0.019	0.019	0.018	0.020	0.020
G319_LN8720_Chthoniid_sp_MJ	0.247	0.249	0.210	0.220	0.191	0.289	0.235	0.242		0.018	0.019	0.020	0.020	0.020	0.020	0.022	0.022	0.023	0.021	0.025	0.022	0.020	0.020	0.024	0.021	0.021	0.021	0.019	0.020	0.024
G324_101086_Tyrannochthonius_sp_MA	0.212	0.212	0.176	0.203	0.179	0.252	0.220	0.178	0.191		0.017	0.018	0.019	0.022	0.019	0.023	0.021	0.020	0.024	0.019	0.022	0.021	0.019	0.018	0.019	0.019	0.017	0.020	0.020	
G328_LN9199_Tyrannochthonius_sp_OP	0.211	0.216	0.187	0.199	0.181	0.208	0.236	0.180	0.209	0.171		0.020	0.020	0.021	0.022	0.021	0.022	0.018	0.022	0.021	0.019	0.019	0.019	0.020	0.021	0.018	0.020	0.020		
G219_Pseudoscorpian_108935	0.216	0.221	0.184	0.179	0.176	0.280	0.226	0.198	0.225	0.187	0.169		0.014	0.022	0.021	0.022	0.024	0.020	0.024	0.023	0.022	0.022	0.016	0.017	0.016	0.018	0.020	0.015	0.017	
G220_Pseudoscorpian_109177	0.211	0.221	0.177	0.195	0.185	0.293	0.206	0.202	0.237	0.191	0.184	0.117		0.022	0.021	0.022	0.021	0.021	0.025	0.022	0.022	0.020	0.017	0.018	0.017	0.018	0.020	0.019	0.018	
G118_Tyrannochthonius	0.275	0.278	0.238	0.238	0.238	0.240	0.261	0.278	0.241	0.252	0.249	0.232	0.235		0.022	0.018	0.022	0.022	0.024	0.022	0.000	0.000	0.022	0.025	0.024	0.023	0.023	0.021	0.021	
EXR1148_J20-6_Ministers_N_Lagy_S4	0.234	0.234	0.216	0.207	0.201	0.000	0.216	0.192	0.243	0.201	0.178	0.216	0.225	0.231		0.022	0.021	0.000	0.024	0.021	0.022	0.022	0.023	0.023	0.024	0.022	0.022	0.022	0.022	
P1012_Hashimoto_Tyan	0.216	0.246	0.183	0.207	0.192	0.197	0.222	0.210	0.210	0.216	0.160	0.189	0.192	0.195	0.197		0.021	0.022	0.023	0.021	0.018	0.018	0.023	0.024	0.022	0.023	0.023	0.019	0.025	
EA0270R_OB24_Lag_B2	0.265	0.268	0.214	0.223	0.229	0.228	0.265	0.232	0.271	0.193	0.202	0.193	0.199	0.265	0.228	0.228		0.021	0.024	0.021	0.022	0.023	0.021	0.021	0.022	0.023	0.021	0.023		
LB084_Hashimoto_Tyrann	0.291	0.288	0.277	0.272	0.259	0.000	0.275	0.246	0.289	0.252	0.208	0.275	0.288	0.240	0.000	0.197	0.228		0.024	0.021	0.022	0.022	0.023	0.025	0.024	0.021	0.023			
EAP0178_OB24_Tyran_B1	0.218	0.221	0.253	0.250	0.241	0.267	0.282	0.268	0.279	0.247	0.226	0.235	0.268	0.291	0.267	0.267	0.280	0.267		0.019	0.024	0.024	0.022	0.023	0.025	0.022	0.023	0.022		
GF0173R_MAC_dep_F_Lag_B2	0.255	0.249	0.208	0.235	0.194	0.189	0.223	0.188	0.223	0.188	0.155	0.205	0.211	0.226	0.189	0.183	0.238	0.189	0.265		0.022	0.022	0.022	0.024	0.022	0.023	0.020	0.022		
JIN0078R_BHP772_Jinaryi_Lagynochthonius	0.277	0.283	0.241	0.241	0.241	0.240	0.263	0.283	0.244	0.255	0.252	0.235	0.238	0.000	0.231	0.195	0.265	0.240	0.291	0.226		0.000	0.022	0.025	0.024	0.023	0.023	0.021	0.022	
EJR0202_2_9_9_ob18_Tyrannochthonius_B2	0.252	0.255	0.217	0.217	0.217	0.231	0.243	0.261	0.223	0.232	0.226	0.214	0.214	0.000	0.231	0.195	0.265	0.231	0.291	0.226	0.000		0.021	0.025	0.024	0.023	0.021	0.020	0.021	
IS01	0.187	0.207	0.204	0.198	0.214	0.308	0.249	0.238	0.230	0.210	0.206	0.198	0.211	0.306	0.240	0.234</td														

**Table 30. Estimates of Evolutionary Divergence between Sequences**

Specimen ID	V201	V217	V206	V209	V202	V211	V213	V219	V205	V208	V207	Indsp	DF18	FZ1	G107	GB0018R	GC0103R	IT72	PSF0090R	Parsu
IV201_DD14MEB0002-20150607-01sc_Pseudoscorpiones		0.009	0.018	0.018	0.022	0.021	0.022	0.021	0.021	0.018	0.020	0.020	0.020	0.021	0.023	0.025	0.025	0.023	0.024	0.021
IV217_RC14MEB0029-20151001-T1-01_Pseudoscorpiones	0.049		0.020	0.019	0.023	0.022	0.021	0.022	0.022	0.020	0.021	0.020	0.020	0.023	0.024	0.025	0.025	0.025	0.025	0.021
IV206_DD14MRR0008-20150808-T1-02_Pseudoscorpiones	0.213	0.227		0.009	0.020	0.019	0.022	0.020	0.018	0.019	0.019	0.019	0.018	0.020	0.021	0.025	0.024	0.022	0.024	0.020
IV209_M2ERC027-t2-03_Pseudoscorpiones	0.207	0.222	0.036		0.020	0.018	0.021	0.020	0.018	0.018	0.019	0.020	0.018	0.020	0.021	0.025	0.024	0.023	0.023	0.020
IV202_DD14MRR0004T1-04_Pseudoscorpiones	0.267	0.260	0.262	0.262		0.022	0.022	0.021	0.021	0.022	0.022	0.022	0.020	0.022	0.026	0.029	0.028	0.023	0.028	0.022
IV211_RC13MEA0279-20150807-T1-02_Pseudoscorpiones	0.227	0.224	0.240	0.227	0.224		0.018	0.018	0.022	0.019	0.021	0.020	0.022	0.021	0.025	0.028	0.028	0.020	0.027	0.020
IV213_DD14MRR0009-20151002-T2-02_Pseudoscorpiones	0.253	0.258	0.249	0.240	0.227	0.131		0.017	0.023	0.020	0.021	0.018	0.021	0.020	0.026	0.030	0.030	0.017	0.028	0.023
IV219_RC14MEB0101-20151001-T1-02_Pseudoscorpiones	0.252	0.254	0.261	0.252	0.242	0.141	0.134		0.022	0.020	0.020	0.020	0.024	0.018	0.025	0.027	0.027	0.016	0.026	0.020
IV205_DD14MRR0005-T2-01_Pseudoscorpiones	0.298	0.304	0.309	0.304	0.282	0.282	0.287	0.289		0.017	0.020	0.021	0.023	0.025	0.027	0.026	0.023	0.026	0.019	
IV208_M2ERC027-t2-03_Pseudoscorpiones	0.264	0.276	0.284	0.276	0.284	0.253	0.256	0.256	0.136		0.012	0.019	0.021	0.022	0.023	0.025	0.025	0.021	0.024	0.019
IV207_DD14MRR0008-20150808-T2-03_Pseudoscorpiones	0.280	0.296	0.313	0.296	0.296	0.260	0.264	0.275	0.167	0.082		0.019	0.021	0.023	0.025	0.026	0.025	0.023	0.025	0.019
EU559564_Indohya_sp._JM-2008	0.211	0.211	0.216	0.211	0.247	0.216	0.229	0.219	0.273	0.244	0.260		0.021	0.022	0.025	0.029	0.027	0.019	0.026	0.020
DF18_8668_Indohya_sp.	0.216	0.218	0.162	0.162	0.236	0.218	0.220	0.254	0.293	0.264	0.282	0.211		0.020	0.022	0.027	0.029	0.021	0.026	0.020
FZ1_Pseudoscorpion_RC13KOOD0302P7T1-1	0.224	0.233	0.231	0.228	0.264	0.221	0.228	0.215	0.296	0.276	0.296	0.228	0.200		0.023	0.024	0.023	0.022	0.025	0.022
G107_Indohya	0.258	0.255	0.176	0.167	0.284	0.284	0.308	0.282	0.340	0.314	0.340	0.252	0.199	0.258		0.028	0.026	0.024	0.024	0.025
GB0018R_Hyidae_B1	0.252	0.255	0.264	0.261	0.337	0.290	0.305	0.305	0.349	0.349	0.361	0.293	0.255	0.238	0.276		0.012	0.028	0.022	0.027
GC0103R_Hyidae	0.255	0.255	0.246	0.249	0.326	0.293	0.302	0.296	0.346	0.343	0.361	0.276	0.258	0.235	0.258	0.053		0.028	0.024	0.027
IT72_BHRC0512-151013-T3-01_Pseudoscorpiones	0.245	0.247	0.263	0.263	0.231	0.113	0.105	0.113	0.285	0.258	0.272	0.191	0.215	0.230	0.268	0.287	0.277		0.027	0.022
PSF0090R_LN2124_Indohya	0.273	0.279	0.258	0.258	0.349	0.311	0.299	0.323	0.378	0.358	0.361	0.287	0.282	0.276	0.287	0.173	0.176	0.283		0.028
JN018204_Paratemnoides_sumatranaus_Atemnidae	0.289	0.298	0.287	0.280	0.276	0.267	0.267	0.282	0.184	0.180	0.198	0.277	0.277	0.308	0.337	0.337	0.323	0.272	0.352	

1. Tamura K., Stecher G., Peterson D., Filipski A., and Kumar S. (2013). MEGA6: Molecular Evolutionary Genetics Analysis version 6.0. Molecular Biology and Evolution 30: 2725-2729.

The number of base differences per site from between sequences are shown. Standard error estimate(s) are shown above the diagonal. The analysis involved 42 nucleotide sequences. Codon positions included were problems to the authors immediately ([www.megasoftware.net](http://www.megasoftware.net)). In no event shall the authors and their employers be liable for any damages, including but not limited to special, consequential, or other damages. Authors specifically disclaim all other warranties expressed or implied, including but not limited to the determination of suitability of this caption text for a specific purpose, use, or application.



# Helix

## Molecular Solutions

School of Animal Biology The University of Western Australia Hackett Entrance No. 4 Hackett Drive Crawley WA 6009	PO Box 155 Leederville WA 6903
t. (08) 6488 4509 f. (08) 6488 1029 abn. 32 133 230 243	w. <a href="http://www.helixsolutions.com.au">www.helixsolutions.com.au</a>

10 October, 2016

Jason Alexander  
Biota Environmental Sciences  
Level 1, 228 Carr Place  
Leederville, WA 6007

Via email

**Re. Report on the molecular systematics of subfauna from the Robe River Valley–historical, Phase 3 and Phase 1 and 2 repeats: Part 3**

Dear Jason,

Following is a summary of the results of the subfauna study we have completed on four taxonomic groups from the Robe River Valley (Amphipoda, Diplura, Diplopoda and Isopoda). Sixteen distinct genetic lineages were detected among the four groups (three Amphipoda, three Diplura, two Diplopoda, nine Isopoda). The 16 lineages likely represent 15 species, up to seven of which have been detected previously in the Pilbara.

Thanks once again for collaborating on this project with Helix. We hope we can continue to provide you with useful information, and feel free to contact us if you have any questions or would like to discuss the results in detail.

Sincerely,

Dr. Terrie Finston, Yvette Hitchen and Dr. Oliver Berry  
Helix Molecular Solutions

## Results

### Amphipoda

#### Preliminary analysis - Reference sequences and outgroups

Twenty-two specimens of amphipods repeated from phases 1 and 2 were sequenced for COI (Table 30). In order to reduce analysis time and to simplify the presentation of results, a preliminary neighbour-joining (NJ) analysis was conducted on the 10 Robe Valley amphipods for which sequences were obtained, and haplotypes were selected from each genetic lineage to include in a model-based phylogenetic analysis.

The neighbour-joining analysis placed the 10 specimens of amphipods for which sequences were obtained into three lineages (Figure 14). Comparisons to the GenBank sequence database indicated that two of the three lineages were most similar to sequences of Melitidae, whereas one lineage was most similar to sequences of Paramelitidae. The Melitidae lineages contained between one and four specimens, and the Paramelitidae lineage contained five specimens (Figure 14). The three lineages differed from one another by between 4.1 and 33.0% mean sequence divergence and the two lineages of Melitidae differed from one another by 4.1% mean sequence divergence (Table 31). Differentiation within lineages ranged from a mean of 0 to 1.4% sequence divergence (Table 32).

For the Paramelitidae, 29 reference sequences were included in the phylogenetic analysis, six GenBank vouchers of Paramelitidae, *Maarrka etheli* (Genbank accession #DQ838031), two *Maarrka weeliwollii* (Genbank accession # DQ838032 and # DQ838033), Paramelitidae sp. 3 (Genbank accession # EF558852) and two references of 'Yilgarus' sp. (Genbank accession # EF118232 and EF118194) as well as 23 specimens from previous surveys of the Central Pilbara, Barrow Island, Lower Shaw River, Fortescue River, and Marillana Creek. Two sequences of the amphipod genus *Niphargus* were used as outgroups as follows: *N. fontanus* (Genbank accession number KC315635) and *N. glenniei* (Genbank accession number KC315646).

For the Melitidae, 33 reference sequences were included in the phylogenetic analysis, two GenBank vouchers of Melitidae, *Nedgia* sp. 1 (Genbank accession #EU304458), and *Norcapensis mandibulis* (Genbank accession # JQ608487) as well as 31 specimens from previous surveys of the Central Pilbara, Barrow Island, Lower Shaw River, Fortescue River, and Marillana Creek. Two sequences of the amphipod genus *Niphargus* were used as outgroups as follows: *N. fontanus* (Genbank accession number KC315635) and *N. glenniei* (Genbank accession number KC315646).

#### *Phylogenetic analysis- Paramelitidae*

The phylogenetic analysis, which included the one representative of Paramelitidae from Robe Valley in addition to 29 reference specimens, placed the Robe Valley specimens in a single distinct lineage that also contained a reference specimen from a previous survey at Barrow Island and thus was assigned to the existing lineage AMP023 (Figure 15).

#### *Differentiation within and between lineages - Paramelitidae*

The Robe Valley Paramelitidae lineage differed from the closest reference lineage (AMP023) by 1.3% (Table 33).

#### *Phylogenetic analysis- Melitidae*

The phylogenetic analysis, which included the two representatives of Melitidae from Robe Valley in addition to 33 reference specimens, placed the Robe Valley specimens in two distinct genetic lineages, one of which also contained a reference specimen from a previous survey at Robe Valley and thus was assigned to the existing lineage AMM023 (Figure 16). The second lineage was not placed with a reference lineage, and was therefore assigned to the new lineage AMM027, however, both Robe Valley lineages were placed in a well-supported clade containing the Genbank reference lineage of *Nedgia* sp. 1 (Figure 16).

#### *Differentiation within and between lineages - Melitidae*

The two lineages of Melitidae differed from one another by 4.1% mean sequence divergence (Table 31). One lineage was genetically identical to a lineage detected previously at Robe

Valley (AMM023) and the second, AMM027 differed from the closest reference lineage (AMM024) by 3.4%, and indeed, a well-supported clade of 11 lineages, which included both of the Robe Valley lineages from the present study and the Genbank voucher specimen of *Nedisia* sp.1, all differed by approximately 5% sequence divergence or less (Table 34).

### Isopoda

#### Preliminary analysis, reference specimens and outgroups

Forty-two specimens of Isopoda were sequenced from historical collections, phase 3 and phase 1/2 repeats (Table 35). Nineteen specimens yielded a DNA sequence. In order to reduce analysis time and to simplify the presentation of results, a preliminary neighbour-joining (NJ) analysis was conducted on the 19 Robe Valley isopods for which sequences were obtained, and haplotypes were selected from each genetic lineage to include in a model-based phylogenetic analysis. Nine distinct genetic lineages were detected in the NJ analysis (Figure 17), and the nine representatives were analysed in a model-based phylogenetic analysis with 48 reference specimens of Isopoda from Genbank and the Pilbara. A search of similar sequences on Genbank and in the Helix database indicated the specimens were most closely matched with Armadillidae and Philosciidae. Hence we included Genbank voucher specimens of both families: *Haloniscus* sp. 10 (Genbank accession #EU364592), *Halonsicus* sp. 12 (Genbank accession #EU364601), *Halonsicus* sp. 21 (Genbank accession #EU364622) *Laevophiloscia yalgoorensis* (Genbank accession #EU364629), and *Troglarmadillo* sp. 6 (Genbank accession # KX656276). Two specimens of the aquatic isopod genus *Pygolabis* *Pygolabis* sp. 1 (Genbank accession # EU107646) and *Pygolabis* sp. 4 (Genbank accession #EU107664), were used as outgroups.

#### Phylogenetic analysis

The phylogenetic analysis, which included the nine representatives from Robe Valley in addition to 48 reference specimens, placed the Robe Valley specimens in nine distinct lineages (Figure 18). Five of the lineages were placed in a clade containing reference specimens of Philosciidae and four of the lineages were placed in a clade containing reference specimens of Armadillidae and *Troglarmadillo* (Figure 18). Three of the nine lineages also contained reference specimens from a previous survey at Robe Valley and thus were assigned to the existing lineages ISP001, ISA009a and ISA008 (Figure 18). The remaining lineages did not contain reference specimens, and thus were assigned to the new lineages ISP050, ISP051, ISP052, ISP053, ISA054 and ISA055 (Figure 18).

#### Differentiation within and between lineages

The Robe Valley lineages of Isopoda differed from one another by a mean of 11.2 to 24.8% sequence divergence (Table 36). Differentiation within lineages ranged from a mean of 0 to 1.0% sequence divergence (Table 37). The Robe valley lineages differed from the reference specimens by between 0 and 28.4% sequence divergence (Table 38).

### Diplura

#### Reference specimens and outgroups

Thirty specimens of historical, phase 3 and phase 1 and 2 repeats of Diplura from Robe Valley were sequenced for COI (Table 39). A neighbour-joining analysis of the five specimens for which sequences were obtained placed the specimens in three distinct lineages (Figure 19). Each lineage contained between one and two specimens (Figure 19). A representative of each of the three lineages was analysed with 34 specimens of Diplura from 13 sites in the Pilbara belonging to five families: Anajapygidae, Campodeidae, Japygidae, Parajapygidae and Projapygidae, as well as five Genbank voucher specimens, Diplura sp., which is most similar to Genbank specimens of Campodeidae (Genbank accession #HQ943342), *Campodea tillyardi* (Genbank accession # AF370844) and *Lepiodocampa weberi* (Genbank accession #HQ882832) from the family Campodeidae, *Parajapyx pauliani* (Genbank accession #JQ692327) from the family Parajapygidae and *Japyx solifugus* (Genbank accession #AY771989) from the family Japygidae. The planthopper *Lycorma delicatula* (Genbank

accession # FJ456942) and a specimen of Fulgoridae (Hemiptera sp.; Genbank accession #GU671563) were used as outgroups.

#### *Phylogenetic analysis*

The phylogenetic analysis, which included the three specimens of Diplura from Robe Valley in addition to 39 reference specimens, placed the Robe Valley specimens in three distinct lineages (Figure 20). The Robe Valley specimens were not placed in lineages containing reference specimens, however, the three lineages were placed in a clade containing reference specimens of Parajapygidae, and were assigned to the new lineages DPA003, DPA005 and DP006 (Figure 20).

#### *Differentiation within and between lineages*

The three lineages from the Robe Valley differed from one another by between 11.9 and 18.8% mean sequence divergence (Table 40). Differentiation between individuals within lineages averaged between 0.3 and 1.8% sequence divergence (Table 41). The three Robe Valley lineages all differed from the nearest reference specimen (JF37 from Mesa H) by between 16.0 and 19.1% sequence divergence (Table 42).

### Diplopoda

#### *Reference specimens and outgroups*

Twenty-six historical and Phase 3 specimens of Diplopoda, assigned to the order Polydesmida on the basis of morphology, were sequenced for COI (Table 43). A neighbour-joining analysis of the eight specimens for which sequences were obtained placed the specimens in two distinct lineages (Figure 21). Each lineage contained between one and seven specimens (Figure 21).

A representative of each of the two lineages was analysed with three Genbank voucher sequences of Diplopoda: *Appalachioria falcifera* (family Xystrodesmidae; Genbank accession #JX437063), *Sellanucheza grandis* (family Paradoxosomatidae; Genbank accession #KR818294), and *Polydesmus* sp (family Polydesmidae; Genbank accession # HQ979247), as well as 48 reference specimens of Diplopoda from 16 sites in the Pilbara. Two specimens of Chilopoda, *Scolopocryptops nigridius* (Genbank accession # JX422680) and *Scolopocryptops rubiginosus* (Genbank accession # JX422682) were used as outgroups.

#### *Phylogenetic analysis*

The phylogenetic analysis, which included the two new representatives from Robe Valley in addition to 48 reference specimens, placed the Robe Valley specimens in two distinct lineages (Figure 22). One Robe Valley lineage also contained a reference lineage from Hardey River, assigned to the family Haplodesmidae, on the basis of morphology and was therefore assigned to the existing lineage DIHAP001 (Figure 22). This lineage was placed in a well-supported clade containing the Genbank reference specimen of Xystrodesmidae (Figure 22). The second Robe Valley lineage did not contain any reference specimens, however it was placed in a well-supported clade with unassigned specimens and specimens assigned to the family Haplodesmidae on the basis of morphology from Red Hill, Hardey River and Buckland Hills (Figure 22).

#### *Differentiation within and between lineages*

The two Robe Valley lineages of Diplopoda differed from one another by 20.7% mean sequence divergence (Table 44). Specimens within lineage differed by x% mean sequence divergence (Table 45). The Robe Valley lineage DIHAP001 of Diplopoda differed from the nearest reference specimen by 1.8% sequence divergence and lineage DIHAP005 differed from the nearest reference specimen by 8.3% sequence divergence (Table 46).

## Conclusions

### Amphipoda

One lineage of Paramelitidae (AMP023) was detected at the Robe River Valley. The lineage was placed in a reference lineage from Barrow Island, differing from that reference lineage by 1.3%, indicating that it represents a species that has been detected previously.

### Paramelitidae

AMP023 = one species, detected previously at Barrow Island

Two lineages of Melitidae were detected at Robe Valley, differing from one another by 4.1% mean sequence divergence. Both were placed in a well-supported clade containing a group of closely related lineages, including *Nedsia* sp. 1, which differed by approximately 5% sequence divergence or less. Thus the group may represent several closely related species, or may represent a single species showing genetic differentiation across its range. Further investigation may be required to resolve relationships among the lineages, but the most likely explanation would be to consider them a single species.

### Melitidae

AMP001 + AMP027 = one species of *Nedsia*, previously detected, but may require further investigation

### Isopoda

Nine distinct genetic lineages of Isopoda were detected at Robe Valley. Three of the lineages (ISP001, ISA009a and ISA008) were placed in reference lineages, differing from those reference lineages by < 3%, indicating that they represent species that have been detected previously.

Two lineages (ISA055 and ISA009q) differed from the nearest reference lineages (ISA005 and ISA009b, respectively, from a previous survey in the Robe Valley) by between 4 and 5%, suggesting that they are likely to belong to those previously-detected species, although further investigation may be required to resolve the relationship between the two lineages.

The remaining five lineages differed from the reference lineages by >10% sequence divergence, indicating that each is likely to represent a new species, which have so far not been detected in the Pilbara, based on the material available for comparison.

### Armadillidae

ISA008 = one species, detected previously at Robe Valley

ISA009a = one species, detected previously at Robe Valley

ISA054 = one species, new

ISA055 = one species, may belong to species ISA005 but requires further investigation

### Philosciidae

ISP001 = one species, detected previously at Robe Valley

ISP050 = one species, new

ISP051 = one species, new

ISP052 = one species, new

ISP053 = one species, new

### Diplura

Three distinct genetic lineages of Diplura were detected at Robe Valley. The three lineages differed from the reference lineages by >15% sequence divergence, indicating that each is likely to represent a new species, which have so far not been detected in the Pilbara, based on the material available for comparison. The lineages were placed in a clade containing Genbank reference and Pilbara specimens of Parajapygidae, thus they are likely to belong to this family.

### Parajapygidae:

DPA003 = one species, new

DPA005 = one species, new

DPA006 = one species, new

## Diplopoda

Two distinct genetic lineages of Diplopoda were detected at Robe Valley in the present study. The two lineages differed from one another by >20% sequence divergence, thus each represents a separate species. One of the lineages differed from a reference lineage by <2% sequence divergence, indicating that the species has been detected previously. The reference specimen was assigned to the family Halplodesmidae on the basis of morphology, however the lineage was placed in a larger clade containing the Genbank specimen of Xystrodesmidae, so we have tentatively placed it in the Haplodesmidae, however further morphological investigation is needed to determine its taxonomic placement. The second lineage from the present study differed from the nearest reference lineage by >8% sequence divergence, this it is likely to represent a new species, which has so far not been detected in the Pilbara, based on the material available for comparison. This lineage was also placed in a clade containing Pilbara specimens of Haplodesmidae thus it may belong to this family.

## Haplodesmidae

DIHAP001 = one species, previously detected at Hardey River

DIHAP005 = one species, new

Table 30. Specimens of Amphipoda used in the present study and the lineage to which they were assigned, based on variation at the COXI gene. nd=no data. Provenance is classified as either historical (H), by phase (P) or as provided by the WAM (WAM); re=repeat.

Specimen ID	Drillhole ID	Provenance	Helix ID	PCR
IV102	Daves bore	P1/2 re	IV102	NoAmp
IV115	TOBRC009	P1/2 re	IV115	AMP023
IV116	TOBRC009	P1/2 re	IV116	AMP023
IV117	TOBRC009	P1/2 re	IV117	AMP023
IV118	TOBRC009	P1/2 re	IV118	AMP023
IV119	TOBRC009	P1/2 re	IV119	AMP023
IV122	Budgie	P1/2 re	IV122	AMM001
IV124	Budgie	P1/2 re	IV124	AMM027
IV131	Daves	P1/2 re	IV131	NoAmp
IV136	TOBRC009	P1/2 re	IV136	contam
IV96	Budgie bore	P1/2 re	IV96	AMM001
IV97	Camp bore	P1/2 re	IV97	AMM001
IV98	Camp bore	P1/2 re	IV98	AMM001
IV99	Daisy well	P1/2 re	IV99	NoAmp
IV101	Daves bore	P1/2 re	IV101	NoAmp
IV103	Daves bore	P1/2 re	IV103	NoAmp
IV110	MB13WARR010	P1/2 re	IV110	NoAmp
IV113	MB13WARR010	P1/2 re	IV113	NoAmp
IV133	RC13MEA0279	P1/2 re	IV133	NoAmp
IV135	TOBRC009	P1/2 re	IV135	NoAmp
IV137	TOBRC009	P1/2 re	IV137	NoAmp
IV138	TOBRC009	P1/2 re	IV138	NoAmp

Table 31. Mean genetic distance (below diagonal) and standard error (above diagonal, in blue) between lineages of Amphipoda detected in the NJ analysis as shown in Figure 14.

Lineage	1	2	3
1		0.008	0.017
2	0.041		0.017
3	0.325	0.330	

Table 32. Mean distance (D) and standard error (s.e.) within lineages of Amphipoda detected in the NJ analysis as shown in Figure 14 and the number (N) of individuals assigned to that lineage. n/c = not calculated, for groups where n=1. Rep=individual selected to represent the lineage in the model-based analysis.

Lineage	D	s.e.	N	Rep
1	0.014	0.004	4	IV97
2	n/c	n/c	1	IV124
3	0.001	0.001	5	IV115

Table 33 (attached). Genetic distances (below diagonal) and standard error (above diagonal, in blue) between specimens of Paramelitidae detected at Robe Valley and the reference lineages as shown in Figure 15.

Table 34 (attached). Genetic distances (below diagonal) and standard error (above diagonal, in blue) between specimens of Melitidae detected at Robe Valley and the reference lineages as shown in Figure 16.

Table 35. Specimens of Isopoda used in the present study and the lineage to which they were assigned, based on variation at the COXI gene. nd=no data. Provenance is classified as either historical (H), by phase (P) or as provided by the WAM (WAM); re=repeat.

Specimen ID	Drillhole ID	Provenance	Helix ID	Lineage
K0989-0712-T2-5	K0989	H	IV356	ISP050
K0989-0712-T2-5	K0989	H	IV357	No Amp
RC12COB0002P1T2-3	RC12COB0002	H	IV358	ISP051
MEBRC00620712T3-2	MEBRC0062	H	IV359	ISP053
MEBRC0005A0712T2-2a	MEBRC0005A	H	IV360	No Amp
MEBRC0005A0712T2-2b	MEBRC0005A	H	IV361	No Amp
MEBRC0005A0712T2-2c	MEBRC0005A	H	IV362	No Amp
MEBRC0005A0712T2-2d	MEBRC0005A	H	IV363	No Amp
MEBRC0005A0712T3-2	MEBRC0005A	H	IV364	No Amp
MEADC2517a-0712-T3-3	MEADC2517a	H	IV365	No Amp
MEK1735a-0712-T1-3	MEK1735a	H	IV366	ISP050
60063		H	IV305	ISA009a
60728		H	IV306	No Amp
60772		H	IV307	No Amp
60730		H	IV308	No Amp
48098		H	IV309	No Amp
42735		H	IV310	No Amp
60773		H	IV311	No Amp
66905		H	IV312	ISP052
60774		H	IV313	No Amp
60720		H	IV314	No Amp
48092		H	IV315	No Amp
66906		H	IV316	ISP053
60769		H	IV317	ISP001
60060		H	IV318	ISA009a
48094		H	IV319	No Amp
DD14MEC0001-20160316-T2-03	DD14MEC0001	P3	IV367	ISA054
GR15MEB0004-20160317-T2-01a	GR15MEB0004	P3	IV368	ISA055
GR15MEB0004-20160317-T2-01b	GR15MEB0004	P3	IV369	Messy seq
GR15MEB0008-20160317-T2-03	GR15MEB0008	P3	IV370	ISA008
RC15MEB0216-20160317-T1-01	RC15MEB0216	P3	IV371	ISA055
RC15MEC0192-20160316-T3-06	RC15MEC0192	P3	IV372	ISA054
RC15MEC0199-20160316-T1-04	RC15MEC0199	P3	IV373	ISA054
RC15MEC0199-20160316-T3-01	RC15MEC0199	P3	IV374	ISA054
60719	M2ERC026	P1/2 re	IV161	ISP001
60722	M2ERC029	P1/2 re	IV164	ISP001
60724	MEARC3811	P1/2 re	IV182	No Amp
60725	MEARC4795	P1/2 re	IV183	contam
60767	M2ERC053	P1/2 re	IV166	ISP001
60770	MEARC4795	P1/2 re	IV184	contam
60771	MEARC4795	P1/2 re	IV185	contam

Table 36. Mean genetic distance (below diagonal) and standard error (above diagonal, in blue) between lineages of Isopoda detected in the NJ analysis as shown in Figure 17.

Lineage	1	2	3	4	5	6	7	8	9
1		<b>0.015</b>	<b>0.016</b>	<b>0.016</b>	<b>0.015</b>	<b>0.016</b>	<b>0.014</b>	<b>0.016</b>	<b>0.016</b>
2	0.151		<b>0.017</b>	<b>0.015</b>	<b>0.015</b>	<b>0.014</b>	<b>0.015</b>	<b>0.017</b>	<b>0.018</b>
3	0.177	0.184		<b>0.015</b>	<b>0.014</b>	<b>0.015</b>	<b>0.016</b>	<b>0.017</b>	<b>0.017</b>
4	0.200	0.199	0.196		<b>0.011</b>	<b>0.015</b>	<b>0.016</b>	<b>0.017</b>	<b>0.017</b>
5	0.205	0.177	0.197	0.113		<b>0.015</b>	<b>0.016</b>	<b>0.016</b>	<b>0.017</b>
6	0.233	0.228	0.224	0.230	0.226		<b>0.015</b>	<b>0.016</b>	<b>0.016</b>
7	0.227	0.244	0.238	0.226	0.215	0.201		<b>0.014</b>	<b>0.015</b>
8	0.219	0.246	0.236	0.233	0.217	0.203	0.165		<b>0.013</b>
9	0.236	0.249	0.248	0.235	0.225	0.214	0.188	0.121	

Table 37. Mean distance (D) and standard error (s.e.) within lineages of Isopoda detected in the NJ analysis as shown in Figure 17 and the number (N) of individuals assigned to that lineage. n/c = not calculated, for groups where n=1. Rep=individual selected to represent the lineage in the model-based analysis.

Lineage	D	s.e.	N	Rep
1	0.000	0.000	4	IV166
2	0.000	0.000	2	IV356
3	n/c	n/c	1	IV358
4	n/c	n/c	1	IV312
5	0.001	0.001	2	IV316
6	0.001	0.001	2	IV368
7	0.010	0.004	2	IV305
8	n/c	n/c	1	IV370
9	0.003	0.001	4	IV372

Table 38 (attached). Genetic distances (below diagonal) and standard error (above diagonal, in blue) between specimens of Isopoda detected at Robe Valley and the reference lineages as shown in Figure 18.

Table 39. Specimens of Diplura used in the present study and the lineage to which they were assigned, based on variation at the COXI gene. nd=no data. Provenance is classified as either historical (H), by phase (P) or as provided by the WAM (WAM); re=repeat.

Specimen ID	Drillhole ID	Provenance	Helix ID	PCR
SSp-2010-209	COBRC0022	H	IV320	NoAmp
SSp-2010-287	COBRC0008	H	IV321	NoAmp
SSp-2010-291	DCBRC_001	H	IV322	NoAmp
SSp-2010-37	COBRC0012	H	IV323	NoAmp
SSp-2010-40	TOBRC0043	H	IV324	NoAmp
SSp-2010-79	COBRC0003	H	IV325	NoAmp
GR15MEB0001-20160317-T2-01	GR15MEB0001	P3	IV236	Contam/Mis-ID?
GR15MEB0008-20160317-T2-01	GR15MEB0008	P3	IV237	contam
GR15MEB0014-20160316-Sc-01	GR15MEB0014	P3	IV238	NoAmp
GR15MEC0001-20160316-T2-01	GR15MEC0001	P3	IV239	NoAmp

GR15MEC0001-20160316-T2-02	GR15MEC0001	P3	IV240	Contam/Mis-ID?
GR15MEC0001-20160316-T2-03	GR15MEC0001	P3	IV241	contam
GR15MEC0001-20160316-T2-04	GR15MEC0001	P3	IV242	NoAmp
GR15MEC0001-20160316-T2-05	GR15MEC0001	P3	IV243	NoAmp
GR15MEC0008-20160316-T2-01	GR15MEC0008	P3	IV244	NoAmp
RC15MEB0171-20160317-T1-01	RC15MEB0171	P3	IV245	DPA003
RC15MEC0001-20160316-T2-01	RC15MEC0001	P3	IV246	NoAmp
RC15MEC0027-20160316-T3-01	RC15MEC0027	P3	IV247	NoAmp
RC15MEC0192-20160316-T1-01	RC15MEC0192	P3	IV248	DPA005
RC15MEC0192-20160316-T1-02	RC15MEC0192	P3	IV249	DPA005
RC15MEC0192-20160316-T1-03	RC15MEC0192	P3	IV250	DPA006
RC15MEC0192-20160316-T3-01	RC15MEC0192	P3	IV251	NoAmp
RC15MEC0192-20160316-T3-02	RC15MEC0192	P3	IV252	NoAmp
RC15MEC0197-20160316-T1-01	RC15MEC0197	P3	IV253	NoAmp
RC15MEC0197-20160316-T2-02A	RC15MEC0197	P3	IV254	NoAmp
RC15MEC0197-20160316-T2-02B	RC15MEC0197	P3	IV255	NoAmp
RC15MEC0200-20160316-T2-01	RC15MEC0200	P3	IV256	Messy seq
RC15MEC0200-20160316-T3-02	RC15MEC0200	P3	IV257	NoAmp
IV158	MEARC5017	P1/2 re	IV158	NoAmp
IV160	MEARC3790	P1/2 re	IV160	NoAmp

Table 40. Mean genetic distance (below diagonal) and standard error (above diagonal, in blue) between lineages of Diplura detected in the NJ analysis as shown in Figure 19.

Lineage	1	2	3
1		0.012	0.014
2	0.119		0.014
3	0.188	0.188	

Table 41. Mean distance (D) and standard error (s.e.) within lineages of Diplura detected in the NJ analysis as shown in Figure 19 and the number (N) of individuals assigned to that lineage. n/c = not calculated, for groups where n=1. Rep=individual selected to represent the lineage in the model-based analysis.

Lineage	D	s.e.	N	Rep
1	0.003	0.002	2	IV248
2	n/c	n/c	1	IV245
3	0.018	0.005	2	IV250

Table 42 (attached). Genetic distances (below diagonal) and standard error (above diagonal, in blue) between specimens of Diplura detected at Robe Valley and the reference lineages as shown in Figure 20.

Table 43. Specimens of Diplopoda used in the present study and the lineage to which they were assigned, based on variation at the COXI gene. nd=no data. Provenance is classified as either historical (H), by phase (P) or as provided by the WAM (WAM); re=repeat.

Specimen ID	Drillhole ID	Provenance	Helix ID	PCR
120194		H	IV296	contam
120162		H	IV297	Messy seq

138444		H	IV298	DIHAP001
138445		H	IV299	Messy Seq
139890		H	IV300	DIHAP001
139891		H	IV301	DIHAP001
139892		H	IV302	DIHAP001
139893		H	IV303	DIHAP001
139894		H	IV304	DIHAP001
120138		H	WAM seq	contam
127096	MEK1685	H	WAM seq	contam
RC14MEB0102-20160317-T3-01	RC14MEB0102	P3	IV375	contam
RC14MEB0102-20160317-T3-02	RC14MEB0102	P3	IV376	contam
RC14MEB0102-20160317-T3-03	RC14MEB0102	P3	IV377	Messy seq
RC14MEB0102-20160317-T3-04	RC14MEB0102	P3	IV378	contam
RC14MEB0102-20160317-T3-05	RC14MEB0102	P3	not sent	-
RC14MEB0115-20160317-T2-01	RC14MEB0115	P3	IV379	DIHAP005
RC15MEC0193-20160316-T1-03	RC15MEC0193	P3	IV380	contam
RC15MEC0193-20160316-T1-04	RC15MEC0193	P3	IV381	contam
RC15MEC0193-20160316-T1-05	RC15MEC0193	P3	IV382	contam
RC15MEC0193-20160316-T3-01	RC15MEC0193	P3	IV383	DIHAP001
RC15MEC0193-20160316-T3-02	RC15MEC0193	P3	empty tube	-
RC15MEC0193-20160316-T3-05	RC15MEC0193	P3	IV384	Messy Seq
RC15MEC0199-20160316-T1-02	RC15MEC0199	P3	IV385	contam
RC15MEC0199-20160316-T1-03	RC15MEC0199	P3	IV386	Messy Seq
RC15MEC0199-20160316-T2-01	RC15MEC0199	P3	IV387	Failed repeat PCR

Table 44. Mean genetic distance (below diagonal) and standard error (above diagonal, in blue) between lineages of Diplopoda detected in the NJ analysis as shown in Figure 21.

Lineage	1	2
1		0.013
2	0.207	

Table 41. Mean distance (D) and standard error (s.e.) within lineages of Diplopoda detected in the NJ analysis as shown in Figure 21 and the number (N) of individuals assigned to that lineage. n/c = not calculated, for groups where n=1. Rep=individual selected to represent the lineage in the model-based analysis.

Lineage	D	s.e.	N	Rep
1	0.007	0.002	7	IV383
2	n/c	n/c	1	IV379

Table 42 (attached). Genetic distances (below diagonal) and standard error (above diagonal, in blue) between specimens of Diplopoda detected at Robe Valley and the reference lineages as shown in Figure 22.

Figure 14. Neighbour-joining analysis of specimens of Amphipoda from the present study. Numbers on major nodes correspond to bootstrap support over 100 iterations; values <50% are not shown. Scale bar= genetic distance. The specimens used to represent each lineage in the model-based phylogenetic analysis are highlighted in yellow.

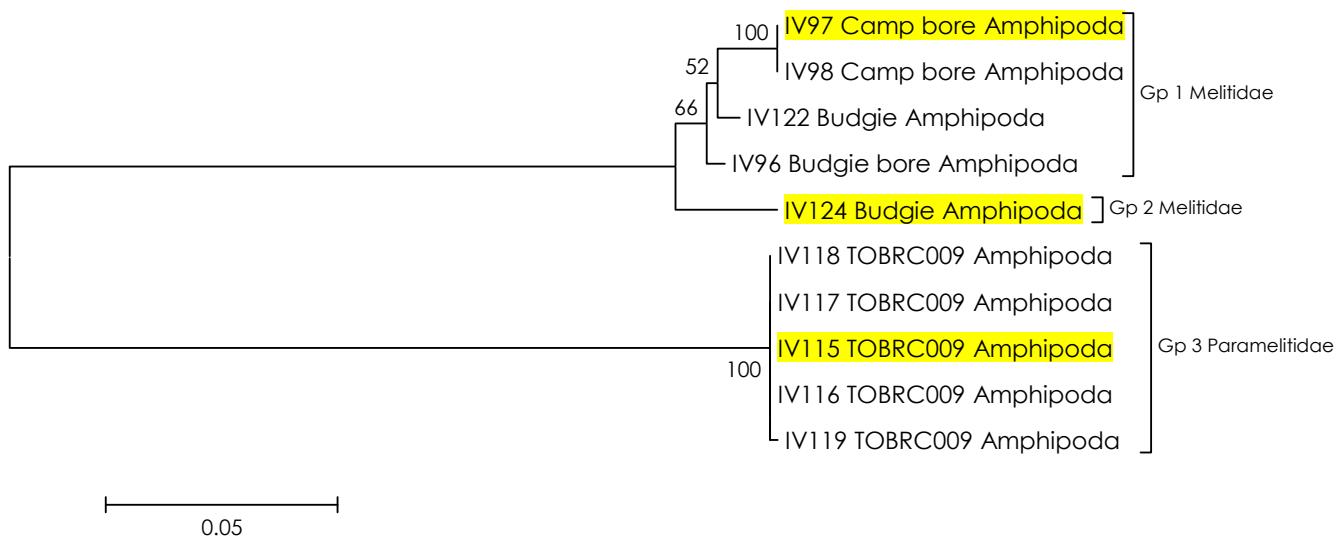


Figure 15. Bayesian analysis of COXI haplotypes of Paramelitidae (Amphipoda) from the present study and reference specimens from previous surveys in the Pilbara. Numbers on major nodes correspond to posterior probabilities; values <50% are not shown. Specimens from the present study are highlighted in yellow; GenBank voucher specimens highlighted in turquoise. Scale bar= number of substitutions per site.

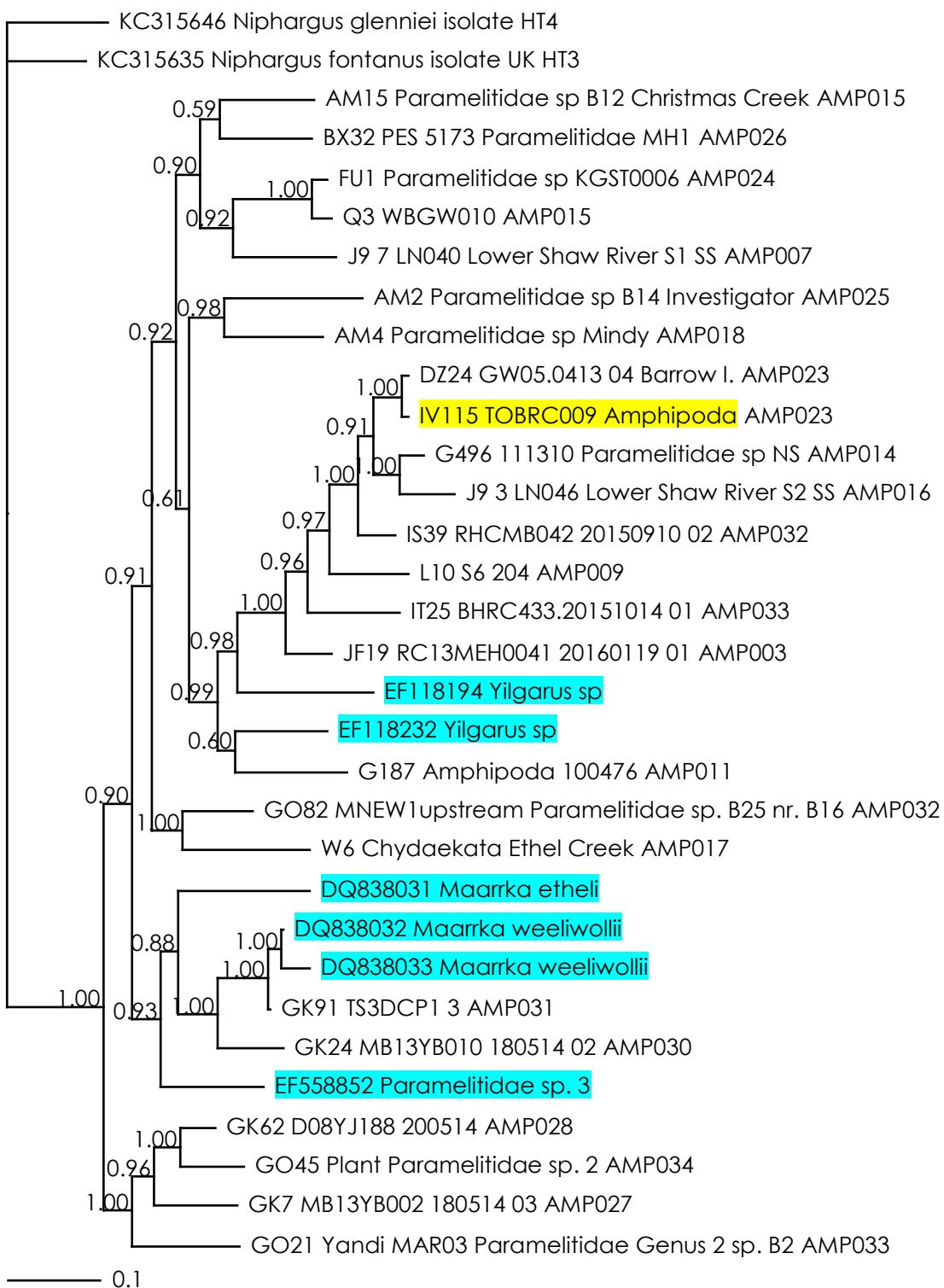


Figure 16. Bayesian analysis of COXI haplotypes of Melitidae (Amphipoda) from the present study and reference specimens from previous surveys in the Pilbara. Numbers on major nodes correspond to posterior probabilities; values <50% are not shown. Specimens from the present study are highlighted in yellow; GenBank voucher specimens highlighted in turquoise. Scale bar= number of substitutions per site. Red box contains putative species, Nedsia sp. 1.

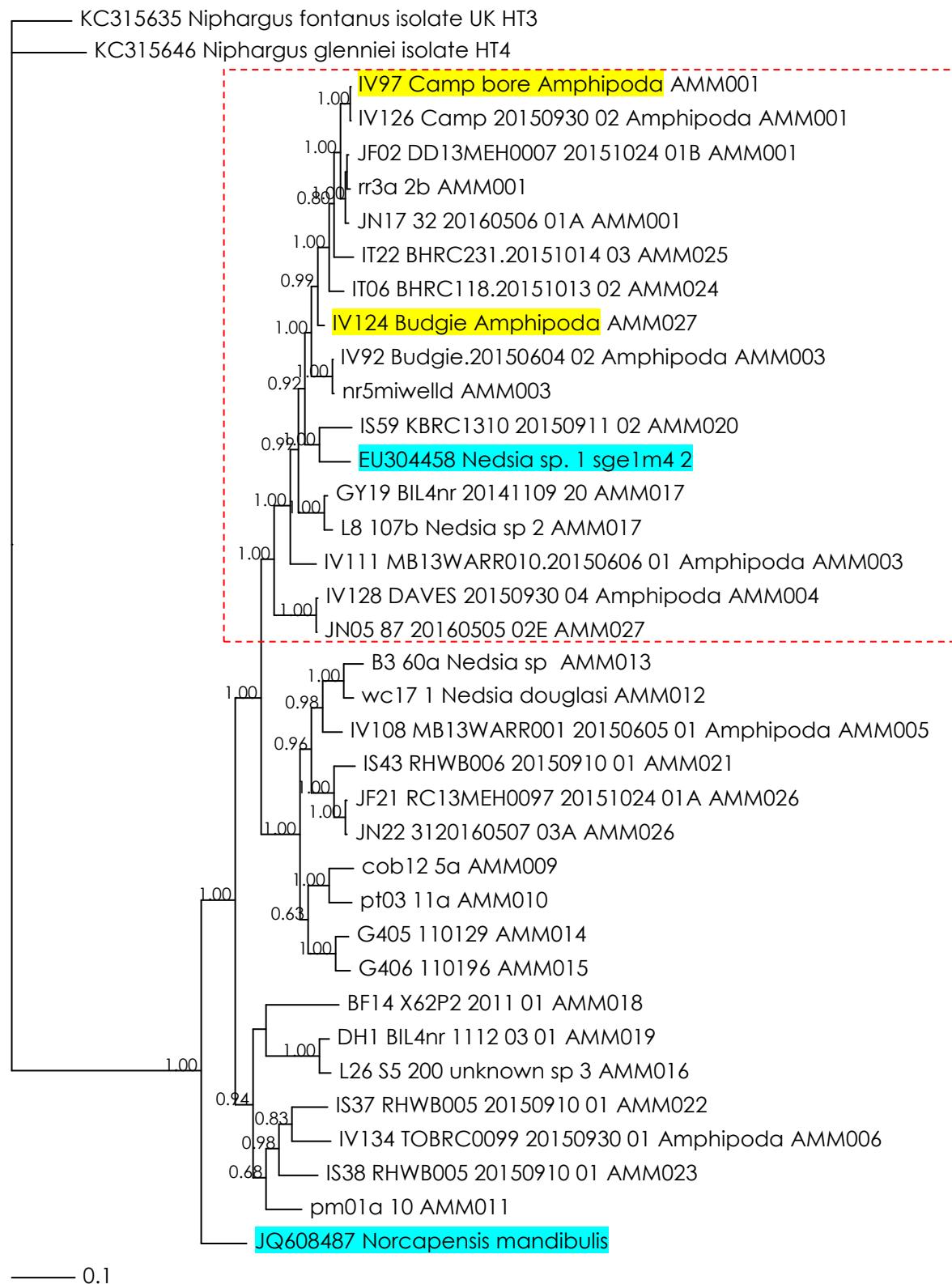


Figure 17. Neighbour-joining analysis of specimens of Isopoda from the present study. Numbers on major nodes correspond to bootstrap support over 100 iterations; values <50% are not shown. Scale bar= genetic distance. The specimens used to represent each lineage in the model-based phylogenetic analysis are highlighted in yellow.

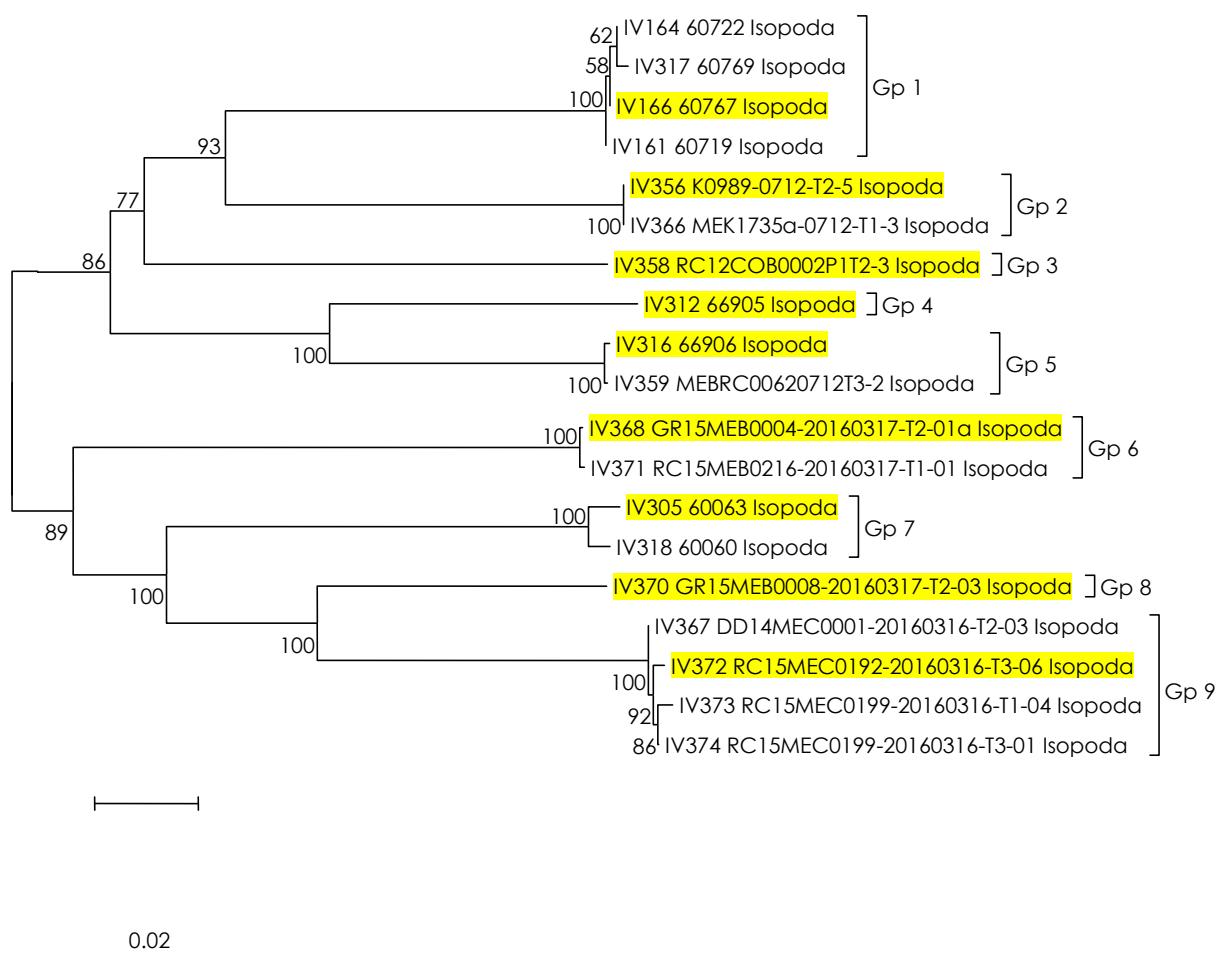


Figure 18. Bayesian analysis of COXI haplotypes of Isopoda from the present study and reference specimens from previous surveys in the Pilbara. Numbers on major nodes correspond to posterior probabilities; values <50% are not shown. Specimens from the present study are highlighted in yellow; GenBank voucher specimens highlighted in turquoise. Scale bar= number of substitutions per site.

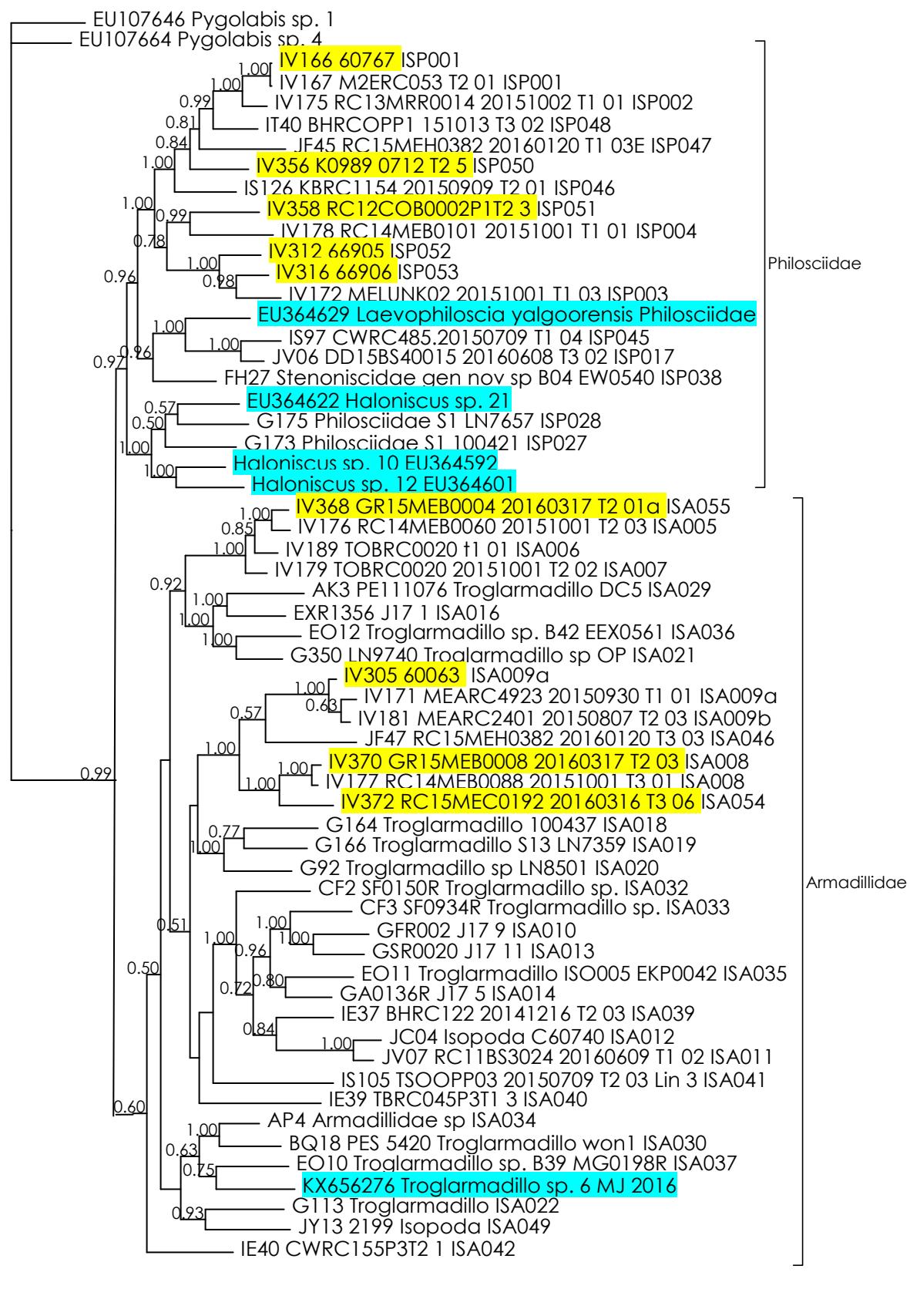


Figure 19. Neighbour-joining analysis of specimens of Diplura from the present study. Numbers on major nodes correspond to bootstrap support over 100 iterations; values <50% are not shown. Scale bar= genetic distance. The specimens used to represent each lineage in the model-based phylogenetic analysis are highlighted in yellow.

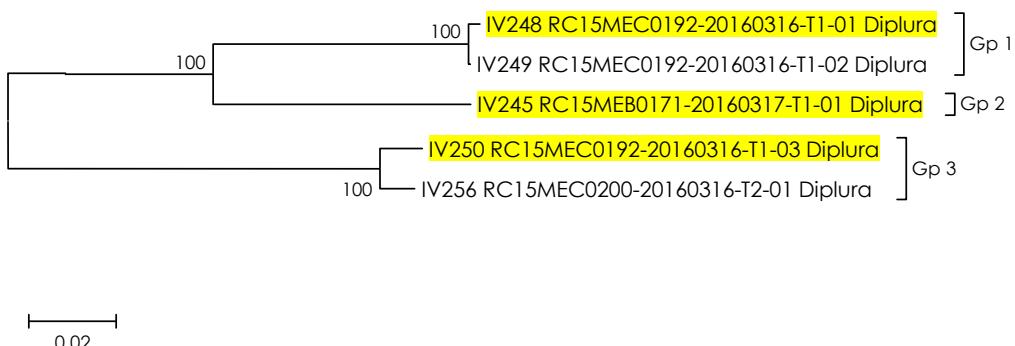


Figure 20. Bayesian analysis of COXI haplotypes of Diplura from the present study and reference specimens from previous surveys in the Pilbara. Numbers on major nodes correspond to posterior probabilities; values <50% are not shown. Specimens from the present study are highlighted in yellow; GenBank voucher specimens highlighted in turquoise. Scale bar= number of substitutions per site.

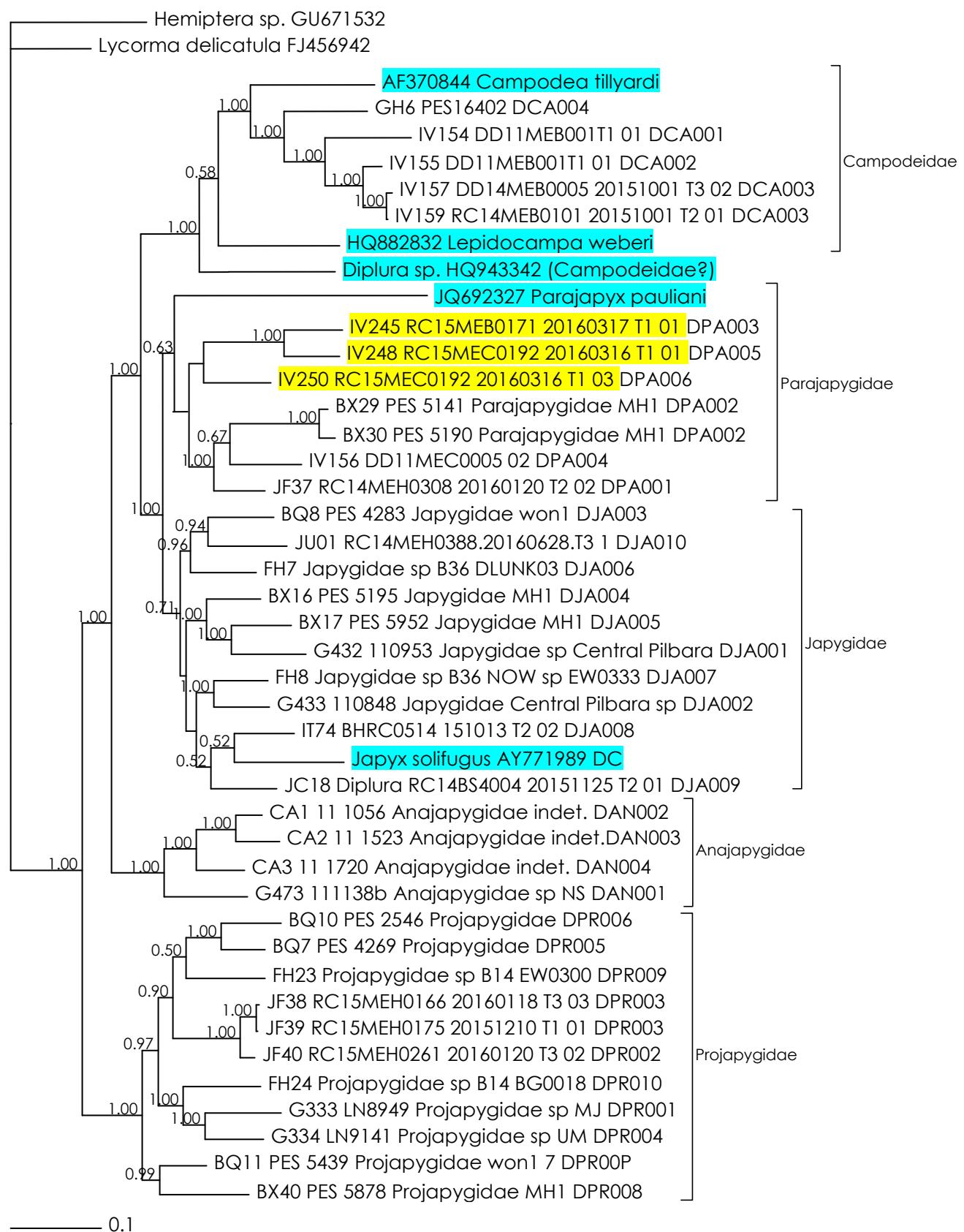


Figure 21. Neighbour-joining analysis of specimens of Diplopoda from the present study. Numbers on major nodes correspond to bootstrap support over 100 iterations; values <50% are not shown. Scale bar= genetic distance. The specimens used to represent each lineage in the model-based phylogenetic analysis are highlighted in yellow.

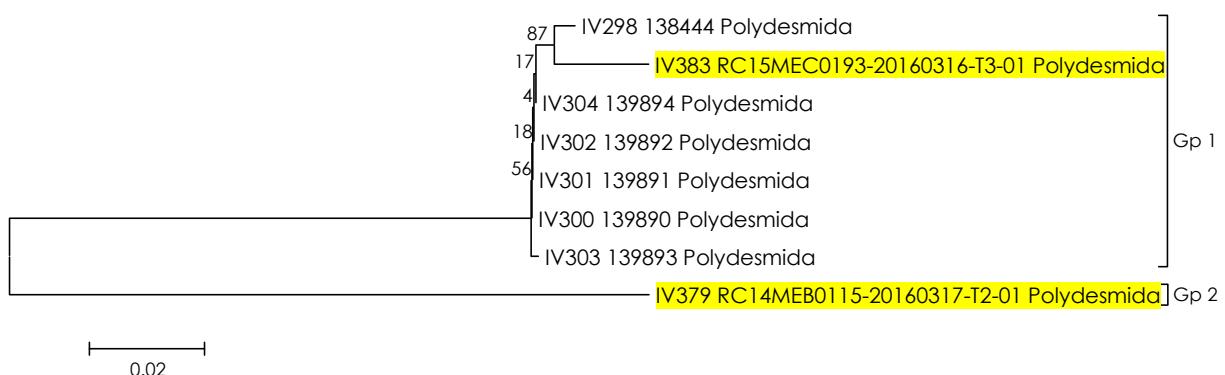
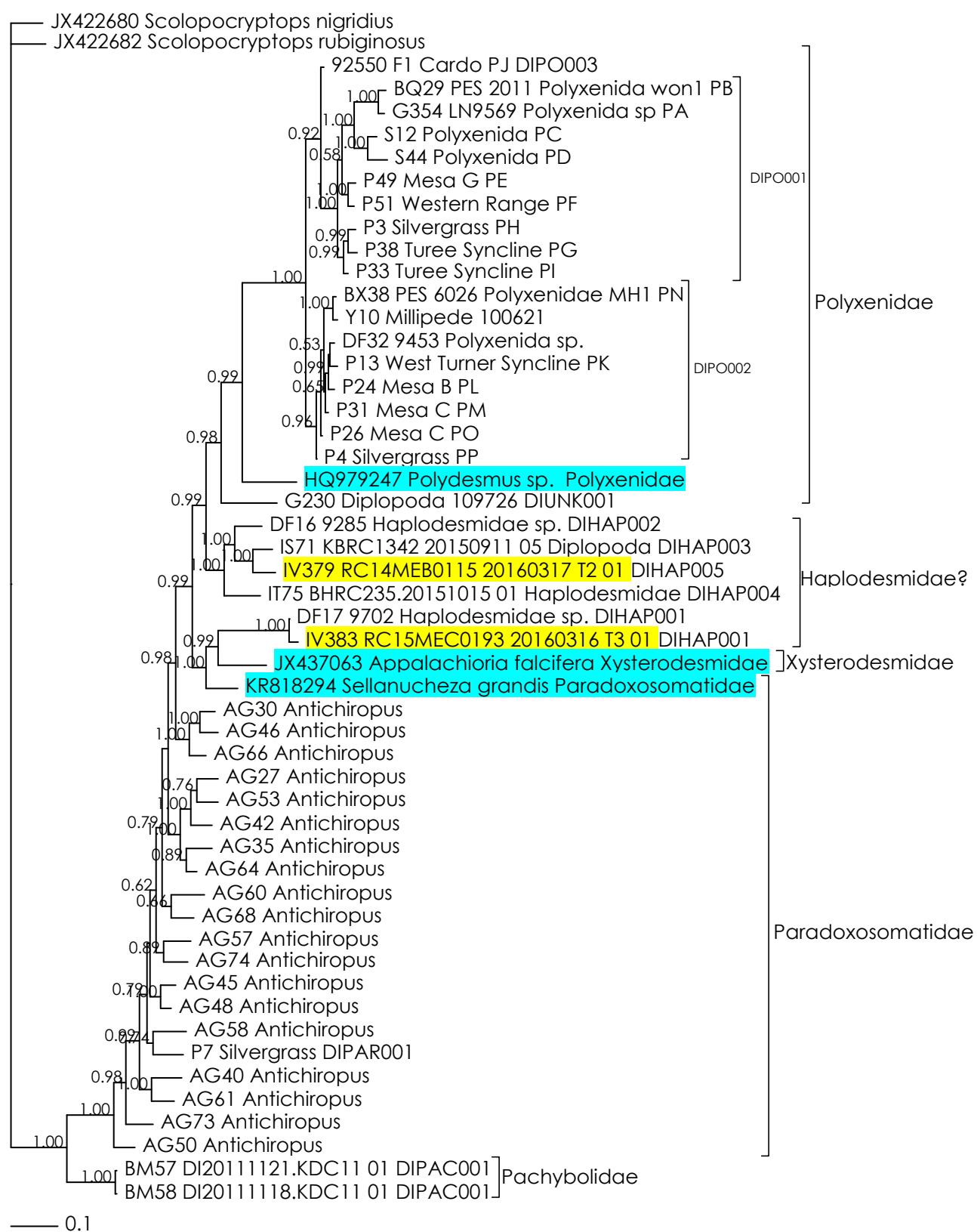


Figure 22. Bayesian analysis of COXI haplotypes of Diplopoda from the present study and reference specimens from previous surveys in the Pilbara. Numbers on major nodes correspond to posterior probabilities; values <50% are not shown. Specimens from the present study are highlighted in yellow; GenBank voucher specimens highlighted in turquoise. Scale bar= number of substitutions per site.



**Table 33. Estimates of Evolutionary Divergence between Sequences**

Lineage	IV115	AM15	AM2	AM4	BX32	Meth	Mww	Mww	DZ24	Yil-sp	Yil-sp	Par-sp3	FU1	G187	G496	GK24	GK62	GK7	GK91	GO21	GO45	GO82	IS39	IT25	J9_3	J9_7	JF19	L10	Q3	W6	
IV115 TOBRC009 Amphipoda		0.015	0.017	0.017	0.016	0.018	0.017	0.017	0.004	0.017	0.016	0.014	0.017	0.017	0.012	0.018	0.015	0.015	0.017	0.017	0.015	0.011	0.018	0.014	0.017	0.012	0.014	0.020	0.016		
AM15 Paramelitidae sp B12 Christmas Creek	0.218		0.014	0.015	0.015	0.014	0.015	0.015	0.015	0.014	0.015	0.014	0.014	0.014	0.014	0.012	0.013	0.013	0.016	0.014	0.015	0.015	0.018	0.017	0.017	0.016	0.017	0.021	0.016		
AM2 Paramelitidae sp B14 Investigator	0.232	0.214		0.015	0.016	0.017	0.018	0.018	0.017	0.017	0.017	0.016	0.015	0.015	0.015	0.015	0.015	0.017	0.015	0.015	0.014	0.016	0.021	0.017	0.017	0.015	0.017	0.021	0.016		
AM4 Paramelitidae sp Mindy	0.240	0.193	0.211		0.017	0.015	0.016	0.018	0.017	0.015	0.017	0.015	0.016	0.013	0.015	0.013	0.015	0.014	0.015	0.017	0.017	0.014	0.016	0.020	0.017	0.018	0.016	0.018	0.023	0.016	
BX32 PES-5173 Paramelitidae MH1	0.220	0.178	0.204	0.195		0.015	0.016	0.016	0.015	0.015	0.017	0.017	0.016	0.014	0.015	0.016	0.016	0.016	0.016	0.016	0.016	0.014	0.017	0.015	0.017	0.015	0.016	0.022	0.016		
DQ838031 Maarrka etheli	0.229	0.231	0.229	0.231	0.233		0.013	0.016	0.018	0.016	0.015	0.014	0.016	0.014	0.016	0.015	0.016	0.014	0.013	0.017	0.018	0.016	0.016	0.020	0.020	0.016	0.016	0.017	0.021	0.017	
DQ838032 Maarrka weelivollii	0.213	0.199	0.234	0.225	0.216	0.194		0.007	0.017	0.014	0.014	0.013	0.015	0.015	0.016	0.012	0.014	0.015	0.005	0.016	0.015	0.016	0.016	0.019	0.017	0.014	0.016	0.018	0.023	0.015	
DQ838033 Maarrka weelivollii	0.217	0.201	0.234	0.229	0.224	0.201	0.030		0.017	0.015	0.013	0.014	0.016	0.017	0.018	0.013	0.015	0.016	0.008	0.016	0.015	0.016	0.016	0.020	0.017	0.014	0.016	0.018	0.023	0.017	
DZ24 GW05.0413-04	0.013	0.212	0.239	0.237	0.224	0.230	0.214	0.218		0.017	0.016	0.014	0.017	0.017	0.012	0.018	0.016	0.015	0.017	0.016	0.017	0.015	0.010	0.018	0.013	0.018	0.012	0.013	0.020	0.016	
EF118194 Yilgarus sp	0.218	0.216	0.254	0.243	0.202	0.236	0.211	0.221	0.209		0.015	0.014	0.015	0.014	0.016	0.014	0.013	0.015	0.014	0.016	0.014	0.015	0.016	0.020	0.016	0.017	0.015	0.016	0.022	0.014	
EF118232 Yilgarus sp	0.208	0.194	0.223	0.212	0.176	0.238	0.200	0.205	0.209	0.197		0.015	0.014	0.015	0.015	0.014	0.014	0.014	0.014	0.014	0.015	0.015	0.015	0.014	0.017	0.016	0.015	0.016	0.020	0.015	
EF558852 Paramelitidae sp. 3	0.208	0.213	0.242	0.236	0.219	0.202	0.194	0.203	0.207	0.211	0.202		0.016	0.014	0.016	0.013	0.013	0.015	0.016	0.014	0.015	0.021	0.018	0.016	0.015	0.017	0.023	0.015			
FU1 Paramelitidae sp KGST0006	0.218	0.175	0.217	0.184	0.194	0.226	0.217	0.224	0.225	0.233	0.197	0.211		0.014	0.016	0.013	0.013	0.016	0.015	0.015	0.014	0.014	0.017	0.022	0.019	0.016	0.016	0.018	0.010	0.018	
G187 Amphipoda 100476 AC	0.209	0.203	0.227	0.210	0.222	0.244	0.224	0.224	0.208	0.213	0.184	0.212	0.213		0.015	0.015	0.013	0.014	0.015	0.016	0.014	0.014	0.015	0.021	0.017	0.017	0.016	0.017	0.018	0.014	
G496 111310 Paramelitidae sp NS AA	0.083	0.212	0.233	0.215	0.212	0.226	0.220	0.226	0.079	0.219	0.205	0.211	0.229	0.208		0.015	0.015	0.014	0.016	0.017	0.017	0.015	0.011	0.018	0.011	0.017	0.012	0.014	0.020	0.015	
GK24 MB13YB010-180514-02	0.213	0.190	0.218	0.221	0.204	0.205	0.140	0.145	0.208	0.202	0.187	0.179	0.212	0.207	0.212		0.013	0.013	0.011	0.015	0.015	0.014	0.014	0.015	0.019	0.017	0.016	0.015	0.017	0.021	0.016
GK62 D08YJ188-200514-01	0.214	0.190	0.239	0.229	0.190	0.237	0.210	0.219	0.213	0.200	0.207	0.207	0.201	0.215	0.227	0.180		0.012	0.013	0.012	0.011	0.015	0.016	0.018	0.018	0.015	0.014	0.017	0.019	0.015	
GK7 MB13YB002-180514-03	0.194	0.205	0.215	0.210	0.177	0.226	0.204	0.216	0.192	0.220	0.207	0.204	0.208	0.211	0.187	0.186	0.128		0.013	0.013	0.013	0.014	0.015	0.018	0.016	0.017	0.013	0.017	0.023	0.016	
GK91 TS3DCP1-3	0.210	0.193	0.224	0.218	0.205	0.193	0.017	0.046	0.210	0.205	0.197	0.184	0.210	0.219	0.211	0.117	0.193	0.184		0.014	0.013	0.014	0.015	0.019	0.017	0.013	0.016	0.018	0.023	0.014	
GO21 Yandi MAR03 Paramelitidae Genus 2 sp. B2	0.237	0.217	0.236	0.244	0.224	0.255	0.242	0.246	0.231	0.228	0.220	0.219	0.221	0.235	0.233	0.216	0.159	0.184	0.222		0.013	0.015	0.017	0.021	0.019	0.017	0.015	0.017	0.020	0.016	
GO45 Plant Paramelitidae sp. 2 (DEC code)	0.226	0.214	0.239	0.257	0.207	0.239	0.214	0.216	0.226	0.225	0.223	0.211	0.211	0.232	0.247	0.194	0.098	0.151	0.197	0.180		0.015	0.016	0.020	0.018	0.016	0.015	0.018	0.020	0.016	
GO82 MNEW1upstream Paramelitidae sp. B25 (nr. B16)	0.219	0.178	0.215	0.193	0.172	0.225	0.198	0.198	0.221	0.227	0.166	0.208	0.180	0.218	0.221	0.191	0.189	0.177	0.180	0.192	0.192		0.016	0.019	0.016	0.020	0.015	0.022	0.014		
IS39 RHCMB042 20150910 02 Amphipoda	0.081	0.217	0.228	0.216	0.219	0.23																									

Table 34. Estimates of Evolutionary Divergence between Sequences

Specimen ID	IV97 Camp bore Amphipoda	IV124 Budgie Amphipoda	B3 60a Nedsia sp 1	BF14 X62P2-2011-01 Amphipoda	cob12 5a	DH1 BIL4nr-1112-03-01 Amphipoda	G405 110129 Paramelitidae	G406 110196 Paramelitidae	GY19 BIL4nr-20141109-20	IS37 RHWB005 20150910 01 Amphipoda	IS38 RHWB005 20150910 01 Amphipoda	IS43 RHWB006 20150910 01 Amphipoda	IS59 KBRC1310 20150911 02 Amphipoda	IT06 BHRC118.20151013-02 Amphipoda	IT22 BHRC231.20151014-03 Amphipoda	IV108 MB13WARR001-20150605-01 Amphipoda lin 5	IV111 MB13WARR010.20150606-01 Amphipoda lin 3	IV126 Camp-20150930-02 Amphipoda lin 1	IV128 DAVES-20150930-04 Amphipoda lin 4	IV134 TOBRC0099-20150930-01 Amphipoda lin 6	IV92 Budgie.20150604-02 Amphipoda lin 2	JF02 DD13MEH0007-20151024-01B Amphipoda	JF21 RC13MEH0097-20151024-01A Amphipoda	JN05 87-20160505-02E Amphipoda	JN22 3120160507-03A Amphipoda	L26 S5-200 unknown sp 3	L8 107b Nedsia sp 2	Norcapensis mandibulis	nr5miwelld	pm01a 10	pt03 11a	rr3a 2b	sge1m4 2	wc17 1 Nedsia douglasi
IV97 Camp bore Amphipoda	0.010	0.013	0.014	0.015	0.017	0.014	0.015	0.016	0.009	0.015	0.013	0.014	0.013	0.017	0.011	0.007	0.011	0.013	0.014	0.010	0.005	0.013	0.009	0.013	0.016	0.016	0.007	0.014	0.017					
IV124 Budgie Amphipoda	0.052	0.012	0.016	0.015	0.015	0.015	0.015	0.017	0.011	0.015	0.014	0.014	0.014	0.014	0.013	0.011	0.009	0.013	0.012	0.014	0.010	0.009	0.013	0.016	0.016	0.009	0.012	0.015						
B3 60a Nedsia sp	0.153	0.139	0.151	0.151	0.151	0.151	0.151	0.151	0.144	0.144	0.144	0.144	0.144	0.144	0.144	0.143	0.143	0.143	0.143	0.143	0.143	0.143	0.143	0.143	0.143	0.143	0.143	0.143	0.143					
BF14 X62P2-2011-01 Amphipoda	0.182	0.185	0.175	0.161	0.161	0.161	0.161	0.161	0.161	0.161	0.161	0.161	0.161	0.161	0.161	0.161	0.161	0.161	0.161	0.161	0.161	0.161	0.161	0.161	0.161	0.161	0.161	0.161						
cob12 5a	0.149	0.139	0.128	0.174	0.171	0.171	0.171	0.171	0.171	0.171	0.171	0.171	0.171	0.171	0.171	0.171	0.171	0.171	0.171	0.171	0.171	0.171	0.171	0.171	0.171	0.171	0.171	0.171						
DH1 BIL4nr-1112-03-01 Amphipoda	0.166	0.175	0.197	0.169	0.187	0.187	0.187	0.187	0.187	0.187	0.187	0.187	0.187	0.187	0.187	0.187	0.187	0.187	0.187	0.187	0.187	0.187	0.187	0.187	0.187	0.187	0.187	0.187						
G405 110129 Paramelitidae	0.139	0.129	0.111	0.180	0.109	0.192	0.008	0.014	0.015	0.015	0.012	0.014	0.014	0.019	0.010	0.014	0.014	0.016	0.013	0.015	0.012	0.016	0.015	0.016	0.015	0.016	0.015	0.016	0.013					
G406 110196 Paramelitidae	0.144	0.133	0.123	0.181	0.113	0.192	0.041	0.015	0.016	0.015	0.012	0.015	0.015	0.019	0.012	0.015	0.016	0.014	0.014	0.016	0.013	0.017	0.016	0.017	0.013	0.018	0.017	0.014						
GY19 BIL4nr-20141109-20	0.078	0.067	0.158	0.173	0.145	0.155	0.144	0.142	0.014	0.013	0.012	0.012	0.009	0.013	0.013	0.012	0.009	0.011	0.014	0.010	0.010	0.014	0.014	0.005	0.015	0.012	0.016	0.015						
IS37 RHWB005 20150910 01 Amphipoda	0.155	0.147	0.170	0.154	0.153	0.137	0.161	0.169	0.149	0.012	0.014	0.014	0.015	0.018	0.014	0.014	0.015	0.014	0.015	0.015	0.014	0.014	0.015	0.014	0.014	0.017	0.018	0.016						
IS38 RHWB005 20150910 01 Amphipoda	0.166	0.155	0.173	0.149	0.181	0.151	0.172	0.178	0.145	0.110	0.016	0.015	0.013	0.020	0.016	0.014	0.013	0.014	0.011	0.012	0.013	0.016	0.014	0.015	0.014	0.018	0.016	0.015						
IS43 RHWB006 20150910 01 Amphipoda	0.142	0.127	0.114	0.178	0.128	0.196	0.117	0.114	0.134	0.158	0.188	0.013	0.014	0.016	0.012	0.013	0.014	0.014	0.016	0.013	0.014	0.009	0.016	0.012	0.016	0.015	0.017	0.013						
IS59 KBRC1310 20150911 02 Amphipoda	0.106	0.085	0.164	0.188	0.153	0.175	0.156	0.161	0.101	0.169	0.169	0.148	0.012	0.016	0.012	0.011	0.011	0.015	0.010	0.011	0.012	0.015	0.012	0.018	0.017	0.013	0.016							
IT06 BHRC118.20151013-02 Amphipoda	0.037	0.034	0.144	0.188	0.141	0.167	0.143	0.147	0.075	0.156	0.164	0.138	0.110	0.011	0.012	0.010	0.007	0.011	0.014	0.010	0.008	0.014	0.011	0.008	0.014	0.015	0.011	0.015						
IT22 BHRC231.20151014-03 Amphipoda	0.048	0.051	0.152	0.195	0.136	0.179	0.150	0.148	0.080	0.164	0.177	0.129	0.103	0.058	0.018	0.013	0.011	0.014	0.020	0.013	0.011	0.015	0.014	0.011	0.015	0.023	0.013	0.019						
IV108 MB13WARR001-20150605-01 Amphipoda lin 5	0.138	0.117	0.081	0.161	0.105	0.188	0.098	0.106	0.145	0.161	0.172	0.099	0.153	0.140	0.140	0.013	0.013	0.014	0.015	0.011	0.013	0.010	0.014	0.013	0.010	0.017	0.014	0.016	0.011					
IV111 MB13WARR010.20150606-01 Amphipoda lin 3	0.090	0.075	0.151	0.181	0.126	0.167	0.140	0.145	0.081	0.155	0.162	0.144	0.093	0.085	0.079	0.147	0.010	0.011	0.014	0.011	0.010	0.012	0.015	0.012	0.016	0.013	0.014	0.014						
IV126 Camp-20150930-02 Amphipoda lin 1	0.000	0.052	0.152	0.183	0.149	0.166	0.139	0.145	0.078	0.155	0.166	0.144	0.104	0.042	0.047	0.139	0.088	0.010	0.013	0.010	0.005	0.013	0.010	0.006	0.014	0.011	0.016	0.012	0.016	0.016				
IV128 DAVES-20150930-04 Amphipoda lin 4	0.101	0.107	0.145	0.186	0.155	0.155	0.148	0.145	0.110	0.153	0.166	0.147	0.107	0.101	0.108	0.142	0.109	0.101	0.013	0.013	0.011	0.014	0.001	0.011	0.014	0.016	0.012	0.017	0.015					
IV134 TOBRC0099-20150930-01 Amphipoda lin 6	0.149	0.143																																

**Table 38. Estimates of Evolutionary Divergence between Sequences**

KX65627 Troglodadillo sp. 6 MJ-2016 0.225 0.236 0.242 0.244 0.219 0.219 0.204 0.209 0.220 0.214 0.200 0.201 0.170 0.184 0.253 0.211 0.230 0.181 0.209 0.208 0.271 0.248 0.204 0.245 0.222 0.248 0.220 0.200 0.222 0.225 0.234 0.222 0.254 0.246 0.235 0.216 0.230 0.197 0.211 0.208 0.217 0.239

1. Tamura K, Stecher G., Peterson D., Filipski A., and Kumar S. (2013). MEGA6: Molecular Evolutionary Genetics Analysis version 6.0. *Molecular Biology and Evolution* 30; 2725-2729. The number of substitutions per site from the tree are shown. Standard errors related to  $\pi$  are shown above the diagonal. The tree analysis included 42 nucleotide sequences.

The number of base differences per site from between sequences are shown. Standard error estimate(s) are shown above the diagonal. The analysis involved 442 nucleotide sequences. Codon positions included were 1st+2nd+3rd+Noncoding. All ambiguous positions were removed for each sequence pair. There were a total of 495 positions in the final dataset. Evolutionary analyses were conducted in MEGA6 [1].

The final dataset. Evolutionary analyses were conducted in MEGA5 [1].  
Disclaimer: Although utmost care has been taken to ensure the correctness of the caption, the caption text is provided "as is" without any warranty of any kind. Authors advise the user to carefully check the caption prior to its use for any

**Table 42. Estimates of Evolutionary Divergence between Sequences**

The number of base differences per site from between sequences are shown. Standard error estimate(s) are shown above the diagonal. The analysis involved 42 nucleotide sequences. Cited from Tamura K., Stecher G., Peterson D., Filipski A., and Kumar S. (2013). MEGAS: Molecular Evolutionary Genetics Analysis version 6.0. *Molecular Biology and Evolution* 30: 2725-2729.

Disclaimer: Although utmost care has been taken to ensure the correctness of the caption, the caption text is provided "as is" without any warranty of any kind. Authors advise the user to carefully check the caption prior to its use for any purpose and report any errors or problems to the authors immediately ([www.megasoftware.net](http://www.megasoftware.net)). In no event shall the authors and their employers be liable for any damages, including but not limited to special,

Disclaimer: Although utmost care has been taken to ensure the correctness of the caption, the caption text is provided 'as is' without any warranty of any kind. Authors advise the user to carefully check the caption prior to its use for any purpose and report any errors or problems to the authors immediately ([www.megasoftware.net](http://www.megasoftware.net)). In no event shall the authors and their employers be liable for any damages, including but not limited to special, consequential, or other damages. Authors specifically disclaim all other warranties expressed or implied, including but not limited to the determination of suitability of this caption text for a specific purpose, use, or application.

Table 42. Estimates of Evolutionary Divergence between Sequences

Specimen ID	IV245 RC15MEB0171-20160317-T1-01 Diplura	IV248 RC15MEC0192-20160316-T1-01 Diplura	IV250 RC15MEC0192-20160316-T1-03 Diplura	AF370844 Campodea tillyardi	BQ10 PES 2546 Projapygidae DL	BQ11 PES 5439 Projapygidae won1 DP	BQ12 PES 4269 Projapygidae DK	BQ13 PES 4283 Japygidae won1 DE	BX16 PES-5195 Japygidae MH1 DQ	BX17 PES-5952 Japygidae MH1 DR	BX29 PES-5141 Parajapygidae MH1 DS	BX30 PES-5190 Parajapygidae MH1 DS	CA1 11:1056 Anajapygidae indet.	CA2 11:1523 Anajapygidae indet.	CA3 11:1720 Anajapygidae indet.	Diplura sp. HQ943342 DA	FH23 Projapygidae sp B14 EW0300	FH24 Projapygidae sp B14 BG0018	FH7 Japygidae sp B36 DLUNK03	FH8 Japygidae sp B36 NOW sp EW0333	G333 LN8949 Projapygidae sp MJ DN	G334 LN9141 Projapygidae sp UM DO	G432 110953 Japygidae sp Central Pilbara DH	G433 110848 Japygidae Central Pilbara sp DG	G473 111138b Anajapygidae sp NS DB	GH6 Anajapygidae Ana-PES16402	HQ882832 Lepidocampa weberi	IT74 BHRC0514-151013-T2-02 Diplura	IV154 DD11MEB001T1-01 Diplura	IV155 DD11MEB001T1-01 Diplura	IV156 DD11MEC0005-02 Diplura	Japyx solifugus AY71989 DC	JC18 Diplura RC14BS4004-20151125-T2-01	JF37 RC14MEH0308-20160120-T2-02 Diplura	JF38 RC15MEH0166-20160118-T3-03 Diplura	JF40 RC15MEH0261-20160120-T3-02 Diplura	JO692327 Parajapyx pauliani voucher HN0405	JU01 RC14MEH0388-20160628-T3-1 Diplura
IV245 RC15MEB0171-20160317-T1-01 Diplura	0.011	0.014	0.015	0.015	0.015	0.015	0.016	0.015	0.015	0.016	0.014	0.014	0.015	0.015	0.015	0.015	0.015	0.015	0.015	0.015	0.015	0.015	0.015	0.015	0.015	0.015	0.015											
IV248 RC15MEC0192-20160316-T1-01 Diplura	0.121	0.015	0.016	0.016	0.017	0.016	0.016	0.015	0.016	0.015	0.014	0.014	0.015	0.015	0.014	0.015	0.015	0.015	0.015	0.015	0.015	0.015	0.015	0.015	0.015	0.015	0.015											
IV250 RC15MEC0192-20160316-T1-03 Diplura	0.191	0.188	0.016	0.016	0.015	0.015	0.013	0.012	0.013	0.013	0.016	0.015	0.014	0.015	0.014	0.015	0.015	0.015	0.015	0.015	0.015	0.015	0.015	0.015	0.015	0.015	0.015											
AF370844 Campodea tillyardi	0.263	0.263	0.271		0.015	0.016	0.017	0.016	0.016	0.014	0.016	0.016	0.017	0.015	0.015	0.015	0.015	0.015	0.015	0.015	0.015	0.015	0.015	0.015	0.015	0.015	0.015											
BQ10 PES 2546 Projapygidae DL	0.282	0.268	0.241	0.280		0.014	0.012	0.017	0.017	0.016	0.016	0.013	0.017	0.016	0.014	0.015	0.015	0.015	0.015	0.015	0.015	0.015	0.015	0.015	0.015	0.015	0.015											
BQ11 PES 5439 Projapygidae won1 DP	0.254	0.254	0.241	0.246	0.162		0.014	0.015	0.016	0.018	0.016	0.015	0.012	0.015	0.014	0.016	0.013	0.012	0.013	0.016	0.016	0.016	0.016	0.016	0.016	0.016	0.016											
BQ7 PES 4269 Projapygidae DK	0.270	0.258	0.248	0.282	0.113	0.156		0.016	0.017	0.016	0.016	0.015	0.016	0.015	0.016	0.016	0.013	0.013	0.017	0.018	0.018	0.017	0.016	0.017	0.016	0.016	0.016											
BQ8 PES 4283 Japygidae won1 DE	0.222	0.200	0.197	0.251	0.252	0.233	0.247		0.012	0.014	0.016	0.017	0.014	0.014	0.016	0.014	0.015	0.016	0.012	0.013	0.016	0.014	0.015	0.015	0.017	0.016	0.014	0.012										
BX16 PES-5195 Japygidae MH1 DQ	0.199	0.215	0.188	0.249	0.246	0.220	0.235	0.138		0.012	0.016	0.016	0.015	0.015	0.015	0.015	0.015	0.015	0.016	0.011	0.013	0.016	0.014	0.015	0.014	0.017	0.017	0.014										
BX17 PES-5952 Japygidae MH1 DR	0.221	0.224	0.196	0.267	0.248	0.238	0.234	0.147	0.130		0.014	0.014	0.017	0.016	0.015	0.016	0.016	0.016	0.013	0.014	0.016	0.013	0.015	0.014	0.014	0.016	0.015	0.014										
BX29 PES-5141 Parajapygidae MH1 DS	0.221	0.218	0.175	0.278	0.246	0.257	0.251	0.210	0.213	0.204		0.006	0.017	0.016	0.015	0.016	0.018	0.016	0.015	0.015	0.017	0.017	0.016	0.017	0.017	0.016	0.015	0.015										
BX30 PES-5190 Parajapygidae MH1 DS	0.215	0.215	0.174	0.274	0.251	0.270	0.256	0.217	0.219	0.208	0.028		0.017	0.016	0.015	0.016	0.015	0.017	0.016	0.016	0.015	0.017	0.017	0.015	0.017	0.016	0.016	0.016										
BX40 PES-5878 Projapygidae MH1 DT	0.274	0.265	0.253	0.287	0.168	0.143	0.168	0.252	0.235	0.262	0.273	0.281		0.016	0.015	0.016	0.014	0.013	0.015	0.016	0.017	0.015	0.017	0.016	0.015	0.015	0.015	0.015										
CA1 11:1056 Anajapygidae indet.	0.235	0.238	0.241	0.263	0.284	0.242	0.275	0.219	0.214	0.245	0.270	0.271	0.262		0.010	0.013	0.015	0.016	0.015	0.016	0.015	0.015	0.015	0.017	0.014	0.016	0.017	0.016	0.017									
CA2 11:1523 Anajapygidae indet.	0.244	0.228	0.254	0.258	0.271	0.239	0.266	0.227	0.235	0.245	0.283	0.280	0.257	0.082		0.013	0.015	0.015	0.015	0.014	0.015	0.015	0.015	0.016	0.015	0.015	0.015	0.015	0.015									
CA3 11:1720 Anajapygidae indet.	0.218	0.235	0.243	0.240	0.251	0.222	0.250	0.224	0.220	0.233	0.261	0.254	0.112	0.134		0.015	0.014	0.014	0.014	0.015	0.015	0.017	0.017	0.017	0.014	0.014	0.015	0.015	0.014									
Diplura sp. HQ943342 DA	0.236	0.245	0.269	0.214	0.283	0.255	0.287	0.216	0.220	0.248	0.263	0.267	0.275	0.231	0.240	0.219		0.017	0.015	0.014	0.015	0.015	0.015	0.017	0.015	0.015	0.015	0.015	0.015	0.015	0.015							
FH23 Projapygidae sp B14 EW0300	0.278	0.271	0.251	0.289	0.166	0.163	0.149	0.224	0.226	0.242	0.261	0.270	0.184	0.255	0.248	0.252	0.271		0.013	0.017	0.015	0.014	0.017	0.017	0.017	0.017	0.016	0.015	0.016	0.015	0.016							
FH24 Projapygidae sp B14 BG0018	0.276	0.271	0.272	0.286	0.178	0.146	0.158	0.251	0.254	0.245	0.274	0.270																										



# Helix

## Molecular Solutions

School of Animal Biology The University of Western Australia Hackett Entrance No. 4 Hackett Drive Crawley WA 6009	PO Box 155 Leederville WA 6903
t. (08) 6488 4509   f. (08) 6488 1029   abn. 32 133 230 243	w. <a href="http://www.helixsolutions.com.au">www.helixsolutions.com.au</a>

8 December, 2016

Jason Alexander  
Biota Environmental Sciences  
Level 1, 228 Carr Place  
Leederville, WA 6007

Via email

**Re. Report on the molecular systematics of subfauna from the Robe River Valley – Phase 4**

Dear Jason,

Following is a summary of the results of the subfauna study we have completed on four (Araneae, Diplura, Chilopoda, Amphipoda) of the eight taxonomic groups from the Robe River Valley phase 4 collections. Sixteen distinct genetic lineages were detected among the four groups so far analysed. Seven of the sixteen lineages have been detected previously in the Pilbara, whereas the remaining nine are new, based on the material available for comparison.

Thanks once again for collaborating on this project with Helix. We hope we can continue to provide you with useful information, and feel free to contact us if you have any questions or would like to discuss the results in detail.

Sincerely,

Dr. Terrie Finston, Yvette Hitchen and Dr. Oliver Berry  
Helix Molecular Solutions

## Background and Objective

Forty specimens of subfauna belonging to four taxonomic groups (Amphipoda, Araneae, Diplura, Chilopoda) were collected from Robe River Valley and sequenced for variation at the mitochondrial COI gene. An additional four taxonomic groups are still to be analysed and will be covered in separate reports. The molecular data were assessed in order to determine the number of species present in each group and compare the results to those obtained during previous surveys that have been undertaken for these groups elsewhere in the Pilbara.

## Executive summary

- Forty specimens from the Robe River Valley belonging to four taxonomic groups were sequenced for variation at the COI gene.
- Sixteen lineages were detected among the four groups.
- Seven of the lineages have been detected previously in the Pilbara, whereas the remaining nine appear to be new, based on the material available for comparison.

## Methods

Forty specimens of subfauna from four taxonomic groups (Amphipoda, Araneae, Diplura, Chilopoda) collected from the Robe River Valley area were sequenced for variation at the mitochondrial cytochrome oxidase subunit I gene (COI) using multiple pairs of primers (LCO1/HCO2, LCO1-long/HCO2-long, NemF1/NemR1 and LCO1/CIN2341).

Sequences were edited using GENEIOUS software (Drummond et al. 2011). Alignment was performed with CLUSTAL W (Thompson et al. 1994) using default parameters. Genetic distances between unique genetic sequences (haplotypes) were measured using uncorrected p-distances (total percentage of nucleotide differences between sequences).

MODELTEST software (Posada and Crandall, 1998) was used to determine the model of sequence evolution that best fitted the data for each taxonomic group. Bayesian analysis was used to construct the phylogenetic trees, incorporating the model as identified in MODELTEST for each taxonomic group. The phylogeny, branch lengths and posterior probabilities were obtained by running two trees simultaneously, each running four simultaneous MCMC chains. The number of cycles needed was determined by the standard deviation of the split frequencies of the two trees. The analysis was paused after every  $1 \times 10^6$  generations and when the standard deviation fell below 0.01, the analysis was stopped. A majority rule consensus tree was constructed after discarding the “burn-in” trees in both analyses. The burn-in value was determined by plotting the posterior probabilities obtained after every generation and identifying the point at which the values reach stationarity (= the asymptote). Trees produced prior to stationarity were discarded.

For the purposes of this report, lineages were defined as haplotypes or groups of haplotypes differing from other such groups by >3% sequence divergence. This cut-off was selected based on bar-coding data, which indicates that intra-specific variation rarely exceeds 3% (Hebert et al., 2003b).

We are currently developing a consistent and unique lineage and species naming system, so all lineages from previous phases will be consolidated in this report to aid in comparisons between phases.

## Results

### Araneae

Two specimens of Araneae from Mesas B and C were sequenced for COI (Table 1). Sequences were obtained from both specimens and these were compared to sequences of Araneae in the Helix and GenBank databases. The specimens were most similar to specimens of Theridiidae, so a subset of reference specimens were selected to include in the phylogenetic analysis, including 31 lineages of Araneae from the Pilbara, five of which were collected during phase 3, as well as seven GenBank reference specimens as follows: Aranidae: *Arachnura scorpiooides*, (GenBank accession #KJ957946 and *Gea theridoides* (Genbank accession #KJ959766), Oonopidae: *Ischnothyreus auritus* (Genbank accession# KR864743) Theridiidae: *Theridion ohlerti* (Genbank accession #GU684645), *Robertus neglectus* (GenBank accession #AY231053),

*Theridion boesonbergi* (Genbank accession #KX537094) and *Coleosoma acutiventer* (Genbank accession # EF050286). Two specimens of Mygalomorphae, *Missulena* sp. WAM T97637 (Genbank accession # KC708097) and *Missulena* sp. WAM T113626 (Genbank accession # KC708079) were used as outgroups.

#### *Phylogenetic analysis*

The phylogenetic analysis, which included the two new specimens from Robe Valley phase 4, in addition to 38 reference specimens, placed the Robe Valley specimens in a single genetically distinct lineage (Figure 1). The lineage was placed in a clade containing Genbank reference specimens of Theridiidae and was assigned to the new lineage AT001 (Figure 1).

#### *Differentiation within and between lineages*

The two phase 4 specimens from lineage AT001 differed from one another by <1% sequence divergence and from the reference specimens by between 11.1 and 28.5% sequence divergence (Table 2).

#### Diplura

##### *Reference specimens and outgroups*

Nine specimens of phase 4 Diplura from Robe Valley were sequenced for COI (Table 3). Comparisons to Genbank and Helix databases showed that the specimens were most closely related to the families Campodeiidae and Parajapygidae, so the nine specimens were analysed with 24 specimens of Diplura from 13 sites in the Pilbara belonging to three families: Campodeidae, Japygidae, and Parajapygidae, as well as five Genbank voucher specimens, *Diplura* sp., which is most similar to Genbank specimens of Campodeidae (Genbank accession #HQ943342), *Campodea tillyardi* (Genbank accession # AF370844) and *Lepiodocampa weberi* (Genbank accession #HQ882832) from the family Campodeidae, *Parajapyx pauliani* (Genbank accession #JQ692327) from the family Parajapygidae and *Japyx solifugus* (Genbank accession #AY771989) from the family Japygidae. The planthopper *Lycorma delicatula* (Genbank accession # FJ456942) and a specimen of Fulgoridae (Hemiptera sp.; Genbank accession #GU671563) were used as outgroups.

#### *Phylogenetic analysis*

The phylogenetic analysis, which included the nine specimens of Diplura from Robe Valley in addition to 29 reference specimens, placed the Robe Valley specimens in four distinct lineages (Figure 2). Seven of the phase 4 specimens were placed in lineages containing reference specimens. Six specimens were placed in the Campodeiidae lineage DCA003 and one specimen was placed in the Parajapygidae lineage DPA006, both of which were detected previously in the Robe Valley (Figure 2). The remaining two specimens were placed in the Parajapygidae clade containing DPA006, and were assigned to the new lineages DPA007 and DP008 (Figure 2).

#### *Differentiation within and between lineages*

The six specimens of Campodeiidae (all within lineage DCA003) differed from one another by <1% sequence divergence (Table 4). The phase 4 specimens of Campodeiidae lineage DCA003 differed from the other reference specimens in DCA003 from previous surveys by between 0.0 and 0.9% sequence divergence, and from the next nearest reference specimen (lineage DCA002) by between 4.8 and 5.7% sequence divergence (Table 4).

The three lineages of Parajapygidae differed from each other by between 4.6 and 15.5% sequence divergence (Table 4). Specimen KD14 differed from the reference specimen of lineage DPA006 (IV250) by 1.5% sequence divergence and specimen KD12 (lineage DPA007) differed from the specimens in lineage DPA006 by between 4.6 and 5.0% sequence divergence (Table 4). Specimen KD15 (lineage DPA008) differed from the nearest reference specimen (IV250) by 15.4% sequence divergence (Table 4).

#### Chilopoda

One specimen of Chilopoda from the Robe Valley, assigned to the family Geophilidae on the basis of morphology, was sequenced for COI (Table 5). The sequence was analysed with nine Genbank vouchers from four families of Chilopoda: Cryptopidae, Geophilidae, Mecistocephalidae (in the superfamily Geophiliomorpha) and Scolopendridae as follows: *Cryptops japonicus* (Genbank accession # AB610777), *Cryptops pictus* (Genbank accession # JF273290) *Cormocephalus multidens* (Genbank accession # KF676531), *Scolopendra multidens* (Genbank accession # AB614405), *Gnathoribautia bonensis* (Genbank accession # KF569297), *Geophilus flavus* (Genbank accession # JN306685), *Stenotaenia linearis* (Genbank accession # KR736251), and *Mecistocephalus multidentatus* (Genbank accession # AB610774) as well as 30 reference specimens of Chilopoda from 12 sites in the Pilbara. Two specimens of Onychophora, *Metaperipatus inae* (Genbank accession # HQ453464) and *Opisthopatus cinctipes* (Genbank accession # NC014273) were used as outgroups.

#### *Phylogenetic analysis*

The phylogenetic analysis, which included the new phase 4 specimen from the Robe Valley, in addition to 39 reference specimens, placed the Robe Valley specimens a single genetically distinct lineage (Figure 3). The specimen was not placed in a lineage containing reference specimens, and was therefore assigned to the new lineage CHI026 (Figure 3). The lineage was placed in a well-supported clade with Genbank and Pilbara specimens of Cryptopidae (Figure 3).

#### *Differentiation within and between lineages*

The new phase 4 Chilopoda lineage from Robe Valley differed the nearest reference specimen (CQ2=lineage CHI013) by 16.8% sequence divergence (Table 6).

#### Amphipoda

##### *Preliminary analysis - Reference sequences and outgroups*

Twenty-eight specimens of amphipods from phases 1 and 2 were sequenced for COI (Table 7). In order to reduce analysis time and to simplify the presentation of results, a preliminary neighbour-joining (NJ) analysis was conducted on the 24 Robe Valley amphipods for which sequences were obtained, and haplotypes were selected from each genetic lineage to include in a model-based phylogenetic analysis.

The neighbour-joining analysis placed the 24 specimens of amphipods into ten lineages (Figure 4). Comparisons to the GenBank sequence database indicated that two lineages each were most similar to sequences of Niphargidae and Paramelitidae, respectively, whereas six lineages were most similar to sequences of Melitidae. The Melitidae lineages contained between one and two specimens, whereas the Niphargidae and Paramelitidae lineage contained between one and seven specimens (Figure 4). The two Niphargidae lineages differed from one another by 24.0% mean sequence divergence and the two lineages of Paramelitidae differed from one another by 13.2% mean sequence divergence (Table 8). The six lineages of Melitidae differed from one another by between 3.7 and 12.2% mean sequence divergence (Table 8). Differentiation within lineages for all three families ranged from 0 to 2.7% mean sequence divergence (Table 9).

The Paramelitidae and Niphargidae were analysed in a single phylogenetic analysis. For the Paramelitidae, 33 reference sequences were included in the phylogenetic analysis, six GenBank vouchers of Paramelitidae, *Maarrka etheli* (Genbank accession # DQ838031), two *Maarrka weeliwollii* (Genbank accession # DQ838032 and # DQ838033), Paramelitidae sp. 3 (Genbank accession # EF558852) and two references of 'Yilgarus' sp. (Genbank accession # EF118232 and EF118194) as well as 27 specimens from previous surveys of the Central Pilbara, Barrow Island, Lower Shaw River, Fortescue River, and Marillana Creek. For the Niphargidae, five reference sequences were included in the analysis, three specimens from previous surveys in the Robe Valley and two Genbank reference sequences of *Niphargus*: *N. fontanus* (Genbank accession number KC315635) and *N. glenniei* (Genbank accession number KC315646). Two sequences of the cladoceran genus *Daphnia* were used as outgroups for the analysis as follows: *Daphnia*

*pulex* (Genbank accession number J150976) and *Daphnia pulicaria* (Genbank accession number JN233925).

For the Melitidae, 35 reference sequences were included in the phylogenetic analysis, two GenBank vouchers of Melitidae, *Nedgia* sp. 1 (Genbank accession #EU304458), and *Norcapensis mandibulalis* (Genbank accession # JQ608487) as well as 33 specimens from previous surveys of the Central Pilbara, Barrow Island, Lower Shaw River, Fortescue River, and Marillana Creek. Two sequences of the amphipod genus *Niphargus* were used as outgroups as follows: *N. fontanus* (Genbank accession number KC315635) and *N. glenniei* (Genbank accession number KC315646).

#### *Phylogenetic analysis- Paramelitidae and Niphargidae*

The phylogenetic analysis, which included the four representatives (two each) of Paramelitidae and Niphargidae from the Robe Valley in addition to 33 and five reference specimens, respectively, revealed the presence of two well-supported major clades, corresponding to the two families (Figure 5). The Robe Valley specimens of Paramelitidae were placed in two distinct lineages, both of which also contained reference specimens from previous surveys in the Pilbara (Figure 5). Specifically, specimen KD63 from TOBRC009 was placed in a lineage containing specimens from previous surveys in the Robe Valley and Barrow Island and thus was assigned to the existing lineage AMP023 and specimen KD48 from Budgie was placed in a lineage containing a specimen from a previous survey at Barrow Island, and was thus assigned to the existing lineage AMP009 (Figure 5). The new Niphargidae specimens from the Robe Valley were placed in two distinct lineages, one of which also contained a reference specimen from a previous survey in the Pilbara (Figure 5). Specifically, specimen KD39 representing specimens from Dave's and Budgie, was placed in a lineage containing specimens from previous surveys in the Robe Valley and thus was assigned to the existing lineage AMN007 (Figure 5). Specimen KD41 from Budgie was placed in a distinct lineage that did not contain any reference specimens, and thus was assigned to the new lineage AMN001 (Figure 5).

#### *Differentiation between lineages – Paramelitidae and Niphargidae*

The Robe Valley Paramelitidae lineage represented by specimen KD63 was genetically identical to reference specimen IV115 (lineage AMP023) and the lineage represented by specimen KD48 differed from the nearest reference specimen (L8; lineage AMP009) by 0.5% sequence divergence (Table 10). The Robe Valley Niphargidae lineage represented by specimen KD39 differed from the nearest reference specimens IV100 and JN08 (lineage AMN008) by 0.3% sequence divergence and the lineage represented by specimen KD41 differed from the nearest reference specimens (IV100 and JN08) by 24.0% sequence divergence (Table 10).

#### *Phylogenetic analysis- Melitidae*

The phylogenetic analysis, which included the six representatives of Melitidae from Robe Valley in addition to 35 reference specimens, placed the Robe Valley specimens in six distinct genetic lineages, two of which also contained reference specimens from previous surveys in the Pilbara (Figure 6). Specifically, specimen KD49 was placed in a lineage containing reference specimens JF02 and rr3a and thus was assigned to the existing lineage AMM001, and specimen KD53 was placed in a lineage containing reference specimens IV92 and nr5miwell, thus was assigned to the existing lineage AMM002 (Figure 6). The remaining four lineages, represented by specimens KD47, KD40, KD44 and KD45 were not placed in lineages containing reference specimens, and were therefore assigned to the new lineages AMM028, AMM029, AMM030 and AMM031, respectively (Figure 6). However, two of the new lineages (KD44/AMM030 and KD45/AMM031) were placed in well-supported clades containing reference lineages (Figure 6). Specifically, KD44 was placed in a clade containing several closely related lineages (AMM001, AMM024, AMM025) and KD45 was placed in a clade containing a reference specimen assigned to lineage AMM027 (Figure 6). Both KD44 and KD45 were placed in a larger clade containing six closely related lineages (AMM001, AMM002, AMM024, AMM025, AMM027 and the new lineage AMM029; Figure 6). The remaining two new lineages (KD47/AMM028 and KD40/AMM029) were placed in clades that were not well-supported, however KD40/AMM029 was placed in the larger, well-supported clade containing KD44/AMM030 and KD45/AMM031 and several other lineages, as described above (Figure 6).

#### Differentiation between lineages - Melitidae

Two specimens assigned to existing lineages differed from the nearest reference lineages by <3% (Table 11). Specifically, KD49/AMM001 differed from the nearest reference specimens JF02 and JN17 by 0.7% sequence divergence and KD53/AMM002 differed from the nearest reference specimens IV92 and nr5miwell by 0 and 0.2% sequence divergence, respectively (Table 11). KD44/AMM030 and KD45/AMM031 differed from the closest reference specimens IT06 and IV124, respectively, by 3.1 and 3.2% sequence divergence, respectively and indeed, a well-supported clade of eight lineages, which included five of the Robe Valley lineages from the present study (AMM001, AMM002, AMM029, AMM030, AMM031), all differed by <5% mean sequence divergence (Table 11; Figure 6). Finally, KD47/AMM028 differed from the closest reference specimen GY19 by 10.6% sequence divergence and KD40/AMM029 differed from the closest reference specimen IT06 by 3.7% sequence divergence (Table 11).

### Conclusions

COI is widely considered to show suitable variation to distinguish species (Hebert et al., 2003a). In a comparison of COI sequences for over 13,000 pairs of taxa, Hebert et al (2003b) found a mean of 11.1% sequence divergence between distinct species. Nearly 80% of the comparisons showed that species pairs differed from one another by greater than 8% sequence divergence. However, a taxon by taxon approach, examining the amount of phylogenetic variation within and between species is the most widely accepted method of defining species.

#### Araneae

A single genetically distinct lineage of Araneae was detected (AT001), containing both specimens from phase 4 and representing a single distinct species, owing to the high level of sequence divergence between it and the reference lineages. The lineage differed from the reference lineages by >10%, indicating that it is likely to be a new species, based on the material available for comparison. The species is likely to belong to the family Theriidae, based on its phylogenetic placement.

One lineage from the previous phase 3 survey (A012) was placed in a clade containing Pilbara specimens assigned on the basis of morphology to the genus *Anapistula* (family Symphytognathidae), as well as Genbank reference specimens of Theriidae, making taxonomic assignment of A012 uncertain. The present analysis placed the Theriidae and the Symphytognathidae in two distinct, reciprocally monophyletic clades. Lineage A012 was placed in the Symphytognathidae clade, increasing our confidence in assigning it to that family.

#### Theriidae (putative)

AT001 = new lineage and species

#### Diplura

Four distinct genetic lineages of Diplura were detected during phase 4 collecting at Robe Valley. One lineage was placed with the Campodeiidae (lineage DCA001) and three with the Parajapygidae (DPA006, DPA007, DPA008).

The lineage of Campodeiidae (DCA001) has been detected previously, indicating that it belongs to species that has been detected previously. The relationship between lineages DCA001 and DCA002 (detected during earlier phases at Robe Valley) requires further consideration. The two lineages differ by between 4.7 and 5.7% sequence divergence. The two lineages may represent two closely related species (recently separated or incipient), or a single species showing genetic variation associated with the geographical distance between collecting sites and the poor dispersal capabilities of the taxon. Sampling from intermediate sites may help resolve this issue. However, it should be noted that the specimens in lineages DCA001 and DCA002 were all collected from drillholes at Mesa B, and sites that are geographically close, in the absence of obvious physical barriers, would be expected to share genotypes, lending weight to the argument for incipient species.

One of the lineages of Parajapygidae, DPA006, has been detected previously, indicating that both belong to species that have been detected previously. Parajapygidae lineage DPA008 differed from the reference lineages by >15% sequence divergence, indicating that it is likely to represent a new species, which has so far not been detected in the Pilbara, based on the material available for comparison. The final lineage of Parajapygidae, DPA007, requires further consideration. It differed from the specimens within lineage DPA006 by between 4.6 and 5.0% sequence divergence, thus the relationship between these two closely related lineages needs further investigation. The two lineages may represent two closely related species (recently separated or incipient), or a single species showing genetic variation associated with the geographical distance between collecting sites and the poor dispersal capabilities of the taxon. Sampling from intermediate sites may help resolve this issue. However, it should be noted that the specimens in lineages DPA006 and DPA007 were all collected from drillholes at Mesa C and sites that are geographically close, in the absence of obvious physical barriers, would be expected to share genotypes, lending weight to the argument for incipient species.

#### Campodeiidae

DCA001 = lineage and species detected previously in the Robe Valley at Mesa B. Relationships between DCA001 and DCA002 require further investigation.

#### Parajapygidae

DPA006 = previously detected lineage and species

DPA007 = new lineage; relationship to DPA006 requires further investigation

DPA008 = new lineage and species

#### Chilopoda

A single distinct lineage of Chilopoda was detected at the Robe River Valley phase 4 (CHI026), representing a single species. The lineage differed from the references by >16.0% sequence divergence, thus the species is likely to be new, based on the material available for comparison. The lineage was placed with the Cryptopidae and appears to belong to that family, in contrast with its assignment to the Geophilidae, on the basis of morphology.

#### Cryptopidae (putative)

CHI026 = new lineage and species

#### Amphipoda

Two lineages each of Niphargidae (AMN008, AMN001) and Paramelitidae (AMP009, AMP023) were detected at the Robe River Valley. One Niphargidae lineage was placed in a reference lineage from the Robe Valley (AMN008), differing from that reference lineage by <1.0%, indicating that it represents a lineage and species that has been detected previously, whereas the second lineage (AMN001) differed from the nearest reference specimens by >10%, indicating that it is a new lineage and species. Both lineages of Paramelitidae (AMP009, AMP023) differed from the nearest reference lineage by <1.0%, indicating that they each represent a lineage and species that has been detected previously.

#### Niphargidae

AMN008 = one species, detected previously in the Robe Valley

AMN001 = new lineage and species

#### Paramelitidae

AMP023 = one species, detected previously at Barrow Island and Robe Valley

AMP009 = one species, detected previously at Barrow Island

Six lineages of Melitidae were detected at Robe Valley, differing from one another by between 3.7 and 12.2% mean sequence divergence. Two of the lineages were assigned to existing lineages (AMM001 and AMM002) and five (AMM001, AMM002, AMM029, AMM030, AMM031) were placed in a well-supported clade containing a group of closely related lineages, which differed by <5% mean sequence divergence. Thus this group may represent several closely related species, or may represent a single species showing genetic differentiation across its range. Further investigation may be required to resolve relationships among the lineages, but

the most likely explanation would be to consider them a single species, owing to the fact that they have a relatively wide distribution (Robe Valley to Barrow Island) and the observed genetic variation may reflect geographic variation associated with a 'stepping stone' pattern of gene exchange – populations that are near-by would be expected to exchange genes, but those on the geographic extremes are not exchanging genes. This clade forms a larger clade with additional lineages, including the Genbank reference specimen of *Nedsia* sp. 1, in which the members differ by 7.4% mean sequence divergence. Again, this group of closely related lineages requires further investigation, however we can assign the lineages to the genus *Nedsia* with some confidence.

#### Melitidae

AMM001	May correspond to one species of <i>Nedsia</i> , but relationships among the clade members requires further investigation. AMM001 and AMM002 have been detected previously, whilst AMM029, AMM030 and AMM031 are new.
AMM002	
AMM029	
AMM030	
AMM031	

AMM028 = new lineage and species

#### References

- Alexander, J. B. , Burger M. A.A., and Harvey, M.S. (2014). A new species of troglobitic *Anatemnus* (Pseudoscorpiones: Atemnidae) from the Pilbara bioregion of Australia. Records of the Western Australian Museum 29: 141 – 148.
- Australian Faunal Directory. <http://www.environment.gov.au/biodiversity/abrs/online-resources/>. Accessed 27 Dec., 2015.
- Bayly, I. A.E, Ellis p. (1969). *Haloniscus searlei* chilton: An aquatic "terrestrial" isopod with remarkable powers of osmotic regulation. Comparative Biochemistry and Physiology 31: 523-528
- Drummond AJ, Ashton B, Buxton S, Cheung M, Cooper A, Duran C, Field M, Heled J, Kearse M, Markowitz S, Moir R, Stones-Havas S, Sturrock S, Thierer T, Wilson A (2011) Geneious v5.4, <http://www.geneious.com/>
- Harvey, M. S., Berry, O. Edward, K. L., Humphreys, G. (2008) Molecular and morphological systematics of hypogean schizomids (Schizomida: Hubbardiidae) in semiarid Australia. Invertebrate Systematics 22: 167-194.
- Hebert, P.D.N., Cywinska, A., Ball, S.L., deWaard J.R. (2003a). Biological identifications through DNA barcodes. Proceedings of the Royal Society of London B 270: 313-321.
- Hebert, P.D.N., Ratnasingham, S., deWaard J.R. (2003b). Barcoding animal life: cytochrome c oxidase subunit 1 divergences among closely related species. Proceedings of the Royal Society of London B (supplement) 270: S96-S99.
- Helix Molecular Solutions (2015). Report on the molecular systematics of Schizomida from The Robe River Valley. Prepared for Biota Environmental Sciences, 5 February.
- Posada, D., Crandall, K.A. (1998). MODELTEST: testing the model of DNA substitution. Bioinformatics 14: 817-818.
- Thompson, J., Higgins, D., and Gibson, T. (1994). CLUSTAL W: improving the sensitivity of progressive multiple sequence alignment through sequence weighting, position-specific gap penalties and weight matrix choice. Nucleic Acids Research 22: 4673–4680. doi:10.1093/nar/ 22.22.4673

Table 1. Specimens of Araneae used in the present study and the lineage to which they were assigned, based on variation at the COI gene. \*=new lineage this study.

Specimen_ID	Drillhole_ID	Cap No.	Helix ID	Lineage
GR15MEB0014.20160915.T1-01	GR15MEB0014	11	KD01	AT001*
RC15MEC0001.20160915.T1-01	RC15MEC0001	74	KD02	AT001*

Table 2 (attached). Genetic distances (below diagonal) and standard error (above diagonal, in blue) between specimens of Araneae detected at Robe Valley and the reference lineages as shown in Figure 1. Distances between the Robe Valley specimens and the reference specimens are highlighted in yellow. Distances between the Robe Valley phase 4 specimens are highlighted in blue.

Table 3. Specimens of Diplura used in the present study and the lineage to which they were assigned, based on variation at the COI gene. \*=new lineage this study.

Specimen_ID	Drillhole_ID	Cap No.	Helix ID	Lineage
GR15MEB0014.20160915.T3-01	GR15MEB0014	13	KD07	DCA003
RC15MEB0115.20160915.T2-01	RC15MEB0115	20	KD08	DCA003
RC15MEB0115.20160915.T2-01	RC15MEB0115	20	KD09	DCA003
RC15MEB0115.20160915.T2-01	RC15MEB0115	20	KD10	DCA003
RC15MEB0115.20160915.T2-01	RC15MEB0115	20	KD11	DCA003
RC15MEC0103.20160915.T1-01	RC15MEC0103	21	KD12	DPA007*
RC14MEB0101.20160915.T2-01	RC14MEB0101	31	KD13	DCA003
RC16MEC0156.20160915.T3-01	RC16MEC0156	72	KD14	DPA006
RC16MEC0118.20160915.T3-01	RC16MEC0118	73	KD15	DPA008*

Table 4 (attached). Genetic distances (below diagonal) and standard error (above diagonal, in blue) between specimens of Diplura detected at Robe Valley and the reference lineages as shown in Figure 2. Distances between the Robe Valley specimens and the reference specimens are highlighted in yellow. Distances between the Robe Valley phase 4 specimens are highlighted in blue.

Table 5. Specimens of Chilopoda used in the present study and the lineage to which they were assigned, based on variation at the COI gene. \*=new lineage this study.

Specimen_ID	Drillhole_ID	Cap No.	Helix ID	Lineage
RC15MEC0168.20160915.T3-02	RC15MEC0168	30	KD16	CHI026*

Table 6 (attached). Genetic distances (below diagonal) and standard error (above diagonal, in blue) between specimens of Chilopoda detected at Robe Valley and the reference lineages as shown in Figure 3. Distances between the Robe Valley specimens and the reference specimens are highlighted in yellow.

Table 7. Specimens of Amphipoda used in the present study and the lineage to which they were assigned, based on variation at the COI gene. \*=new lineage this study.

Specimen ID	Drillhole ID	Cap	Helix ID	Lineage
DAVES-20150930-04	DAVES	4	KD38	AMN008
Budgie-20150930-01	Budgie	7	KD39	AMN008
Budgie-20150930-01	Budgie		KD40	AMM029*
Budgie-20150930-01	Budgie		KD41	AMN001*
Budgie-20150930-01	Budgie		KD42	AMN008
Budgie-20150930-01	Budgie		KD43	AMN008
Budgie-20150930-01	Budgie		KD44	AMM030*
Budgie-20150930-01	Budgie		KD45	AMM031*
Budgie-20150930-01	Budgie		KD46	
Budgie-20150930-01	Budgie		KD47	AMM028*
Budgie-20150930-01	Budgie		KD48	AMP009
Budgie-20150930-01	Budgie		KD49	AMM001
Budgie-20150930-01	Budgie		KD50	AMM030*
Budgie-20150930-01	Budgie		KD51	AMN008
Budgie.20150604-02	Budgie	7	KD52	
Budgie.20150604-02	Budgie		KD53	AMM002
Budgie.20150604-02	Budgie		KD54	
Budgie.20150604-02	Budgie		KD55	AMM031*
Budgie.20150604-02	Budgie	7	KD56	AMN008
Budgie.20150604-02	Budgie	7a	KD57	AMN008
TOBRC0099-20150930-01	TOBRC0099	18	KD58	AMP023
TOBRC0099-20150930-01	TOBRC0099		KD59	AMP023
TOBRC0099-20150930-01	TOBRC0099		KD60	AMP023
TOBRC0099-20150930-01	TOBRC0099		KD61	AMP023
TOBRC0099-20150930-01	TOBRC0099		KD62	AMP023
TOBRC0099-20150930-01	TOBRC0099		KD63	AMP023
TOBRC0099-20150930-01	TOBRC0099		KD64	AMP023
Daves-20150604-01	DAVES	1a	KD65	

Table 8. Mean genetic distance (p-distances) between lineages of amphipods as shown in Figure 4. Distances between lineages within families are highlighted in blue.

lineage	Niphargidae		Paramelitidae		Melitidae					
	1	2	3	4	5	6	7	8	9	10
Gp 1		0.015	0.015	0.016	0.017	0.017	0.017	0.017	0.017	0.018
Gp 2	0.240		0.018	0.018	0.018	0.018	0.018	0.017	0.017	0.018
Gp 3	0.264	0.300		0.013	0.018	0.016	0.017	0.017	0.017	0.018
Gp 4	0.276	0.304	0.132		0.017	0.017	0.018	0.018	0.017	0.018
Gp 5	0.306	0.317	0.327	0.310		0.012	0.014	0.014	0.013	0.014
Gp 6	0.311	0.334	0.322	0.321	0.106		0.010	0.009	0.007	0.009
Gp 7	0.325	0.330	0.336	0.329	0.115	0.070		0.009	0.008	0.009
Gp 8	0.319	0.334	0.323	0.327	0.122	0.072	0.062		0.006	0.007
Gp 9	0.322	0.334	0.324	0.318	0.110	0.048	0.041	0.037		0.005
Gp 10	0.338	0.354	0.332	0.329	0.118	0.058	0.070	0.062	0.040	

Table 9. Mean genetic distance (p-distances) and standard errors within lineages of amphipods as shown in Figure 4. N= number of specimens in the lineage and rep= specimen selected to represent the lineage in the model-based phylogenetic analysis.

lineage	D	s.e.	N	rep
Gp 1	0.004	0.002	7	KD39
Gp 2	n/c	n/c	1	KD49
Gp 3	n/c	n/c	1	KD48
Gp 4	0.000	0.000	7	KD63
Gp 5	n/c	n/c	1	KD47
Gp 6	n/c	n/c	1	KD53
Gp 7	n/c	n/c	1	KD40
Gp 8	n/c	n/c	1	KD49
Gp 9	0.016	0.005	2	KD44
Gp 10	0.027	0.007	2	KD45

Table 10 (attached). Genetic distances (below diagonal) and standard error (above diagonal, in blue) between specimens of Niphargidae and Paramelitidae (Amphipoda) detected at Robe Valley and the reference lineages as shown in Figure 5. Distances between the Robe Valley specimens and the reference specimens are highlighted in yellow.

Table 11 (attached). Genetic distances (below diagonal) and standard error (above diagonal, in blue) between specimens of Melitidae (Amphipoda) detected at Robe Valley and the reference lineages as shown in Figure 6. Distances between the Robe Valley specimens and the reference specimens are highlighted in yellow.

Appendix 1. All specimens, assigned to lineages, from phases 1-4. Lineages with name changes are highlighted in yellow. Phase is classified as either historical (H), by phase (P) or as provided by the WAM (WAM); re=repeat. \*=new lineage this study. Renamed lineages are highlighted in yellow.

Specimen_ID	Drillhole_ID	Taxon	P	Helix ID	Lineage	Renamed lineage
SSp-2010-253	DCBRC-017	Araneae	H	IV345	AO014	AO014
SSp-2010-75	DCBRC-040	Araneae	H	IV346	AO014	AO014
MEBRC0016P1T1-2	MEBRC0016	Araneae	P3	IV272	AO015	AO015
110817		Araneae	P3	IV273	contam	
127038		Araneae	P3	IV274	No amp	
127039		Araneae	P3	IV275	AA001	AA001
138441		Araneae	P3	IV276	A012	A012
GR15MEB0014.20160915.T1-01	GR15MEB0014	Araneae	P4	KD01	AT001	AT001*
RC15MEC0001.20160915.T1-01	RC15MEC0001	Araneae	P4	KD02	AT001	AT001*
SSp-2010-209	COBRC0022	Diplura	H	IV320	NoAmp	
SSp-2010-287	COBRC0008	Diplura	H	IV321	NoAmp	
SSp-2010-291	DCBRC_001	Diplura	H	IV322	NoAmp	
SSp-2010-37	COBRC0012	Diplura	H	IV323	NoAmp	
SSp-2010-40	TOBRC0043	Diplura	H	IV324	NoAmp	
SSp-2010-79	COBRC0003	Diplura	H	IV325	NoAmp	
DD11MEB001T1-01	DD11MEB001	Diplura	P1	IV154	Lin 1	DCA001
DD11MEB001T1-01	DD11MEB001	Diplura	P1	IV155	Lin 2	DCA002
DD11MEC0005-02	DD14MEB0005	Diplura	P1	IV156	Lin 4	DPA004
DD14MEB0005-20151001-T3-02	DD14MEB0005	Diplura	P2	IV157	Lin 3	DCA003
MEARC5017-20151001-T2-01	MEARC5017	Diplura	P2	IV158	nd	
RC14MEB0101-20151001-T2-01	RC14MEB0101	Diplura	P2	IV159	Lin 3	DCA003
MEARC3790-20150807-T2-03	MEARC3790	Diplura	P1	IV160	nd	
GR15MEB0001-20160317-T2-01	GR15MEB0001	Diplura	P3	IV236	Contam/Mis-ID?	
GR15MEB0008-20160317-T2-01	GR15MEB0008	Diplura	P3	IV237	contam	
GR15MEB0014-20160316-Sc-01	GR15MEB0014	Diplura	P3	IV238	NoAmp	
GR15MEC0001-20160316-T2-01	GR15MEC0001	Diplura	P3	IV239	NoAmp	
GR15MEC0001-20160316-T2-02	GR15MEC0001	Diplura	P3	IV240	Contam/Mis-ID?	
GR15MEC0001-20160316-T2-03	GR15MEC0001	Diplura	P3	IV241	contam	
GR15MEC0001-20160316-T2-04	GR15MEC0001	Diplura	P3	IV242	NoAmp	
GR15MEC0001-20160316-T2-05	GR15MEC0001	Diplura	P3	IV243	NoAmp	
GR15MEC0008-20160316-T2-01	GR15MEC0008	Diplura	P3	IV244	NoAmp	
RC15MEB0171-20160317-T1-01	RC15MEB0171	Diplura	P3	IV245	DPA003	DPA003
RC15MEC0001-20160316-T2-01	RC15MEC0001	Diplura	P3	IV246	NoAmp	
RC15MEC0027-20160316-T3-01	RC15MEC0027	Diplura	P3	IV247	NoAmp	
RC15MEC0192-20160316-T1-01	RC15MEC0192	Diplura	P3	IV248	DPA005	DPA005
RC15MEC0192-20160316-T1-02	RC15MEC0192	Diplura	P3	IV249	DPA005	DPA005
RC15MEC0192-20160316-T1-03	RC15MEC0192	Diplura	P3	IV250	DPA006	DPA006
RC15MEC0192-20160316-T3-01	RC15MEC0192	Diplura	P3	IV251	NoAmp	
RC15MEC0192-20160316-T3-02	RC15MEC0192	Diplura	P3	IV252	NoAmp	
RC15MEC0197-20160316-T1-01	RC15MEC0197	Diplura	P3	IV253	NoAmp	
RC15MEC0197-20160316-T2-02A	RC15MEC0197	Diplura	P3	IV254	NoAmp	
RC15MEC0197-20160316-T2-02B	RC15MEC0197	Diplura	P3	IV255	NoAmp	
RC15MEC0200-20160316-T2-01	RC15MEC0200	Diplura	P3	IV256	Messy seq	
RC15MEC0200-20160316-T3-02	RC15MEC0200	Diplura	P3	IV257	NoAmp	

GR15MEB0014.20160915.T3-01	GR15MEB0014	Diplura	P4	KD07	DCA003	DCA003
RC15MEB0115.20160915.T2-01	RC15MEB0115	Diplura	P4	KD08	DCA003	DCA003
RC15MEB0115.20160915.T2-01	RC15MEB0115	Diplura	P4	KD09	DCA003	DCA003
RC15MEB0115.20160915.T2-01	RC15MEB0115	Diplura	P4	KD10	DCA003	DCA003
RC15MEB0115.20160915.T2-01	RC15MEB0115	Diplura	P4	KD11	DCA003	DCA003
RC15MEC0103.20160915.T1-01	RC15MEC0103	Diplura	P4	KD12	DPA007*	DPA007*
RC14MEB0101.20160915.T2-01	RC14MEB0101	Diplura	P4	KD13	DCA003	DCA003
RC16MEC0156.20160915.T3-01	RC16MEC0156	Diplura	P4	KD14	DPA006	DPA006
RC16MEC0118.20160915.T3-01	RC16MEC0118	Diplura	P4	KD15	DPA008*	DPA008*
DD14MRR0004T1-01	DD14MRR0004	Chilopoda	P1	IV139	Lineage 1	CHI001
DD14MRR0004T1-01	DD14MRR0004	Chilopoda	P1	IV140	Lineage 1	CHI001
DD14MRR0005-T1-04	DD14MRR0005	Chilopoda	P1	IV141	Lineage 1	CHI001
DD14MEL0001-20151001-T1-01	DD14MEL0001	Chilopoda	P2	IV142	nd	
MEARC4383-20151001-T2-01	MEARC4383	Chilopoda	P2	IV143	Lineage 2	CHI002
SSp-2010-325		Chilopoda	H	IV347	Failed repeat PCR	
93283		Chilopoda	H	93283	NoAmp	
93287		Chilopoda	H	93287	NoAmp	
93778		Chilopoda	H	93778	NoAmp	
93780		Chilopoda	H	93780	NoAmp	
98714		Chilopoda	H	98714	NoAmp	
120191		Chilopoda	H	120191	CHI021	CHI021
132678		Chilopoda	H	132678	CHI022	CHI022
93779		Chilopoda	H	93779	CHI024	CHI024
RC14MEB0115-20160317-T2-02	RC14MEB0115	Chilopoda	P3	IV231	CHI023	CHI023
138572		Chilopoda	P1/2 re	IV142	CHI025	CHI025
RC15MEC0168.20160915.T3-02	RC15MEC0168	Chilopoda	4	KD16	CHI026	CHI026*
DAVES-20150930-04	DAVES	Amphipoda	P2	KD38	AMN008	AMN008
Budgie-20150930-01	Budgie	Amphipoda	P2	KD39	AMN008	AMN008
Budgie-20150930-01	Budgie	Amphipoda	P2	KD40	AMM029*	AMM029*
Budgie-20150930-01	Budgie	Amphipoda	P2	KD41	AMN001*	AMN001*
Budgie-20150930-01	Budgie	Amphipoda	P2	KD42	AMN008	AMN008
Budgie-20150930-01	Budgie	Amphipoda	P2	KD43	AMN008	AMN008
Budgie-20150930-01	Budgie	Amphipoda	P2	KD44	AMM030*	AMM030*
Budgie-20150930-01	Budgie	Amphipoda	P2	KD45	AMM031*	AMM031*
Budgie-20150930-01	Budgie	Amphipoda	P2	KD46		
Budgie-20150930-01	Budgie	Amphipoda	P2	KD47	AMM028*	AMM028*
Budgie-20150930-01	Budgie	Amphipoda	P2	KD48	AMP009	AMP009
Budgie-20150930-01	Budgie	Amphipoda	P2	KD49	AMM001	AMM001
Budgie-20150930-01	Budgie	Amphipoda	P2	KD50	AMM030*	AMM030*
Budgie-20150930-01	Budgie	Amphipoda	P2	KD51	AMN008	AMN008
Budgie.20150604-02	Budgie	Amphipoda	P1	KD52		
Budgie.20150604-02	Budgie	Amphipoda	P1	KD53	AMM002	AMM002
Budgie.20150604-02	Budgie	Amphipoda	P1	KD54		
Budgie.20150604-02	Budgie	Amphipoda	P1	KD55	AMM031*	AMM031*
Budgie.20150604-02	Budgie	Amphipoda	P1	KD56	AMN008	AMN008
Budgie.20150604-02	Budgie	Amphipoda	P1	KD57	AMN008	AMN008
TOBRC0099-20150930-01	TOBRC0099	Amphipoda	P2	KD58	AMP023	AMP023
TOBRC0099-20150930-01	TOBRC0099	Amphipoda	P2	KD59	AMP023	AMP023
TOBRC0099-20150930-01	TOBRC0099	Amphipoda	P2	KD60	AMP023	AMP023
TOBRC0099-20150930-01	TOBRC0099	Amphipoda	P2	KD61	AMP023	AMP023
TOBRC0099-20150930-01	TOBRC0099	Amphipoda	P2	KD62	AMP023	AMP023

TOBRC0099-20150930-01	TOBRC0099	Amphipoda	P2	KD63	AMP023	AMP023
TOBRC0099-20150930-01	TOBRC0099	Amphipoda	P2	KD64	AMP023	AMP023
Daves-20150604-01	DAVES	Amphipoda	P1	KD65		
Budgie.20150604-02	Budgie	Amphipoda	P1	IV92	Lineage 2	AMM002
Budgie.20150604-02	Budgie	Amphipoda	P1	IV93	Lineage 1	AMM001
Budgie.20150604-02	Budgie	Amphipoda	P1	IV94	Lineage 8	AMN008
Budgie.20150604-02	Budgie	Amphipoda	P1	IV95	Lineage 8	AMN008
Budgie.20150604-02	Budgie	Amphipoda	P1	IV96	nd	
Camp-20150604-02	Camp	Amphipoda	P1	IV97	nd	
Camp-20150604-02	Camp	Amphipoda	P1	IV98	nd	
Daisy-20150604-02	Daisy	Amphipoda	P1	IV99	nd	
Daves-20150604-01	Daves	Amphipoda	P1	IV100	Lineage 8	AMN008
Daves-20150604-01	Daves	Amphipoda	P1	IV101	nd	
Daves-20150604-01	Daves	Amphipoda	P1	IV102	nd	
Daves-20150604-01	Daves	Amphipoda	P1	IV103	nd	
Daves-20150604-01	Daves	Amphipoda	P1	IV104	Lineage 8	AMN008
MB13WARR001-20150605-01	MB13WARR001	Amphipoda	P1	IV105	Lineage 5	AMM005
MB13WARR001-20150605-01	MB13WARR001	Amphipoda	P1	IV106	Lineage 5	AMM005
MB13WARR001-20150605-01	MB13WARR001	Amphipoda	P1	IV107	Lineage 5	AMM005
MB13WARR001-20150605-01	MB13WARR001	Amphipoda	P1	IV108	Lineage 5	AMM005
MB13WARR001-20150605-01	MB13WARR001	Amphipoda	P1	IV109	Lineage 5	AMM005
MB13WARR010.20150606-01	MB13WARR010	Amphipoda	P1	IV110	nd	
MB13WARR010.20150606-01	MB13WARR010	Amphipoda	P1	IV111	Lineage 3	AMM003
MB13WARR010.20150606-01	MB13WARR010	Amphipoda	P1	IV112	Lineage 3	AMM003
MB13WARR010.20150606-01	MB13WARR010	Amphipoda	P1	IV113	nd	
MB13WARR010.20150606-01	MB13WARR010	Amphipoda	P1	IV114	Lineage 3	AMM003
TOBRC009-20150605-01	TOBRC009	Amphipoda	P1	IV115	nd	
TOBRC009-20150605-01	TOBRC009	Amphipoda	P1	IV116	nd	
TOBRC009-20150605-01	TOBRC009	Amphipoda	P1	IV117	nd	
TOBRC009-20150605-01	TOBRC009	Amphipoda	P1	IV118	nd	
TOBRC009-20150605-01	TOBRC009	Amphipoda	P1	IV119	nd	
Budgie-20150930-01	Budgie	Amphipoda	P1	IV120	Lineage 1	AMM001
Budgie-20150930-01	Budgie	Amphipoda	P1	IV121	Lineage 1	AMM001
Budgie-20150930-01	Budgie	Amphipoda	P1	IV122	nd	
Budgie-20150930-01	Budgie	Amphipoda	P1	IV123	Lineage 1	AMM001
Budgie-20150930-01	Budgie	Amphipoda	P1	IV124	nd	
Camp-20150930-02	Camp	Amphipoda	P2	IV125	Lineage 1	AMM001
Camp-20150930-02	Camp	Amphipoda	P2	IV126	Lineage 1	AMM001
Daisy-201509-02	Daisy	Amphipoda	P2	IV127	Lineage 2	AMM002
DAVES-20150930-04	Daves	Amphipoda	P2	IV128	Lineage 4	AMM004
DAVES-20150930-04	Daves	Amphipoda	P2	IV129	Lineage 7	AMN007
DAVES-20150930-04	Daves	Amphipoda	P2	IV130	Lineage 8	AMM008
DAVES-20150930-04	Daves	Amphipoda	P2	IV131	nd	
DAVES-20150930-04	Daves	Amphipoda	P2	IV132	Lineage 4	AMM004
RC13MEA0279-20150930-02	RC13MEA0279	Amphipoda	P2	IV133	nd	
TOBRC0099-20150930-01	TOBRC0099	Amphipoda	P2	IV134	Lineage 6	AMM006
TOBRC0099-20150930-01	TOBRC0099	Amphipoda	P2	IV135	nd	
TOBRC0099-20150930-01	TOBRC0099	Amphipoda	P2	IV136	nd	
TOBRC0099-20150930-01	TOBRC0099	Amphipoda	P2	IV137	nd	
TOBRC0099-20150930-01	TOBRC0099	Amphipoda	P2	IV138	nd	
Daves bore	Daves bore	Amphipoda	P1/2 re	IV102	NoAmp	NoAmp

TOBRC009	TOBRC009	Amphipoda	P1/2 re	IV115	AMP023	AMP023
TOBRC009	TOBRC009	Amphipoda	P1/2 re	IV116	AMP023	AMP023
TOBRC009	TOBRC009	Amphipoda	P1/2 re	IV117	AMP023	AMP023
TOBRC009	TOBRC009	Amphipoda	P1/2 re	IV118	AMP023	AMP023
TOBRC009	TOBRC009	Amphipoda	P1/2 re	IV119	AMP023	AMP023
Budgie	Budgie	Amphipoda	P1/2 re	IV122	AMM001	AMM001
Budgie	Budgie	Amphipoda	P1/2 re	IV124	AMM027	AMM027
Daves	Daves	Amphipoda	P1/2 re	IV131	NoAmp	NoAmp
TOBRC009	TOBRC009	Amphipoda	P1/2 re	IV136	contam	contam
Budgie bore	Budgie bore	Amphipoda	P1/2 re	IV96	AMM001	AMM001
Camp bore	Camp bore	Amphipoda	P1/2 re	IV97	AMM001	AMM001
Camp bore	Camp bore	Amphipoda	P1/2 re	IV98	AMM001	AMM001
Daisy well	Daisy well	Amphipoda	P1/2 re	IV99	NoAmp	NoAmp
Daves bore	Daves bore	Amphipoda	P1/2 re	IV101	NoAmp	NoAmp
Daves bore	Daves bore	Amphipoda	P1/2 re	IV103	NoAmp	NoAmp
MB13WARR010	MB13WARR010	Amphipoda	P1/2 re	IV110	NoAmp	NoAmp
MB13WARR010	MB13WARR010	Amphipoda	P1/2 re	IV113	NoAmp	NoAmp
RC13MEA0279	RC13MEA0279	Amphipoda	P1/2 re	IV133	NoAmp	NoAmp
TOBRC009	TOBRC009	Amphipoda	P1/2 re	IV135	NoAmp	NoAmp
TOBRC009	TOBRC009	Amphipoda	P1/2 re	IV137	NoAmp	NoAmp
TOBRC009	TOBRC009	Amphipoda	P1/2 re	IV138	NoAmp	NoAmp

Figure 1. Bayesian analysis of COI haplotypes of Araneae from the present study and reference specimens from Genbank and previous surveys in the Pilbara. Numbers on major nodes correspond to posterior probabilities; values <50% are not shown. Specimens from the present study are highlighted in yellow; specimens from previous phases at Robe Valley are highlighted in green; GenBank voucher specimens highlighted in turquoise. Scale bar= number of substitutions per site. Red boxes enclose species with high confidence.

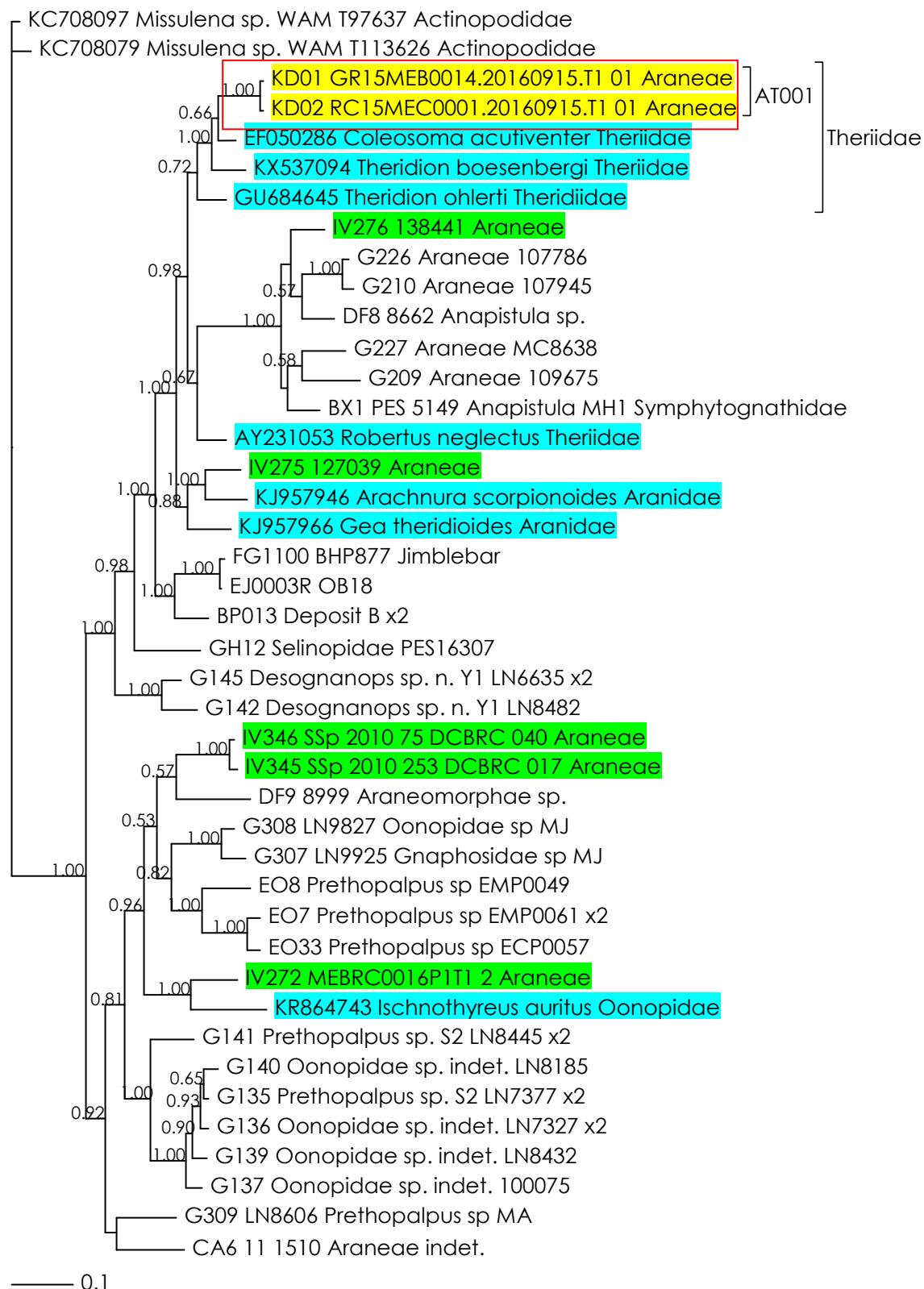


Figure 2. Bayesian analysis of COI haplotypes of Diplura from the present study and reference specimens from Genbank and previous surveys in the Pilbara. Numbers on major nodes correspond to posterior probabilities; values <50% are not shown. Specimens from the present study are highlighted in yellow; specimens from previous phases at Robe Valley are highlighted in green; GenBank voucher specimens highlighted in turquoise. Scale bar= number of substitutions per site. Red boxes with solid lines enclose species with high confidence; red boxes with dashed lines represent groups requiring further investigation.

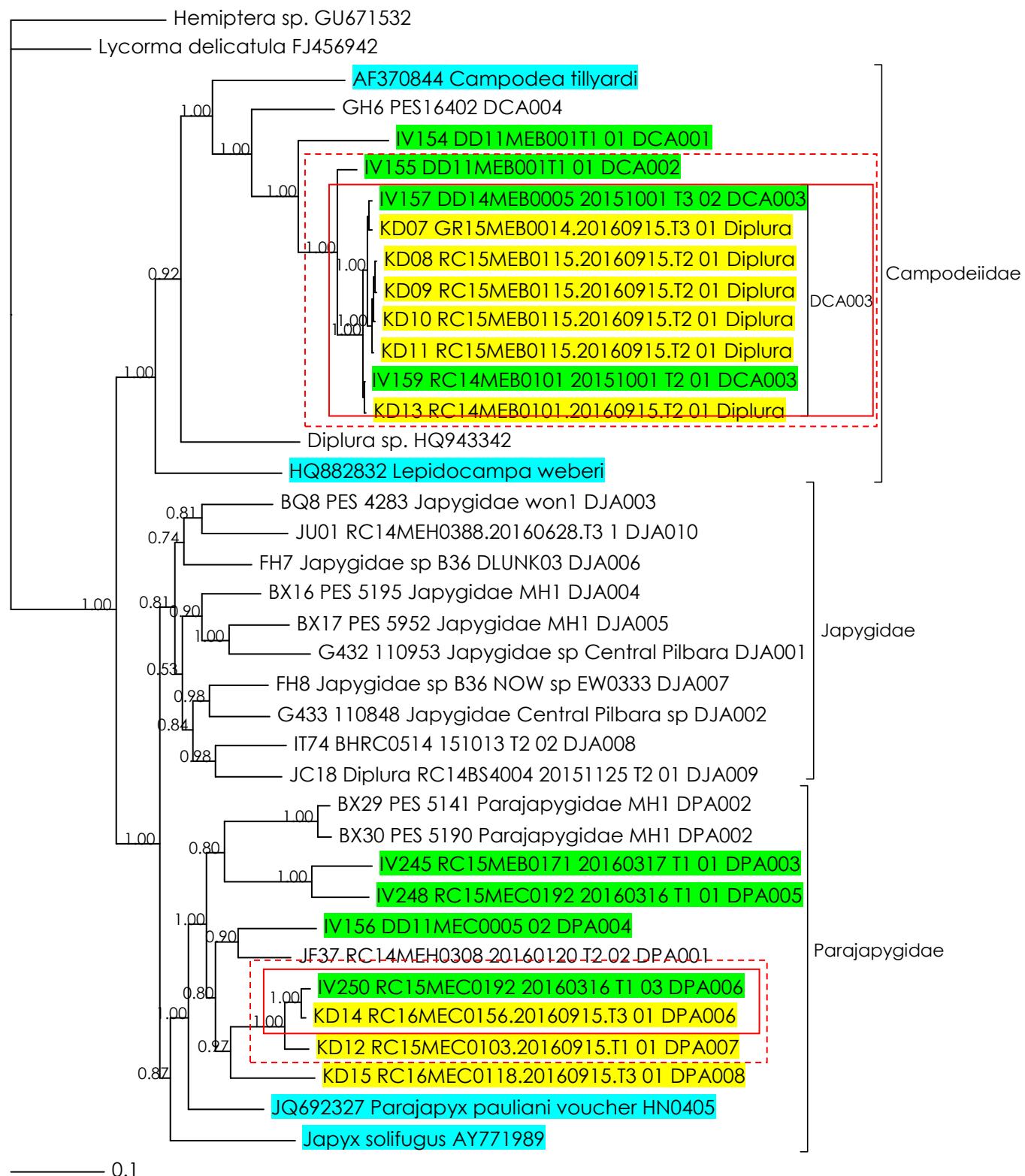


Figure 3. Bayesian analysis of COI haplotypes of Chilopoda from the present study and reference specimens from Genbank and previous surveys in the Pilbara. Numbers on major nodes correspond to posterior probabilities; values <50% are not shown. Specimens from the present study are highlighted in yellow; specimens from previous phases at Robe Valley are highlighted in green; GenBank voucher specimens highlighted in turquoise. Scale bar= number of substitutions per site.

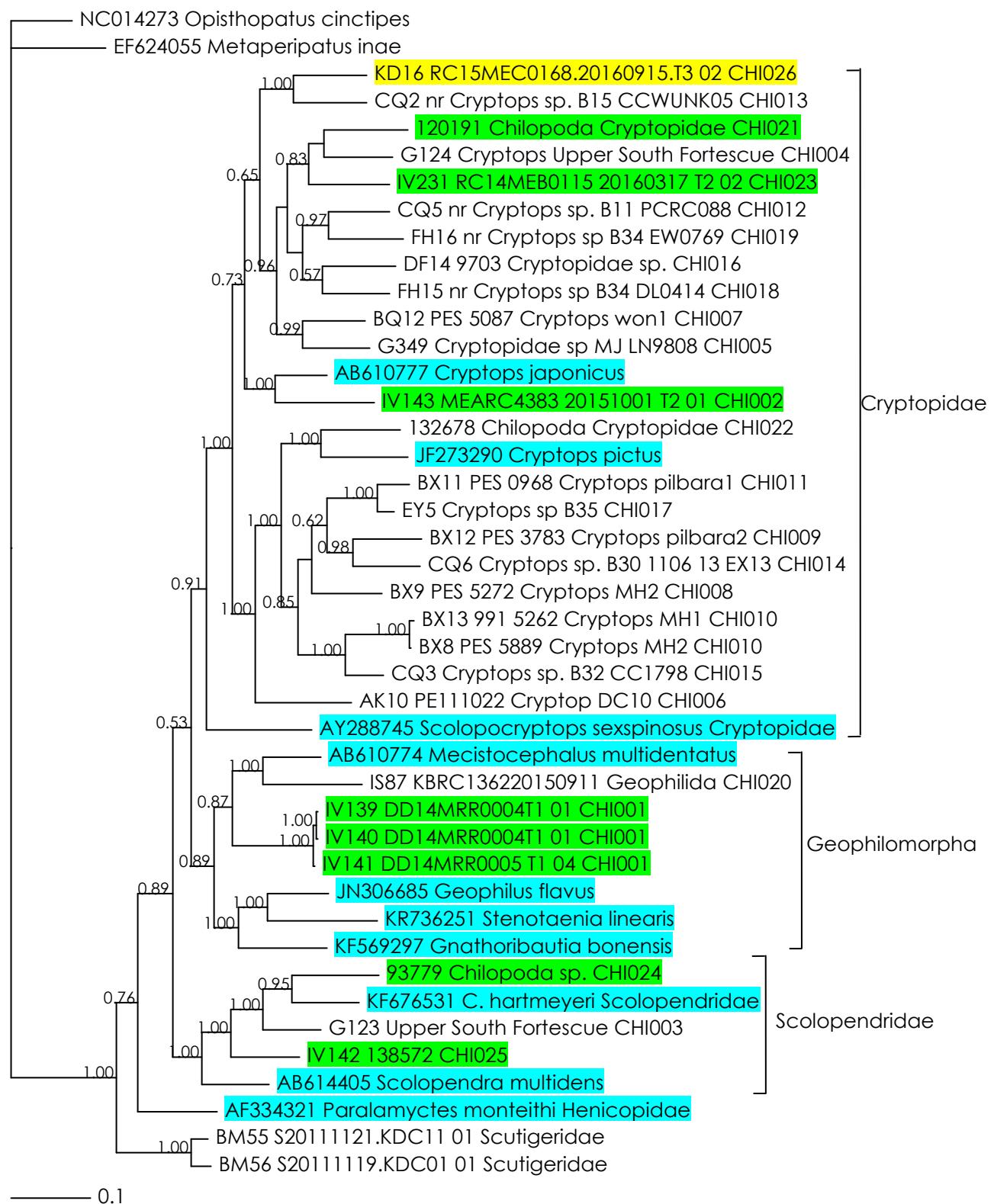


Figure 4. Neighbour-joining analysis of specimens of Amphipoda from the present study. Numbers on major nodes correspond to bootstrap support over 100 iterations; values <50% are not shown. Scale bar= genetic distance. The specimens used to represent each lineage in the model-based phylogenetic analysis are highlighted in yellow.

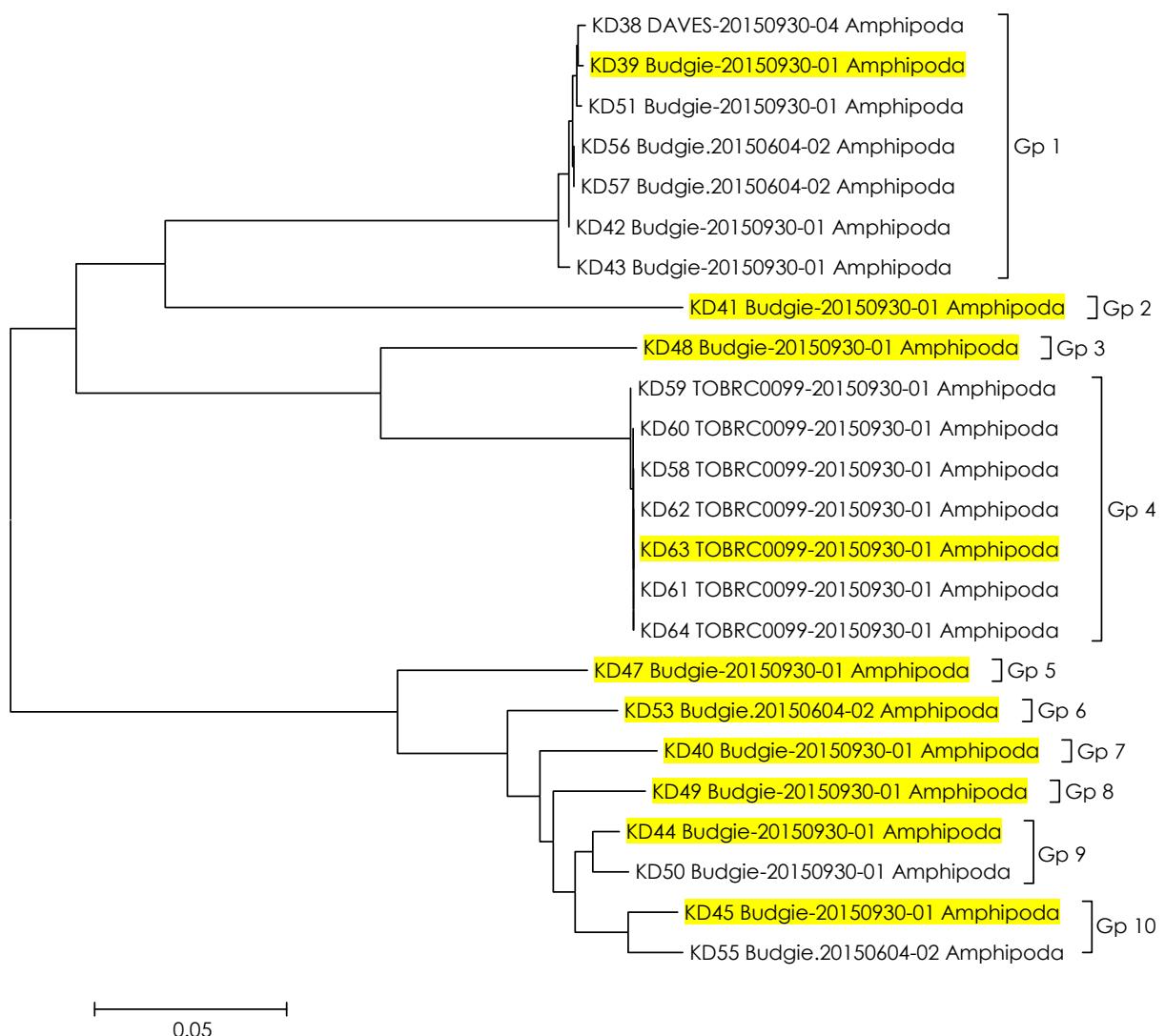


Figure 5. Bayesian analysis of COI haplotypes of Paramelitidae and Niphargidae (Amphipoda) from the present study and reference specimens from Genbank and previous surveys in the Pilbara. Numbers on major nodes correspond to posterior probabilities; values <50% are not shown. Specimens from the present study are highlighted in yellow; specimens from previous phases at Robe Valley are highlighted in green; GenBank voucher specimens highlighted in turquoise. Scale bar= number of substitutions per site. Red boxes with solid lines enclose species with high confidence.

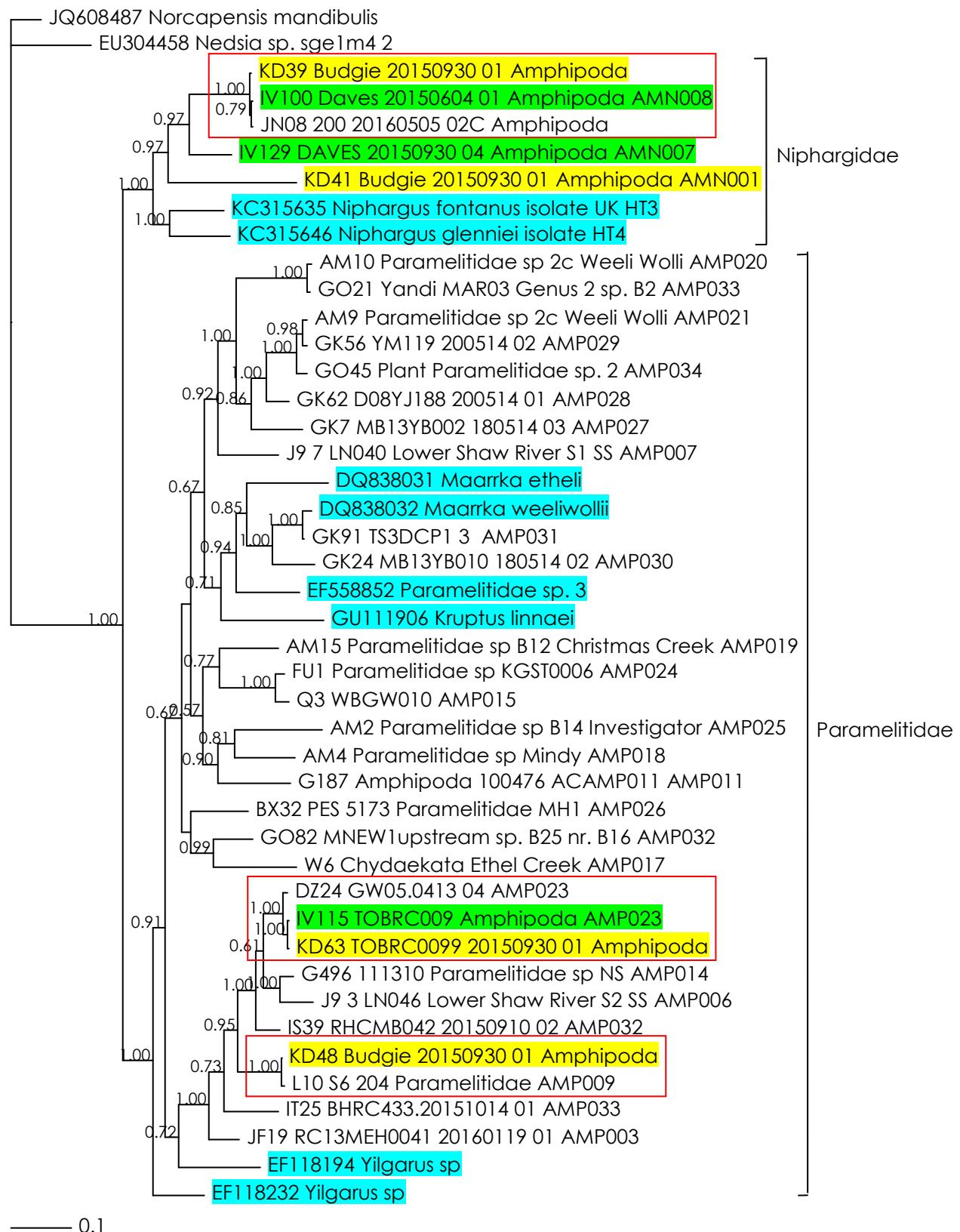


Figure 6. Bayesian analysis of COI haplotypes of Melitidae (Amphipoda) from the present study and reference specimens from Genbank and previous surveys in the Pilbara. Numbers on major nodes correspond to posterior probabilities; values <50% are not shown. Specimens from the present study are highlighted in yellow; specimens from previous phases at Robe Valley are highlighted in green; GenBank voucher specimens highlighted in turquoise. Scale bar= number of substitutions per site. Red boxes with dashed lines represent groups requiring further investigation.



**Table 2. Estimates of Evolutionary Divergence between Sequences**

1. Tamura K., Stecher G., Peterson D., Filipski A., and Kumar S. (2013). MEGA6: Molecular Evolutionary Genetics Analysis version 6.0. Molecular Biology and Evolution 30: 2725-2729.

The number of base differences per site from between sequences are shown. Standard error estimate(s) are shown above the diagonal. The analysis involved 42 nucleotide sequences. Codon positions included were 1st+2nd+3rd+Noncoding. All ambiguous positions were removed for each sequence pair. There were a total of 495 positions in the final dataset. Evolutionary analyses were conducted in MEGA6 [1].

Table 4: Estimates of Evolutionary Divergence between Sequences

Specimen ID	KD07 GR15MEB0014.20160915.T3-01 Diplura	KD08 RC15MEB0115.20160915.T2-01 Diplura	KD09 RC15MEB0115.20160915.T2-01 Diplura	KD10 RC15MEB0115.20160915.T2-01 Diplura	KD11 RC15MEB0115.20160915.T2-01 Diplura	KD12 RC15MEC0103.20160915.T1-01 Diplura	KD13 RC14MEC0118.20160915.T3-01 Diplura	KD14 RC16MEC0156.20160915.T3-01 Diplura	KD15 RC16MEC0118.20160915.T3-01 Diplura	AF370844 Campodea tillyardi	BQ8 PES 4283 Japygidae won1 DJA003	BX16 PES-5195 Japygidae MH1 DJA004	BX17 PES-5952 Japygidae MH1 DJA005	BX29 PES-5141 Parajapygidae MH1 DPA002	BX30 PES-5190 Parajapygidae MH1 DPA002	Diplura sp. HQ943342	FH7 Japygidae sp B36 DLUNK03 DJA006	FH8 Japygidae sp B36 NOW sp EW0333 DJA007	G432 110953 Japygidae sp Central Pilbara DJA001	G433 110848 Japygidae Central Pilbara sp DJA002	GH6 Anajapygidae Ana-PES16402 DCA004	IT74 BHRC0514-151013-T2-02 DJA008	IV154 DD11MEB001T1-01 DCA001	IV155 DD11MEB001T1-01 DCA002	IV156 DD11MEC0005-02 DPA004	IV157 DD14MEB0005-20151001-T3-02 DCA003	IV159 RC14MEB0101-20151001-T2-01 DCA003	IV245 RC15MEB0171-20160317-T1-01 DPA003	IV248 RC15MEC0192-20160316-T1-01 DPA005	IV250 RC15MEC0192-20160316-T1-03 DPA006	Japyx solifugus AY771989	JC18 Diplura RC14BS4004-20151125-T2-01 DJA009	JF37 RC14MEH0308-20160120-T2-02 DPA001	JQ692327 Parajapyx pauliani voucher HN0405	JU01 RC14MEH0388.20160628.T3-1 DJA010
KD07 GR15MEB0014.20160915.T3-01 Diplura	<b>0.002</b>	<b>0.002</b>	<b>0.002</b>	<b>0.002</b>	<b>0.017</b>	<b>0.003</b>	<b>0.017</b>	<b>0.017</b>	<b>0.014</b>	<b>0.017</b>	<b>0.015</b>	<b>0.017</b>	<b>0.015</b>	<b>0.016</b>	<b>0.014</b>	<b>0.015</b>	<b>0.017</b>	<b>0.018</b>	<b>0.017</b>	<b>0.014</b>	<b>0.015</b>	<b>0.015</b>	<b>0.016</b>	<b>0.017</b>	<b>0.017</b>										
KD08 RC15MEB0115.20160915.T2-01 Diplura	0.006	<b>0.000</b>	<b>0.000</b>	<b>0.000</b>	<b>0.018</b>	<b>0.004</b>	<b>0.017</b>	<b>0.017</b>	<b>0.014</b>	<b>0.017</b>	<b>0.016</b>	<b>0.016</b>	<b>0.016</b>	<b>0.016</b>	<b>0.014</b>	<b>0.015</b>	<b>0.017</b>	<b>0.018</b>	<b>0.017</b>	<b>0.014</b>	<b>0.015</b>	<b>0.015</b>	<b>0.016</b>	<b>0.017</b>	<b>0.017</b>										
KD09 RC15MEB0115.20160915.T2-01 Diplura	0.006	<b>0.000</b>	<b>0.000</b>	<b>0.000</b>	<b>0.018</b>	<b>0.004</b>	<b>0.017</b>	<b>0.017</b>	<b>0.014</b>	<b>0.017</b>	<b>0.016</b>	<b>0.016</b>	<b>0.016</b>	<b>0.016</b>	<b>0.014</b>	<b>0.015</b>	<b>0.017</b>	<b>0.018</b>	<b>0.017</b>	<b>0.014</b>	<b>0.015</b>	<b>0.015</b>	<b>0.016</b>	<b>0.017</b>	<b>0.017</b>										
KD10 RC15MEB0115.20160915.T2-01 Diplura	0.006	<b>0.000</b>	<b>0.000</b>	<b>0.000</b>	<b>0.018</b>	<b>0.004</b>	<b>0.017</b>	<b>0.017</b>	<b>0.014</b>	<b>0.017</b>	<b>0.016</b>	<b>0.016</b>	<b>0.016</b>	<b>0.016</b>	<b>0.014</b>	<b>0.015</b>	<b>0.017</b>	<b>0.018</b>	<b>0.017</b>	<b>0.014</b>	<b>0.015</b>	<b>0.015</b>	<b>0.016</b>	<b>0.017</b>	<b>0.017</b>										
KD11 RC15MEB0115.20160915.T2-01 Diplura	0.006	<b>0.000</b>	<b>0.000</b>	<b>0.000</b>	<b>0.018</b>	<b>0.004</b>	<b>0.017</b>	<b>0.017</b>	<b>0.014</b>	<b>0.017</b>	<b>0.016</b>	<b>0.016</b>	<b>0.016</b>	<b>0.016</b>	<b>0.014</b>	<b>0.015</b>	<b>0.017</b>	<b>0.018</b>	<b>0.017</b>	<b>0.014</b>	<b>0.015</b>	<b>0.015</b>	<b>0.016</b>	<b>0.017</b>	<b>0.017</b>										
KD12 RC15MEC0103.20160915.T1-01 Diplura	0.261	0.265	0.265	0.265	<b>0.017</b>	<b>0.008</b>	<b>0.012</b>	<b>0.018</b>	<b>0.014</b>	<b>0.015</b>	<b>0.015</b>	<b>0.014</b>	<b>0.014</b>	<b>0.016</b>	<b>0.014</b>	<b>0.015</b>	<b>0.015</b>	<b>0.014</b>	<b>0.017</b>	<b>0.014</b>	<b>0.015</b>	<b>0.015</b>	<b>0.016</b>	<b>0.017</b>	<b>0.017</b>										
KD13 RC14MEB0101.20160915.T2-01 Diplura	0.006	0.009	0.009	0.009	0.262	<b>0.017</b>	<b>0.016</b>	<b>0.014</b>	<b>0.017</b>	<b>0.015</b>	<b>0.017</b>	<b>0.016</b>	<b>0.016</b>	<b>0.014</b>	<b>0.016</b>	<b>0.015</b>	<b>0.017</b>	<b>0.014</b>	<b>0.015</b>	<b>0.016</b>	<b>0.017</b>	<b>0.017</b>	<b>0.017</b>	<b>0.017</b>	<b>0.017</b>										
KD14 RC16MEC0156.20160915.T3-01 Diplura	0.242	0.244	0.244	0.244	0.046	0.244	<b>0.013</b>	<b>0.017</b>	<b>0.014</b>	<b>0.015</b>	<b>0.015</b>	<b>0.014</b>	<b>0.014</b>	<b>0.016</b>	<b>0.015</b>	<b>0.015</b>	<b>0.017</b>	<b>0.015</b>	<b>0.019</b>	<b>0.018</b>	<b>0.014</b>	<b>0.017</b>	<b>0.017</b>	<b>0.015</b>	<b>0.014</b>	<b>0.014</b>									
KD15 RC16MEC0118.20160915.T3-01 Diplura	0.247	0.250	0.250	0.250	0.150	0.246	0.155	<b>0.018</b>	<b>0.014</b>	<b>0.014</b>	<b>0.015</b>	<b>0.014</b>	<b>0.013</b>	<b>0.017</b>	<b>0.012</b>	<b>0.013</b>	<b>0.014</b>	<b>0.014</b>	<b>0.016</b>	<b>0.014</b>	<b>0.019</b>	<b>0.017</b>	<b>0.015</b>	<b>0.015</b>	<b>0.015</b>										
AF370844 Campodea tillyardi	0.216	0.214	0.214	0.214	0.269	0.214	0.266	0.283	<b>0.019</b>	<b>0.019</b>	<b>0.017</b>	<b>0.018</b>	<b>0.018</b>	<b>0.016</b>	<b>0.017</b>	<b>0.019</b>	<b>0.017</b>	<b>0.018</b>	<b>0.014</b>	<b>0.015</b>	<b>0.019</b>	<b>0.016</b>	<b>0.018</b>	<b>0.017</b>	<b>0.019</b>										
BQ8 PES 4283 Japygidae won1 DJA003	0.230	0.227	0.227	0.227	0.197	0.227	0.191	0.189	0.251	<b>0.013</b>	<b>0.011</b>	<b>0.015</b>	<b>0.014</b>	<b>0.018</b>	<b>0.012</b>	<b>0.012</b>	<b>0.013</b>	<b>0.018</b>	<b>0.016</b>	<b>0.014</b>	<b>0.019</b>	<b>0.018</b>	<b>0.014</b>	<b>0.015</b>	<b>0.014</b>										
BX16 PES-5195 Japygidae MH1 DJA004	0.214	0.215	0.215	0.215	0.186	0.212	0.183	0.195	0.249	0.138	<b>0.011</b>	<b>0.015</b>	<b>0.015</b>	<b>0.016</b>	<b>0.012</b>	<b>0.012</b>	<b>0.013</b>	<b>0.016</b>	<b>0.014</b>	<b>0.016</b>	<b>0.018</b>	<b>0.016</b>	<b>0.015</b>	<b>0.013</b>	<b>0.013</b>										
BX17 PES-5952 Japygidae MH1 DJA005	0.227	0.227	0.227	0.227	0.200	0.227	0.196	0.210	0.267	0.147	0.130	<b>0.015</b>	<b>0.014</b>	<b>0.017</b>	<b>0.013</b>	<b>0.013</b>	<b>0.012</b>	<b>0.012</b>	<b>0.017</b>	<b>0.016</b>	<b>0.012</b>	<b>0.017</b>	<b>0.018</b>	<b>0.016</b>	<b>0.015</b>										
BX29 PES-5141 Parajapygidae MH1 DPA002	0.264	0.261	0.261	0.261	0.191	0.261	0.181	0.181	0.278	0.210	0.213	0.204	<b>0.006</b>	<b>0.018</b>	<b>0.014</b>	<b>0.014</b>	<b>0.013</b>	<b>0.016</b>	<b>0.014</b>	<b>0.017</b>	<b>0.018</b>	<b>0.016</b>	<b>0.015</b>	<b>0.015</b>	<b>0.015</b>										
BX30 PES-5190 Parajapygidae MH1 DPA002	0.261	0.258	0.258	0.258	0.186	0.258	0.183	0.179	0.274	0.217	0.219	0.208	0.028	<b>0.017</b>	<b>0.013</b>	<b>0.015</b>	<b>0.014</b>	<b>0.016</b>	<b>0.015</b>	<b>0.017</b>	<b>0.017</b>	<b>0.014</b>	<b>0.016</b>	<b>0.</b>											

Table 6. Estimates of Evolutionary Divergence between Sequences

Specimen ID	KD16 RC15MEC0168.20160915.T3-02 Geophilida	120191 Chilopoda Cryptopidae CHI021	132678 Chilopoda Cryptopidae CHI022	93779 Chilopoda Cryptopidae sp. CHI024	AB610774 Mecistocephalus multidentatus	AB614405 Scolopendra japonicus	AB610777 Cryptops japonicus	AB614405 Scolopendra multidens	AF334321 Paralamyctes monteithi Henicopidae	AK10 PE111022 Cryptop DC10 CHI006	AY288745 Scolopocryptops sexspinosus Cryptopidae	BM55 S20111121.KDC11-01 Scutigeridae	BM56 S20111119.KDC01-01 Scutigeridae	BQ12 PES 5087 Cryptops won1 CHI007	BX11 PES-0968 Cryptops pilbara1 CHI011	BX12 PES-3783 Cryptops pilbara2 CHI009	BX13 991-5262 Cryptops MH1 CHI010	BX8 PES-5889 Cryptops MH2 CHI010	BX9 PES-5272 Cryptops MH2 CHI008	CQ2 nr Cryptopidae sp. B15 CCWUNK05 CHI013	CQ3 Cryptopidae sp. B32 CC1798 CHI015	CQ5 nr Cryptopidae sp. B30 1106 13 EX13 CHI014	DF14 9703 Cryptopidae sp. CHI016	EY5 Cryptops sp B35 CHI017	FH15 nr Cryptopidae sp B34 DL0414 CHI018	FH16 nr Cryptopidae sp B34 EW0769 CHI019	G123 Cryptops Upper South Fortescue CHI003	G124 Cryptops Upper South Fortescue CHI004	G349 Cryptopidae sp MJ LN9808 CHI005	IS87 KBRC136220150911T2 03 Geophilida sp CHI020	IV139 DD14MRR0004T1-01 CHI001	IV140 DD14MRR0004T1-01 CHI001	IV141 DD14MRR0005-T1-04 CHI001	JN306685 Geophilus flavus	KF69297 Gnathoribautia bonensis	KF676531 Cormocephalus hartmeyeri Scolopendridae	KR736251 Stenotaenia linearis	JF273290 Cryptops pictus
KD16 RC15MEC0168.20160915.T3-02 Geophilida	0.021	0.022	0.016	0.019	0.018	0.018	0.017	0.017	0.018	0.019	0.019	0.020	0.020	0.017	0.017	0.018	0.019	0.019	0.019	0.016	0.016	0.016	0.016	0.016	0.016	0.016	0.016											
120191 Chilopoda Cryptopidae CHI021	0.210	0.023	0.021	0.020	0.021	0.022	0.019	0.020	0.018	0.019	0.019	0.020	0.022	0.023	0.021	0.021	0.020	0.020	0.020	0.019	0.021	0.017	0.017	0.026	0.020	0.019	0.023	0.022										
132678 Chilopoda Cryptopidae CHI022	0.221	0.235	0.022	0.021	0.023	0.024	0.020	0.021	0.023	0.022	0.022	0.021	0.020	0.022	0.023	0.024	0.021	0.021	0.022	0.023	0.022	0.023	0.021	0.021	0.022	0.020	0.019	0.024	0.021									
93779 Chilopoda Cryptopidae sp. CHI024	0.226	0.256	0.270	0.019	0.018	0.018	0.020	0.018	0.019	0.016	0.017	0.016	0.019	0.017	0.017	0.019	0.017	0.017	0.016	0.020	0.016	0.017	0.015	0.017	0.019	0.017	0.019	0.018										
AB610774 Mecistocephalus multidentatus	0.239	0.227	0.262	0.258	0.018	0.016	0.016	0.018	0.017	0.017	0.017	0.018	0.017	0.017	0.017	0.018	0.016	0.017	0.016	0.016	0.016	0.016	0.017	0.016	0.016	0.016	0.017	0.018										
AB610777 Cryptops japonicus	0.190	0.205	0.222	0.234	0.216	0.017	0.017	0.017	0.016	0.017	0.018	0.017	0.019	0.017	0.015	0.015	0.017	0.016	0.016	0.018	0.019	0.014	0.018	0.018	0.016	0.017	0.019	0.018										
AB614405 Scolopendra multidens	0.229	0.270	0.277	0.196	0.216	0.234	0.018	0.017	0.015	0.017	0.017	0.019	0.016	0.018	0.019	0.020	0.018	0.019	0.015	0.018	0.018	0.017	0.017	0.018	0.017	0.018	0.020	0.019										
AF334321 Paralamyctes monteithi Henicopidae	0.220	0.234	0.249	0.220	0.198	0.195	0.206	0.017	0.016	0.016	0.016	0.017	0.019	0.018	0.019	0.019	0.017	0.017	0.016	0.017	0.019	0.019	0.018	0.019	0.018	0.020	0.019	0.019										
AK10 PE111022 Cryptop DC10 CHI006	0.204	0.224	0.200	0.236	0.250	0.192	0.223	0.213	0.019	0.018	0.018	0.019	0.020	0.018	0.019	0.019	0.017	0.017	0.016	0.017	0.018	0.020	0.020	0.020	0.020	0.018	0.019	0.019										
AY288745 Scolopocryptops sexspinosus Cryptopidae	0.223	0.208	0.220	0.232	0.223	0.211	0.204	0.206	0.218	0.017	0.018	0.018	0.020	0.021	0.021	0.018	0.019	0.018	0.019	0.017	0.017	0.016	0.017	0.017	0.018	0.020	0.021											
BM55 S20111121.KDC11-01 Scutigeridae	0.216	0.238	0.277	0.221	0.245	0.228	0.225	0.188	0.227	0.225	0.008	0.018	0.018	0.019	0.017	0.017	0.017	0.016	0.016	0.016	0.016	0.020	0.020	0.016	0.017	0.018	0.019	0.018										
BM56 S20111119.KDC01-01 Scutigeridae	0.218	0.233	0.272	0.224	0.242	0.220	0.217	0.191	0.232	0.223	0.047	0.019	0.020	0.019	0.017	0.017	0.019	0.018	0.016	0.017	0.022	0.017	0.018	0.016	0.018	0.020	0.019											
BQ12 PES 5087 Cryptops won1 CHI007	0.191	0.192	0.210	0.244	0.226	0.184	0.245	0.213	0.198	0.190	0.241	0.234	0.017	0.019	0.021	0.021	0.019	0.019	0.018	0.016	0.020	0.020	0.019	0.018	0.019	0.018	0.020											
BX11 PES-0968 Cryptops pilbara1 CHI011	0.210	0.226	0.198	0.281	0.240	0.209	0.242	0.224	0.194	0.214	0.231	0.233	0.213	0.018	0.019	0.019	0.017	0.017	0.017	0.018	0.011	0.018	0.020	0.018	0.019	0.016	0.021	0.020										
BX12 PES-3783 Cryptops pilbara2 CHI009	0.197	0.233	0.209	0.263	0.229	0.211	0.258	0.247	0.219	0.240	0.229	0.239	0.233	0.169	0.017	0.017	0.016	0.016	0.017	0.019	0.020	0.018	0.017	0.018	0.017	0.019	0.018											
BX13 991-5262 Cryptops MH1 CHI010	0.234	0.226	0.221	0.270	0.246	0.211	0.254	0.251	0.218	0.239	0.244	0.251	0.236	0.201	0.184	0.002	0.018	0.018	0.013	0.017	0.015	0.019	0.022	0.019	0.020	0.018	0.016	0.019										
BX8 PES-5889 Cryptops MH2 CHI010	0.231	0.226	0.211	0.269	0.248	0.211	0.252	0.253	0.215	0.244	0.242	0.250	0.233	0.201	0.181	0.006	0.018	0.018	0.013	0.017	0.016	0.018	0.022	0.018	0.017	0.017	0.016	0.018										
BX9 PES-5272 Cryptops MH2 CHI008	0.228	0.225	0.210	0.278	0.247	0.199	0.252	0.215	0.208	0.213	0.244	0.236	0.218	0.173	0.186	0.175	0.175	0.019	0.018	0.018	0.016	0.020	0.020	0.019	0.018	0.020	0.019											
CQ2 nr Cryptopidae sp. B15 CCWUNK05 CHI013	0.168	0.219	0.228	0.250	0.228	0.199	0.243	0.249	0.207	0.230	0.220	0.231	0																									

Table 10. Estimates of Evolutionary Divergence between Sequences

Specimen ID	KD39 Budgie-20150930-01 Amphipoda	KD41 Budgie-20150930-01 Amphipoda	KD48 Budgie-20150930-01 Amphipoda	KD63 TOBRC0099-20150930-01 Amphipoda	AM10 Paramelitidae sp 2c Weeli Woll AMP020	AM15 Paramelitidae sp B12 Christmas Creek AMP019	AM2 Paramelitidae sp B14 Investigator AMP025	AM4 Paramelitidae sp Mindy AMP018	AM9 Paramelitidae sp 2c Weeli Woll AMP021	BX32 PE5-5173 Paramelitidae MH1 AMP026	DQ838031 Maarrka weeliwollii	DZ24 GW05.0413-04 AMP023	EF118194 Yilgarus sp	EF118232 Yilgarus sp	EF558852 Paramelitidae sp. 3	EU1 Paramelitidae sp KGS10006 AMP024	G187 Amphipoda 100476 ACAMP011 AMP011	G496 111310 Paramelitidae sp NS AMP014	GK24 MB13YB010-180514-02 AMP030	GK56 YM119-200514-02 AMP029	GK62 D08YJ188-200514-01 AMP028	GK7 MB13YB002-180514-03 AMP027	GK91 TS3DCP1-3 AMP031	GO21 Yandi MAR03 Paramelitidae Genus 2 sp B2 AMP033	GO45 Plant Paramelitidae sp. 2 AMP034	IS39 RHCMB042 20150910 02 AMP032	IV100 Daves-20150604-01 Amphipoda lin 8	IV15 TOBRC0099 Amphipoda AMP023	IV19 Lower Shaw River S2 SS AMP006	J9 3 LN040 Lower Shaw River S1 SS AMP007	JF19 RC13MEH041-20160119-01 AMP003	JN08 200-20160505-02C Amphipoda	KC315635 Niphargus fontanus isolate UK HT3	KC315646 Niphargus glenniei isolate HT4	L10 S6-204 Paramelitidae AMP009	Q3 WBGW010 AMP015	W6 Chykaeta Ethel Creek AMP017
KD39 Budgie-20150930-01 Amphipoda	0.015	0.016	0.015	0.015	0.015	0.015	0.015	0.015	0.017	0.014	0.016	0.017	0.015	0.016	0.017	0.016	0.017	0.016	0.017	0.016	0.017	0.016	0.017	0.016	0.017	0.016	0.017	0.016	0.017	0.016	0.017						
KD41 Budgie-20150930-01 Amphipoda	0.237	0.018	0.016	0.016	0.016	0.016	0.016	0.016	0.017	0.017	0.018	0.019	0.017	0.016	0.018	0.017	0.017	0.016	0.017	0.016	0.017	0.016	0.017	0.016	0.017	0.016	0.017	0.016	0.017	0.016	0.017						
KD48 Budgie-20150930-01 Amphipoda	0.261	0.300	0.013	0.016	0.014	0.016	0.016	0.016	0.017	0.015	0.016	0.015	0.015	0.014	0.015	0.015	0.017	0.016	0.017	0.016	0.017	0.016	0.017	0.016	0.017	0.016	0.017	0.016	0.017	0.016	0.017						
KD63 TOBRC0099-20150930-01 Amphipoda	0.280	0.304	0.133	0.016	0.014	0.016	0.018	0.017	0.017	0.017	0.015	0.005	0.015	0.015	0.014	0.017	0.014	0.010	0.014	0.016	0.016	0.016	0.017	0.016	0.017	0.016	0.017	0.016	0.017	0.016	0.017						
AM10 Paramelitidae sp 2c Weeli Woll AMP020	0.245	0.266	0.252	0.241	0.014	0.015	0.015	0.014	0.015	0.017	0.016	0.015	0.014	0.014	0.015	0.015	0.014	0.014	0.013	0.014	0.015	0.014	0.014	0.015	0.016	0.015	0.016	0.015	0.016	0.015	0.016	0.015	0.016				
AM15 Paramelitidae sp B12 Christmas Creek AMP019	0.250	0.289	0.223	0.220	0.217	0.014	0.015	0.014	0.015	0.015	0.015	0.014	0.013	0.014	0.014	0.015	0.014	0.014	0.013	0.015	0.015	0.014	0.014	0.015	0.014	0.015	0.015	0.015	0.015	0.015	0.015	0.015	0.015	0.015	0.015		
AM2 Paramelitidae sp B14 Investigator AMP025	0.295	0.319	0.225	0.235	0.238	0.214	0.015	0.016	0.016	0.016	0.016	0.015	0.017	0.014	0.014	0.016	0.015	0.017	0.014	0.014	0.015	0.016	0.017	0.016	0.017	0.015	0.016	0.015	0.016	0.015	0.016	0.015	0.016	0.015	0.016		
AM4 Paramelitidae sp Mindy AMP018	0.266	0.321	0.204	0.241	0.245	0.193	0.211	0.015	0.016	0.015	0.016	0.018	0.015	0.017	0.015	0.016	0.015	0.014	0.015	0.015	0.016	0.015	0.017	0.016	0.017	0.015	0.016	0.017	0.016	0.017	0.015	0.016	0.017	0.015	0.016		
AM9 Paramelitidae sp 2c Weeli Woll AMP021	0.270	0.299	0.220	0.232	0.190	0.208	0.238	0.245	0.017	0.016	0.016	0.016	0.015	0.015	0.016	0.015	0.017	0.016	0.016	0.017	0.016	0.017	0.016	0.017	0.016	0.017	0.016	0.017	0.016	0.017	0.016	0.017	0.015	0.016	0.017		
BX32 PE5-5173 Paramelitidae MH1 AMP026	0.274	0.285	0.212	0.223	0.226	0.178	0.204	0.195	0.207	0.017	0.017	0.017	0.016	0.017	0.018	0.017	0.018	0.017	0.016	0.017	0.016	0.017	0.016	0.017	0.016	0.017	0.016	0.017	0.016	0.017	0.016	0.017	0.016	0.017			
DQ838031 Maarrka etheli	0.304	0.320	0.220	0.230	0.254	0.231	0.229	0.231	0.233	0.014	0.017	0.017	0.015	0.016	0.016	0.016	0.015	0.016	0.015	0.016	0.015	0.017	0.016	0.017	0.016	0.017	0.016	0.017	0.016	0.017	0.016	0.017	0.016	0.017			
DQ838032 Maarrka weeliwollii	0.264	0.299	0.202	0.216	0.243	0.199	0.234	0.225	0.203	0.216	0.194	0.015	0.016	0.015	0.014	0.017	0.017	0.014	0.013	0.016	0.016	0.017	0.016	0.017	0.016	0.017	0.016	0.017	0.016	0.017	0.016	0.017	0.016	0.017			
DZ24 GW05.0413-04 AMP023	0.280	0.302	0.131	0.013	0.233	0.212	0.239	0.237	0.231	0.224	0.230	0.214	0.014	0.015	0.015	0.014	0.011	0.015	0.016	0.016	0.014	0.015	0.016	0.017	0.016	0.017	0.016	0.017	0.016	0.017	0.016	0.017	0.016	0.017			
EF118194 Yilgarus sp	0.264	0.301	0.236	0.217	0.228	0.216	0.254	0.243	0.228	0.202	0.236	0.211	0.209	0.014	0.016	0.015	0.016	0.015	0.016	0.017	0.016	0.015	0.016	0.017	0.016	0.017	0.016	0.017	0.016	0.017	0.016	0.017	0.016	0.017			
EF118232 Yilgarus sp	0.263	0.297	0.196	0.207	0.220	0.194	0.223	0.212	0.217	0.176	0.238	0.200	0.209	0.197	0.015	0.015	0.015	0.015	0.015	0.016	0.017	0.016	0.015	0.016	0.017	0.016	0.017	0.016	0.017	0.016	0.017	0.016	0.017	0.016	0.017		
EF558852 Paramelitidae sp. 3	0.260	0.293	0.222	0.209	0.222	0.213	0.242	0.236	0.204	0.219	0.202	0.207	0.211	0.202	0.015	0.017	0.014	0.015	0.014	0.015	0.016	0.015	0.015	0.016	0.017	0.016	0.017	0.016	0.017</								

**Table 11. Estimates of Evolutionary Divergence between Sequences**

1. Tamura K., Stecher G., Peterson D., Filipski A., and Kumar S. (2013). MEGA6: Molecular Evolutionary Genetics Analysis version 6.0. Molecular Biology and Evolution 30: 2725-2729.

The number of base differences per site from between sequences are shown. Standard error estimate(s) are shown above the diagonal. The analysis involved 42 nucleotide sequences. Codon positions included were 1st+2nd+3rd+Noncoding. All ambiguous positions were removed for each sequence pair. There were a total of 495 positions in the final dataset. Evolutionary analyses were conducted in MEGA6 [1].

Disclaimer: Although utmost care has been taken to ensure the correctness of the caption, the caption text is provided "as is" without any warranty of any kind. Authors advise the user to carefully check the caption prior to its use for any purpose and report any errors or problems to the authors immediately ([www.megasoftware.net](http://www.megasoftware.net)). In no event shall the authors and their employers be liable for any damages, including but not limited to special, consequential, or other damages. Authors specifically disclaim all other warranties expressed or implied, including but not limited to the determination of suitability of this caption text for a specific purpose, use, or application.



# Helix

## Molecular Solutions

School of Animal Biology The University of Western Australia  
Hackett Entrance No. 4 Hackett Drive Crawley WA 6009

PO Box 155  
Leederville WA 6903

t. (08) 6488 4509

f. (08) 6488 1029

abn. 32 133 230 243

w. [www.helixsolutions.com.au](http://www.helixsolutions.com.au)

12 February, 2017

Jason Alexander  
Biota Environmental Sciences  
Level 1, 228 Carr Place  
Leederville, WA 6007

Via email

**Re. Report on the molecular systematics of Amphipoda from the Robe River Valley – Phase 5**

Dear Jason,

Following is a summary of the results of the Amphipoda study we have completed from the Robe River Valley phase 5 collections. Seven distinct genetic lineages from three families (Melitidae, Niphargidae, Paramelitidae) were detected in the phase 5 collections, all of which have been detected previously in the Pilbara.

Thanks once again for collaborating on this project with Helix. We hope we can continue to provide you with useful information, and feel free to contact us if you have any questions or would like to discuss the results in detail.

Sincerely,

Dr. Terrie Finston, Yvette Hitchen and Dr. Oliver Berry  
Helix Molecular Solutions

## Background and Objective

Seventy-eight specimens of Amphipoda were collected from Robe River Valley during phase 5 and sequenced for variation at the mitochondrial COI gene. The molecular data were assessed in order to determine the number of species present in each group and compare the results to those obtained during previous surveys that have been undertaken for these groups elsewhere in the Pilbara.

## Executive summary

- Seventy-eight specimens of amphipods from the Robe River Valley phase 5 were sequenced for variation at the COI gene.
- Seven distinct genetic lineages from three families (Melitidae, Niphargidae, Paramelitidae) were detected among the 66 specimens for which sequences were obtained.
- All seven of the lineages have been detected previously in the Pilbara.

## Methods

Seventy-eight specimens of Amphipoda from four drillholes in the Robe River Valley area were sequenced for variation at the mitochondrial cytochrome oxidase subunit I gene (COI) using multiple pairs of primers (LCO1/HCO2, LCO1-long/HCO2-long, NemF1/NemR1 and LCO1/CIN2341).

Sequences were edited using GENEIOUS software (Drummond et al. 2011). Alignment was performed with CLUSTAL W (Thompson et al. 1994) using default parameters. Genetic distances between unique genetic sequences (haplotypes) were measured using uncorrected p-distances (total percentage of nucleotide differences between sequences).

MODELTEST software (Posada and Crandall, 1998) was used to determine the model of sequence evolution that best fitted the data for each taxonomic group. Bayesian analysis was used to construct the phylogenetic trees, incorporating the model as identified in MODELTEST for each taxonomic group. The phylogeny, branch lengths and posterior probabilities were obtained by running two trees simultaneously, each running four simultaneous MCMC chains. The number of cycles needed was determined by the standard deviation of the split frequencies of the two trees. The analysis was paused after every  $1 \times 10^6$  generations and when the standard deviation fell below 0.01, the analysis was stopped. A majority rule consensus tree was constructed after discarding the “burn-in” trees in both analyses. The burn-in value was determined by plotting the posterior probabilities obtained after every generation and identifying the point at which the values reach stationarity (= the asymptote). Trees produced prior to stationarity were discarded.

For the purposes of this report, lineages were defined as haplotypes or groups of haplotypes differing from other such groups by >3% sequence divergence. This cut-off was selected based on bar-coding data, which indicates that intra-specific variation rarely exceeds 3% (Hebert et al., 2003b).

## Results

### Preliminary analysis - Reference sequences and outgroups

Seventy-eight specimens of amphipods from phase 5 were sequenced for COI (Table 1; Appendix 1). In order to reduce analysis time and to simplify the presentation of results, a preliminary neighbour-joining (NJ) analysis was conducted on the 66 Robe Valley amphipods for which sequences were obtained, and haplotypes were selected from each genetic lineage to include in a model-based phylogenetic analysis.

The neighbour-joining analysis placed the 66 specimens of amphipods into seven lineages (Figure 1). Comparisons to the GenBank sequence database indicated that one lineage each was most similar to sequences of Niphargidae and Paramelitidae, whereas five lineages were most similar to sequences of Melitidae. The Melitidae and Niphargidae lineages contained between one and three specimens, whereas the Paramelitidae lineage contained 54 specimens (Figure 1). The five lineages of Melitidae differed from one another by between 6.0

and 17.1% mean sequence divergence (Table 2). Differentiation within lineages for all three families ranged from 0 to 2.0% mean sequence divergence (Table 3).

The Paramelitidae and Niphargidae were analysed in a single phylogenetic analysis. For the Paramelitidae, 35 reference sequences were included in the phylogenetic analysis, six GenBank vouchers of Paramelitidae, *Maarrka etheli* (Genbank accession #DQ838031), two *Maarrka weeliwollii* (Genbank accession # DQ838032 and # DQ838033), Paramelitidae sp. 3 (Genbank accession # EF558852) and two references of 'Yilgarus' sp. (Genbank accession # EF118232 and EF118194) as well as 29 specimens from previous surveys of the Central Pilbara, Barrow Island, Lower Shaw River, Fortescue River, and Marillana Creek. For the Niphargidae, seven reference sequences were included in the analysis, five specimens from previous surveys in the Robe Valley and two Genbank reference sequences of *Niphargus*: *N. fontanus* (Genbank accession number KC315635) and *N. glenniei* (Genbank accession number KC315646). Two sequences of Melitidae, *Nedsia* sp. 1 (Genbank accession #EU304458), and *Norcapensis mandibulus* (Genbank accession # JQ608487)

For the Melitidae, 41 reference sequences were included in the phylogenetic analysis, two GenBank vouchers of Melitidae, *Nedsia* sp. 1 (Genbank accession #EU304458), and *Norcapensis mandibulus* (Genbank accession # JQ608487) as well as 39 specimens from previous surveys of the Central Pilbara, Barrow Island, Lower Shaw River, Fortescue River, and Marillana Creek. Two sequences of the amphipod genus *Niphargus* were used as outgroups as follows: *N. fontanus* (Genbank accession number KC315635) and *N. glenniei* (Genbank accession number KC315646).

#### *Phylogenetic analysis- Paramelitidae and Niphargidae*

The phylogenetic analysis, which included the two representatives (one each) of Paramelitidae and Niphargidae from the Robe Valley phase 5, in addition to 35 and seven reference specimens, respectively, revealed the presence of two well-supported major clades, corresponding to the two families (Figure 2). The phase 5 Robe Valley specimen of Paramelitidae was placed in a single distinct lineage, which also contained reference specimens from previous surveys in the Pilbara (Figure 2). Specifically, specimen KJ43 from MB16WARR was placed in a lineage containing specimens from previous surveys in the Robe Valley and Barrow Island and thus was assigned to the existing lineage AMP023 (Figure 2). The phase 5 Niphargidae specimen from the Robe Valley was placed in a single distinct lineage, which also contained reference specimens from previous surveys in the Robe Valley (Figure 2). Specifically, specimen KJ64 from Budgie bore, was placed in a lineage containing specimens from previous surveys in the Robe Valley and thus was assigned to the existing lineage AMN008 (Figure 2).

#### *Differentiation between lineages – Paramelitidae and Niphargidae*

The Robe Valley Paramelitidae lineage represented by specimen KJ43 differed from the nearest reference specimens DZ24, IV115 and KD63 (lineage AMP023) by between 0.5 and 0.8% sequence divergence and from the next nearest reference specimen by 8.5% sequence divergence (Table 4). The Robe Valley Niphargidae lineage (specimen KJ64) differed from the nearest reference specimens KD39, IV100 and JN08 (lineage AMN008) by between 0.5 and 0.6% sequence divergence and from the next nearest reference specimen by 15.1% sequence divergence (Table 4).

#### *Phylogenetic analysis- Melitidae*

The phylogenetic analysis, which included the five representatives of Melitidae from phase 5 Robe Valley in addition to 41 reference specimens, placed the Robe Valley specimens in five distinct genetic lineages, all of which also contained reference specimens from previous surveys in the Pilbara (Figure 3). Specifically, specimen KJ65 was placed in a lineage containing reference specimens IV97, IV126, JN17, KD49, JF02 and rr3a and thus was assigned to the existing lineage AMM001, and specimen KJ73 was placed in a lineage containing reference specimens KD45 and KD55 and thus was assigned to the existing lineage AMM031 (Figure 3). Specimen KJ70 was placed in a lineage with reference specimens KD53, IV92 and nr5miwell, thus was assigned to the existing lineage AMM002 and specimen KJ72 was placed in a lineage

containing reference specimen KD47 and thus was assigned to the existing lineage AMM028 (Figure 3). Specimen KJ63 was placed in a lineage containing reference specimen IV134 and thus was assigned to the existing lineage AMM006 (Figure 3).

Specimens KJ65, KJ70 and KJ73 were placed in a larger clade containing eight closely related lineages from the Robe Valley (AMM001, AMM002, AMM024, AMM025, AMM027, AMM029, AMM030 and AMM031; Figure 3).

#### Differentiation between lineages - Melitidae

All five specimens representing the five lineages collected in phase 5 were assigned to existing lineages and differed from the nearest reference specimens by <3% (Table 5). Specifically, KJ65/AMM001 differed from the nearest reference specimens IV97, IV126, JN17, KD49, JF02 and rr3a by between 0.6 and 2.8% sequence divergence and KJ73/AMM031 differed from the nearest reference specimens KD45 and KD55 by between 2.1 and 3.0% sequence divergence (Table 5). KJ70/AMM002 differed from the nearest reference specimens KD53, IV92 and nr5miwell by 0.2% sequence divergence (Table 5). KJ72/AMM028 differed from reference specimen KD47 by 0.2% sequence divergence and KJ63/AMM006 was genetically identical to reference specimen IV134 (Table 5).

The genetic distance between specimens in the large well-supported clade comprising the eight closely related lineages (enclosed by a dashed red box in Figure 3) ranged from 0 – 7.7% and the mean was 4.9% sequence divergence.

#### Conclusions

COI is widely considered to show suitable variation to distinguish species (Hebert et al., 2003a). In a comparison of COI sequences for over 13,000 pairs of taxa, Hebert et al (2003b) found a mean of 11.1% sequence divergence between distinct species. Nearly 80% of the comparisons showed that species pairs differed from one another by greater than 8% sequence divergence. However, a taxon by taxon approach, examining the amount of phylogenetic variation within and between species is the most widely accepted method of defining species.

One lineage each of Niphargidae (AMN008) and Paramelitidae (AMP023) were detected at the Robe River Valley. Both specimens were placed in existing reference lineages, differing from those lineages by <1.0% and from the next nearest reference specimens by 8.5% or greater, indicating that each represents a distinct lineage and species that has been detected previously.

#### Niphargidae

AMN008 = one species from Budgie bore, detected previously in the Robe Valley

#### Paramelitidae

AMP023 = one species from MB16WARR, detected previously at Barrow Island and Robe Valley

Five lineages of Melitidae were detected at Robe Valley, differing from one another by between 6.0 and 17% mean sequence divergence, indicating that each is likely to represent a distinct species (however see following comments). All five of the lineages were assigned to existing lineages (AMM001, AMM002, AMM006, AMM028 and AMM031).

Three of the five lineages detected in phase 5 (AMM001, AMM002, AMM031) were placed in a well-supported clade containing a group of closely related specimens (enclosed by a dashed red box in Figure 3), which differed by <5% mean sequence divergence (range = 0 – 7.7%). Thus this group may represent several closely related species (as shown by solid red boxes in Figure 3), or may represent a single species showing genetic differentiation across its range. Further investigation may be required to resolve relationships among the lineages, but the most likely explanation would be to consider them a single species, owing to the fact that they have a relatively wide distribution (Robe Valley to Barrow Island) and the observed genetic variation may reflect geographic variation associated with a 'stepping stone' pattern of gene exchange – populations that are near-by would be expected to exchange genes, but those on the geographic extremes are not exchanging genes. This clade forms a larger clade with additional

lineages, including the Genbank reference specimen of *Nedsia* sp. 1, allowing us to assign the lineages to the genus *Nedsia* with some confidence.

**Melitidae**

AMM001 } Detected in Dave's and Budgie bores. May correspond to one species of  
AMM002 } *Nedsia*, but relationships among the clade members requires further  
AMM031 } investigation. All have been detected previously.

AMM006 = one species from RC13TOB, detected previously in the Robe Valley

AMM028 = one species from Budgie bore, detected previously in the Robe Valley

**References**

Alexander, J. B., Burger M. A.A., and Harvey, M.S. (2014). A new species of troglobitic *Anatemnus* (Pseudoscorpiones: Atemnidae) from the Pilbara bioregion of Australia. Records of the Western Australian Museum 29: 141 – 148.

Australian Faunal Directory. <http://www.environment.gov.au/biodiversity/abrs/online-resources/>. Accessed 27 Dec., 2015.

Bayly, I. A.E, Ellis p. (1969). *Haloniscus searlei* chilton: An aquatic "terrestrial" isopod with remarkable powers of osmotic regulation. Comparative Biochemistry and Physiology 31: 523-528

Drummond AJ, Ashton B, Buxton S, Cheung M, Cooper A, Duran C, Field M, Heled J, Kearse M, Markowitz S, Moir R, Stones-Havas S, Sturrock S, Thierer T, Wilson A (2011) Geneious v5.4, <http://www.geneious.com/>

Harvey, M. S., Berry, O. Edward, K. L., Humphreys, G. (2008) Molecular and morphological systematics of hypogean schizomids (Schizomida: Hubbardiidae) in semiarid Australia. Invertebrate Systematics 22: 167-194.

Hebert, P.D.N., Cywinska, A., Ball, S.L., deWaard J.R. (2003a). Biological identifications through DNA barcodes. Proceedings of the Royal Society of London B 270: 313-321.

Hebert, P.D.N., Ratnasingham, S., deWaard J.R. (2003b). Barcoding animal life: cytochrome c oxidase subunit 1 divergences among closely related species. Proceedings of the Royal Society of London B (supplement) 270: S96-S99.

Helix Molecular Solutions (2015). Report on the molecular systematics of Schizomida from The Robe River Valley. Prepared for Biota Environmental Sciences, 5 February.

Posada, D., Crandall, K.A. (1998). MODELTEST: testing the model of DNA substitution. Bioinformatics 14: 817-818.

Thompson, J., Higgins, D., and Gibson, T. (1994). CLUSTAL W: improving the sensitivity of progressive multiple sequence alignment through sequence weighting, position-specific gap penalties and weight matrix choice. Nucleic Acids Research 22: 4673–4680.  
doi:10.1093/nar/ 22.22.4673

Table 1. Specimens of Amphipoda used in the present study and the lineage to which they were assigned, based on variation at the COI gene.

Tracking Number	Cap #	N	Helix ID	Lineage
Davesbore-20161207-01	1	2	KJ01	AMM031
Davesbore-20161207-01			KJ02	AMM031
MB16WARR0009-01	5	35	KJ03	AMP023
MB16WARR0009-01			KJ04	AMP023
MB16WARR0009-01			KJ05	AMP023
MB16WARR0009-01			KJ06	AMP023
MB16WARR0009-01			KJ07	AMP023
MB16WARR0009-01			KJ08	AMP023
MB16WARR0009-01			KJ09	AMP023
MB16WARR0009-01			KJ10	AMP023
MB16WARR0009-01			KJ11	AMP023
MB16WARR0009-01			KJ12	AMP023
MB16WARR0009-01			KJ13	AMP023
MB16WARR0009-01			KJ14	AMP023
MB16WARR0009-01			KJ15	AMP023
MB16WARR0009-01			KJ16	AMP023
MB16WARR0009-01			KJ17	AMP023
MB16WARR0009-01			KJ18	AMP023
MB16WARR0009-01			KJ19	AMP023
MB16WARR0009-01			KJ20	AMP023
MB16WARR0009-01			KJ21	AMP023
MB16WARR0009-01			KJ22	AMP023
MB16WARR0009-01			KJ23	AMP023
MB16WARR0009-01			KJ24	AMP023
MB16WARR0009-01			KJ25	AMP023
MB16WARR0009-01			KJ26	AMP023
MB16WARR0009-01			KJ27	AMP023
MB16WARR0009-01			KJ28	AMP023
MB16WARR0009-01			KJ29	AMP023
MB16WARR0009-01			KJ30	AMP023
MB16WARR0009-01			KJ31	No data
MB16WARR0009-01			KJ32	AMP023
MB16WARR0009-01			KJ33	AMP023
MB16WARR0009-01			KJ34	AMP023
MB16WARR0009-01			KJ35	AMP023
MB16WARR0009-01			KJ36	AMP023
MB16WARR0009-01			KJ37	AMP023
MB16WARR0009-02	7	18	KJ38	AMP023
MB16WARR0009-02			KJ39	AMP023
MB16WARR0009-02			KJ40	AMP023
MB16WARR0009-02			KJ41	AMP023
MB16WARR0009-02			KJ42	AMP023

MB16WARR0009-02			KJ43	AMP023
MB16WARR0009-02			KJ44	AMP023
MB16WARR0009-02			KJ45	AMP023
MB16WARR0009-02			KJ46	No data
MB16WARR0009-02			KJ47	No data
MB16WARR0009-02			KJ48	AMP023
MB16WARR0009-02			KJ49	AMP023
MB16WARR0009-02			KJ50	AMP023
MB16WARR0009-02			KJ51	AMP023
MB16WARR0009-02			KJ52	AMP023
MB16WARR0009-02			KJ53	No data
MB16WARR0009-02			KJ54	AMP023
MB16WARR0009-02			KJ55	No data
MB16WARR0009-05	9	13 (only 7 in tube)	KJ56	AMP023
MB16WARR0009-05			KJ57	AMP023
MB16WARR0009-05			KJ58	AMP023
MB16WARR0009-05			KJ59	AMP023
MB16WARR0009-05			KJ60	AMP023
MB16WARR0009-05			KJ61	AMP023
MB16WARR0009-05			KJ62	No data
RC13TOB0023-20161210-02	18	1	KJ63	AMM006
Budgiebore-20161210-01	11	10 (only 9 in the tube)	KJ64	AMN008
Budgiebore-20161210-01			KJ65	AMM001
Budgiebore-20161210-01			KJ66	No data
Budgiebore-20161210-01			KJ67	No data
Budgiebore-20161210-01			KJ68	No data
Budgiebore-20161210-01			KJ69	No data
Budgiebore-20161210-01			KJ70	AMM002
Budgiebore-20161210-01			KJ71	AMM002
Budgiebore-20161210-01			KJ72	AMM028
Budgiebore-20161210-03	13	1	KJ73	AMM031
Budgiebore-20161210-07	17	5	KJ74	No data
Budgiebore-20161210-07			KJ75	No data
Budgiebore-20161210-07			KJ76	AMM031
Budgiebore-20161210-07			KJ77	AMM028
Budgiebore-20161210-07			KJ78	AMM031

Table 2. Mean genetic distance (p-distances) between lineages of amphipods as shown in Figure 1. Distances between lineages within families are highlighted in yellow.

	Para	Niph	Melitidae				
	1	2	3	4	5	6	7
Gp 1		<b>0.018</b>	<b>0.018</b>	<b>0.016</b>	<b>0.018</b>	<b>0.018</b>	<b>0.017</b>
Gp 2	0.274		<b>0.017</b>	<b>0.018</b>	<b>0.017</b>	<b>0.016</b>	<b>0.018</b>
Gp 3	0.342	0.308		<b>0.013</b>	<b>0.012</b>	<b>0.013</b>	<b>0.013</b>
Gp 4	0.318	0.318	0.171		<b>0.011</b>	<b>0.013</b>	<b>0.013</b>
Gp 5	0.313	0.309	0.147	0.103		<b>0.008</b>	<b>0.009</b>
Gp 6	0.317	0.306	<b>0.145</b>	0.123	0.066		<b>0.008</b>
Gp 7	0.328	0.314	<b>0.146</b>	0.121	0.070	0.060	

Table 3. Mean genetic distance (p-distances) and standard errors within lineages of amphipods as shown in Figure 1. N= number of specimens in the lineage and rep= specimen selected to represent the lineage in the model-based phylogenetic analysis.

Lineage	D	s.e.	N	Rep
Gp 1	0.000	0.000	54	KJ43
Gp 2	n/c	n/c	1	KJ64
Gp 3	n/c	n/c	1	KJ63
Gp 4	0.020	0.006	2	KJ72
Gp 5	0.000	0.000	2	KJ70
Gp 6	0.015	0.004	3	KJ73
Gp 7	0.013	0.004	3	KJ65

Table 4 (attached). Genetic distances (below diagonal) and standard error (above diagonal, in blue) between specimens of Niphargidae and Paramelitidae (Amphipoda) detected at Robe Valley and the reference lineages as shown in Figure 2. Distances between the Robe Valley specimens and the reference specimens are highlighted in yellow.

Table 5 (attached). Genetic distances (below diagonal) and standard error (above diagonal, in blue) between specimens of Melitidae (Amphipoda) detected at Robe Valley and the reference lineages as shown in Figure 3. Distances between the Robe Valley specimens and the reference specimens are highlighted in yellow.

Appendix 1. All specimens, assigned to lineages, from phases 1-5. Lineages with name changes are highlighted in yellow. Phase is classified as either historical (H), by phase (P) or as provided by the WAM (WAM); re=repeat. \*=new lineage this study.

Specimen_ID	Drillhole_ID	TAXON	P	Helix ID	Lineage	Renamed lineage
SSp-2010-253	DCBRC-017	Araneae	H	IV345	AO014	AO014
SSp-2010-75	DCBRC-040	Araneae	H	IV346	AO014	AO014
MEBRC0016P1T1-2	MEBRC0016	Araneae	P3	IV272	AO015	AO015
110817		Araneae	P3	IV273	contam	
127038		Araneae	P3	IV274	No amp	
127039		Araneae	P3	IV275	AA001	AA001
138441		Araneae	P3	IV276	A012	A012
GR15MEB0014.20160915.T1-01	GR15MEB0014	Araneae	P4	KD01	AT001	AT001*
RC15MEC0001.20160915.T1-01	RC15MEC0001	Araneae	P4	KD02	AT001	AT001*
SSp-2010-209	COBRC0022	Diplura	H	IV320	NoAmp	
SSp-2010-287	COBRC0008	Diplura	H	IV321	NoAmp	
SSp-2010-291	DCBRC_001	Diplura	H	IV322	NoAmp	
SSp-2010-37	COBRC0012	Diplura	H	IV323	NoAmp	
SSp-2010-40	TOBRC0043	Diplura	H	IV324	NoAmp	
SSp-2010-79	COBRC0003	Diplura	H	IV325	NoAmp	
DD11MEB001T1-01	DD11MEB001	Diplura	P1	IV154	Lin 1	DCA001
DD11MEB001T1-01	DD11MEB001	Diplura	P1	IV155	Lin 2	DCA002
DD11MEC0005-02	DD14MEB0005	Diplura	P1	IV156	Lin 4	DPA004
DD14MEB0005-20151001-T3-02	DD14MEB0005	Diplura	P2	IV157	Lin 3	DCA003
MEARC5017-20151001-T2-01	MEARC5017	Diplura	P2	IV158	nd	
RC14MEB0101-20151001-T2-01	RC14MEB0101	Diplura	P2	IV159	Lin 3	DCA003
MEARC3790-20150807-T2-03	MEARC3790	Diplura	P1	IV160	nd	
GR15MEB0001-20160317-T2-01	GR15MEB0001	Diplura	P3	IV236	Contam/Mis-ID?	
GR15MEB0008-20160317-T2-01	GR15MEB0008	Diplura	P3	IV237	contam	
GR15MEB0014-20160316-Sc-01	GR15MEB0014	Diplura	P3	IV238	NoAmp	
GR15MEC0001-20160316-T2-01	GR15MEC0001	Diplura	P3	IV239	NoAmp	
GR15MEC0001-20160316-T2-02	GR15MEC0001	Diplura	P3	IV240	Contam/Mis-ID?	
GR15MEC0001-20160316-T2-03	GR15MEC0001	Diplura	P3	IV241	contam	
GR15MEC0001-20160316-T2-04	GR15MEC0001	Diplura	P3	IV242	NoAmp	
GR15MEC0001-20160316-T2-05	GR15MEC0001	Diplura	P3	IV243	NoAmp	
GR15MEC0008-20160316-T2-01	GR15MEC0008	Diplura	P3	IV244	NoAmp	
RC15MEB0171-20160317-T1-01	RC15MEB0171	Diplura	P3	IV245	DPA003	DPA003
RC15MEC0001-20160316-T2-01	RC15MEC0001	Diplura	P3	IV246	NoAmp	
RC15MEC0027-20160316-T3-01	RC15MEC0027	Diplura	P3	IV247	NoAmp	
RC15MEC0192-20160316-T1-01	RC15MEC0192	Diplura	P3	IV248	DPA005	DPA005
RC15MEC0192-20160316-T1-02	RC15MEC0192	Diplura	P3	IV249	DPA005	DPA005
RC15MEC0192-20160316-T1-03	RC15MEC0192	Diplura	P3	IV250	DPA006	DPA006
RC15MEC0192-20160316-T3-01	RC15MEC0192	Diplura	P3	IV251	NoAmp	
RC15MEC0192-20160316-T3-02	RC15MEC0192	Diplura	P3	IV252	NoAmp	
RC15MEC0197-20160316-T1-01	RC15MEC0197	Diplura	P3	IV253	NoAmp	
RC15MEC0197-20160316-T2-02A	RC15MEC0197	Diplura	P3	IV254	NoAmp	
RC15MEC0197-20160316-T2-02B	RC15MEC0197	Diplura	P3	IV255	NoAmp	
RC15MEC0200-20160316-T2-01	RC15MEC0200	Diplura	P3	IV256	Messy seq	
RC15MEC0200-20160316-T3-02	RC15MEC0200	Diplura	P3	IV257	NoAmp	
GR15MEB0014.20160915.T3-01	GR15MEB0014	Diplura	P4	KD07	DCA003	DCA003
RC15MEB0115.20160915.T2-01	RC15MEB0115	Diplura	P4	KD08	DCA003	DCA003

RC15MEB0115.20160915.T2-01	RC15MEB0115	Diplura	P4	KD09	DCA003	DCA003
RC15MEB0115.20160915.T2-01	RC15MEB0115	Diplura	P4	KD10	DCA003	DCA003
RC15MEB0115.20160915.T2-01	RC15MEB0115	Diplura	P4	KD11	DCA003	DCA003
RC15MEC0103.20160915.T1-01	RC15MEC0103	Diplura	P4	KD12	DPA007*	DPA007*
RC14MEB0101.20160915.T2-01	RC14MEB0101	Diplura	P4	KD13	DCA003	DCA003
RC16MEC0156.20160915.T3-01	RC16MEC0156	Diplura	P4	KD14	DPA006	DPA006
RC16MEC0118.20160915.T3-01	RC16MEC0118	Diplura	P4	KD15	DPA008*	DPA008*
DD14MRR0004T1-01	DD14MRR0004	Chilopoda	P1	IV139	Lineage 1	CHI001
DD14MRR0004T1-01	DD14MRR0004	Chilopoda	P1	IV140	Lineage 1	CHI001
DD14MRR0005-T1-04	DD14MRR0005	Chilopoda	P1	IV141	Lineage 1	CHI001
DD14MEL0001-20151001-T1-01	DD14MEL0001	Chilopoda	P2	IV142	nd	
MEARC4383-20151001-T2-01	MEARC4383	Chilopoda	P2	IV143	Lineage 2	CHI002
SSp-2010-325		Chilopoda	H	IV347	Failed repeat PCR	
93283		Chilopoda	H	93283	NoAmp	
93287		Chilopoda	H	93287	NoAmp	
93778		Chilopoda	H	93778	NoAmp	
93780		Chilopoda	H	93780	NoAmp	
98714		Chilopoda	H	98714	NoAmp	
120191		Chilopoda	H	120191	CHI021	CHI021
132678		Chilopoda	H	132678	CHI022	CHI022
93779		Chilopoda	H	93779	CHI024	CHI024
RC14MEB0115-20160317-T2-02	RC14MEB0115	Chilopoda	P3	IV231	CHI023	CHI023
138572		Chilopoda	P1/2 re	IV142	CHI025	CHI025
RC15MEC0168.20160915.T3-02	RC15MEC0168	Chilopoda	4	KD16	CHI026	CHI026*
DAVES-20150930-04	DAVES	Amphipoda	P2	KD38	AMN008	AMN008
Budgie-20150930-01	Budgie	Amphipoda	P2	KD39	AMN008	AMN008
Budgie-20150930-01	Budgie	Amphipoda	P2	KD40	AMM029*	AMM029*
Budgie-20150930-01	Budgie	Amphipoda	P2	KD41	AMN001*	AMN001*
Budgie-20150930-01	Budgie	Amphipoda	P2	KD42	AMN008	AMN008
Budgie-20150930-01	Budgie	Amphipoda	P2	KD43	AMN008	AMN008
Budgie-20150930-01	Budgie	Amphipoda	P2	KD44	AMM030*	AMM030*
Budgie-20150930-01	Budgie	Amphipoda	P2	KD45	AMM031*	AMM031*
Budgie-20150930-01	Budgie	Amphipoda	P2	KD46		
Budgie-20150930-01	Budgie	Amphipoda	P2	KD47	AMM028*	AMM028*
Budgie-20150930-01	Budgie	Amphipoda	P2	KD48	AMP009	AMP009
Budgie-20150930-01	Budgie	Amphipoda	P2	KD49	AMM001	AMM001
Budgie-20150930-01	Budgie	Amphipoda	P2	KD50	AMM030*	AMM030*
Budgie-20150930-01	Budgie	Amphipoda	P2	KD51	AMN008	AMN008
Budgie.20150604-02	Budgie	Amphipoda	P1	KD52		
Budgie.20150604-02	Budgie	Amphipoda	P1	KD53	AMM002	AMM002
Budgie.20150604-02	Budgie	Amphipoda	P1	KD54		
Budgie.20150604-02	Budgie	Amphipoda	P1	KD55	AMM031*	AMM031*
Budgie.20150604-02	Budgie	Amphipoda	P1	KD56	AMN008	AMN008
Budgie.20150604-02	Budgie	Amphipoda	P1	KD57	AMN008	AMN008
TOBRC0099-20150930-01	TOBRC0099	Amphipoda	P2	KD58	AMP023	AMP023
TOBRC0099-20150930-01	TOBRC0099	Amphipoda	P2	KD59	AMP023	AMP023
TOBRC0099-20150930-01	TOBRC0099	Amphipoda	P2	KD60	AMP023	AMP023
TOBRC0099-20150930-01	TOBRC0099	Amphipoda	P2	KD61	AMP023	AMP023
TOBRC0099-20150930-01	TOBRC0099	Amphipoda	P2	KD62	AMP023	AMP023
TOBRC0099-20150930-01	TOBRC0099	Amphipoda	P2	KD63	AMP023	AMP023
TOBRC0099-20150930-01	TOBRC0099	Amphipoda	P2	KD64	AMP023	AMP023

Daves-20150604-01	DAVES	Amphipoda	P1	KD65		
Budgie.20150604-02	Budgie	Amphipoda	P1	IV92	Lineage 2	AMM002
Budgie.20150604-02	Budgie	Amphipoda	P1	IV93	Lineage 1	AMM001
Budgie.20150604-02	Budgie	Amphipoda	P1	IV94	Lineage 8	AMN008
Budgie.20150604-02	Budgie	Amphipoda	P1	IV95	Lineage 8	AMN008
Budgie.20150604-02	Budgie	Amphipoda	P1	IV96	nd	
Camp-20150604-02	Camp	Amphipoda	P1	IV97	nd	
Camp-20150604-02	Camp	Amphipoda	P1	IV98	nd	
Daisy-20150604-02	Daisy	Amphipoda	P1	IV99	nd	
Daves-20150604-01	Daves	Amphipoda	P1	IV100	Lineage 8	AMN008
Daves-20150604-01	Daves	Amphipoda	P1	IV101	nd	
Daves-20150604-01	Daves	Amphipoda	P1	IV102	nd	
Daves-20150604-01	Daves	Amphipoda	P1	IV103	nd	
Daves-20150604-01	Daves	Amphipoda	P1	IV104	Lineage 8	AMN008
MB13WARR001-20150605-01	MB13WARR001	Amphipoda	P1	IV105	Lineage 5	AMM005
MB13WARR001-20150605-01	MB13WARR001	Amphipoda	P1	IV106	Lineage 5	AMM005
MB13WARR001-20150605-01	MB13WARR001	Amphipoda	P1	IV107	Lineage 5	AMM005
MB13WARR001-20150605-01	MB13WARR001	Amphipoda	P1	IV108	Lineage 5	AMM005
MB13WARR001-20150605-01	MB13WARR001	Amphipoda	P1	IV109	Lineage 5	AMM005
MB13WARR010.20150606-01	MB13WARR010	Amphipoda	P1	IV110	nd	
MB13WARR010.20150606-01	MB13WARR010	Amphipoda	P1	IV111	Lineage 3	AMM003
MB13WARR010.20150606-01	MB13WARR010	Amphipoda	P1	IV112	Lineage 3	AMM003
MB13WARR010.20150606-01	MB13WARR010	Amphipoda	P1	IV113	nd	
MB13WARR010.20150606-01	MB13WARR010	Amphipoda	P1	IV114	Lineage 3	AMM003
TOBRC009-20150605-01	TOBRC009	Amphipoda	P1	IV115	nd	
TOBRC009-20150605-01	TOBRC009	Amphipoda	P1	IV116	nd	
TOBRC009-20150605-01	TOBRC009	Amphipoda	P1	IV117	nd	
TOBRC009-20150605-01	TOBRC009	Amphipoda	P1	IV118	nd	
TOBRC009-20150605-01	TOBRC009	Amphipoda	P1	IV119	nd	
Budgie-20150930-01	Budgie	Amphipoda	P1	IV120	Lineage 1	AMM001
Budgie-20150930-01	Budgie	Amphipoda	P1	IV121	Lineage 1	AMM001
Budgie-20150930-01	Budgie	Amphipoda	P1	IV122	nd	
Budgie-20150930-01	Budgie	Amphipoda	P1	IV123	Lineage 1	AMM001
Budgie-20150930-01	Budgie	Amphipoda	P1	IV124	nd	
Camp-20150930-02	Camp	Amphipoda	P2	IV125	Lineage 1	AMM001
Camp-20150930-02	Camp	Amphipoda	P2	IV126	Lineage 1	AMM001
Daisy-201509-02	Daisy	Amphipoda	P2	IV127	Lineage 2	AMM002
DAVES-20150930-04	Daves	Amphipoda	P2	IV128	Lineage 4	AMM004
DAVES-20150930-04	Daves	Amphipoda	P2	IV129	Lineage 7	AMN007
DAVES-20150930-04	Daves	Amphipoda	P2	IV130	Lineage 8	AMM008
DAVES-20150930-04	Daves	Amphipoda	P2	IV131	nd	
DAVES-20150930-04	Daves	Amphipoda	P2	IV132	Lineage 4	AMM004
RC13MEA0279-20150930-02	RC13MEA0279	Amphipoda	P2	IV133	nd	
TOBRC0099-20150930-01	TOBRC0099	Amphipoda	P2	IV134	Lineage 6	AMM006
TOBRC0099-20150930-01	TOBRC0099	Amphipoda	P2	IV135	nd	
TOBRC0099-20150930-01	TOBRC0099	Amphipoda	P2	IV136	nd	
TOBRC0099-20150930-01	TOBRC0099	Amphipoda	P2	IV137	nd	
TOBRC0099-20150930-01	TOBRC0099	Amphipoda	P2	IV138	nd	
Daves bore	Daves bore	Amphipoda	P1/2 re	IV102	NoAmp	NoAmp
TOBRC009	TOBRC009	Amphipoda	P1/2 re	IV115	AMP023	AMP023
TOBRC009	TOBRC009	Amphipoda	P1/2 re	IV116	AMP023	AMP023

TOBRC009	TOBRC009	Amphipoda	P1/2 re	IV117	AMP023	AMP023
TOBRC009	TOBRC009	Amphipoda	P1/2 re	IV118	AMP023	AMP023
TOBRC009	TOBRC009	Amphipoda	P1/2 re	IV119	AMP023	AMP023
Budgie	Budgie	Amphipoda	P1/2 re	IV122	AMM001	AMM001
Budgie	Budgie	Amphipoda	P1/2 re	IV124	AMM027	AMM027
Daves	Daves	Amphipoda	P1/2 re	IV131	NoAmp	NoAmp
TOBRC009	TOBRC009	Amphipoda	P1/2 re	IV136	contam	contam
Budgie bore	Budgie bore	Amphipoda	P1/2 re	IV96	AMM001	AMM001
Camp bore	Camp bore	Amphipoda	P1/2 re	IV97	AMM001	AMM001
Camp bore	Camp bore	Amphipoda	P1/2 re	IV98	AMM001	AMM001
Daisy well	Daisy well	Amphipoda	P1/2 re	IV99	NoAmp	NoAmp
Daves bore	Daves bore	Amphipoda	P1/2 re	IV101	NoAmp	NoAmp
Daves bore	Daves bore	Amphipoda	P1/2 re	IV103	NoAmp	NoAmp
MB13WARR010	MB13WARR010	Amphipoda	P1/2 re	IV110	NoAmp	NoAmp
MB13WARR010	MB13WARR010	Amphipoda	P1/2 re	IV113	NoAmp	NoAmp
RC13MEA0279	RC13MEA0279	Amphipoda	P1/2 re	IV133	NoAmp	NoAmp
TOBRC009	TOBRC009	Amphipoda	P1/2 re	IV135	NoAmp	NoAmp
TOBRC009	TOBRC009	Amphipoda	P1/2 re	IV137	NoAmp	NoAmp
TOBRC009	TOBRC009	Amphipoda	P1/2 re	IV138	NoAmp	NoAmp
GR15MEB0003.20160915.T3-01	GR15MEB0003	Coleoptera	4	KD03	CCU004	CCU004
RC15MEB0216.20160915.T3-02	RC15MEB0216	Coleoptera	4	KD04	CCU004	CCU004
GR15MEC0019.20160915.T2-01	GR15MEC0019	Coleoptera	4	KD05	CCU004	CCU004
GR15MEB0022.20160915.T3-01	GR15MEB0022	Coleoptera	4	KD06	Contam.	Contam.
MEK1478P7T2-2	MEK1478	Coleoptera	H	IV395	CCU007	CCU007
MEK1478P7T2-2	MEK1478	Coleoptera	H	IV396	CCU007	CCU007
MEK1718P7T3-2	MEK1718	Coleoptera	H	IV397	CCU007	CCU007
MEK1718P7T3-2	MEK1718	Coleoptera	H	IV398	CCU007	CCU007
MEK1718P7T3-2	MEK1718	Coleoptera	H	IV399	CCU007	CCU007
MEK1721P7T1-3	MEK1721	Coleoptera	H	IV400	CPT003	CPT003
MEK1721P7T1-3	MEK1721	Coleoptera	H	IV401	CPT003	CPT003
MEK1721P7T1-3	MEK1721	Coleoptera	H	IV402	CPT003	CPT003
MEK1721P7T1-3	MEK1721	Coleoptera	H	IV403	CPT003	CPT003
MEK1721P7T1-3	MEK1721	Coleoptera	H	IV404	CPT003	CPT003
MEK1721P7T1-3	MEK1721	Coleoptera	H	IV405	CPT003	CPT003
MEK1721P7T1-3	MEK1721	Coleoptera	H	IV406	CPT003	CPT003
MEK1721P7T1-3	MEK1721	Coleoptera	H	IV407	CPT003	CPT003
MEK1721P7T1-3	MEK1721	Coleoptera	H	IV408	CPT003	CPT003
MEK1721P7T1-3	MEK1721	Coleoptera	H	IV409	CPT003	CPT003
K0968P7T3-3	K0968	Coleoptera	H	IV410	CPT003	CPT003
MEGRC0495P6T2-3	MEGRC0495	Coleoptera	H	IV411	CUN003	CUN003
MEGRC0495P6T2-3	MEGRC0495	Coleoptera	H	IV412	CUN003	CUN003
MEGRC0097P6T1-5	MEGRC0097	Coleoptera	H	IV413	CUN003	CUN003
MEARC2657P1T1-3	MEARC2657	Coleoptera	H	IV414	CCU004	CCU004
RC08SILV0683p3t1-1	RC08SILV0683	Coleoptera	H	IV415	CCA013	CCA013
D08BU075P1T1-4	D08BU075	Coleoptera	H	IV416	CUN001	CUN001
D08BU075P1T1-4	D08BU075	Coleoptera	H	IV417	CUN001	CUN001
D08BU075P1T1-4	D08BU075	Coleoptera	H	IV418	CUN001	CUN001
D08BU075P1T1-4	D08BU075	Coleoptera	H	IV419	CUN001	CUN001
D08BU075P1T1-4	D08BU075	Coleoptera	H	IV420	CUN001	CUN001
D08BU075P1T1-4	D08BU075	Coleoptera	H	IV421	CUN001	CUN001
E004FP3T1-4	E004F	Coleoptera	H	IV422	CAN001	CAN001

BUNW01114P1T2-3	BUNW01114	Coleoptera	H	IV423	CUN002	CUN002
RHRC013P1T3-3	RHRC013	Coleoptera	H	IV424	CAN001	CAN001
RC15MEB0107-20160317-T2-02	RC15MEB0107	Coleoptera	P3	IV232	CCA012	CCA012
RC15MEC0192-20160316-T2-03	RC15MEC0192	Coleoptera	P3	IV233	CCU004	CCU004
RC15MEC0192-20160316-T3-03	RC15MEC0192	Coleoptera	P3	IV234	CCU004	CCU004
RC15MEC0192-20160316-T3-04	RC15MEC0192	Coleoptera	P3	IV235	CCU004	CCU004
MEARC5093-20151001-T1-03	MEARC5093	Coleoptera	P1/2 re	IV388	CUN003	CUN003
MEARC5093-20151001-T2-02	MEARC5093	Coleoptera	P1/2 re	IV389	CST002	CST002
DD14MEC0006T2-02	DD14MEC0006	Coleoptera	P1/2 re	IV390	CST002	CST002
DD14MEC0006T2-02	DD14MEC0006	Coleoptera	P1/2 re	IV391	CST002	CST002
DD14MEC0006T2-02	DD14MEC0006	Coleoptera	P1/2 re	IV392	CST002	CST002
DD14MEC0006T2-02	DD14MEC0006	Coleoptera	P1/2 re	IV393	CST002	CST002
DD14MEC0006T2-02	DD14MEC0006	Coleoptera	P1/2 re	IV394	CST002	CST002
IV149	RC14MEB0068	Coleoptera	P1/2 re	IV149	CCU004	CCU004
Davesbore-20161207-01	Daves bore	Amphipoda	5	KJ01	AMM031	
Davesbore-20161207-01	Daves bore	Amphipoda	5	KJ02	AMM031	
MB16WARR0009-01	MB16WARR0009	Amphipoda	5	KJ03	AMP023	
MB16WARR0009-01	MB16WARR0009	Amphipoda	5	KJ04	AMP023	
MB16WARR0009-01	MB16WARR0009	Amphipoda	5	KJ05	AMP023	
MB16WARR0009-01	MB16WARR0009	Amphipoda	5	KJ06	AMP023	
MB16WARR0009-01	MB16WARR0009	Amphipoda	5	KJ07	AMP023	
MB16WARR0009-01	MB16WARR0009	Amphipoda	5	KJ08	AMP023	
MB16WARR0009-01	MB16WARR0009	Amphipoda	5	KJ09	AMP023	
MB16WARR0009-01	MB16WARR0009	Amphipoda	5	KJ10	AMP023	
MB16WARR0009-01	MB16WARR0009	Amphipoda	5	KJ11	AMP023	
MB16WARR0009-01	MB16WARR0009	Amphipoda	5	KJ12	AMP023	
MB16WARR0009-01	MB16WARR0009	Amphipoda	5	KJ13	AMP023	
MB16WARR0009-01	MB16WARR0009	Amphipoda	5	KJ14	AMP023	
MB16WARR0009-01	MB16WARR0009	Amphipoda	5	KJ15	AMP023	
MB16WARR0009-01	MB16WARR0009	Amphipoda	5	KJ16	AMP023	
MB16WARR0009-01	MB16WARR0009	Amphipoda	5	KJ17	AMP023	
MB16WARR0009-01	MB16WARR0009	Amphipoda	5	KJ18	AMP023	
MB16WARR0009-01	MB16WARR0009	Amphipoda	5	KJ19	AMP023	
MB16WARR0009-01	MB16WARR0009	Amphipoda	5	KJ20	AMP023	
MB16WARR0009-01	MB16WARR0009	Amphipoda	5	KJ21	AMP023	
MB16WARR0009-01	MB16WARR0009	Amphipoda	5	KJ22	AMP023	
MB16WARR0009-01	MB16WARR0009	Amphipoda	5	KJ23	AMP023	
MB16WARR0009-01	MB16WARR0009	Amphipoda	5	KJ24	AMP023	
MB16WARR0009-01	MB16WARR0009	Amphipoda	5	KJ25	AMP023	
MB16WARR0009-01	MB16WARR0009	Amphipoda	5	KJ26	AMP023	
MB16WARR0009-01	MB16WARR0009	Amphipoda	5	KJ27	AMP023	
MB16WARR0009-01	MB16WARR0009	Amphipoda	5	KJ28	AMP023	
MB16WARR0009-01	MB16WARR0009	Amphipoda	5	KJ29	AMP023	
MB16WARR0009-01	MB16WARR0009	Amphipoda	5	KJ30	AMP023	
MB16WARR0009-01	MB16WARR0009	Amphipoda	5	KJ31	No data	
MB16WARR0009-01	MB16WARR0009	Amphipoda	5	KJ32	AMP023	
MB16WARR0009-01	MB16WARR0009	Amphipoda	5	KJ33	AMP023	
MB16WARR0009-01	MB16WARR0009	Amphipoda	5	KJ34	AMP023	
MB16WARR0009-01	MB16WARR0009	Amphipoda	5	KJ35	AMP023	
MB16WARR0009-01	MB16WARR0009	Amphipoda	5	KJ36	AMP023	
MB16WARR0009-01	MB16WARR0009	Amphipoda	5	KJ37	AMP023	

MB16WARR0009-02	MB16WARR0009	Amphipoda	5	KJ38	AMP023	
MB16WARR0009-02	MB16WARR0009	Amphipoda	5	KJ39	AMP023	
MB16WARR0009-02	MB16WARR0009	Amphipoda	5	KJ40	AMP023	
MB16WARR0009-02	MB16WARR0009	Amphipoda	5	KJ41	AMP023	
MB16WARR0009-02	MB16WARR0009	Amphipoda	5	KJ42	AMP023	
MB16WARR0009-02	MB16WARR0009	Amphipoda	5	KJ43	AMP023	
MB16WARR0009-02	MB16WARR0009	Amphipoda	5	KJ44	AMP023	
MB16WARR0009-02	MB16WARR0009	Amphipoda	5	KJ45	AMP023	
MB16WARR0009-02	MB16WARR0009	Amphipoda	5	KJ46	No data	
MB16WARR0009-02	MB16WARR0009	Amphipoda	5	KJ47	No data	
MB16WARR0009-02	MB16WARR0009	Amphipoda	5	KJ48	AMP023	
MB16WARR0009-02	MB16WARR0009	Amphipoda	5	KJ49	AMP023	
MB16WARR0009-02	MB16WARR0009	Amphipoda	5	KJ50	AMP023	
MB16WARR0009-02	MB16WARR0009	Amphipoda	5	KJ51	AMP023	
MB16WARR0009-02	MB16WARR0009	Amphipoda	5	KJ52	AMP023	
MB16WARR0009-02	MB16WARR0009	Amphipoda	5	KJ53	No data	
MB16WARR0009-02	MB16WARR0009	Amphipoda	5	KJ54	AMP023	
MB16WARR0009-02	MB16WARR0009	Amphipoda	5	KJ55	No data	
MB16WARR0009-05	MB16WARR0009	Amphipoda	5	KJ56	AMP023	
MB16WARR0009-05	MB16WARR0009	Amphipoda	5	KJ57	AMP023	
MB16WARR0009-05	MB16WARR0009	Amphipoda	5	KJ58	AMP023	
MB16WARR0009-05	MB16WARR0009	Amphipoda	5	KJ59	AMP023	
MB16WARR0009-05	MB16WARR0009	Amphipoda	5	KJ60	AMP023	
MB16WARR0009-05	MB16WARR0009	Amphipoda	5	KJ61	AMP023	
MB16WARR0009-05	MB16WARR0009	Amphipoda	5	KJ62	No data	
RC13TOB0023-20161210-02	RC13TOB0023	Amphipoda	5	KJ63	AMM006	
Budgiebore-20161210-01	Budgie bore	Amphipoda	5	KJ64	AMN008	
Budgiebore-20161210-01	Budgie bore	Amphipoda	5	KJ65	AMM001	
Budgiebore-20161210-01	Budgie bore	Amphipoda	5	KJ66	No data	
Budgiebore-20161210-01	Budgie bore	Amphipoda	5	KJ67	No data	
Budgiebore-20161210-01	Budgie bore	Amphipoda	5	KJ68	No data	
Budgiebore-20161210-01	Budgie bore	Amphipoda	5	KJ69	No data	
Budgiebore-20161210-01	Budgie bore	Amphipoda	5	KJ70	AMM002	
Budgiebore-20161210-01	Budgie bore	Amphipoda	5	KJ71	AMM002	
Budgiebore-20161210-01	Budgie bore	Amphipoda	5	KJ72	AMM028	
Budgiebore-20161210-03	Budgie bore	Amphipoda	5	KJ73	AMM031	
Budgiebore-20161210-07	Budgie bore	Amphipoda	5	KJ74	No data	
Budgiebore-20161210-07	Budgie bore	Amphipoda	5	KJ75	No data	
Budgiebore-20161210-07	Budgie bore	Amphipoda	5	KJ76	AMM031	
Budgiebore-20161210-07	Budgie bore	Amphipoda	5	KJ77	AMM028	
Budgiebore-20161210-07	Budgie bore	Amphipoda	5	KJ78	AMM031	

Figure 1. Neighbour-joining analysis of specimens of Amphipoda from the present study. Numbers on major nodes correspond to bootstrap support over 100 iterations; values <50% are not shown. Scale bar= genetic distance. The specimens used to represent each lineage in the model-based phylogenetic analysis are highlighted in yellow.

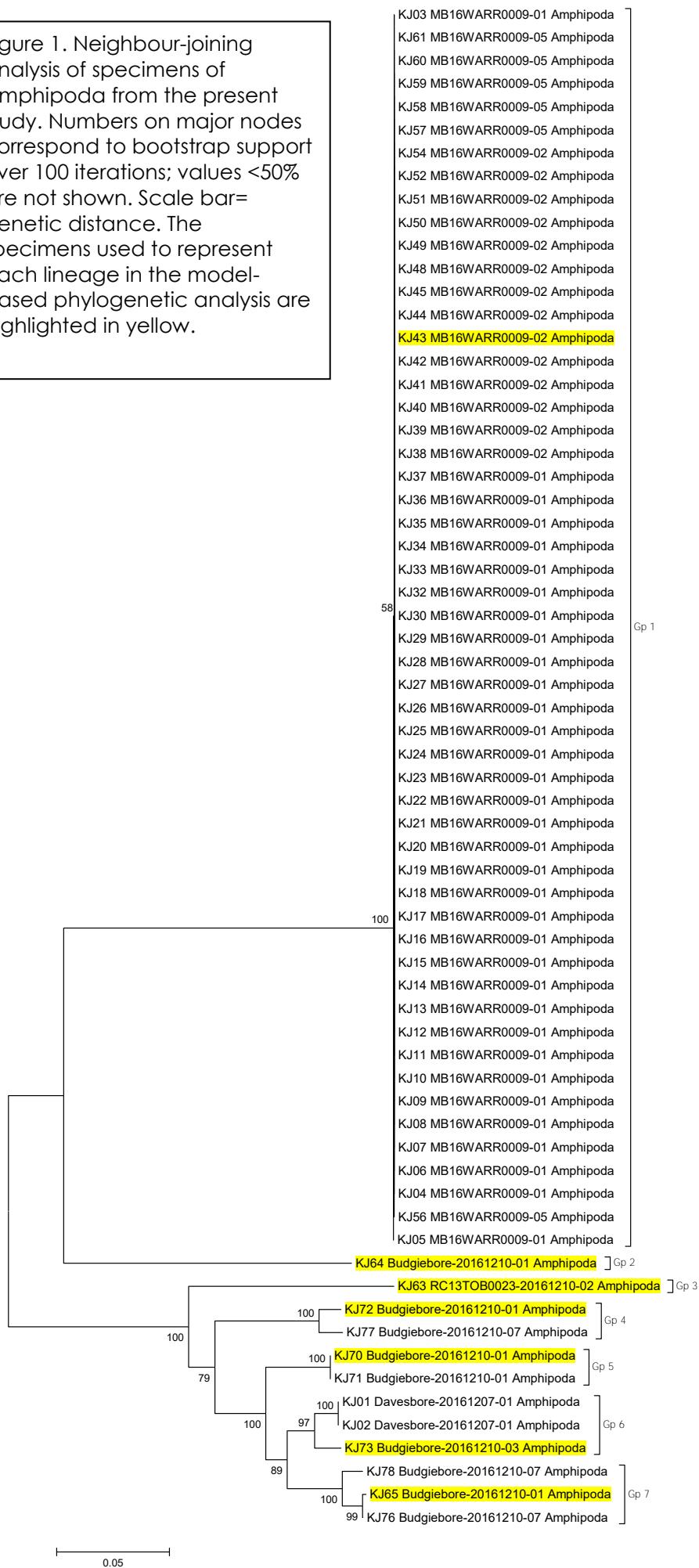


Figure 2. Bayesian analysis of COI haplotypes of Paramelitidae and Niphargidae (Amphipoda) from the present study and reference specimens from Genbank and previous surveys in the Pilbara. Numbers on major nodes correspond to posterior probabilities; values <50% are not shown. Specimens from the present study are highlighted in yellow; specimens from previous phases at Robe Valley are highlighted in green; GenBank voucher specimens highlighted in turquoise. Scale bar= number of substitutions per site. Red boxes enclose species with high confidence.

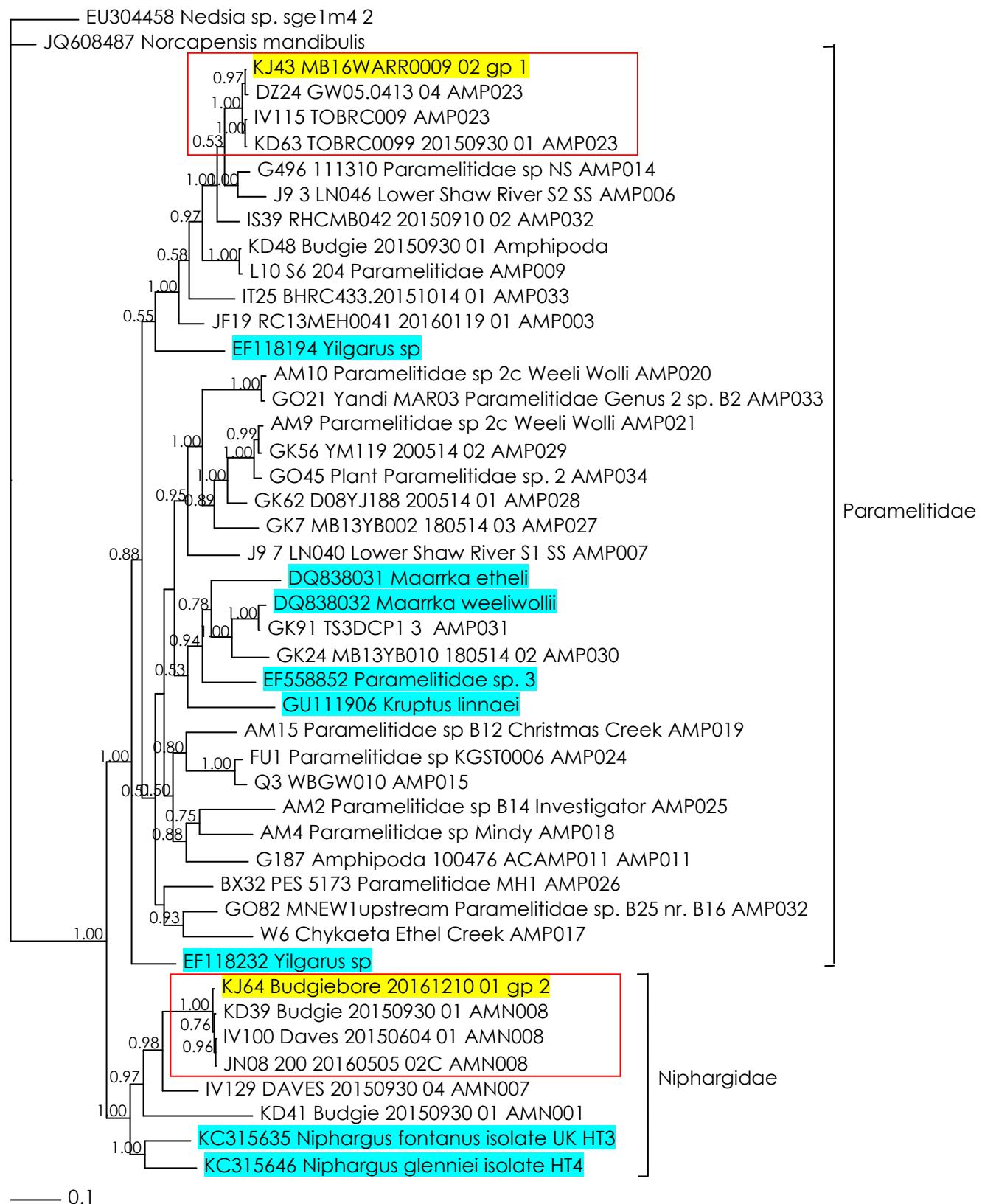
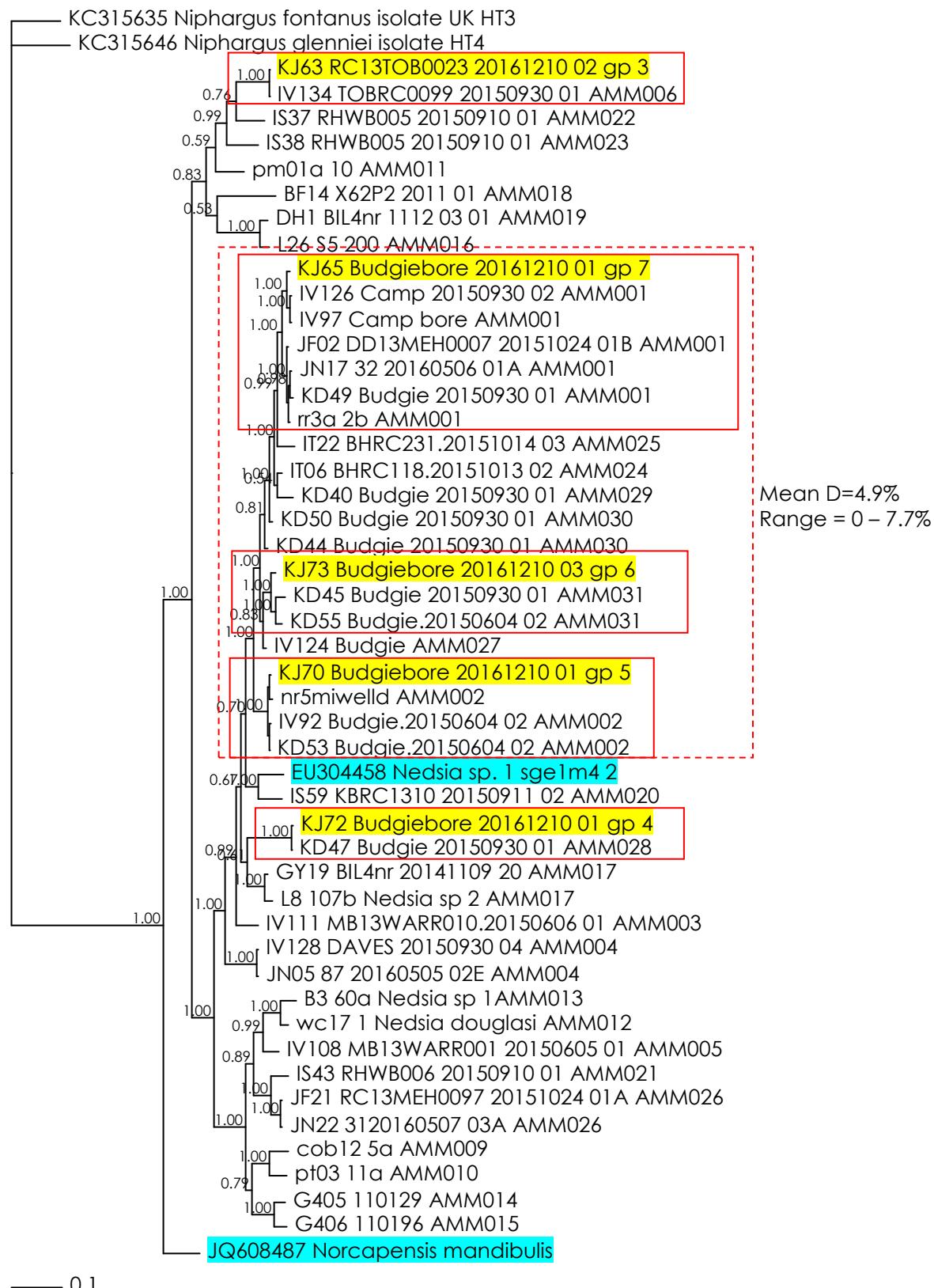


Figure 3. Bayesian analysis of COI haplotypes of Melitidae (Amphipoda) from the present study and reference specimens from Genbank and previous surveys in the Pilbara. Numbers on major nodes correspond to posterior probabilities; values <50% are not shown. Specimens from the present study are highlighted in yellow; specimens from previous phases at Robe Valley are highlighted in green; GenBank voucher specimens highlighted in turquoise. Scale bar= number of substitutions per site. Red boxes with dashed lines represent groups requiring further investigation.



— 0.1

**Table 4. Estimates of Evolutionary Divergence between Sequences**

1. Tamura K., Stecher G., Peterson D., Filipski A., and Kumar S. (2013). MEGA6: Molecular Evolutionary Genetics Analysis version 6.0. *Molecular Biology and Evolution* 30: 2725-2729.

The number of base differences per site from between sequences are shown. Standard error estimate(s) are shown above the diagonal. The analysis involved 42 nucleotide sequences. Codon positions included were 1st+2nd+3rd+Noncoding. All ambiguous positions were removed for each sequence pair. There were a total of 495 positions in the final dataset. Evolutionary analyses were conducted in MEGA6 [1].

Disclaimer: Although utmost care has been taken to ensure the correctness of the caption, the caption text is provided "as is" without any warranty of any kind. Authors advise the user to carefully check the caption prior to its use for any purpose and report any errors or problems to the authors immediately ([www.megasoftware.net](http://www.megasoftware.net)). In no event shall the authors and their employers be liable for any damages, including but not limited to special, consequential, or other damages. Authors specifically disclaim all other warranties expressed or implied, including but not limited to the determinations of suitability of this caption text for a specific purpose, use, or application.

**Table 5. Estimates of Evolutionary Divergence between Sequences**

1. Tamura K., Stecher G., Peterson D., Filipski A., and Kumar S. (2013). MEGA6: Molecular Evolutionary Genetics Analysis version 6.0. Molecular Biology and Evolution 30: 2725-2729.

The number of base differences per site from between sequences are shown. Standard error estimate(s) are shown above the diagonal. The analysis involved 42 nucleotide sequences. Codon positions included were 1st+2nd+3rd+Noncoding. All ambiguous positions were removed for each sequence pair. There were a total of 495 positions in the final dataset. Evolutionary analyses were conducted in MEGA6 [1].



# Helix

## Molecular Solutions

School of Animal Biology The University of Western Australia  
Hackett Entrance No. 4 Hackett Drive Crawley WA 6009

PO Box 155  
Leederville WA 6903

t. (08) 6488 4509

f. (08) 6488 1029

abn. 32 133 230 243

w. [www.helixsolutions.com.au](http://www.helixsolutions.com.au)

19 May, 2017

Jason Alexander  
Biota Environmental Sciences  
Level 1, 228 Carr Place  
Leederville, WA 6007

Via email

**Re. Report on the molecular systematics of Amphipoda from Warramboo, and Mesas A, C and K (Biota 1080c)**

Dear Jason,

Following is a summary of the results of the Amphipoda study we have completed from Mesa C. Four distinct genetic lineages from two families (Melitidae, Niphargidae) were detected in the collections, all of which have been detected previously in the Pilbara.

Thanks once again for collaborating on this project with Helix. We hope we can continue to provide you with useful information, and feel free to contact us if you have any questions or would like to discuss the results in detail.

Sincerely,

Dr. Terrie Finston, Yvette Hitchin and Dr. Oliver Berry  
Helix Molecular Solutions

## Background and Objective

Twenty-eight specimens of Amphipoda were collected from Mesa C and sequenced for variation at the mitochondrial COI gene. The molecular data were assessed in order to determine the number of species present and compare the results to those obtained during previous surveys in the Pilbara.

## Executive summary

- Twenty-eight specimens of amphipods from Mesa C were sequenced for variation at the COI gene.
- Four distinct genetic lineages (three Melitidae, one Niphargidae) were detected among the 24 specimens for which sequences were obtained.
- All four of the lineages have been detected previously in the Pilbara.

## Methods

Twenty-eight specimens of Amphipoda from eight drillholes at Mesa C were sequenced for variation at the mitochondrial cytochrome oxidase subunit I gene (COI) using primers LCO1/HCO2.

Sequences were edited using GENEIOUS software (Drummond et al. 2011). Alignment was performed with CLUSTAL W (Thompson et al. 1994) using default parameters. Genetic distances between unique genetic sequences (haplotypes) were measured using uncorrected p-distances (total percentage of nucleotide differences between sequences).

MODELTEST software (Posada and Crandall, 1998) was used to determine the model of sequence evolution that best fitted the data for each taxonomic group. Bayesian analysis was used to construct the phylogenetic trees, incorporating the model as identified in MODELTEST for each taxonomic group. The phylogeny, branch lengths and posterior probabilities were obtained by running two trees simultaneously, each running four simultaneous MCMC chains. The number of cycles needed was determined by the standard deviation of the split frequencies of the two trees. The analysis was paused after every  $1 \times 10^6$  generations and when the standard deviation fell below 0.01, the analysis was stopped. A majority rule consensus tree was constructed after discarding the “burn-in” trees in both analyses. The burn-in value was determined by plotting the posterior probabilities obtained after every generation and identifying the point at which the values reach stationarity (= the asymptote). Trees produced prior to stationarity were discarded.

For the purposes of this report, lineages were defined as haplotypes or groups of haplotypes differing from other such groups by >3% sequence divergence. This cut-off was selected based on bar-coding data, which indicates that intra-specific variation rarely exceeds 2-3% (Hebert et al., 2003b).

## Results

### Preliminary analysis - Reference sequences and outgroups

Twenty-eight specimens of amphipods from Mesa C were sequenced for COI (Table 1; Appendix 1). In order to reduce analysis time and to simplify the presentation of results, a preliminary neighbour-joining (NJ) analysis was conducted on the 24 amphipods for which sequences were obtained, and haplotypes were selected from each genetic lineage to include in a model-based phylogenetic analysis.

The neighbour-joining analysis placed the 24 specimens of amphipods into four lineages (Figure 1). Comparisons to the GenBank sequence database indicated that three lineages were most similar to sequences of Melitidae and one was most similar to Niphargidae. The Niphargidae lineage contained three specimens, whereas the Melitidae lineages contained between four and ten specimens (Figure 1). The three lineages of Melitidae differed from one another by between 9.9 and 14.1% mean sequence divergence (Table 2). There was no variation within any of the four lineages (Table 3).

The Melitidae and Niphargidae were analysed in separate phylogenetic analyses. For the Niphargidae, twelve reference sequences were included in the analysis, ten specimens from previous surveys in the Robe Valley, and two Genbank reference sequences of *Niphargus*: *N. fontanus* (Genbank accession number KC315635) and *N. glenniei* (Genbank accession number KC315646). Two sequences of Paramelitidae, *Maarrka weeliwollii* (Genbank accession # DQ838032), and *Yilgarus* sp (Genbank accession # EF118232) were used as outgroups.

For the Melitidae, 48 reference sequences were included in the phylogenetic analysis, two GenBank vouchers of Melitidae, *Nedsia* sp. 1 (Genbank accession #EU304458), and *Norcapensis mandibulis* (Genbank accession # JQ608487) as well as 46 specimens from previous surveys of the Robe Valley, Central Pilbara, Barrow Island, Lower Shaw River, Fortescue River, and Marillana Creek. Two sequences of the amphipod genus *Niphargus* were used as outgroups as follows: *N. fontanus* (Genbank accession number KC315635) and *N. glenniei* (Genbank accession number KC315646).

#### *Phylogenetic analysis- Niphargidae*

The phylogenetic analysis, which included the one representative of Niphargidae from Mesa C in addition to twelve reference specimens, placed the new Mesa C specimen in a lineage containing five reference specimens from Dave's and Budgie bores and thus was assigned to the existing lineage AMN008 (Figure 2).

#### *Differentiation between lineages –Niphargidae*

The Mesa C Niphargidae lineage, represented by specimen LI20, differed from the nearest reference specimens KJ64, KD39, KE07, IV100 and JN08 (lineage AMN008) by between 0.3 and 0.8% sequence divergence (Table 4).

#### *Phylogenetic analysis- Melitidae*

The phylogenetic analysis, which included the three representatives of Melitidae from Mesa C, in addition to 48 reference specimens, placed the Mesa C specimens in three distinct genetic lineages, all of which also contained reference specimens from previous surveys in the Pilbara (Figure 3). Specifically, specimen LI25 was placed in a lineage containing reference specimens KE05, KJ73, KD45 and KD55 and thus was assigned to the existing lineage AMM031 (Figure 3). Specimen LI11 was placed in a lineage with reference specimens KE10, IV128 and JN05, and thus was assigned to the existing lineage AMM004 and specimen LI10 was placed in a lineage containing reference specimens JF21 and JN22 and thus was assigned to the existing lineage AMM026 (Figure 3).

Specimens LI25 was placed in a larger clade containing eight closely related lineages from the Robe Valley (AMM001, AMM002, AMM024, AMM025, AMM027, AMM029, AMM030 and AMM031; Figure 3).

#### *Differentiation between lineages - Melitidae*

The three meltid lineages detected at Mesa C were assigned to existing lineages and differed from the nearest reference specimens by <2.5%, with the exception of LI25, which differed from reference specimens in lineage AMM031 to which it was assigned by 0 – 3.5% (Table 5). Specimen LI10 differed from the nearest reference specimens JF21 and JN22 by between 1.3 and 1.4% sequence divergence and LI11 differed from the nearest reference specimens IV128, JN05 and KE10 by between 0.2 and 0.3% sequence divergence (Table 5).

The genetic distance between specimens in the large well-supported clade comprising the eight closely related lineages (enclosed by a dashed red box in Figure 3) ranged from 0 – 7.8% and the mean was 4.9% sequence divergence.

### **Conclusions**

COI is widely considered to show suitable variation to distinguish species (Hebert et al., 2003a). In a comparison of COI sequences for over 13,000 pairs of taxa, Hebert et al (2003b) found a mean of 11.1% sequence divergence between distinct species. Nearly 80% of the comparisons showed that species pairs differed from one another by greater than 8% sequence divergence.

However, a taxon by taxon approach, examining the amount of phylogenetic variation within and between species is the most widely accepted method of defining species.

#### Niphargidae

One lineage of Niphargidae, AMN008, was detected at Mesa C during the current collection phase. The lineage has been detected previously at Mesa C and other sites in the Robe Valley.

**AMN008** = species detected previously in the Robe Valley at Dave's and Budgie bores in the Robe Valley.

#### Melitidae

Three lineages of Melitidae were detected at Mesa C, differing from one another by between 9.9 and 14.1% mean sequence divergence, indicating that each is likely to represent a distinct species. All three of the lineages were assigned to existing lineages (AMM004, AMM026 and AMM031).

One of the three lineages detected at Mesa C (AMM031) was placed in a well-supported clade containing a group of closely related specimens (enclosed by a dashed red box in Figure 3), which differed by <5% mean sequence divergence (range = 0 – 7.8%). Thus this group may represent several closely related species, or may represent a single species showing genetic differentiation across its range. Further investigation may be required to resolve relationships among the lineages, but the most likely explanation would be to consider them a single species, owing to the fact that the clade has a relatively wide distribution (Robe Valley to Barrow Island) and the observed genetic variation may reflect geographic variation associated with a 'stepping stone' pattern of gene exchange – populations that are near-by would be expected to exchange genes, but those on the geographic extremes are not exchanging genes. This clade forms a larger clade with additional lineages, including the Genbank reference specimen of *Nedsia* sp. 1, allowing us to assign the lineages to the genus *Nedsia* with some confidence.

**AMM004** = species detected previously at Mesa H and Dave's bore in the Robe Valley.

**AMM026** = species detected previously at Mesa H and Red Hill

**AMM031** = species detected at Mesa H as well as Budgie bore in the Robe Valley. Belongs to a large clade that may correspond to one species of *Nedsia*, but relationships among the clade members requires further investigation.

#### **References**

- Drummond AJ, Ashton B, Buxton S, Cheung M, Cooper A, Duran C, Field M, Heled J, Kearse M, Markowitz S, Moir R, Stones-Havas S, Sturrock S, Thierer T, Wilson A (2011) Geneious v5.4, <http://www.geneious.com/>
- Hebert, P.D.N., Cywinska, A., Ball, S.L., deWaard J.R. (2003a). Biological identifications through DNA barcodes. Proceedings of the Royal Society of London B 270: 313-321.
- Hebert, P.D.N., Ratnasingham, S., deWaard J.R. (2003b). Barcoding animal life: cytochrome c oxidase subunit 1 divergences among closely related species. Proceedings of the Royal Society of London B (supplement) 270: S96-S99.
- Posada, D., Crandall, K.A. (1998). MODELTEST: testing the model of DNA substitution. Bioinformatics 14: 817-818.
- Thompson, J., Higgins, D., and Gibson, T. (1994). CLUSTAL W: improving the sensitivity of progressive multiple sequence alignment through sequence weighting, position-specific gap penalties and weight matrix choice. Nucleic Acids Research 22: 4673–4680.  
doi:10.1093/nar/ 22.22.4673

Table 1. Specimens of Amphipoda used in the present study and the lineage to which they were assigned, based on variation at the COI gene.

Tracking Number	Taxonomy	Cap #	N	Helix ID	Lineage
MB16MEC0007-20170308-01	Amphipoda	16	2	LI01	AMM004
MB16MEC0007-20170308-01	Amphipoda	16	2	LI02	AMM004
MB16MEC0008-20170308-01	Amphipoda	2	2	LI03	No amp
MB16MEC0008-20170308-01	Amphipoda	2	2	LI04	No amp
MB16MEC0009-170308-2	Amphipoda	6	14	LI05	AMM026
MB16MEC0009-170308-2	Amphipoda	6	14	LI06	AMM004
MB16MEC0009-170308-2	Amphipoda	6	14	LI07	AMM026
MB16MEC0009-170308-2	Amphipoda	6	14	LI08	AMM004
MB16MEC0009-170308-2	Amphipoda	6	14	LI09	AMM026
MB16MEC0009-170308-2	Amphipoda	6	14	LI10	AMM026
MB16MEC0009-170308-2	Amphipoda	6	14	LI11	AMM004
MB16MEC0009-170308-2	Amphipoda	6	14	LI12	AMM026
MB16MEC0009-170308-2	Amphipoda	6	14	LI13	AMM004
MB16MEC0009-170308-2	Amphipoda	6	14	LI14	AMM026
MB16MEC0009-170308-2	Amphipoda	6	14	LI15	AMM026
MB16MEC0009-170308-2	Amphipoda	6	14	LI16	No amp
MB16MEC0009-170308-2	Amphipoda	6	14	LI17	No amp
MB16MEC0009-170308-2	Amphipoda	6	14	LI18	AMM004
MEAWO4086-20170308-01	Amphipoda	12	4	LI19	AMN008
MEAWO4086-20170308-01	Amphipoda	12		LI20	AMN008
MEAWO4086-20170308-01	Amphipoda	12		LI21	AMN008
MEAWO4086-20170308-01	Amphipoda	12		LI22	AMM031
RC15MEC0027-20170309-01	Amphipoda	23	1	LI23	AMM004
RC15MEC0200-20170308-01	Amphipoda	9	1	LI24	AMM031
RC15MEC0200-20170308-01	Amphipoda	9		LI25	AMM031
RC15MEC0200-20170308-01	Amphipoda	9		LI26	AMM031
RC16MEC0102-170308-1	Amphipoda	10	1	LI27	AMM004
WB16MEC0002-20170309-01	Amphipoda	17	1	LI28	AMM004

Table 2. Mean genetic distance (p-distances) between lineages of amphipods as shown in Figure 1. Distances between lineages within families are highlighted in yellow.  
Niph=Niphargidae.

	<b>Melitidae</b>			<b>Niph</b>
Lineage	1	2	3	4
Gp 1		0.010	0.011	0.019
Gp 2	0.099		0.012	0.018
Gp 3	0.141	0.136		0.019
Gp 4	0.341	0.324	0.303	

Table 3. Mean genetic distance (p-distances) and standard errors within lineages of amphipods as shown in Figure 1. N= number of specimens in the lineage and rep= specimen selected to represent the lineage in the model-based phylogenetic analysis.

<b>Lineage</b>	<b>D</b>	<b>s.e.</b>	<b>N</b>	<b>Rep</b>
Gp 1	0.000	0.000	10	LI11
Gp 2	0.000	0.000	4	LI25
Gp 3	0.000	0.000	7	LI10
Gp 4	0.000	0.000	3	LI20

Table 4. Genetic distances (below diagonal) and standard error (above diagonal, in blue) between specimens of Niphargidae (Amphipoda) detected at Mesa C and the reference lineages as shown in Figure 2. Distances between the Mesa C specimens and the reference specimens are highlighted in yellow.

Specimen ID	LI20	IV100	IV129	JN08	KD39	KD41	KE07	KE18	KE28	KE33	KJ64
LI20 MEAWO4086-20170308-01		0.003	0.013	0.003	0.002	0.017	0.003	0.015	0.013	0.013	0.003
IV100 Daves-20150604-01 AMN008	0.005		0.013	0.000	0.002	0.017	0.000	0.014	0.013	0.012	0.003
IV129 DAVES-20150930-04 AMN007	0.159	0.149		0.013	0.013	0.016	0.013	0.014	0.008	0.013	0.013
JN08 200-20160505-02C AMN008	0.005	0.000	0.149		0.002	0.017	0.000	0.014	0.013	0.012	0.003
KD39 Budgie-20150930-01 AMN008	0.003	0.003	0.156	0.003		0.017	0.002	0.015	0.013	0.012	0.003
KD41 Budgie-20150930-01 AMN001	0.245	0.240	0.246	0.240	0.237		0.017	0.016	0.017	0.017	0.017
KE07 200-20160910-01 AMN008	0.005	0.000	0.149	0.000	0.003	0.241		0.014	0.013	0.012	0.003
KE18 RR1-20160910-01 AMN002	0.199	0.189	0.173	0.189	0.191	0.258	0.189		0.016	0.014	0.014
KE28 32-20160910-02 AMN003	0.163	0.156	0.063	0.156	0.163	0.253	0.156	0.184		0.014	0.013
KE33 25-20160910-01 AMN004	0.128	0.121	0.151	0.121	0.123	0.245	0.121	0.183	0.156		0.013
KJ64 Budgiebore-20161210-01 AMN008	0.008	0.006	0.151	0.006	0.006	0.243	0.006	0.187	0.158	0.122	

Table 5 (attached). Genetic distances (below diagonal) and standard error (above diagonal, in blue) between specimens of Melitidae (Amphipoda) detected at Mesa C and the reference lineages as shown in Figure 3. Distances between the Mesa C specimens and the reference specimens are highlighted in yellow.

Figure 1. Neighbour-joining analysis of specimens of Amphipoda from the present study. Numbers on major nodes correspond to bootstrap support over 100 iterations; values <50% are not shown. Scale bar= genetic distance. The specimens used to represent each lineage in the model-based phylogenetic analysis are highlighted in yellow.

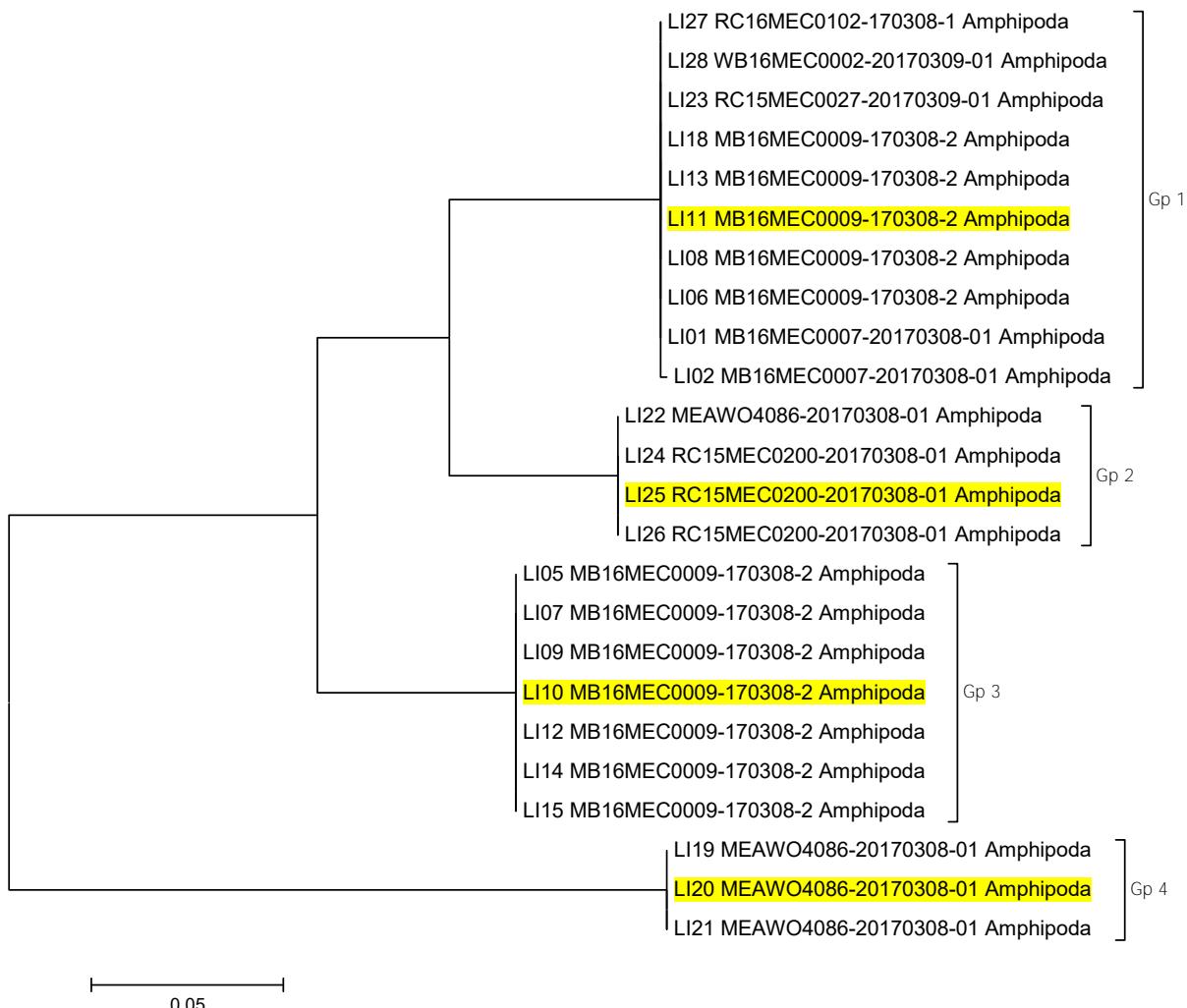


Figure 2. Bayesian analysis of COI haplotypes of Niphargidae (Amphipoda) from the present study and reference specimens from Genbank and previous surveys in the Pilbara. Numbers on major nodes correspond to posterior probabilities; values <50% are not shown. Specimens from the present study are highlighted in yellow; GenBank voucher specimens highlighted in turquoise. Scale bar= number of substitutions per site. Red boxes enclose species with high confidence.

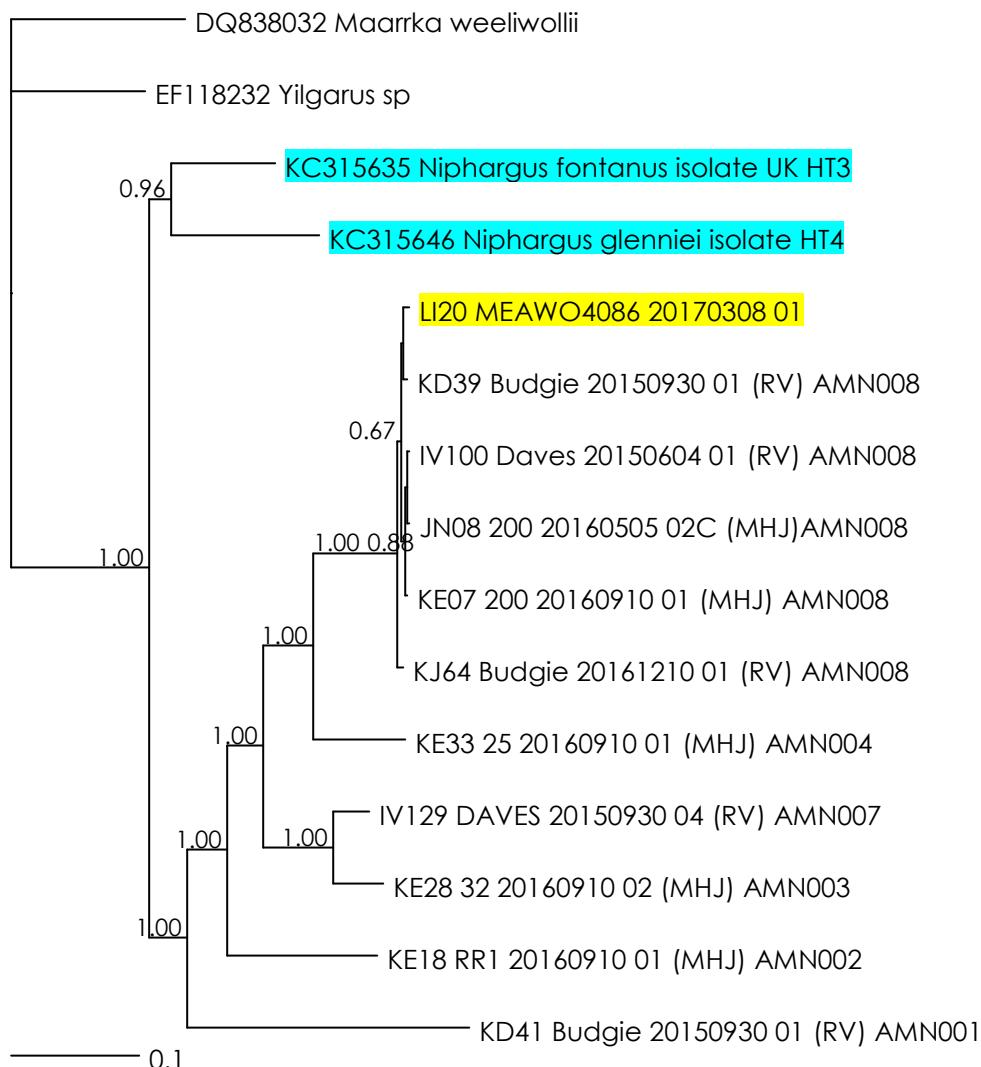
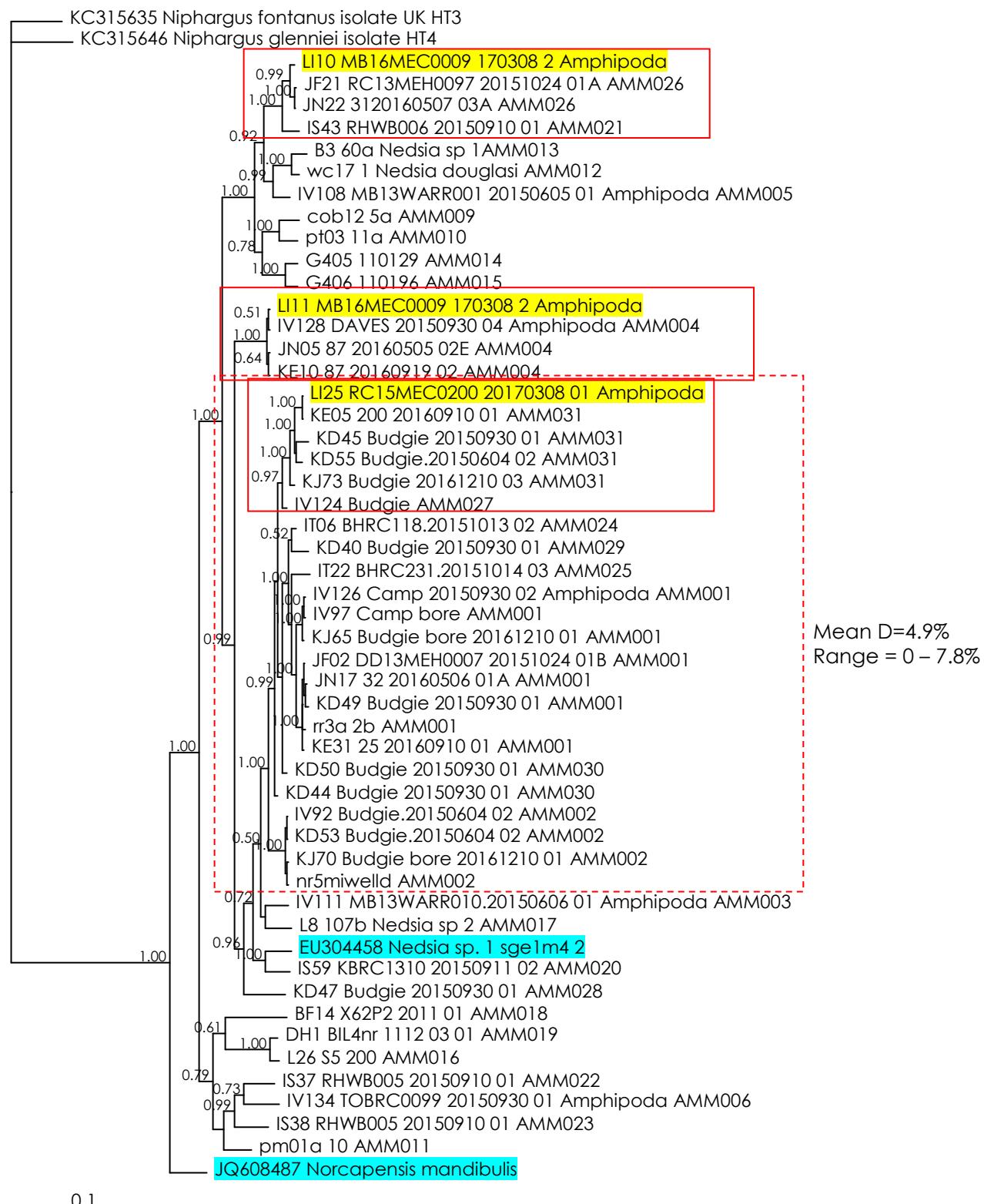


Figure 3. Bayesian analysis of COI haplotypes of Melitidae (Amphipoda) from the present study and reference specimens from Genbank and previous surveys in the Pilbara. Numbers on major nodes correspond to posterior probabilities; values <50% are not shown. Specimens from the present study are highlighted in yellow; GenBank voucher specimens highlighted in turquoise. Scale bar= number of substitutions per site. Red boxes with dashed lines represent groups requiring further investigation.



**RTIO007---: WAM Molecular Systematics Unit**

**Molecular analysis of Amphipoda from the Robe River  
Valley: Mesa H and Mesa B/C, Western Australia  
(Rio Tinto/ WRM – Robe Valley Aquatic Amphipods)**

Report to Rio Tinto

16 June 2017

Karen Cullen, Mark S. Harvey

Department of Terrestrial Zoology, Western Australian Museum,  
Locked Bag 49, Welshpool DC, Western Australia 6986, Australia



*Although identifications in this report were consistent with the best available information and current scientific thinking at the time of identification the use of this report is at the risk of the user. Any liability to users of this report for loss of any kind arising out of the use of this report or the information and identifications it contains is expressly disclaimed.*

## SUMMARY

---

Sixty-three specimens from the Robe River (Mesa H & Mesa B/C) initially identified as *Nedsia* (Amphipoda, Melitidae) by *Wetland Research & Management* (WRM) were extracted for sequencing. Molecular analyses were conducted to inform the number of species present, and to compare the results with those obtained during previous surveys in the Robe Valley undertaken by Biota Environmental Sciences.

Fourteen specimens from seven locations produced good quality COI sequences which were analysed against other Amphipoda specimens (encompassing eight lineages of Eriopisidae, two of Paramelitidae, and five lineages of Niphargidae) originally sequenced by Helix Molecular Solutions, together with sequences obtained from Genbank #JN233925, #EU304458, and # DQ267095. Neighbour-joining and Maximum likelihood (RAxML) analyses were undertaken.

From these 14 specimens, it is likely that there are three lineages of Amphipoda, two lineages belonging to the family Eriopisidae (Lowry & Myers, 2013: originally Melitidae), and likely belonging to the genus *Nedsia*, and one belonging to Paramelitidae (most likely a species of *Chydaekata*; WAM lineage **AMP-Par-001**).

One of the Eriopisidae lineages aligns with a species already identified by Helix as AMM-001 (Hereby referred to as WAM Lineage **AMP-Eri-001**). The other lineage (represented by two specimens from two different locations), is closely related, but supported by a separate clade (Bootstrap support > 78%; WAM Lineage **AMP-Eri-001A**). This lineage differs from AMP-Eri-001 from between 3.62% and 6.64%. More taxonomic work would be required to determine whether individuals within this lineage constitute a separate species as phylogenetic analysis was based on sequence data from a single gene only.

## **BACKGROUND AND OBJECTIVE**

Wetland Research & Management (WRM) collected amphipods from Robe River and Mungarathoona Creek hyporheic and benthic habitats (Mesa H and Mesa B/C) between 28 April – 7 May 2016. These samples were not able to be assigned to a species based on morphological criteria, and 186 specimens were deposited at the Western Australian museum on 20 March 2017 for molecular analysis (Appendix 2).

The purpose of this project was to undertake sub-sampling and sequence for variation at the mitochondrial COI gene. Molecular analysis was undertaken in order to determine whether these species match those identified during previous surveys of stygobitic amphipods from the Robe Valley previously collected and sequenced by Helix Molecular Solutions for Biota Environmental Sciences. Comparison of molecular data of target samples with reference samples will be undertaken to determine:

- a) The identity and distribution of the WRM samples, and
- b) Whether the range of previously identified stygobitic amphipods can be extended.

## **METHODS**

Sixty-three amphipod specimens were subsampled at the WA Museum using Leica dissecting microscopes (MZ6, MZ16) and samples placed directly into ATL buffer for extraction using a commercially available DNA extraction kit (QIAGEN DN-easy). DNA barcoding sequences (Cytochrome Oxidase I; COI) were amplified by PCR using Folmer's PCR primers (LCO1490, HCO2198) in the WA Museum's Molecular Systematics Unit and sequenced by the Australian Genomic Research Facility (AGRIF) Perth node. Sequences were edited, aligned and analysed using GENEIOUS software version 10.1.2 (Kearse et al., 2012), against 67 historical sequences provided by Helix Molecular Solutions from five separate jobs (328, 340, 352, 383 and 387; see Finston et al., 2017, 2016a, 2016b, 2016c, and 2016d). Sequences obtained from Genbank were used for the outgroup (*Daphnia pulicaria* [JN233925]), as well as reference sequences of *Nedgia* sp. 1 [EU304458] and *Chydaekata acuminata* [DQ267095].

Maximum likelihood analyses with 100 rapid bootstrap replicates was performed in RAxML (Randomised Accelerated Maximum Likelihood) version 8.2.7 software (Stamatakis, 2014), using the GTR Gamma model of sequence evolution and default settings. To be consistent with Helix reports, lineages were defined as haplotypes or groups of haplotypes differing from other such groups by >3% sequence divergence (See Finston et al. 2017, Herbert et al., 2003).

## RESULTS

---

A summary of specimen identifications together with lineage information is presented in Table 1. The consensus Maximum Likelihood Phylogenetic tree including representative samples from each major Helix reference lineage is shown in Figure 1. A full Maximum Likelihood Phylogenetic tree is included in Appendix 1, showing all samples included in the analysis. Summary information for all queried WRM specimens are provided in Appendix 2. A complete table of genetic distances (% Identity) can be supplied as supplementary information if required.

Although 63 specimens were sent for sequencing, only 14 specimens produced good quality COI sequences. The remaining sequences either failed or showed evidence of contamination and were excluded from the analysis. The final analysis included 14 specimens from 7 locations (See Table 1), as well as reference Amphipoda from eight lineages of Eriopisidae, two of Paramelitidae, and five lineages of Niphargidae originally sequenced by Helix Molecular solutions. Sequences obtained from Genbank were used as outgroup (*Daphnia pulicaria* [JN233925]), as well as, reference sequences of *Nedsia* sp. 1 [EU304458] and *Chydaekata acuminata* [DQ267095].

From these 14 specimens, it is likely that there are three lineages of Amphipoda, two lineages belonging to the family Eriopisidae (likely belonging to the genus *Nedsia*), and one belonging to Paramelitidae (most likely a species of *Chydaekata*; WAM lineage **AMP-Par-001**). This specimen (WAMC70269) differed from the closest Paramelitidae (KE16\_RR1-20160910-01 – Lineage AMP035) by 23.9%.

One of the Eriopisidae lineages was genetically identical to a lineage already identified by Helix as AMM-001 (Hereby referred to as WAM Lineage **AMP-Eri-001**). The other lineage (represented by two specimens from two different locations), is closely related, but supported by a separate clade (Bootstrap support > 78%; WAM Lineage **AMP-Eri-001A**). WAMC70317 and WAMC70279 (AMP-Eri-001A) differed from the nearest reference specimen IV93 (AMP-Eri-001) from between 6.8% and 4.71% respectively, but from WAMC70290 by 4.29% and 3.62%. Further analysis is needed to determine whether these specimens constitute a different species, or whether they belong to the Helix AMM001 lineage (Here referred to as WAM-Eriop-001).

With the information we have at hand, no discernable pattern could be seen in the molecular data relating to sampling type (Benthic vs Hyphoreic sweeps).

**Table 1. Summary of WRM specimen identifications**

Taxonomy				#	WAM No.	Sampling	Location
Family	Genetic Lineage	Species Name	Helix Lineage				
Eriopisidae	AMP-Eri-001	Nedsia AMP-Eri-001	AMM001	11	C70280	Benthos Kick-sweep	Mesa H, Robe River, RRD4
					C70281		
					C70282		
					C70283		
					C70289	Hyporheos Sweep	Mesa H, Robe River, RRU3
					C70290		Mesa H, Robe River, RRU6
					C70296		
					C70297		
					C70301		Mesa B/C, Mungarathoona Cr, MCPE5
					C70303		
	AMP-Eri-001A	Nedsia AMP-Eri-001A	N/A	2	C70319	Benthos Kick-sweep	Mesa B/C, Mungarathoona Cr, MCR3
					C70317	Benthos Kick-sweep	Mesa B/C, Mungarathoona Cr, MCR3
					C70279	Hyporheos Sweep	Mesa H, Robe River, RRD4
Paramelitidae	AMP-Par-001	Chydaekata AMP-Par-001	N/A	1	C70269	Hyporheos Sweep	Mesa H, Robe River, RRD3

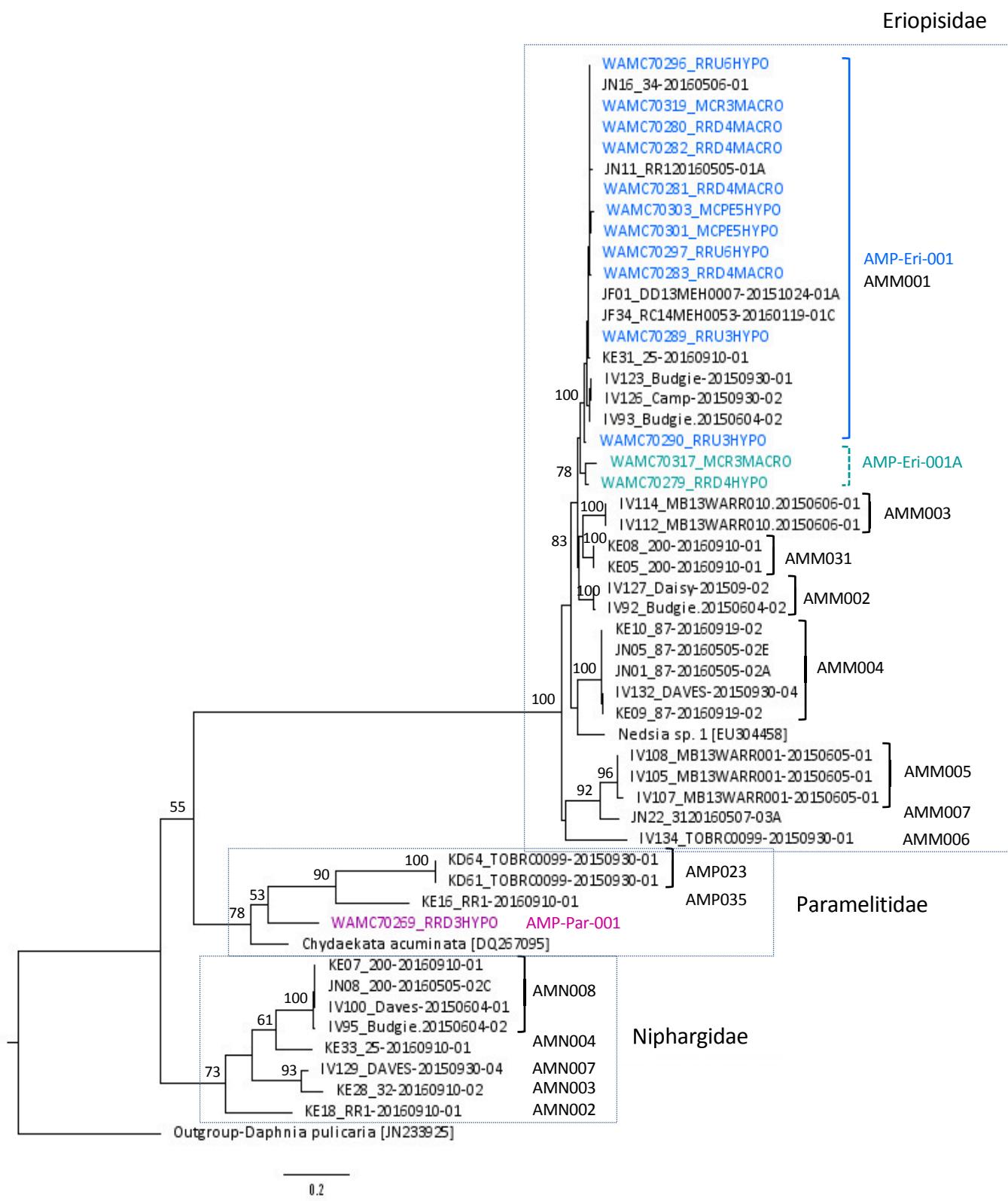


Figure 1. Maximum Likelihood of COI haplotypes of Amphipoda from the present study and a sub-set of reference specimens from Helix Molecular solutions and Genbank. >50% support based on 100 bootstrap replicates are shown for major nodes.

## **CONCLUSIONS**

---

Specimens collected by WRM in benthic and hyporheic habitats along the Robe River (Mesa H and Mesa B/C) are shown to belong to at least one lineage already previously identified (AMP-Eri-001/ Helix AMM001) within the family Eriopisidae and belonging to the genus *Nedsia*, and one lineage within the family Paramelitidae, which has not been previously identified by Helix (AMP-Par-001). Two specimens form another lineage AMP-Eri-001A, which is closely related to AMP-Eri-001 (ranging from 3.6-6.6% genetic difference). The genetic distance between samples collected within the same site (MCR3), WAMC70317 and WAMC70319, was 6.17%, which suggests that the genetic divergences are not associated with geographic variation. However, more data are required to determine whether these specimens constitute a distinct species, or whether they belong to a single species (AMP-Eri-001) showing high genetic diversity. Further investigation would be required to answer this, including increasing the sample sizes, analysis of multiple gene regions, as well as, morphological examination of specimens belonging to the separate lineages.

Not all specimens were able to be amplified and many sequences showed evidence of contamination. This could be due to a number of reasons and most likely due to the degraded nature of the specimens. It would be possible to re-design primers to reduce the potential for contamination being sequenced over the target DNA. Samples could also be re-extracted, but primer design would ultimately be required to enable target DNA to be isolated at a higher success rate. To provide a robust dataset, we would suggest that a sub-set of samples be re-sequenced with specific primers from sites which could not be included in this report. Ideally, additional genes should be sequenced for both study and reference samples, to ultimately resolve the taxonomic questions arising from this report.

## APPENDIX 1.

Eriopisidae

**WAMC70282\_RRD4MACRO**  
**WAMC70295\_RRU6HYPO**  
**JN16\_34-20160506-01**  
**JN13\_RR120160505-01C**  
**WAMC70280\_RRD4MACRO**  
**JN12\_RR120160505-01B**  
**WAMC70319\_MCR3MACRO**  
**JN20\_32-20160506-01D**  
**JN11\_RR120160505-01A**  
**JN21\_32-20160506-01E**  
**WAMC70303\_MCPESHYPO**  
**WAMC70301\_MCPESHYPO**  
**JN24\_3120160507-03C**  
**JN17\_32-20160506-01A**  
**JN23\_3120160507-03B**  
**WAMC70281\_RRD4MACRO**  
**JN25\_3120160507-03D**  
**WAMC70297\_RRU6HYPO**  
**WAMC70283\_RRD4MACRO**  
**JF22\_RC13MEH0097-20151024-01B**  
**JF34\_RC14MEH0053-20160119-01C**  
**JF20\_RC13MEH0041-20151024-01**  
**JF19\_RC13MEH0041-20160119-01**  
**JF18\_RC13MEH0007-20151024-03**  
**JF05\_DD13MEH0007-20151024-01E**  
**JF01\_DD13MEH0007-20151024-01A**  
**WAMC70289\_RRU3HYPO**  
**JF12\_RC12JIM0019-20160119-01B**  
**KE31\_25-20160910-01**  
**IV126\_Camp-20150930-02**  
**IV123\_Budgie-20150930-01**  
**IV120\_Budgie-20150930-01**  
**IV93\_Budgie-20150604-02**  
**WAMC70290\_RRU3HYPO**  
**WAMC70317\_MCR3MACRO**  
**WAMC70279\_RRD4HYPO**  
**IV111\_MB13WARR010.20150606-01**  
**IV112\_MB13WARR010.20150606-01**  
**IV114\_MB13WARR010.20150606-01**  
**KE08\_200-20160910-01**  
**KE05\_200-20160910-01**  
**IV92\_Budgie.20150604-02**  
**IV127\_Daisy-201509-02**  
**JN05\_87-20160505-02E**  
**JN03\_87-20160505-02C**  
**KE10\_87-20160919-02**  
**JN04\_87-20160505-02D**  
**KE12\_87-20160919-02**  
**JN01\_87-20160505-02A**  
**JN02\_87-20160505-02B**  
**KE09\_87-20160919-02**  
**IV128\_DAVES-20150930-04**  
**JN06\_200-20160505-02A**  
**IV132\_DAVES-20150930-04**  
**JN10\_200-20160505-02E**  
**Nedisia sp. 1 [EU304458]**  
**IV105\_MB13WARR001-20150605-01**  
**IV108\_MB13WARR001-20150605-01**  
**IV107\_MB13WARR001-20150605-01**  
**JN22\_3120160507-03A**  
**IV134\_TOBRC0099-20150930-01**

Paramelitidae

**KD64\_TOBRC0099-20150930-01**  
**KD63\_TOBRC0099-20150930-01**  
**KD62\_TOBRC0099-20150930-01**  
**KD58\_TOBRC0099-20150930-01**  
**KD61\_TOBRC0099-20150930-01**  
**KD59\_TOBRC0099-20150930-01**  
**KD60\_TOBRC0099-20150930-01**

**KE16\_RR1-20160910-01**

**WAMC70269\_RRD3HYPO**

**Chydaekata acuminata [DQ267095]**

Niphargidae

**JN08\_200-20160505-02C**  
**IV130\_DAVES-20150930-04**  
**JN09\_200-20150505-02D**  
**IV100\_Daves-20150604-01**  
**JN07\_200-20160505-02B**  
**KE07\_200-20160910-01**  
**IV94\_Budgie.20150604-02**  
**IV95\_Budgie.20150604-02**  
**KE33\_25-20160910-01**  
**IV129\_DAVES-20150930-04**  
**KE28\_32-20160910-02**  
**KE18\_RR1-20160910-01**

**Outgroup-Daphnia pulicaria [JN233925]**

0.2

Maximum Likelihood of COI haplotypes of Amphipoda, including samples from the present study and all relevant reference specimens from Helix Molecular Solutions. Genbank sequences are shown in parentheses.

**APPENDIX 2. SPECIMEN DATA FOR AMPHIPODA COLLECTED FROM THE ROBE RIVER VALLEY.**

Specimens included in Molecular analysis are highlighted in yellow.

REGNO	FLDNO	ORDER	INFRAORDER	FAMILY	GENUS	SPECIES	STATE	SITE	LATITUDE	LONGITUDE	TOTAL
70259	RRD1HYPO-1	Amphipoda	Hadziida	Eriopisidae	Nedsia		WA	Mesa H, Robe River	21°43'07.32"S	116°11'54.80"E	20
70260	RRD1HYPO-2	Amphipoda	Hadziida	Eriopisidae	Nedsia		WA	Mesa H, Robe River	21°43'07.32"S	116°11'54.80"E	1
70261	RRD1HYPO-3	Amphipoda	Hadziida	Eriopisidae	Nedsia		WA	Mesa H, Robe River	21°43'07.32"S	116°11'54.80"E	1
70262	RRD1HYPO-4	Amphipoda	Hadziida	Eriopisidae	Nedsia		WA	Mesa H, Robe River	21°43'07.32"S	116°11'54.80"E	1
70263	RRD1HYPO-5	Amphipoda	Hadziida	Eriopisidae	Nedsia		WA	Mesa H, Robe River	21°43'07.32"S	116°11'54.80"E	1
70264	RRD2HYPO-1	Amphipoda	Hadziida	Eriopisidae	Nedsia		WA	Mesa H, Robe River	21°43'09.22"S	116°11'24.68"E	8
70265	RRD2HYPO-2	Amphipoda	Hadziida	Eriopisidae	Nedsia		WA	Mesa H, Robe River	21°43'09.22"S	116°11'24.68"E	1
70266	RRD2HYPO-3	Amphipoda	Hadziida	Eriopisidae	Nedsia		WA	Mesa H, Robe River	21°43'09.22"S	116°11'24.68"E	1
70267	RRD2HYPO-4	Amphipoda	Hadziida	Eriopisidae	Nedsia		WA	Mesa H, Robe River	21°43'09.22"S	116°11'24.68"E	1
70268	RRD2HYPO-5	Amphipoda	Hadziida	Eriopisidae	Nedsia		WA	Mesa H, Robe River	21°43'09.22"S	116°11'24.68"E	1
70269	RRD3HYPO-1	Amphipoda	Hadziida	Paramelitidae	Chydaekata	AMP-Par-001	WA	Mesa H, Robe River	21°43'09.65"S	116°10'52.10"E	12
70270	RRD3HYPO-2	Amphipoda	Hadziida	Eriopisidae	Nedsia		WA	Mesa H, Robe River	21°43'09.65"S	116°10'52.10"E	1
70271	RRD3HYPO-3	Amphipoda	Hadziida	Eriopisidae	Nedsia		WA	Mesa H, Robe River	21°43'09.65"S	116°10'52.10"E	1
70272	RRD3HYPO-4	Amphipoda	Hadziida	Eriopisidae	Nedsia		WA	Mesa H, Robe River	21°43'09.65"S	116°10'52.10"E	1
70273	RRD3HYPO-5	Amphipoda	Hadziida	Eriopisidae	Nedsia		WA	Mesa H, Robe River	21°43'09.65"S	116°10'52.10"E	1
70274	RRD3MACRO-1	Amphipoda	Hadziida	Eriopisidae	Nedsia		WA	Mesa H, Robe River	21°43'09.65"S	116°10'52.10"E	5
70275	RRD3MACRO-2	Amphipoda	Hadziida	Eriopisidae	Nedsia		WA	Mesa H, Robe River	21°43'09.65"S	116°10'52.10"E	1
70276	RRD3MACRO-3	Amphipoda	Hadziida	Eriopisidae	Nedsia		WA	Mesa H, Robe River	21°43'09.65"S	116°10'52.10"E	1
70277	RRD3MACRO-4	Amphipoda	Hadziida	Eriopisidae	Nedsia		WA	Mesa H, Robe River	21°43'09.65"S	116°10'52.10"E	1
70278	RRD3MACRO-5	Amphipoda	Hadziida	Eriopisidae	Nedsia		WA	Mesa H, Robe River	21°43'09.65"S	116°10'52.10"E	1
70279	RRD4HYPO-1	Amphipoda	Hadziida	Eriopisidae	Nedsia	AMP-Eri-001A	WA	Mesa H, Robe River	21°43'21.85"S	116°10'21.05"E	1
70280	RRD4MACRO-1	Amphipoda	Hadziida	Eriopisidae	Nedsia	AMP-Eri-001	WA	Mesa H, Robe River	21°43'21.85"S	116°10'21.05"E	6
70281	RRD4MACRO-2	Amphipoda	Hadziida	Eriopisidae	Nedsia	AMP-Eri-001	WA	Mesa H, Robe River	21°43'21.85"S	116°10'21.05"E	1
70282	RRD4MACRO-3	Amphipoda	Hadziida	Eriopisidae	Nedsia	AMP-Eri-001	WA	Mesa H, Robe River	21°43'21.85"S	116°10'21.05"E	1
70283	RRD4MACRO-4	Amphipoda	Hadziida	Eriopisidae	Nedsia	AMP-Eri-001	WA	Mesa H, Robe River	21°43'21.85"S	116°10'21.05"E	1
70284	RRD4MACRO-5	Amphipoda	Hadziida	Eriopisidae	Nedsia		WA	Mesa H, Robe River	21°43'21.85"S	116°10'21.05"E	1
70285	RRU1HYPO-1	Amphipoda					WA	Mesa H, Robe River	21°40'22.30"S	116°22'40.05"E	1
70286	RRU3HYPO-1	Amphipoda	Hadziida	Eriopisidae	Nedsia		WA	Mesa H, Robe River	21°41'16.66"S	116°19'55.70"	4
70287	RRU3HYPO-2	Amphipoda	Hadziida	Eriopisidae	Nedsia		WA	Mesa H, Robe River	21°41'16.66"S	116°19'55.70"	1
70288	RRU3HYPO-3	Amphipoda	Hadziida	Eriopisidae	Nedsia		WA	Mesa H, Robe River	21°41'16.66"S	116°19'55.70"	1
70289	RRU3HYPO-4	Amphipoda	Hadziida	Eriopisidae	Nedsia	AMP-Eri-001	WA	Mesa H, Robe River	21°41'16.66"S	116°19'55.70"	1
70290	RRU3HYPO-5	Amphipoda	Hadziida	Eriopisidae	Nedsia	AMP-Eri-001	WA	Mesa H, Robe River	21°41'16.66"S	116°19'55.70"	1
70291	RRU4HYPO-1	Amphipoda	Hadziida	Eriopisidae	Nedsia		WA	Mesa H, Robe River	21°41'20.48"S	116°19'12.71"E	1
70292	RRU5HYPO-1	Amphipoda					WA	Mesa H, Robe River	21°41'23.51"S	116°18'41.10"E	1

REGNO	FLDNO	ORDER	INFRAORDER	FAMILY	GENUS	SPECIES	STATE	SITE	LATITUDE	LONGITUDE	TOTAL
70293	RRU5HYPO-2	Amphipoda					WA	Mesa H, Robe River	21°41`23.51"S	116°18`41.10"E	1
70294	RRU5HYPO-3	Amphipoda					WA	Mesa H, Robe River	21°41`23.51"S	116°18`41.10"E	1
70295	RRU5HYPO-4	Amphipoda					WA	Mesa H, Robe River	21°41`23.51"S	116°18`41.10"E	1
70296	RRU6HYPO-1	Amphipoda	Hadziida	Eriopisidae	Nedsia	AMP-Eri-001	WA	Mesa H, Robe River	21°41`31.06"S	116°18`20.56"E	26
70297	RRU6HYPO-2	Amphipoda	Hadziida	Eriopisidae	Nedsia	AMP-Eri-001	WA	Mesa H, Robe River	21°41`31.06"S	116°18`20.56"E	1
70298	RRU6HYPO-3	Amphipoda	Hadziida	Eriopisidae	Nedsia		WA	Mesa H, Robe River	21°41`31.06"S	116°18`20.56"E	1
70299	RRU6HYPO-4	Amphipoda	Hadziida	Eriopisidae	Nedsia		WA	Mesa H, Robe River	21°41`31.06"S	116°18`20.56"E	1
70300	RRU6HYPO-5	Amphipoda	Hadziida	Eriopisidae	Nedsia		WA	Mesa H, Robe River	21°41`31.06"S	116°18`20.56"E	1
70301	MCPE5HYPO-1	Amphipoda	Hadziida	Eriopisidae	Nedsia	AMP-Eri-001	WA	Mesa B/C, Mungarathoona Creek	21°39`48.40"S	115°57`43.29"E	10
70302	MCPE5HYPO-2	Amphipoda	Hadziida	Eriopisidae			WA	Mesa B/C, Mungarathoona Creek	21°39`48.40"S	115°57`43.29"E	1
70303	MCPE5HYPO-3	Amphipoda	Hadziida	Eriopisidae	Nedsia	AMP-Eri-001	WA	Mesa B/C, Mungarathoona Creek	21°39`48.40"S	115°57`43.29"E	1
70304	MCPE5HYPO-4	Amphipoda	Hadziida	Eriopisidae			WA	Mesa B/C, Mungarathoona Creek	21°39`48.40"S	115°57`43.29"E	1
70305	MCPE5HYPO-5	Amphipoda	Hadziida	Eriopisidae			WA	Mesa B/C, Mungarathoona Creek	21°39`48.40"S	115°57`43.29"E	1
70306	MCPE5MACRO-1	Amphipoda					WA	Mesa B/C, Mungarathoona Creek	21°39`48.40"S	115°57`43.29"E	1
70307	MCPE6HYPO-1	Amphipoda	Hadziida	Eriopisidae			WA	Mesa B/C, Mungarathoona Creek	21°39`27.41"S	115°57`34.64"E	16
70308	MCPE6HYPO-2	Amphipoda	Hadziida	Eriopisidae			WA	Mesa B/C, Mungarathoona Creek	21°39`27.41"S	115°57`34.64"E	1
70309	MCPE6HYPO-3	Amphipoda	Hadziida	Eriopisidae			WA	Mesa B/C, Mungarathoona Creek	21°39`27.41"S	115°57`34.64"E	1
70310	MCPE6HYPO-4	Amphipoda	Hadziida	Eriopisidae			WA	Mesa B/C, Mungarathoona Creek	21°39`27.41"S	115°57`34.64"E	1
70311	MCPE6HYPO-5	Amphipoda	Hadziida	Eriopisidae			WA	Mesa B/C, Mungarathoona Creek	21°39`27.41"S	115°57`34.64"E	1
70312	MCR2HYPO-1	Amphipoda	Hadziida	Eriopisidae			WA	Mesa B/C, Mungarathoona Creek	21°45`00.69"S	116° 2`24.91"E	1
70313	MCR3HYPO-1	Amphipoda					WA	Mesa B/C, Mungarathoona Creek	21°45`01.52"S	116° 1`54.20"E	1
70314	MCR3HYPO-2	Amphipoda					WA	Mesa B/C, Mungarathoona Creek	21°45`01.52"S	116° 1`54.20"E	1
70315	MCR3HYPO-3	Amphipoda					WA	Mesa B/C, Mungarathoona Creek	21°45`01.52"S	116° 1`54.20"E	1
70316	MCR3HYPO-4	Amphipoda					WA	Mesa B/C, Mungarathoona Creek	21°45`01.52"S	116° 1`54.20"E	1
70317	MCR3MACRO-1	Amphipoda	Hadziida	Eriopisidae	Nedsia	AMP-Eri-001A	WA	Mesa B/C, Mungarathoona Creek	21°45`01.52"S	116° 1`54.20"E	26
70318	MCR3MACRO-2	Amphipoda	Hadziida	Eriopisidae	Nedsia		WA	Mesa B/C, Mungarathoona Creek	21°45`01.52"S	116° 1`54.20"E	1
70319	MCR3MACRO-3	Amphipoda	Hadziida	Eriopisidae	Nedsia	AMP-Eri-001	WA	Mesa B/C, Mungarathoona Creek	21°45`01.52"S	116° 1`54.20"E	1
70320	MCR3MACRO-4	Amphipoda	Hadziida	Eriopisidae	Nedsia		WA	Mesa B/C, Mungarathoona Creek	21°45`01.52"S	116° 1`54.20"E	1
70321	MCR3MACRO-5	Amphipoda	Hadziida	Eriopisidae	Nedsia		WA	Mesa B/C, Mungarathoona Creek	21°45`01.52"S	116° 1`54.20"E	1

## **REFERENCES**

---

- Finston, T., Y. Hitchen, and O. Berry (2017). Report on the molecular systematics of Amphipoda from Mesa H – Phase 4. Unpublished report prepared for Biota Environmental Sciences, March 2017.
- Finston, T., Y. Hitchen, and O. Berry (2016a). Report on the molecular systematics of subfauna from the Robe River Valley – Phase 4. Unpublished report prepared for Biota Environmental Sciences, December 2016.
- Finston, T., Y. Hitchen, and O. Berry (2016b). Report on the molecular systematics of subfauna from the Robe River Valley – historical, Phase 3 and Phase 1 and 2 repeats: Part 3. Unpublished report prepared for Biota Environmental Sciences, October 2016.
- Finston, T., Y. Hitchen, and O. Berry (2016c). Report on the molecular systematics of subfauna from Mesas H and J. Unpublished report prepared for Biota Environmental Sciences, June 2016.
- Finston, T., Y. Hitchen, and O. Berry (2016d). Report on the molecular systematics of subfauna from Mesa H and J. Prepared for Biota Environmental Sciences, March 2016.
- Folmer, O., M. Black, W. Hoeh, R. Lutz, and R. Vrijenhoek (1994). DNA primers for amplification of mitochondrial cytochrome c oxidase subunit I from diverse metazoan invertebrates. *Molecular Marine Biology and Biotechnology*, **3**: 294-299.
- Herbert, P.D.N., S. Ratnasingham., J.R. deWaard. (2003). Barcoding animal life: cytochrome c oxidase subunit I divergences among closely related species. *Proceedings of the Royal Society of London B (supplement)* **270**:S96-S99.
- Kearse, M., Moir, R., Wilson, A., Stones-Havas, S., Cheung, M., Sturrock, S., Buxton, S., Cooper, A., Markowitz, S., Duran, C., Thierer, T., Ashton, B., Mentjies, P., & Drummond, A. (2012). Geneious Basic: an integrated and extendable desktop software platform for the organization and analysis of sequence data. *Bioinformatics* **28**(12): 1647-1649.
- Lowry, J.K and A.A. Myers (2013) A Phylogeny and Classification of the Senticaudata subord. nov. (Crustacea: Amphipoda). *Zootaxa* **3610**: 1-080.
- Stamatakis, A. 2014. RAxML Version 8: A tool for Phylogenetic Analysis and Post-Analysis of Large Phylogenies. *Bioinformatics* [open access](#).

	JN233925	DQ267095	KE09	KE10	KE05	KE08	KE31	KE18	KE28	KE07	KE33	KE16	KD61	KD64	EU304458	IV129	IV95	IV100	IV134	IV105	IV108	IV107	IV132	IV112	IV114	IV92	
JN233925		69.33	62.63	62.79	63.55	63.55	63.86	66.92	67.99	69.07	69.53	68.61	66.51	66.51	62.76	67.99	68.76	69.07	62.17	64.47	64.47	64.47	62.63	61.87	61.87	62.79	
DQ267095	69.33		67.73	67.88	68.34	68.34	68.8	75.19	74.58	73.52	75.65	78.23	76.77	76.77	66.6	75.49	73.36	73.52	69.56	68.95	68.95	68.95	67.73	68.04	68.04	68.19	
KE09	62.63	67.73		99.85	89.82	89.82	89.82	67.78	68.69	66.87	68.09	65.65	65.54	65.54	89.06	69.91	67.02	66.87	84.5	85.71	85.71	84.8	100	88.91	88.91	88.91	
KE10	62.79	67.88	99.85		89.97	89.97	89.97	67.93	68.84	67.02	68.24	65.81	65.38	65.38	89.25	70.06	67.17	67.02	84.65	85.87	85.87	84.95	99.85	89.06	89.06	89.06	
KE05	63.55	68.34	89.82	89.97		100	94.07	68.24	68.84	68.09	68.84	66.57	67.47	67.47	89.06	70.36	68.39	68.09	84.95	85.87	85.87	86.02	89.82	91.79	91.79	93.31	
KE08	63.55	68.34	89.82	89.97	100		94.07	68.24	68.84	68.09	68.84	66.57	67.47	67.47	89.06	70.36	68.39	68.09	84.95	85.87	85.87	86.02	89.82	91.79	91.79	93.31	
KE31	63.86	68.8	89.82	89.97	94.07	94.07		67.93	68.24	68.09	68.24	65.5	67.15	67.15	89.64	69.91	68.39	68.09	84.8	85.26	85.26	85.56	89.82	91.03	91.03	93.31	
KE18	66.92	75.19	67.78	67.93	68.24	68.24	67.93		80.85	80.4	81	75.99	72.62	72.62	66.6	82.07	80.55	80.4	67.78	67.02	67.02	67.02	67.78	68.09	68.09	68.54	
KE28	67.99	74.58	68.69	68.84	68.84	68.84	68.84		80.85	83.74	83.74	76.29	72.79	72.79	69.48	93.47	83.59	83.74	70.52	68.84	68.84	68.69	69.45	69.45	69.45	70.21	
KE07	69.07	73.52	66.87	67.02	68.09	68.09	68.09		80.4	83.74		87.39	74.77	72.14	72.14	65.64	84.5	99.39	100	69	69.45	69.45	69.15	66.87	69.15	69.15	69
KE33	69.53	75.65	68.09	68.24	68.84	68.84	68.24		81	83.74	87.39		74.47	73.75	73.75	68.33	84.35	87.23	87.39	69.45	68.69	68.69	68.39	68.09	68.69	68.69	69.45
KE16	68.61	78.23	65.65	65.81	66.57	66.57	65.5	75.99	76.29	74.77	74.47		78.42	78.42	66.03	77.05	74.92	74.77	67.17	66.72	66.72	66.87	65.65	67.48	67.48	66.41	
KD61	66.51	76.77	65.54	65.38	67.47	67.47	67.15	72.62	72.79	72.14	73.75	78.42		100	65.07	71.5	71.98	72.14	64.9	65.22	65.22	65.54	65.54	67.31	67.31	67.95	
KD64	66.51	76.77	65.54	65.38	67.47	67.47	67.15	72.62	72.79	72.14	73.75	78.42		100		65.07	71.5	71.98	72.14	64.9	65.22	65.22	65.54	65.54	67.31	67.31	67.95
EU304458	62.76	66.6	89.06	89.25	89.06	89.06	89.64	66.6	69.48	65.64	68.33	66.03	65.07	65.07		70.63	65.83	65.64	83.49	84.64	84.64	84.64	89.06	90.02	90.02	90.21	
IV129	67.99	75.49	69.91	70.06	70.36	70.36	69.91	82.07	93.47	84.5	84.35	77.05	71.5	71.5	70.63		84.35	84.5	72.49	70.21	70.21	70.06	69.91	70.97	70.97	70.82	
IV95	68.76	73.36	67.02	67.17	68.39	68.39	68.39		80.55	83.59	99.39	87.23	74.92	71.98	71.98	65.83	84.35		99.39	69	69.76	69.76	69.45	67.02	69.45	69.45	69
IV100	69.07	73.52	66.87	67.02	68.09	68.09	68.09		80.4	83.74	100	87.39	74.77	72.14	72.14	65.64	84.5	99.39		69	69.45	69.45	69.15	66.87	69.15	69.15	69
IV134	62.17	69.56	84.5	84.65	84.95	84.95	84.8	67.78	70.52	69	69.45	67.17	64.9	64.9	83.49	72.49	69	69		83.89	83.89	83.43	84.5	84.65	84.65	84.95	
IV105	64.47	68.95	85.71	85.87	85.87	85.26	67.02	68.84	69.45	68.69	66.72	65.22	65.22	84.64	70.21	69.76	69.45	83.89		100	98.33	85.71	84.65	84.65	85.71		
IV108	64.47	68.95	85.71	85.87	85.87	85.26	67.02	68.84	69.45	68.69	66.72	65.22	65.22	84.64	70.21	69.76	69.45	83.89	100		98.33	85.71	84.65	84.65	85.71		
IV107	64.47	68.95	84.8	84.95	86.02	86.02	85.56	67.02	68.69	69.15	68.39	66.87	65.54	65.54	84.64	70.06	69.45	69.15	83.43	98.33	98.33		84.8	84.5	84.5	85.41	
IV132	62.63	67.73	100	99.85	89.82	89.82	89.82	67.78	68.69	66.87	68.09	65.65	65.54	65.54	89.06	69.91	67.02	66.87	84.5	85.71	85.71	84.8		88.91	88.91	88.91	
IV112	61.87	68.04	88.91	89.06	91.79	91.79	91.03	68.09	69.45	69.15	68.69	67.48	67.31	67.31	90.02	70.97	69.45	69.15	84.65	84.65	84.65	84.5	88.91		100	92.1	
IV114	61.87	68.04	88.91	89.06	91.79	91.79	91.03	68.09	69.45	69.15	68.69	67.48	67.31	67.31	90.02	70.97	69.45	69.15	84.65	84.65	84.65	84.5	88.91		100	92.1	
IV92	62.79	68.19	88.91	89.06	93.31	93.31	93.31	68.54	70.21	69	69.45	66.41	67.95	67.95	90.21	70.82	69	69	84.95	85.71	85.71	85.41	88.91	92.1	92.1	92.1	
IV127	62.94	68.34	88.75	88.91	93.47	93.47	93.47	68.69	70.06	68.84	69.3	66.57	68.12	68.12	90.02	70.67	68.84	68.84	84.8	85.56	85.56	85.56	88.75				

IV127	JF01	JF34	IV93	IV123	IV126	JN01	JN05	JN08	JN11	JN16	JN22	WAMC70269	WAMC70317	WAMC70279	WAMC70290	WAMC70303	WAMC70319	WAMC70301	WAMC70297	WAMC70283	WAMC70281	WAMC70296	WAMC70280	WAMC70282	WAMC70289
62.94	64.01	64.01	64.01	64.01	64.01	62.79	62.79	69.07	64.47	64.17	62.79	66.77	62.91	64.17	63.36	64.24	64.17	64.32	64.2	64.01	64.01	64.17	64.17	64.01	
68.34	68.65	68.65	68.49	68.49	68.49	67.88	67.88	73.52	68.34	68.49	68.95	84.02	68.05	68.8	68.45	67.96	68.49	68.49	68.53	68.34	68.65	68.49	68.49	68.65	
88.75	89.67	89.67	89.97	89.51	89.51	99.85	99.85	66.87	88.91	89.67	86.32	69	88.05	90.73	90.3	89.67	89.67	89.97	89.7	89.51	89.82	89.67	89.67	89.67	
88.91	89.82	89.82	90.12	89.67	89.67	100	100	67.02	89.06	89.82	86.47	68.84	88.2	90.88	90.46	89.82	89.82	90.12	89.86	89.67	89.97	89.82	89.82	89.82	
93.47	94.22	94.22	93.31	93.16	93.16	89.97	89.97	68.09	93.31	93.92	85.11	67.17	91.95	93.62	93.89	93.39	93.92	93.62	93.96	93.62	93.77	93.92	93.92	94.22	
93.47	94.22	94.22	93.31	93.16	93.16	89.97	89.97	68.09	93.31	93.92	85.11	67.17	91.95	93.62	93.89	93.39	93.92	93.62	93.96	93.62	93.77	93.92	93.92	94.22	
93.47	99.85	99.85	98.18	97.87	97.87	89.97	89.97	68.09	98.78	99.54	85.71	67.48	93.52	95.59	98.09	98.56	99.54	99.24	99.58	99.24	99.39	99.54	99.54	99.85	
68.69	68.09	68.09	68.69	68.39	68.39	67.93	67.93	80.4	67.48	67.93	67.17	74.01	65.7	67.48	67.72	67.4	67.93	68.09	67.97	67.78	67.78	67.93	67.93	68.09	
70.06	68.39	68.39	68.69	68.54	68.54	68.84	68.84	83.74	67.63	68.24	68.69	74.01	68.2	69.3	68.03	67.71	68.24	68.24	68.28	68.24	68.09	68.24	68.24	68.39	
68.84	68.24	68.69	68.54	68.54	67.02	67.02	100	67.48	67.93	69.3	71.73	66.33	67.93	67.56	67.48	67.93	68.09	67.97	68.09	67.78	67.93	67.93	67.93	68.24	
69.3	68.39	68.39	68.69	68.54	68.54	68.24	68.24	87.39	67.78	68.09	68.69	74.01	67.58	68.69	68.19	67.93	68.09	68.24	68.24	67.93	68.09	68.09	68.09	68.39	
66.57	65.65	65.65	65.96	65.96	65.96	65.81	65.81	74.77	65.81	65.65	66.11	76.14	65.23	66.26	65.69	65.27	65.65	65.81	65.69	65.5	65.81	65.65	65.65	65.65	
68.12	66.99	66.99	66.67	66.83	66.83	65.38	65.38	72.14	66.83	66.83	66.99	76.97	66.87	67.15	67.27	66.51	66.83	66.67	66.83	66.67	66.83	66.83	66.83	66.99	
68.12	66.99	66.99	66.67	66.83	66.83	65.38	65.38	72.14	66.83	66.83	66.99	76.97	66.87	67.15	67.27	66.51	66.83	66.67	66.83	66.67	66.83	66.83	66.83	66.99	
90.02	89.83	89.83	89.44	88.87	88.87	89.25	89.25	65.64	89.44	89.64	84.84	68.33	89.49	90.79	90.16	89.44	89.64	89.64	89.25	89.44	89.64	89.64	89.64	89.83	
70.67	70.06	70.36	70.21	70.21	70.06	70.06	70.06	84.5	69.3	69.91	70.06	75.23	68.98	70.67	69.43	69.22	69.91	69.91	69.95	69.6	70.06	69.91	69.91	70.06	
68.84	68.54	68.54	69	68.84	68.84	67.17	67.17	99.39	67.78	68.24	69.3	71.58	66.48	68.09	67.87	67.78	68.24	68.39	68.28	68.39	68.09	68.24	68.24	68.54	
68.84	68.24	68.69	68.54	68.54	67.02	67.02	100	67.48	67.93	69.3	71.73	66.33	67.93	67.56	67.48	67.93	68.09	67.97	68.09	67.78	67.93	67.93	67.93	68.24	
84.8	84.95	84.95	85.11	84.65	84.65	84.65	84.65	69	84.8	84.95	83.28	69.45	84.3	85.26	85.32	84.57	84.95	85.11	84.99	84.5	84.8	84.95	84.95	84.95	
85.56	85.41	85.41	85.71	85.26	85.26	85.87	85.87	69.45	85.11	85.26	91.79	68.54	83.83	85.11	85.79	85.11	85.26	85.26	85.3	84.8	85.11	85.26	85.26	85.41	
85.56	85.41	85.41	85.71	85.26	85.26	85.87	85.87	69.45	85.11	85.26	91.79	68.54	83.83	85.11	85.79	85.11	85.26	85.26	85.3	84.8	85.11	85.26	85.26	85.41	
85.56	85.71	85.71	86.02	85.56	85.56	84.95	84.95	69.15	85.41	85.56	90.73	68.24	84.3	85.56	85.56	85.6	85.11	85.41	85.56	85.56	85.56	85.56	85.71		
88.75	89.67	89.97	89.51	89.51	89.85	99.85	99.85	66.87	88.91	89.67	86.32	69	88.05	90.73	90.3	89.67	89.67	89.97	89.7	89.51	89.82	89.67	89.67	89.67	
92.25	91.19	91.19	91.03	90.88	90.88	89.06	89.06	69.06	69.15	90.58	91.19	86.02	67.93	89.92	91.95	91.71	90.35	91.19	90.88	91.22	91.03	91.03	91.19	91.19	
92.25	91.19	91.19	91.03	90.88	90.88	89.06	89.06	69.06	69.15	90.58	91.19	86.02	67.93	89.92	91.95	91.71	90.35	91.19	90.88	91.22	91.03	91.03	91.19	91.19	
99.85	93.47	93.47	92.86	92.55	92.55	89.06	89.06	69	92.86	93.16	86.47	68.24	91.64	93.77	93.57	92.78	93.16	93.16	93.2	93.16	93.01	93.16	93.16	93.47	
93.62	93.62	93.01	92.71	92.71	88.91	88.91	68.84	93.01	93.31	86.32	68.09	91.8	93.92	93.73	92.93	93.31	93.31	93.35	93.31	93.16	93.31	93.31	93.62		
93.62		100	98.33	98.02	98.02	89.82	89.82	68.24	98.94	99.7	85.87	67.63	93.67	95.74	98.25	98.71	99.7	99.39	99.73	99.39	99.54				



## Appendix 3

### WAM SRE Categories





## APPENDIX 1. WAM SHORT-RANGE ENDEMIC CATEGORIES

	Taxonomic Certainty	Taxonomic Uncertainty
Distribution < 10 000km <sup>2</sup>	<b>Confirmed SRE</b> <ul style="list-style-type: none"> <li>A known distribution of &lt; 10 000km<sup>2</sup>.</li> <li>The taxonomy is well known.</li> <li>The group is well represented in collections and/ or via comprehensive sampling.</li> </ul>	<b>Potential SRE</b> <ul style="list-style-type: none"> <li>Patchy sampling has resulted in incomplete knowledge of the geographic distribution of the group.</li> <li>We have incomplete taxonomic knowledge.</li> <li>The group is not well represented in collections.</li> <li>This category is most applicable to situations where there are gaps in our knowledge of the taxon.</li> </ul>
Distribution > 10 000km <sup>2</sup>	<b>Widespread (not an SRE)</b> <ul style="list-style-type: none"> <li>A known distribution of &gt; 10 000km<sup>2</sup>.</li> <li>The taxonomy is well known.</li> <li>The group is well represented in collections and/ or via comprehensive sampling.</li> </ul>	<b>Sub-categories for this SRE designation are outlined below</b>

### SRE SUB-CATEGORIES

If a taxon is determined to be a “Potential SRE”, the following sub-categories will further elucidate this status.

#### A. Data Deficient:

- There is insufficient data available to determine SRE status.
- Factors that fall under this category include:
  - New species.
  - Lack of geographic information.
  - Lack of taxonomic information.
  - The group may be poorly represented in collections.
  - The individuals sampled (e.g. juveniles) may prevent identification to species level.

#### B. Habitat Indicators:

- It is becoming increasingly clear that habitat data can elucidate SRE status.
- Where habitat is known to be associated with SRE taxa and vice versa, it will be noted here.

#### C. Morphology Indicators:

- A suite of morphological characters are characteristic of SRE taxa.
- Where morphological characters are known to be associated with SRE taxa and vice-versa, it will be noted here.

#### D. Molecular Evidence:

- If molecular work has been done on this taxon (or a close relative), it may reveal patterns congruent or incongruent with SRE status.

#### E. Research & Expertise:

- Previous research and/ or WAM expertise elucidates taxon SRE status.
- This category takes into account the expert knowledge held within the WAM.



## Appendix 4

### Report on the Morphological Identification of Collected Inermipes





**Barrow Island and mainland Pilbara Copepoda Morphological Assessment**  
**7 March, 2017**

**Prepared by:**

Tom Karanovic  
Assistant Professor  
Sungkyunkwan University  
General Studies Building, r. 51311  
Suwon 440-746  
KOREA  
email: [Tomislav.karanovic@utas.edu.au](mailto:Tomislav.karanovic@utas.edu.au)

**Prepared for:**

Dr Jason Alexander  
Biota Environmental Sciences Pty Ltd  
Level 1, 228 Carr Place, Leederville Western Australia 6007  
PO Box 155 Leederville WA 6903  
t: +61 8 9328 1900 f: +61 8 9328 6138

**Total Number of Samples:** 5 vials

**RESULTS:**

WA, Pilbara, Barrow Island, 20°46'34"S, 115°28'03"E, 3 May 2011, J. Alexander, Biota GW07-0511-02, WAM C60637

*Inermipes humphreysi* Lee & Huys, 2002 – 5 specimens (all in alcohol and all damaged)

WA, Pilbara, Barrow Island, 20°46'34"S, 115°28'03"E, 10 Nov 2012, J. Alexander & N. Watson, Biota GW07-1112-01, WAM C60860

*Inermipes humphreysi* Lee & Huys, 2002 – 14 specimens (1 female dissected on 1 slide; others in alcohol and 10 of them damaged)

WA, Pilbara, Barrow Island, 20°46'34"S, 115°28'03"E, 9 May 2012, J. Alexander & J. Caimes, Biota GW07P3-02, WAM C60861

*Inermipes humphreysi* Lee & Huys, 2002 – 3 specimens (all juveniles, all in alcohol, and all undamaged)

WA, Pilbara, Warramboo, 53 km west of Pannawonica, 21°39'10.73"S, 115°48'33.11"E, 5 June 2015, J. Alexander & P. Brooshoof, Biota RC13MEA0279-20150605-02, WAM C67614

*Inermipes humphreysi* Lee & Huys, 2002 – 3 specimens (1 female dissected on 1 slide; 2 juveniles in alcohol all in good condition)

WA, Pilbara, Bungaroo Creek, 32 km SE of Pannawonica, 21°54'58.42"S, 116°24'43.70"E, 25 July 200, J. Alexander & C. O'Neill, Biota BC1473-151, WAM C61519

*Lucionitocrella yalleenensis* Karanovic & Hancock, 2009 – 1 damaged male, dissected on 1 slide

**SYSTEMATIC LIST:**

Syphylum Crustacea Brünich, 1772

Class Maxillopoda Dahl, 1956

Subclass Copepoda H. Milne Edwards, 1840

Family Ameiridae Monard, 1927

Subfamily Ameirinae Monard, 1927

Genus *Inermipes* Lee & Huys, 2002

1. *Inermipes humphreysi* Lee & Huys, 2002

Genus *Lucionitocrella* Karanovic & Hancock, 2009

2. *Lucionitocrella yalleenensis* Karanovic & Hancock, 2009

**COMMENTS:**

Your samples contained representatives of only two ameirid species, both belonging to monospecific genera. The only male of *L. yalleenensis*, one female of *I. humphreysi* from Barrow Island, and one female of *I. humphreysi* from Warramboo were dissected and mounted on one slide each, to check details of their morphology. There is no morphological difference between *I. humphreysi* specimens from Barrow Island and Warramboo, even in minute details of somite ornamentation; their appendage armature is also identical, as is their habitus shape and size.

To my knowledge this is the first record of *I. humphreysi* outside of Barrow Island (see Lee & Huys 2002). Also, this is the first record of *L. yalleenensis* outside its type locality, Yalleen Station (see Karanovic & Hanckok 2009). The only specimen of the latter species was damaged (antennulae missing, most segments of the first swimming leg broken off), but there was no doubt that I had an adult male (well-developed spermatophore observed) and I could not find any morphological difference in armature or ornamentation between it and the type material.

Please, note that all vials except one contained less specimens than stated on the labels and in the WAM Specimen Invoice sheet. Also, many specimens were damaged, and they were not kept in small insert vials inside larger vials. This is not a good practice, as these small and gentle subterranean harpacticoids could easily be damaged by large cardboard labels (four in each vial!). I made sure to carefully wash all labels, vials, and pipettes, so there is no possibility that I have lost any. They are either kept on slides somewhere or lost during processing and counting by people who handled these samples before me.

## L. REFERENCES

- Karanovic, T. & Hancock, P. (2009)** On the diagnostic characters of the genus *Stygonitocrella* (Copepoda, Harpacticoida), with descriptions of seven new species from Australian subterranean waters. Zootaxa, 2324, 1-85.
- Lee, W. & Huys, R. (2002)** A new genus of groundwater Ameiridae (Copepoda, Harpacticoida) from boreholes in Western Australia and the artificial status of *Stygonitocrella* Petkovski, 1976. Bulletin of the Natural History Museum London, 68: 9-50.

With best wishes,

Tom Karanovic

Seoul, 7 March 2017

## Appendix 5

Desktop Review: Study Comparison;  
Stygobitic Fauna Species List; and  
Conservation Significance





Summary of previous surveys completed within the study area.

	Current Study (Warramboo)	Current Study (Mesa C)	Department of Parks and Wildlife; Pilbara Regional Stygofauna Surveys	Biota (2004a) Mesa A and Bungaroo Creek Exploration Areas Subterranean Fauna Survey	Biota (2006b) Mesa A, Warramboo and Yarraloola Borefield Development	Biota (2015a) Bungaroo Subterranean Fauna Desktop Assessment	Biota (2016b) Bungaroo Coastal Waters Project Stygofauna Monitoring 2015	Biota (2016a) Bungaroo Coastal Waters Project Stygofauna Monitoring 2016	WAM (2017) Molecular analysis of Amphipoda from the Robe River Valley *
Phases	3	2	9	1	1	14	2	2	-
Area Focus	Warramboo	Mesa C	Robe Valley	Mesa A and Bungaroo	Warramboo, Yarraloola	Bungaroo	Bungaroo	Bungaroo	Robe Valley
Survey Timing	Jun 2015 – Dec 2016	Dec 2016 – Mar 2017	2002 – 2005	Dec 2003	Oct 2005	Dec 2003 – Oct 2014	May – Oct 2015	May – Sep 2016	-
Rain 3 months preceding (mm)	254.8	3.0	0.2	21	92.4	21	279.4	65.2	-
Sites sampled	26	23	23 ^	36	54	122	26	31	13
Number of orders recorded	8	6	10 ^	3	5	15	8	13	1
Oligochaeta	X		X	X	X	X	X	X	
Polychaeta			X						
Hydrachnidia			X			X			
Synbranchiformes						X		X	
Diplopoda									X
Amphipoda	X	X		X	X	X	X	X	X
Copepoda	X	X	X	X	X	X	X	X	
Isopoda	X	X	X			X	X	X	
Ostracoda		X	X		X	X	X	X	
Syncarida	X		X			X	X	X	
Thermosbaenacea	X	X	X		X	X	X	X	
Sorbeoconcha		X				X	X	X	
Nematoda	X		X			X			
Nemertea						X			
Platyhelminthes	X					X		X	
Protozoa						X			
Rotifera			X			X			

\* genetics report on amphipod specimens only. No sampling completed as part of the report.

^ Within the study area

Year	Site	Phylum	Class	Order	Family	Species	#	Notes
2002	PSS015	Annelida	Oligochaeta	Tubificida	Phreodrilidae	Phreodrilidae sp. 'dissimilar ventral chaetae'	20	Widespread
2002	PSS015	Arthropoda	Arachnida	Sarcoptiformes	-	Oribatida group 4	1	
2002	PSS015	Crustacea	Copepoda	Calanoida	Stygoridgewayiidae	Stygoridgewayia trispinosa	17	
2002	PSS015	Crustacea	Copepoda	Cyclopoida	Cyclopidae	Apocyclops dengizicus	1	
2002	PSS015	Crustacea	Copepoda	Cyclopoida	Cyclopidae	Halicyclops rochai	1	
2002	PSS015	Crustacea	Copepoda	Harpacticoida	Ameiridae	Stygonitocrella trispinosa	7	
2002	PSS015	Crustacea	Copepoda	Harpacticoida	Ectinosomatidae	Pseudectinosoma galassiae	9	
2002	PSS015	Crustacea	Malacostraca	Amphipoda	Bogidiellidae	Bogidiellidae sp. '1'	1	
2002	PSS015	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Nedsia hurlberti	1	
2002	PSS015	Crustacea	Malacostraca	Amphipoda	Paramelitidae	Paramelitidae sp. 'indet'	1	Indeterminate Species
2002	PSS015	Crustacea	Malacostraca	Bathynellacea	Parabathynellidae	Atopobathynella sp. 'A'	2	
2002	PSS015	Crustacea	Malacostraca	Thermosbaenacea	Halosbaenidae	Halosbaena tulki	1	
2002	PSS015	Crustacea	Ostracoda	Podocopida	Candonidae	Areacandona astrepte	3	
2002	PSS015	Crustacea	Ostracoda	Podocopida	Candonidae	Humphreyscandona pilbarae	1	
2002	PSS015	Crustacea	Ostracoda	Podocopida	Candonidae	Meridescandona sp. '2'	1	
2002	PSS015	Crustacea	Ostracoda	Podocopida	Limnocytheridae	Gomphodella hirsuta	1	
2002	PSS015	Nematoda	-	-	-	Nematoda sp. '2'	1	
2002	PSS015	Rotifera	Bdelloidea	-	-	Bdelloidea sp. 'indet'	2	Indeterminate Species
2002	PSS016	Annelida	Oligochaeta	Tubificida	Enchytraeidae	Enchytraeidae sp. '1' (PSS)	1	
2002	PSS016	Annelida	Oligochaeta	Tubificida	Enchytraeidae	Enchytraeus Pilbara sp. '2'	74	
2002	PSS016	Annelida	Polychaeta	Phyllodocida	Nereididae	Namanereis sp. 'indet'	1	Indeterminate Species
2002	PSS016	Arthropoda	Arachnida	Sarcoptiformes	-	Oribatida group 1	11	
2002	PSS016	Arthropoda	Arachnida	Trombidiformes	Arrenuridae	Arrenurus sp. 'indet'	1	Indeterminate Species
2002	PSS016	Arthropoda	Arachnida	Trombidiformes	Arrenuridae	Arrenurus sp. 'nov. 2'	3	
2002	PSS016	Arthropoda	Arachnida	Trombidiformes	Pezidae	Peza sp. 'indet'	2	
2002	PSS016	Crustacea	Copepoda	Calanoida	Stygoridgewayiidae	Stygoridgewayia trispinosa	30	
2002	PSS016	Crustacea	Copepoda	Cyclopoida	Cyclopidae	Diacyclops humphreysi unispinosus	56	Widespread
2002	PSS016	Crustacea	Copepoda	Cyclopoida	Cyclopidae	Halicyclops rochai	18	
2002	PSS016	Crustacea	Copepoda	Cyclopoida	Cyclopidae	Orbuscyclops westaustraliensis	3	
2002	PSS016	Crustacea	Copepoda	Harpacticoida	Ameiridae	Stygonitocrella trispinosa	12	
2002	PSS016	Crustacea	Copepoda	Harpacticoida	Ectinosomatidae	Pseudectinosoma galassiae	2	
2002	PSS016	Crustacea	Copepoda	Harpacticoida	Miraciidae	Schizopera roberiverensis	3	
2002	PSS016	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Nedsia sp. 'Indet'	18	Indeterminate Species
2002	PSS016	Crustacea	Malacostraca	Amphipoda	Paramelitidae	Pilbarus millsii	1	
2002	PSS016	Crustacea	Malacostraca	Bathynellacea	Parabathynellidae	Atopobathynella sp. 'A'	4	
2002	PSS016	Crustacea	Malacostraca	Isopoda	Olibrinidae	Adoniscus sp. 'indet'	13	Indeterminate Species
2002	PSS016	Crustacea	Malacostraca	Isopoda	Oniscidae	Oniscidae sp. 'indet'	6	Indeterminate Species
2002	PSS016	Crustacea	Ostracoda	Podocopida	Candonidae	Areacandona astrepte	1	
2002	PSS016	Crustacea	Ostracoda	Podocopida	Candonidae	Deminutiocandona aenigma	1	
2002	PSS016	Crustacea	Ostracoda	Podocopida	Candonidae	Humphreyscandona imperfecta	2	

Year	Site	Phylum	Class	Order	Family	Species	#	Notes
2002	PSS016	Crustacea	Ostracoda	Podocopida	Candonidae	Meridiescandona sp. '2'	1	
2002	PSS016	Crustacea	Ostracoda	Podocopida	Candonidae	Origocandona sp. '2'	1	
2002	PSS016	Crustacea	Ostracoda	Podocopida	Limnocytheridae	Gomphodella hirsuta	1	
2002	PSS016	Nematoda	-	-	-	Nematoda sp. '11'	1	
2002	PSS016	Nematoda	-	-	-	Nematoda sp. '3'	1	
2002	PSS016	Rotifera	Bdelloidea	-	-	Bdelloidea sp. 'indet'	3	Indeterminate Species
2002	PSS017	Annelida	Oligochaeta	Tubificida	Phreodrilidae	Phreodrilid sp. 'similar ventral chaetae'	2	
2002	PSS017	Crustacea	Copepoda	Calanoida	Stygoridgewayiidae	Stygoridgewayia trispinosa	3	
2002	PSS017	Crustacea	Copepoda	Cyclopoida	Cyclopidae	Diacyclops humphreysi unispinosus	3	Widespread
2002	PSS017	Crustacea	Copepoda	Cyclopoida	Cyclopidae	Halicyclops rochai	3	
2002	PSS017	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Nedsia hurlberti	1	
2002	PSS017	Crustacea	Ostracoda	Podocopida	Candonidae	Humphreyscandona fovea	2	
2002	PSS017	Crustacea	Ostracoda	Podocopida	Candonidae	Humphreyscandona pilbarae	2	
2003	PSS015	Arthropoda	Arachnida	Trombidiformes	Mideopsidae	Guineaxonopsis sp. 'S1'	1	
2003	PSS015	Crustacea	Copepoda	Calanoida	Stygoridgewayiidae	Stygoridgewayia trispinosa	29	
2003	PSS015	Crustacea	Copepoda	Cyclopoida	Cyclopidae	Halicyclops rochai	2	
2003	PSS015	Crustacea	Copepoda	Harpacticoida	Ectinosomatidae	Pseudectinosoma sp. 'indet'	1	Indeterminate Species
2003	PSS015	Crustacea	Copepoda	Harpacticoida	Miraciidae	Schizopera roberiverensis	1	
2003	PSS015	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Eriopisidae sp. '1 (PSS)'	1	Widespread
2003	PSS015	Crustacea	Malacostraca	Bathynellacea	Parabathynellidae	Atopobathynella sp. 'A'	1	
2003	PSS015	Crustacea	Ostracoda	Podocopida	Candonidae	Areacandona sp. '4'	1	
2003	PSS015	Crustacea	Ostracoda	Podocopida	Candonidae	Humphreyscandona pilbarae	1	
2003	PSS015	Crustacea	Ostracoda	Podocopida	Candonidae	Meridiescandona sp. '2'	3	
2003	PSS015	Crustacea	Ostracoda	Podocopida	Limnocytheridae	Gomphodella hirsuta	1	
2003	PSS016	Annelida	Oligochaeta	Tubificida	Phreodrilidae	Phreodrilidae sp. 'dissimilar ventral chaetae'	5	Widespread
2003	PSS016	Annelida	Oligochaeta	Tubificida	Tubificidae	Tubificidae sp. '2A'	20	
2003	PSS016	Arthropoda	Arachnida	Sarcoptiformes	-	Oribatida group 1	5	
2003	PSS016	Crustacea	Copepoda	Calanoida	Stygoridgewayiidae	Stygoridgewayia trispinosa	50	
2003	PSS016	Crustacea	Copepoda	Cyclopoida	Cyclopidae	Diacyclops humphreysi unispinosus	20	Widespread
2003	PSS016	Crustacea	Copepoda	Harpacticoida	Ectinosomatidae	Pseudectinosoma galassiae	1	
2003	PSS016	Crustacea	Copepoda	Harpacticoida	Miraciidae	Schizopera roberiverensis	4	
2003	PSS016	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Nedsia hurlberti	38	
2003	PSS016	Crustacea	Malacostraca	Isopoda	Oniscidae	Oniscidae sp. 'indet'	1	Indeterminate Species
2003	PSS016	Crustacea	Ostracoda	Podocopida	Candonidae	Areacandona astrepte	30	
2003	PSS016	Crustacea	Ostracoda	Podocopida	Candonidae	Deminutiocandona aenigma	1	
2003	PSS016	Rotifera	Bdelloidea	-	-	Bdelloidea sp. 'indet'	9	Indeterminate Species
2003	PSS072	Crustacea	Copepoda	Calanoida	Stygoridgewayiidae	Stygoridgewayia trispinosa	13	
2003	PSS072	Crustacea	Copepoda	Calanoida	Stygoridgewayiidae	Stygoridgewayia trispinosa	87	
2003	PSS072	Crustacea	Copepoda	Cyclopoida	Cyclopidae	Diacyclops humphreysi unispinosus	19	Widespread
2003	PSS072	Crustacea	Copepoda	Cyclopoida	Cyclopidae	Halicyclops rochai	13	

Year	Site	Phylum	Class	Order	Family	Species	#	Notes
2003	PSS072	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Orbuscyclops westaustraliensis</i>	2	
2003	PSS072	Crustacea	Copepoda	Harpacticoida	Ameiridae	<i>Stygonitocrella trispinosa</i>	9	
2003	PSS072	Crustacea	Copepoda	Harpacticoida	Ectinosomatidae	<i>Pseudectinosoma galassiae</i>	1	
2003	PSS072	Crustacea	Copepoda	Harpacticoida	Miraciidae	<i>Schizopera</i> sp. 'indet'	3	Indeterminate Species
2003	PSS072	Crustacea	Malacostraca	Amphipoda	Bogidiellidae	<i>Bogidiellidae</i> sp. '1'	2	
2003	PSS072	Crustacea	Malacostraca	Amphipoda	Eriopisidae	<i>Nedsia</i> sp. 'Indet'	10	Indeterminate Species
2003	PSS072	Crustacea	Malacostraca	Amphipoda	Eriopisidae	<i>Nedsia</i> sp. 'Indet'	19	Indeterminate Species
2003	PSS072	Crustacea	Malacostraca	Thermosbaenacea	Thermosbaenacidae	<i>Halosbaena tulki</i>	1	
2003	PSS072	Crustacea	Malacostraca	Thermosbaenacea	Thermosbaenacidae	<i>Halosbaena tulki</i>	15	
2003	PSS072	Crustacea	Ostracoda	Podocopida	Candonidae	<i>Humphreyscandona imperfecta</i>	6	
2003	PSS072	Crustacea	Ostracoda	Podocopida	Candonidae	<i>Humphreyscandona woutersi</i>	2	
2003	PSS072	Crustacea	Ostracoda	Podocopida	Candonidae	<i>Meridiescandona</i> sp. '2'	1	
2003	PSS072	Crustacea	Ostracoda	Podocopida	Candonidae	<i>Meridiescandona</i> sp. '2'	20	
2003	PSS072	Crustacea	Ostracoda	Podocopida	Candonidae	<i>Pilbaracandona rosa</i>	2	
2003	PSS073	Crustacea	Copepoda	Calanoida	Stygoridgewayiidae	<i>Stygoridgewayia trispinosa</i>	90	
2003	PSS073	Crustacea	Copepoda	Calanoida	Stygoridgewayiidae	<i>Stygoridgewayia trispinosa</i>	55	
2003	PSS073	Crustacea	Malacostraca	Amphipoda	Bogidiellidae	<i>Bogidiellidae</i> sp. '1'	1	
2003	PSS073	Crustacea	Malacostraca	Amphipoda	Eriopisidae	<i>Eriopisidae</i> sp. 'indet'	1	Indeterminate Species
2003	PSS073	Crustacea	Malacostraca	Amphipoda	Eriopisidae	<i>Nedsia hurlberti</i>	23	
2003	PSS073	Crustacea	Malacostraca	Amphipoda	Paramelitidae	<i>Paramelitidae</i> sp. 'indet'	3	Indeterminate Species
2003	PSS073	Crustacea	Malacostraca	Thermosbaenacea	Halosbaenidae	<i>Halosbaena tulki</i>	2	
2003	PSS073	Crustacea	Ostracoda	Podocopida	Candonidae	<i>Areacandona scanloni</i>	1	Widespread
2003	PSS073	Crustacea	Ostracoda	Podocopida	Candonidae	<i>Humphreyscandona woutersi</i>	6	
2003	PSS073	Crustacea	Ostracoda	Podocopida	Candonidae	<i>Humphreyscandona woutersi</i>	20	
2003	PSS073	Crustacea	Ostracoda	Podocopida	Candonidae	<i>Pilbaracandona rosa</i>	1	
2003	PSS073	Crustacea	Ostracoda	Podocopida	Candonidae	<i>Pilbaracandona rosa</i>	1	
2003	PSS074	Crustacea	Copepoda	Calanoida	Stygoridgewayiidae	<i>Stygoridgewayia trispinosa</i>	5	
2003	PSS074	Crustacea	Copepoda	Calanoida	Stygoridgewayiidae	<i>Stygoridgewayia trispinosa</i>	93	
2003	PSS074	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Halicyclops rochai</i>	4	
2003	PSS074	Crustacea	Copepoda	Harpacticoida	Canthocamptidae	<i>Elaphoidella humphreysi</i>	2	
2003	PSS074	Crustacea	Malacostraca	Amphipoda	Bogidiellidae	<i>Bogidiellidae</i> sp. '1'	3	
2003	PSS074	Crustacea	Malacostraca	Amphipoda	Bogidiellidae	<i>Bogidiellidae</i> sp. '1'	3	
2003	PSS074	Crustacea	Malacostraca	Amphipoda	Eriopisidae	<i>Nedsia</i> sp. 'Indet'	1	Indeterminate Species
2003	PSS074	Crustacea	Malacostraca	Amphipoda	Eriopisidae	<i>Nedsia</i> sp. 'Indet'	4	Indeterminate Species
2003	PSS074	Crustacea	Malacostraca	Bathynellacea	Parabathynellidae	<i>Brevisomabathynella</i> sp. 'indet'	1	Indeterminate Species
2003	PSS074	Crustacea	Malacostraca	Thermosbaenacea	Halosbaenidae	<i>Halosbaena tulki</i>	1	
2003	PSS074	Crustacea	Ostracoda	Podocopida	Candonidae	<i>Humphreyscandona woutersi</i>	108	
2003	PSS074	Crustacea	Ostracoda	Podocopida	Candonidae	<i>Humphreyscandona woutersi</i>	3	
2003	PSS074	Crustacea	Ostracoda	Podocopida	Candonidae	<i>Meridiescandona</i> sp. '2'	5	
2003	PSS074	Crustacea	Ostracoda	Podocopida	Candonidae	<i>Meridiescandona</i> sp. '2'	3	
2003	PSS074	Crustacea	Ostracoda	Podocopida	Limnocytheridae	<i>Gomphodella</i> sp. 'indet'	2	Indeterminate Species

Year	Site	Phylum	Class	Order	Family	Species	#	Notes
2003	PSS074	Crustacea	Ostracoda		-	Ostracoda sp. 'indet'	107	Indeterminate Species
2003	PSS075	Crustacea	Copepoda	Calanoida	Stygoridgewayiidae	Stygoridgewayia trispinosa	5	
2003	PSS075	Crustacea	Copepoda	Calanoida	Stygoridgewayiidae	Stygoridgewayia trispinosa	4	
2003	PSS075	Crustacea	Copepoda	Harpacticoida	Canthocamptidae	Elaphoidella humphreysi	1	
2003	PSS075	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Eriopisidae sp. '1 (PSS)'	2	Widespread
2003	PSS075	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Eriopisidae sp. 'indet'	1	Indeterminate Species
2003	PSS075	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Nedsia sp. 'Indet'	2	Indeterminate Species
2003	PSS075	Crustacea	Malacostraca	Amphipoda	Paramelitidae	Paramelitidae sp. 'indet'	1	Indeterminate Species
2003	PSS075	Crustacea	Malacostraca	Isopoda	Cirolanidae	Haptolana yarraloola	1	
2003	PSS075	Crustacea	Ostracoda	Podocopida	Candonidae	Humphreyscandona imperfecta	2	
2003	PSS075	Crustacea	Ostracoda	Podocopida	Candonidae	Humphreyscandona woutersi	17	
2003	PSS075	Crustacea	Ostracoda	Podocopida	Candonidae	Humphreyscandona woutersi	9	
2003	PSS075	Crustacea	Ostracoda	Podocopida	Candonidae	Pilbaracandona rosa	2	
2003	PSS075	Crustacea	Ostracoda	Podocopida	Limnocytheridae	Gomphodella sp. 'indet'	3	Indeterminate Species
2003	PSS088	Annelida	Oligochaeta	Tubificida	Phreodrilidae	Phreodrilidae sp. 'dissimilar ventral chaetae'	3	Widespread
2003	PSS088	Crustacea	Copepoda	Calanoida	Stygoridgewayiidae	Stygoridgewayia trispinosa	1	
2003	PSS088	Crustacea	Copepoda	Cyclopoida	Cyclopidae	Diacyclops humphreysi unispinosus	7	Widespread
2003	PSS088	Crustacea	Copepoda	Cyclopoida	Cyclopidae	Halicyclops rochai	11	
2003	PSS088	Crustacea	Copepoda	Harpacticoida	Ameiridae	Stygonitocrella unispinosa	4	Widespread
2003	PSS088	Crustacea	Copepoda	Harpacticoida	Parastenocarididae	Parastenocaris jane	1	
2003	PSS088	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Nedsia sp. '24'	7	
2003	PSS088	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Nedsia sp. '24'	16	
2003	PSS088	Crustacea	Ostracoda	Podocopida	Candonidae	Areacandona triangulum	9	
2003	PSS088	Crustacea	Ostracoda	Podocopida	Candonidae	Areacandona triangulum	1	
2003	PSS088	Crustacea	Ostracoda	Podocopida	Candonidae	Deminutiocandona atope	6	
2003	PSS088	Crustacea	Ostracoda	Podocopida	Candonidae	Deminutiocandona atope	4	
2003	PSS088	Crustacea	Ostracoda	Podocopida	Candonidae	Humphreyscandona woutersi	2	
2003	PSS088	Crustacea	Ostracoda	Podocopida	Candonidae	Pilbaracandona rosa	1	
2003	PSS088	Crustacea	Ostracoda	Podocopida	Candonidae	Pilbaracandona rosa	2	
2003	PSS089*	Arthropoda	Arachnida	Sarcoptiformes	-	Oribatida group 1	1	
2003	PSS089*	Crustacea	Copepoda	Calanoida	Stygoridgewayiidae	Stygoridgewayia trispinosa	23	
2003	PSS089*	Crustacea	Copepoda	Calanoida	Stygoridgewayiidae	Stygoridgewayia trispinosa	50	
2003	PSS089*	Crustacea	Copepoda	Cyclopoida	Cyclopidae	Diacyclops humphreysi humphreysi	5	
2003	PSS089*	Crustacea	Copepoda	Cyclopoida	Cyclopidae	Diacyclops humphreysi unispinosus	19	Widespread
2003	PSS089*	Crustacea	Copepoda	Cyclopoida	Cyclopidae	Halicyclops rochai	2	
2003	PSS089*	Crustacea	Copepoda	Harpacticoida	Ameiridae	Stygonitocrella trispinosa	4	
2003	PSS089*	Crustacea	Copepoda	Harpacticoida	Canthocamptidae	Elaphoidella humphreysi	3	
2003	PSS089*	Crustacea	Copepoda	Harpacticoida	Miraciidae	Schizopera roberiverensis	7	
2003	PSS089*	Crustacea	Malacostraca	Amphipoda	Bogidiellidae	Bogidiellidae sp. '1'	5	
2003	PSS089*	Crustacea	Malacostraca	Amphipoda	Bogidiellidae	Bogidiellidae sp. '1'	4	
2003	PSS089*	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Nedsia hurlberti	3	

Year	Site	Phylum	Class	Order	Family	Species	#	Notes
2003	PSS089*	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Nedsia sp. 'Indet'	5	Indeterminate Species
2003	PSS089*	Crustacea	Malacostraca	Amphipoda	Paramelitidae	Paramelitidae sp. '2'	4	
2003	PSS089*	Crustacea	Malacostraca	Amphipoda	Paramelitidae	Pilbarus millsi	10	
2003	PSS089*	Crustacea	Malacostraca	Isopoda	Cirolanidae	Haptolana yarraloola	2	
2003	PSS089*	Crustacea	Malacostraca	Isopoda	Cirolanidae	Haptolana yarraloola	3	
2003	PSS089*	Crustacea	Malacostraca	Isopoda	Cirolanidae	Kagalana tonde	2	
2003	PSS089*	Crustacea	Malacostraca	Thermosbaenacea	Halosbaenidae	Halosbaena tulki	20	
2003	PSS089*	Crustacea	Malacostraca	Thermosbaenacea	Halosbaenidae	Halosbaena tulki	12	
2003	PSS089*	Crustacea	Ostracoda	Podocopida	Candonidae	Humphreyscandona woutersi	4	
2003	PSS089*	Crustacea	Ostracoda	Podocopida	Candonidae	Humphreyscandona woutersi	8	
2003	PSS089*	Crustacea	Ostracoda	Podocopida	Candonidae	Meridescandona sp. '2'	2	
2003	PSS089*	Mollusca	Gastropoda	Sorbeoconcha	Hydrobiidae	Hydrobiidae sp. 'indet'	9	Indeterminate Species
2003	PSS089*	Nematoda	-	-	-	Nematoda sp. 'indet'	2	Indeterminate Species
2003	PSS155	Annelida	Oligochaeta	Tubificida	Phreodrilidae	Phreodrilid sp. 'similar ventral chaetae'	5	
2003	PSS155	Crustacea	Copepoda	Calanoida	Stygoridgewayiidae	Stygoridgewayia trispinosa	4	
2003	PSS155	Crustacea	Copepoda	Cyclopoida	Cyclopidae	Diacyclops cockingi	33	
2003	PSS157	Crustacea	Copepoda	Harpacticoida	Canthocamptidae	Elaphoidella humphreysi	4	
2003	PSS158	Crustacea	Copepoda	Calanoida	Stygoridgewayiidae	Stygoridgewayia trispinosa	6	
2003	PSS158	Crustacea	Copepoda	Cyclopoida	Cyclopidae	Diacyclops sobeprolatus	8	Widespread
2003	PSS158	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Nedsia sp. 'Indet'	8	Indeterminate Species
2003	PSS158	Crustacea	Ostracoda	Podocopida	Candonidae	Humphreyscandona waldockae	1	
2003	PSS159	Crustacea	Copepoda	Calanoida	Stygoridgewayiidae	Stygoridgewayia trispinosa	1	
2003	PSS159	Crustacea	Copepoda	Cyclopoida	Cyclopidae	Diacyclops humphreysi unispinosus	1	Widespread
2003	PSS159	Crustacea	Ostracoda	Podocopida	Candonidae	Areacandona triangulum	2	
2003	PSS160	Annelida	Oligochaeta	Tubificida	Tubificidae	Tubificidae sp. '3'	5	
2003	PSS160	Crustacea	Copepoda	Calanoida	Stygoridgewayiidae	Stygoridgewayia trispinosa	35	
2003	PSS160	Crustacea	Copepoda	Cyclopoida	Cyclopidae	Halicyclops (Rochacyclops) sp. 'calm'	3	
2003	PSS160	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Nedsia sp. 'Indet'	18	Indeterminate Species
2003	PSS160	Crustacea	Ostracoda	Podocopida	Candonidae	Areacandona triangulum	4	
2003	PSS160	Crustacea	Ostracoda	Podocopida	Candonidae	Humphreyscandona fovea	3	
2003	PSS160	Crustacea	Ostracoda	Podocopida	Candonidae	Humphreyscandona waldockae	1	
2003	PSS160	Crustacea	Ostracoda	Podocopida	Candonidae	Pilbaracandona rosa	10	
2003	PSS161	Annelida	Oligochaeta	Tubificida	Tubificidae	Tubificidae sp. '2A'	4	
2003	PSS161	Aphanoneura	Polychaeta	Aphaneura	Aeolosomatidae	Aeolosoma sp. '1'	2	
2003	PSS161	Crustacea	Copepoda	Calanoida	Stygoridgewayiidae	Stygoridgewayia trispinosa	69	
2003	PSS161	Crustacea	Copepoda	Calanoida	Stygoridgewayiidae	Stygoridgewayia trispinosa	50	
2003	PSS161	Crustacea	Copepoda	Cyclopoida	Cyclopidae	Halicyclops rochai	3	
2003	PSS161	Crustacea	Copepoda	Cyclopoida	Cyclopidae	Halicyclops rochai	5	
2003	PSS161	Crustacea	Copepoda	Harpacticoida	Canthocamptidae	Elaphoidella humphreysi	1	

Year	Site	Phylum	Class	Order	Family	Species	#	Notes
2003	PSS161	Crustacea	Copepoda	Harpacticoida	Canthocamptidae	<i>Elaphoidella humphreysi</i>	1	
2003	PSS161	Crustacea	Malacostraca	Amphipoda	Eriopisidae	<i>Nedsia</i> sp. 'Indet'	4	Indeterminate Species
2003	PSS161	Crustacea	Malacostraca	Amphipoda	Eriopisidae	<i>Nedsia</i> sp. 'Indet'	3	Indeterminate Species
2003	PSS161	Crustacea	Malacostraca	Thermosbaenacea	Halosbaenidae	<i>Halosbaena tulki</i>	33	
2003	PSS161	Crustacea	Malacostraca	Thermosbaenacea	Halosbaenidae	<i>Halosbaena tulki</i>	19	
2003	PSS161	Crustacea	Ostracoda	Podocopida	Candonidae	<i>Humphreyscandona woutersi</i>	6	
2003	PSS161	Crustacea	Ostracoda	Podocopida	Candonidae	<i>Humphreyscandona woutersi</i>	3	
2003	PSS161	Crustacea	Ostracoda	Podocopida	Candonidae	<i>Pilbaracandona temporaria</i>	2	
2003	PSS161	Crustacea	Ostracoda	Podocopida	Candonidae	<i>Pilbaracandona temporaria</i>	3	
2003	PSS161	Crustacea	Ostracoda	Podocopida	Cyprididae	<i>Cyprætta seurati</i>	20	Widespread
2003	PSS161	Rotifera	Bdelloidea	-	-	<i>Bdelloidea</i> sp. 'indet'	2	Indeterminate Species
2003	PSS161	Rotifera	Bdelloidea	-	-	<i>Bdelloidea</i> sp. 'indet'	1	Indeterminate Species
2003	PSS161	Rotifera	Bdelloidea	Philodinida	Philodinidae	<i>Dissotrocha</i> sp. 'indet'	1	Indeterminate Species
2003	PSS161	Rotifera	Bdelloidea	Philodinida	Philodinidae	<i>Dissotrocha</i> sp. 'indet'	11	Indeterminate Species
2003	PSS163	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Metacyclops pilbaricus</i>	35	Widespread
2003	PSS163	Crustacea	Malacostraca	Amphipoda	Eriopisidae	<i>Nedsia</i> sp. 'Indet'	239	Indeterminate Species
2003	PSS163	Crustacea	Malacostraca	Bathynellacea	Bathynellidae	<i>Bathynella</i> sp. 2	1	Widespread
2003	PSS164	Crustacea	Ostracoda	Podocopida	Cyprididae	<i>Cyprætta</i> sp. '4'	1	Potential SRE species
2003	PSS201*	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Halicyclops rochai</i>	1	
2003	PSS201*	Crustacea	Malacostraca	Amphipoda	Bogidiellidae	<i>Bogidiellidae</i> sp. '1'	2	
2003	PSS201*	Crustacea	Malacostraca	Amphipoda	Eriopisidae	<i>Nedsia</i> sp. '24'	1	
2003	PSS201*	Crustacea	Malacostraca	Amphipoda	Paramelitidae	<i>Paramelitidae</i> sp. '2'	1	
2003	PSS201*	Crustacea	Malacostraca	Thermosbaenacea	Halosbaenidae	<i>Halosbaena tulki</i>	2	
2003	PSS201*	Crustacea	Malacostraca	Thermosbaenacea	Halosbaenidae	<i>Halosbaena tulki</i>	4	
2003	PSS201*	Crustacea	Ostracoda	Podocopida	Candonidae	<i>Humphreyscandona woutersi</i>	2	
2003	PSS201*	Crustacea	Ostracoda	Podocopida	Candonidae	<i>Humphreyscandona woutersi</i>	1	
2003	PSS201^	Crustacea	Ostracoda		-	<i>Ostracoda</i> sp. 'indet'	1	Indeterminate Species
2003	PSS201*	Mollusca	Gastropoda	Basommatophora	Planorbidae	<i>Planorbidae</i> sp. 'indet'	1	Indeterminate Species
2003	PSS201*	Mollusca	Gastropoda	Basommatophora	Planorbidae	<i>Planorbidae</i> sp. 'indet'	1	Indeterminate Species
2004	PSS017	Aphanoneura	Polychaeta	Aphaneura	Aeolosomatidae	<i>Aeolosoma</i> sp. '3'	3	
2004	PSS017	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Diacyclops einslei</i>	10	
2004	PSS017	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Microcyclops varicans</i>	10	Widespread
2004	PSS017	Crustacea	Malacostraca	Amphipoda	Paramelitidae	<i>Paramelitidae</i> sp. 'indet'	1	Indeterminate Species
2004	PSS017	Crustacea	Ostracoda	Podocopida	Candonidae	<i>Humphreyscandona fovea</i>	8	
2004	PSS017	Crustacea	Ostracoda	Podocopida	Candonidae	<i>Humphreyscandona woutersi</i>	17	
2004	PSS155	Annelida	Oligochaeta	Tubificida	Phreodrilidae	<i>Phreodrilid</i> sp. 'similar ventral chaetae'	1	
2004	PSS158	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Diacyclops sobeprolatus</i>	4	Widespread
2004	PSS158	Crustacea	Ostracoda	Podocopida	Candonidae	<i>Areacandona triangulum</i>	5	
2004	PSS158	Crustacea	Ostracoda	Podocopida	Candonidae	<i>Humphreyscandona capillus</i>	5	
2004	PSS159	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Diacyclops humphreysi unispinosus</i>	7	Widespread
2004	PSS159	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Halicyclops (Rochacyclops) sp.</i>	7	

Year	Site	Phylum	Class	Order	Family	Species	#	Notes
						'calm'		
2004	PSS159	Crustacea	Malacostraca	Amphipoda	Paramelitidae	<i>Pilbarus millsi</i>	1	
2004	PSS159	Crustacea	Ostracoda	Podocopida	Candonidae	<i>Areacandona triangulum</i>	2	
2004	PSS160	Annelida	Oligochaeta	Tubificida	Tubificidae	<i>Tubificidae sp. '3'</i>	17	
2004	PSS160	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Halicyclops (Rochacyclops) sp.</i> 'calm'	1	
2004	PSS160	Crustacea	Malacostraca	Amphipoda	Eriopisidae	<i>Nedsia hurlberti</i>	5	
2004	PSS160	Crustacea	Malacostraca	Amphipoda	Eriopisidae	<i>Nedsia sculptilis</i>	1	
2004	PSS160	Crustacea	Ostracoda	Podocopida	Candonidae	<i>Areacandona lepte</i>	4	
2004	PSS160	Crustacea	Ostracoda	Podocopida	Candonidae	<i>Humphreyscandona sp. 2</i>	2	
2004	PSS163	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Diacyclops sobeprolatus</i>	2	Widespread
2004	PSS163	Crustacea	Malacostraca	Amphipoda	Eriopisidae	<i>Eriopisidae sp. '1' (PSS)</i>	1	Widespread
2004	PSS163	Crustacea	Malacostraca	Amphipoda	Eriopisidae	<i>Nedsia sp. 'Indet'</i>	1	Indeterminate Species
2004	PSS164	Annelida	Oligochaeta	Tubificida	Phreodrilidae	<i>Phreodrilidae sp. 'dissimilar ventral chaetae'</i>	2	Widespread
2004	PSS164	Annelida	Oligochaeta	Tubificida	Phreodrilidae	<i>Phreodrilus n. sp. 'WA32'</i>	1	Potential SRE species
2004	PSS164	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Diacyclops sobeprolatus</i>	1	Widespread
2004	PSS164	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Microcyclops varicans</i>	1	Widespread
2004	PSS164	Crustacea	Copepoda	Harpacticoida	Ameiridae	<i>Parapseudoleptomesochra tureei</i>	12	Widespread
2004	PSS164	Crustacea	Copepoda	Harpacticoida	Ameiridae	<i>Stygonitocrella unispinosa</i>	12	Widespread
2004	PSS164	Crustacea	Ostracoda	Podocopida	Candonidae	<i>Areacandona scanloni</i>	5	Widespread
2004	PSS164	Crustacea	Ostracoda	Podocopida	Cyprididae	<i>Cypretta seurati</i>	1	Widespread
2004	PSS375	Annelida	Oligochaeta	Tubificida	Phreodrilidae	<i>Phreodrilidae sp. 'indet'</i>	69	Indeterminate Species
2004	PSS375	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Diacyclops humphreysi humphreysi</i>	1	
2004	PSS375	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Diacyclops sobeprolatus</i>	4	Widespread
2004	PSS375	Crustacea	Copepoda	Harpacticoida	Parastenocarididae	<i>Parastenocaris sp. 'indet'</i>	2	Indeterminate Species
2004	PSS375	Crustacea	Malacostraca	Amphipoda	Paramelitidae	<i>Pilbarus millsi</i>	11	
2004	PSS375	Crustacea	Ostracoda	Podocopida	Candonidae	<i>Humphreyscandona akaina</i>	91	
2005	Ashley Well	Crustacea	Copepoda	Calanoida	Centropagidae	<i>Gladioferens sp. 'indet'</i>	1	Indeterminate Species
2005	BC019	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Diacyclops humphreysi humphreysi</i>	11	
2005	BC429	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Diacyclops sp. 'indet'</i>	3	Indeterminate Species
2005	BF 2-1	Crustacea	Copepoda	Cyclopoida	-	<i>Cyclopoida sp. 'indet'</i>	2	Indeterminate Species
2005	BF 2-1	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Thermocyclops decipiens</i>	10	
2005	BHP Town Bore	Crustacea	Copepoda	Calanoida	-	<i>Calanoida sp. 'indet'</i>	14	Indeterminate Species
2005	BHP Town Bore	Crustacea	Malacostraca	Amphipoda	-	<i>Amphipoda sp. 'indet'</i>	3	Indeterminate Species
2005	BHP Town Bore	Crustacea	Malacostraca	Thermosbaenacea	Halosbaenidae	<i>Halosbaena tulki</i>	10	
2005	BUNDD0731	Crustacea	Copepoda	Cyclopoida	-	<i>Cyclopoida sp. 'indet'</i>	18	Indeterminate Species
2005	BUNDD0731	Crustacea	Malacostraca	Amphipoda	-	<i>Amphipoda sp. 'indet'</i>	8	Indeterminate Species
2005	BUNMD0887	Crustacea	Copepoda	Cyclopoida	-	<i>Cyclopoida sp. 'indet'</i>	8	Indeterminate Species

Year	Site	Phylum	Class	Order	Family	Species	#	Notes
2005	BUNMD0887	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Halicyclops rochai</i>	1	
2005	BUNMD0887	Crustacea	Malacostraca	Bathynellacea	-	<i>Bathynellacea</i> sp. 'indet'	1	Indeterminate Species
2005	BUNW00766	Crustacea	Malacostraca	Amphipoda	-	Amphipoda sp. 'indet'	1	Indeterminate Species
2005	Macks Bore	Crustacea	Copepoda	Calanoida	-	Calanoida sp. 'indet'	3	Indeterminate Species
2005	MEARC3167	Annelida	Oligochaeta	-	-	<i>Oligochaeta</i> sp. 'indet'	20	Indeterminate Species
2005	Nr Five Mile Well	Crustacea	Copepoda	Cyclopoida	-	Cyclopoida sp. 'indet'	1	Indeterminate Species
2005	Nr Five Mile Well	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Paracyclops chiltoni</i>	2	
2005	Nr Five Mile Well	Crustacea	Malacostraca	Amphipoda	Eriopisidae	<i>Nedsia</i> sp. 'AMM001/029/030'	6	
2005	Nr Five Mile Well	Crustacea	Malacostraca	Thermosbaenacea	Halosbaenidae	<i>Halosbaena tulki</i>	3	
2005	Perseverance Well	Crustacea	Malacostraca	Amphipoda	-	Amphipoda sp. 'indet'	4	Indeterminate Species
2005	PSS375	Aphanoneura	Polychaeta	Aphaneura	Aeolosomatidae	<i>Aeolosoma</i> sp. '1'	7	
2005	PSS375	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Diacyclops humphreysi humphreysi</i>	5	
2005	PSS375	Crustacea	Malacostraca	Amphipoda	Paramelitidae	<i>Pilbarus millsi</i>	26	
2005	PSS375	Crustacea	Ostracoda	Podocopida	Candonidae	<i>Humphreyscandona akaina</i>	22	
2005	Robe River 16A	Annelida	Oligochaeta	-	-	<i>Oligochaeta</i> sp. 'indet'	1	Indeterminate Species
2005	Robe River 16A	Crustacea	Malacostraca	Amphipoda	-	Amphipoda sp. 'indet'	37	Indeterminate Species
2005	Robe River 3A	Crustacea	Copepoda	Calanoida	-	Calanoida sp. 'indet'	47	Indeterminate Species
2005	Robe River 3A	Crustacea	Malacostraca	Amphipoda	Eriopisidae	<i>Nedsia</i> sp. 'AMM001/029/030'	6	
2005	Robe River 3A	Crustacea	Malacostraca	Thermosbaenacea	Halosbaenidae	<i>Halosbaena tulki</i>	14	
2005	Robe River 4	Crustacea	Malacostraca	Amphipoda	-	Amphipoda sp. 'indet'	20	Indeterminate Species
2005	Robe River 4A	Crustacea	Copepoda	Calanoida	-	Calanoida sp. 'indet'	30	Indeterminate Species
2005	Robe River 4A	Crustacea	Malacostraca	Amphipoda	-	Amphipoda sp. 'indet'	8	Indeterminate Species
2005	Robe River 4P	Crustacea	Copepoda	Calanoida	-	Calanoida sp. 'indet'	7	Indeterminate Species
2005	Robe River 4P	Crustacea	Malacostraca	Amphipoda	-	Amphipoda sp. 'indet'	3	Indeterminate Species
2005	Robe River 4P	Crustacea	Ostracoda	-	-	<i>Ostracoda</i> sp. 'indet'	13	Indeterminate Species
2005	Robe River 6A	Crustacea	Malacostraca	Amphipoda	-	Amphipoda sp. 'indet'	1	Indeterminate Species
2005	Robe River Coastal Plain 1A	Crustacea	Copepoda	Calanoida	-	Calanoida sp. 'indet'	26	Indeterminate Species
2005	Robe River Coastal Plain 1A	Crustacea	Malacostraca	Thermosbaenacea	Halosbaenidae	<i>Halosbaena tulki</i>	4	
2005	Robe River Coastal Plain 4	Crustacea	Copepoda	Calanoida	-	Calanoida sp. 'indet'	32	Indeterminate Species

Year	Site	Phylum	Class	Order	Family	Species	#	Notes
2005	Sheryl Bore 13Y	Crustacea	Copepoda	Calanoida	-	Calanoida sp. 'indet'	2	Indeterminate Species
2005	Sheryl Bore 13Y	Crustacea	Malacostraca	Amphipoda	-	Amphipoda sp. 'indet'	1	Indeterminate Species
2005	Varanus Well	Crustacea	Malacostraca	Amphipoda	-	Amphipoda sp. 'indet'	1	Indeterminate Species
2005	Wongoo Bore	Crustacea	Malacostraca	Amphipoda	-	Amphipoda sp. 'indet'	1	Indeterminate Species
2005	Woolshed Wel	Crustacea	Copepoda	Calanoida	-	Calanoida sp. 'indet'	2	Indeterminate Species
2005	Woolshed Well	Crustacea	Malacostraca	Thermosbaenacea	Halosbaenidae	Halosbaena tulki	2	
2007	BC210	Crustacea	Copepoda	Cyclopoida	Cyclopidae	Microcycllops varicans	29	Widespread
2007	BC225	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Nedsia sculptilis group	1	
2007	BC225	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Nedsia sculptilis group	1	
2007	BC228	Crustacea	Copepoda	Cyclopoida	Cyclopidae	Diacyclops humphreysi	7	
2007	BC228	Crustacea	Copepoda	Cyclopoida	Cyclopidae	Diacyclops humphreysi humphreysi	7	
2007	BC434	Crustacea	Copepoda	Cyclopoida	Cyclopidae	Diacyclops humphreysi	12	
2007	BC434	Crustacea	Copepoda	Cyclopoida	Cyclopidae	Diacyclops humphreysi humphreysi	12	
2007	BC434	Crustacea	Copepoda	Cyclopoida	Cyclopidae	Diacyclops sobeprolatus	10	Widespread
2007	BUNMD1227	Arthropoda	Arachnida	Trombidiformes	Mideopsidae	Tiramideopsis sp. 'indet'	1	Indeterminate Species
2007	BUNMD1227	Arthropoda	Arachnida	Trombidiformes	Mideopsidae	Tiramideopsis sp. 'indet'	1	Indeterminate Species
2007	BUNMD1227	Crustacea	Copepoda	Cyclopoida	Cyclopidae	Diacyclops humphreysi	5	
2007	BUNMD1227	Crustacea	Copepoda	Cyclopoida	Cyclopidae	Diacyclops humphreysi humphreysi	5	
2007	BUNMD1227	Crustacea	Copepoda	Cyclopoida	Cyclopidae	Diacyclops sobeprolatus	5	Widespread
2008	BC186	Arthropoda	Arachnida	Sarcoptiformes	-	Sarcoptiformes group 1 (PSW)	3	
2008	BC186	Crustacea	Copepoda	Calanoida	Ridgewayiidae	Stygoridgewayia trispinosa	16	
2008	BC186	Crustacea	Copepoda	Calanoida	Ridgewayiidae	Stygoridgewayia westralienensis	5	
2008	BC186	Crustacea	Copepoda	Cyclopoida	Cyclopidae	Halicyclops rochai	4	
2008	BC186	Crustacea	Copepoda	Cyclopoida	Cyclopidae	Halicyclops rochai	2	
2008	BC186	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Nedsia sp. 'indet'	4	Indeterminate Species
2008	BC186	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Nedsia sp. 'indet'	3	Indeterminate Species
2008	BC186	Crustacea	Malacostraca	Amphipoda	Paramelitidae	Paramelitidae sp. '2 (DEC)'	1	
2008	BC186	Crustacea	Malacostraca	Thermosbaenacea	Halosbaenidae	Halosbaena tulki	1	
2008	BC186	Crustacea	Malacostraca	Thermosbaenacea	Halosbaenidae	Halosbaena tulki	5	
2008	BC186	Platyhelminthes	Turbellaria	-	-	Turbellaria sp. 'indet'	1	Indeterminate Species
2008	BC194	Crustacea	Copepoda	Cyclopoida	Cyclopidae	Thermocyclops aberrans	4	
2008	BC210	Annelida	Oligochaeta	Tubificida	Naididae	Pristina aequiseta	1	
2008	BC210	Crustacea	Copepoda	Cyclopoida	Cyclopidae	Mesocyclops darwini	27	
2008	BC210	Crustacea	Copepoda	Cyclopoida	Cyclopidae	Microcycllops varicans	13	Widespread
2008	BC210	Crustacea	Copepoda	Cyclopoida	Cyclopidae	Microcycllops varicans	1	Widespread
2008	BC210	Crustacea	Ostracoda	Podocopida	Cyprididae	Plesiocypridopsis sp. 'indet'	3	Indeterminate Species
2008	BC225	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Nedsia sculptilis group	2	
2008	BC225	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Nedsia sp. 'indet'	1	Indeterminate Species
2008	BC225	Crustacea	Malacostraca	Thermosbaenacea	Halosbaenidae	Halosbaena tulki	1	

Year	Site	Phylum	Class	Order	Family	Species	#	Notes
2008	BC228	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Metacyclops pilbaricus</i>	1	Widespread
2008	BC282	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Thermocyclops aberrans</i>	16	
2008	BC282	Crustacea	Malacostraca	Amphipoda	Eriopisidae	<i>Nedsia</i> sp. 'indet'	1	Indeterminate Species
2008	BC282	Crustacea	Ostracoda	Podocopida	Cyprididae	<i>Plesiocypridopsis</i> sp. 'indet'	5	Indeterminate Species
2008	BC406	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Diacyclops humphreysi humphreysi</i>	2	
2008	BC406	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Halicyclops rochai</i>	2	
2008	BC434	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Diacyclops humphreysi humphreysi</i>	19	
2008	BUNDD1687	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Diacyclops humphreysi humphreysi</i>	1	
2008	BUNDD1687	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Thermocyclops aberrans</i>	9	
2008	BUNDD1687	Crustacea	Malacostraca	Amphipoda	Eriopisidae	<i>Nedsia sculptilis</i> group	1	
2008	BUNDD1687	Crustacea	Malacostraca	Amphipoda	Eriopisidae	<i>Nedsia</i> sp. 'indet'	1	Indeterminate Species
2008	BUNWB13	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Metacyclops pilbaricus</i>	2	Widespread
2008	BUNWB13	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Metacyclops pilbaricus</i>	1	Widespread
2008	BUNWB13	Crustacea	Malacostraca	Amphipoda	Eriopisidae	<i>Nedsia sculptilis</i> group	2	
2008	BUNWB13	Crustacea	Malacostraca	Bathynellacea	Parabathynellidae	<i>Notobathynella</i> sp. 'indet'	2	Indeterminate Species
2008	BUNWB13	Mollusca	Gastropoda	Sorbeoconcha	Hydrobiidae	<i>Hydrobiidae</i> sp. '1'	60	
2008	BUNWB13	Mollusca	Gastropoda	Sorbeoconcha	Hydrobiidae	<i>Hydrobiidae</i> sp. '1'	50	
2008	BUNWO0773	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Diacyclops humphreysi humphreysi</i>	5	
2008	BUNWO0773	Crustacea	Malacostraca	Amphipoda	Eriopisidae	<i>Nedsia sculptilis</i> group	5	
2008	BUNWO0773	Crustacea	Ostracoda	Podocopida	Candonidae	<i>Areacandonia triangulum</i>	1	
2008	Hyporheic 03	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Microcyclops varicans</i>	2	Widespread
2008	Hyporheic 03	Platyhelminthes	Turbellaria	-	-	<i>Turbellaria</i> sp. 'indet'	1	Indeterminate Species
2008	Hyporheic 04	Arthropoda	Arachnida	Sarcoptiformes	-	<i>Sarcoptiformes</i> group 1 (PSW)	1	
2008	Hyporheic 04	Nematoda	-	-	-	<i>Nematoda</i> sp. 'indet'	2	Indeterminate Species
2008	JIMDR094	Crustacea	Copepoda	Calanoida	Ridgewayiidae	<i>Stygoridgewayia trispinosa</i>	4	
2008	JIMDR094	Crustacea	Malacostraca	Amphipoda	Eriopisidae	<i>Nedsia sculptilis</i> group	8	
2008	Un-named04	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Mesocyclops darwini</i>	1	
2009	BC1473	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Diacyclops humphreysi humphreysi</i>	200	
2009	BC1473	Crustacea	Copepoda	Harpacticoida	Ameridae	<i>Lucionitocrella yalleenensis</i>	2	Indeterminate Species
2009	BC1473	Crustacea	Malacostraca	Amphipoda	Eriopisidae	<i>Nedsia sculptilis</i> group	1	
2009	BC1473	Crustacea	Malacostraca	Bathynellacea	Parabathynellidae	<i>Hexabathynella</i> sp. 'indet'	1	Indeterminate Species
2009	BC186	Annelida	Oligochaeta	Tubificida	Enchytraeidae	<i>Enchytraeidae</i> sp. '1 (PSS)'	9	
2009	BC186	Chordata	Actinopterygii	Synbranchiformes	Synbranchidae	<i>Ophisternon candidum</i>	1	
2009	BC186	Crustacea	Copepoda	Calanoida	Ridgewayiidae	<i>Stygoridgewayia trispinosa</i>	8	
2009	BC186	Crustacea	Copepoda	Calanoida	Ridgewayiidae	<i>Stygoridgewayia trispinosa</i>	25	
2009	BC186	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Diacyclops humphreysi humphreysi</i>	1	
2009	BC186	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Diacyclops sobeprolatus</i>	3	Widespread
2009	BC186	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Halicyclops rochai</i>	13	
2009	BC186	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Halicyclops rochai</i>	27	
2009	BC186	Crustacea	Copepoda	Harpacticoida	Canthocamptidae	<i>Elaphoidella humphreysi</i>	3	
2009	BC186	Crustacea	Malacostraca	Amphipoda	Bogidiellidae	<i>Bogidiellidae</i> sp. 'indet'	1	Indeterminate Species
2009	BC186	Crustacea	Malacostraca	Amphipoda	Paramelitidae	<i>Paramelitidae</i> sp. '2 (DEC)'	9	

Year	Site	Phylum	Class	Order	Family	Species	#	Notes
2009	BC186	Crustacea	Malacostraca	Amphipoda	Paramelitidae	Paramelitidae sp. '2 (DEC)'	1	
2009	BC186	Crustacea	Malacostraca	Thermosbaenacea	Halosbaenidae	Halosbaena tulki	32	
2009	BC186	Crustacea	Malacostraca	Thermosbaenacea	Halosbaenidae	Halosbaena tulki	49	
2009	BC186	Crustacea	Ostracoda	Podocopida	Candonidae	Humphreyscandona janeae	3	
2009	BC186	Nematoda	-	-	-	Nematoda sp. 'indet'	25	Indeterminate Species
2009	BC186	Nemertea	-	-	-	Nemertea sp. 'indet'	1	Indeterminate Species
2009	BC186	Platyhelminthes	Turbellaria	-	-	Turbellaria sp. 'indet'	1	Indeterminate Species
2009	BC210	Annelida	Oligochaeta	Tubificida	Naididae	Pristina aequiseta	11	
2009	BC210	Crustacea	Copepoda	Cyclopoida	Cyclopidae	Mesocyclops darwini	12	
2009	BC210	Crustacea	Copepoda	Cyclopoida	Cyclopidae	Mesocyclops darwini	10	
2009	BC210	Crustacea	Copepoda	Cyclopoida	Cyclopidae	Microcyclops varicans	1	Widespread
2009	BC210	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Nedsia sculptilis group	1	
2009	BC212	Crustacea	Copepoda	Cyclopoida	Cyclopidae	Diacyclops humphreysi humphreysi	1	
2009	BC212	Platyhelminthes	Turbellaria	-	-	Turbellaria sp. 'indet'	11	Indeterminate Species
2009	BC212	Protozoa	-	-	-	Protozoa sp. 'indet'	13	Indeterminate Species
2009	BC225	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Eriopisidae sp. '1 (PSS)'	1	Widespread
2009	BC228	Crustacea	Copepoda	Cyclopoida	Cyclopidae	Diacyclops humphreysi humphreysi	2	
2009	BC282	Crustacea	Ostracoda	Podocopida	Cyprididae	Cyprætta seurati	11	Widespread
2009	BC292	Crustacea	Copepoda	Cyclopoida	Cyclopidae	Halicyclops rochai	1	
2009	BC292	Crustacea	Copepoda	Cyclopoida	Cyclopidae	Metacyclops pilbaricus	1	Widespread
2009	BC292	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Eriopisidae sp. '1 (PSS)'	1	Widespread
2009	BC292	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Nedsia hurlberti	8	
2009	BC401	Annelida	Oligochaeta	Tubificida	Enchytraidae	Enchytraeidae sp. 'indet'	1	Indeterminate Species
2009	BC401	Crustacea	Copepoda	Cyclopoida	Cyclopidae	Diacyclops humphreysi humphreysi	3	
2009	BC401	Crustacea	Copepoda	Cyclopoida	Cyclopidae	Diacyclops humphreysi humphreysi	1	
2009	BC401	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Nedsia sp. 'indet'	1	Indeterminate Species
2009	BC401	Crustacea	Malacostraca	Thermosbaenacea	Halosbaenidae	Halosbaena tulki	1	
2009	BC401	Mollusca	Gastropoda	Sorbeoconcha	Hydrobiidae	Hydrobiidae sp. '1'	1	
2009	BC401	Platyhelminthes	Turbellaria	-	-	Turbellaria sp. 'indet'	4	Indeterminate Species
2009	BC401	Protozoa	-	-	-	Protozoa sp. 'indet'	1	Indeterminate Species
2009	BUNDD1687	Crustacea	Copepoda	Cyclopoida	Cyclopidae	Thermocyclops aberrans	17	
2009	BUNDD1687	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Nedsia hurlberti	1	
2009	BUNWB08	Annelida	Oligochaeta	Tubificida	Naididae	Pristina aequiseta	1	
2009	BUNWB08	Arthropoda	Arachnida	Sarcoptiformes	-	Sarcoptiformes group 1 (PSW)	5	
2009	BUNWB08	Crustacea	Copepoda	Cyclopoida	Cyclopidae	Microcyclops varicans	1	Widespread
2009	BUNWB08	Crustacea	Malacostraca	Amphipoda	-	Amphipoda sp. 'indet'	1	Indeterminate Species
2009	BUNWB10	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Eriopisidae sp. '1 (PSS)'	1	Widespread
2009	BUNWB13	Crustacea	Copepoda	Cyclopoida	Cyclopidae	Diacyclops humphreysi humphreysi	2	
2009	BUNWB13	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Nedsia sp. 'indet'	2	Indeterminate Species
2009	BUNWB13	Mollusca	Gastropoda	Sorbeoconcha	Hydrobiidae	Hydrobiidae sp. '1'	201	
2009	BUNWO0773	Annelida	Oligochaeta	Tubificida	Tubificidae	Tubificidae sp. 'indet'	1	Indeterminate Species

Year	Site	Phylum	Class	Order	Family	Species	#	Notes
2009	BUNWO0773	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Diacyclops humphreysi humphreysi</i>	6	
2009	BUNWO0773	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Diacyclops humphreysi humphreysi</i>	2	
2009	BUNWO0773	Crustacea	Copepoda	Harpacticoida	Canthocamptidae	<i>Elaphoidella humphreysi</i>	1	
2009	BUNWO0773	Crustacea	Ostracoda	Podocopida	Candonidae	<i>Areacandona triangulum</i>	6	
2009	BUNWO0774	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Diacyclops humphreysi humphreysi</i>	30	
2009	BUNWO0774	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Diacyclops humphreysi humphreysi</i>	25	
2009	BUNWO0774	Crustacea	Ostracoda	Podocopida	Candonidae	<i>Areacandona triangulum</i>	2	
2009	BUNWO0774	Crustacea	Ostracoda	Podocopida	Candonidae	<i>Humphreyscandona janeae</i>	2	
2009	BUNWO1104	Crustacea	Malacostraca	Amphipoda	Eriopisidae	<i>Nedsia sculptilis</i> group	4	
2009	BUWMD1500	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Diacyclops humphreysi humphreysi</i>	1	
2009	D08BU021	Crustacea	Malacostraca	Amphipoda	Eriopisidae	<i>Nedsia sculptilis</i> group	12	
2009	J154	Crustacea	Malacostraca	Amphipoda	Eriopisidae	<i>Nedsia</i> sp. 'indet'	1	Indeterminate Species
2009	JIMDR094	Crustacea	Malacostraca	Amphipoda	Eriopisidae	<i>Nedsia hurlberti</i>	10	
2009	JIMDR094	Crustacea	Malacostraca	Amphipoda	Paramelitidae	<i>Paramelitidae</i> sp. '2 (DEC)'	1	
2009	JIMWE0003	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Halicyclops rochai</i>	3	
2009	JIMWE0003	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Halicyclops rochai</i>	18	
2009	JIMWE0003	Crustacea	Malacostraca	Amphipoda	Bogidiellidae	<i>Bogidiellidae</i> sp. 'indet'	1	Indeterminate Species
2009	JIMWE0003	Crustacea	Malacostraca	Amphipoda	Eriopisidae	<i>Nedsia hurlberti</i>	2	
2009	JIMWE0003	Crustacea	Malacostraca	Amphipoda	Eriopisidae	<i>Nedsia</i> sp. 'indet'	1	Indeterminate Species
2009	JIMWE0003	Crustacea	Malacostraca	Amphipoda	Paramelitidae	<i>Paramelitidae</i> sp. '2 (DEC)'	1	
2009	JIMWE0004	Crustacea	Copepoda	Calanoida	Ridgewayiidae	<i>Stygoridgewayia trispinosa</i>	1	
2009	JIMWE0004	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Halicyclops rochai</i>	8	
2009	JIMWE0004	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Halicyclops rochai</i>	5	
2009	JIMWE0004	Crustacea	Malacostraca	Amphipoda	Eriopisidae	<i>Nedsia hurlberti</i>	12	
2009	JIMWE0004	Crustacea	Malacostraca	Amphipoda	Eriopisidae	<i>Nedsia</i> sp. 'indet'	2	Indeterminate Species
2009	JIMWE0004	Crustacea	Malacostraca	Amphipoda	Paramelitidae	<i>Paramelitidae</i> sp. '2 (DEC)'	3	
2009	JIMWE0004	Crustacea	Malacostraca	Amphipoda	Paramelitidae	<i>Paramelitidae</i> sp. '2 (DEC)'	3	
2009	JIMWE0004	Crustacea	Ostracoda	Podocopida	Candonidae	<i>Areacandona bluffi</i>	1	
2010	BC156	Crustacea	Copepoda	Calanoida	Ridgewayiidae	<i>Stygoridgewayia trispinosa</i>	2	
2010	BC156	Crustacea	Copepoda	Cyclopoida	Cyclopiidae	<i>Halicyclops rochai</i>	20	
2010	BC156	Crustacea	Malacostraca	Amphipoda	Eriopisidae	<i>Nedsia hurlberti</i>	8	
2010	BC156	Platyhelminthes	Turbellaria	-	-	<i>Turbellaria</i> sp. 'indet'	19	Indeterminate Species
2010	BC186	Annelida	Oligochaeta	Tubificida	Enchytraeidae	<i>Enchytraeidae</i> sp. '1 (PSS)'	3	
2010	BC186	Crustacea	Copepoda	Calanoida	Ridgewayiidae	<i>Stygoridgewayia trispinosa</i>	7	
2010	BC186	Crustacea	Copepoda	Calanoida	Ridgewayiidae	<i>Stygoridgewayia trispinosa</i>	11	
2010	BC186	Crustacea	Copepoda	Cyclopoida	Cyclopiidae	<i>Halicyclops rochai</i>	17	
2010	BC186	Crustacea	Copepoda	Cyclopoida	Cyclopiidae	<i>Halicyclops rochai</i>	3	
2010	BC186	Crustacea	Copepoda	Harpacticoida	Canthocamptidae	<i>Elaphoidella humphreysi</i>	2	
2010	BC186	Crustacea	Malacostraca	Amphipoda	Eriopisidae	<i>Nedsia hurlberti</i>	1	
2010	BC186	Crustacea	Malacostraca	Amphipoda	Paramelitidae	<i>Paramelitidae</i> sp. '2 (DEC)'	1	
2010	BC186	Crustacea	Malacostraca	Thermosbaenacea	Halosbaenidae	<i>Halosbaena tulki</i>	4	
2010	BC186	Crustacea	Malacostraca	Thermosbaenacea	Halosbaenidae	<i>Halosbaena tulki</i>	4	

Year	Site	Phylum	Class	Order	Family	Species	#	Notes
2010	BC210	Crustacea	Copepoda	Cyclopoida	Cyclopiidae	<i>Microcycllops varicans</i>	5	Widespread
2010	BC210	Crustacea	Copepoda	Cyclopoida	Cyclopiidae	<i>Microcycllops varicans</i>	4	Widespread
2010	BC282	Crustacea	Copepoda	Cyclopoida	Cyclopiidae	<i>Halicyclops rochai</i>	1	
2010	BC282	Crustacea	Malacostraca	Amphipoda	Eriopisidae	<i>Nedsia hurlberti</i>	30	
2010	BC401	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Eriopisidae sp. '1 (PSS)'	1	Widespread
2010	BC401	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Eriopisidae sp. '1 (PSS)'	1	Widespread
2010	BC401	Crustacea	Malacostraca	Amphipoda	Eriopisidae	<i>Nedsia sculptilis</i> group	2	
2010	BC401	Crustacea	Malacostraca	Amphipoda	Eriopisidae	<i>Nedsia sculptilis</i> group	1	
2010	BUNWB13	Crustacea	Malacostraca	Amphipoda	Eriopisidae	<i>Nedsia sculptilis</i> group	5	
2010	BUNWB13	Crustacea	Malacostraca	Amphipoda	Eriopisidae	<i>Nedsia sculptilis</i> group	2	
2010	BUNWB13	Mollusca	Gastropoda	Sorbeoconcha	Hydrobiidae	Hydrobiidae sp. '1'	38	
2010	BUNWB13	Mollusca	Gastropoda	Sorbeoconcha	Hydrobiidae	Hydrobiidae sp. '1'	35	
2010	BUNWE01	Crustacea	Copepoda	Calanoida	Ridgewayiidae	<i>Stygoridgewayia trispinosa</i>	14	
2010	BUNWE01	Crustacea	Malacostraca	Amphipoda	Eriopisidae	<i>Nedsia</i> sp. 'indet'	1	Indeterminate Species
2010	D08BU021	Crustacea	Copepoda	Cyclopoida	Cyclopiidae	<i>Microcycllops varicans</i>	2	Widespread
2010	D08BU021	Crustacea	Malacostraca	Amphipoda	Eriopisidae	<i>Nedsia sculptilis</i> group	8	
2010	D08BU021	Crustacea	Malacostraca	Amphipoda	Eriopisidae	<i>Nedsia sculptilis</i> group	10	
2010	JIMDD080	Crustacea	Malacostraca	Amphipoda	Eriopisidae	<i>Nedsia hurlberti</i>	3	
2010	JIMDR094	Crustacea	Malacostraca	Amphipoda	Eriopisidae	<i>Nedsia hurlberti</i>	4	
2010	JIMWE0003	Crustacea	Copepoda	Cyclopoida	Cyclopiidae	<i>Halicyclops rochai</i>	14	
2010	JIMWE0003	Crustacea	Copepoda	Cyclopoida	Cyclopiidae	<i>Halicyclops rochai</i>	4	
2010	JIMWE0003	Crustacea	Malacostraca	Amphipoda	Bogidiellidae	Bogidiellidae sp. 'indet'	1	Indeterminate Species
2010	JIMWE0003	Crustacea	Malacostraca	Amphipoda	Eriopisidae	<i>Nedsia hurlberti</i>	1	
2010	JIMWE0003	Crustacea	Malacostraca	Amphipoda	Eriopisidae	<i>Nedsia hurlberti</i>	1	
2010	JIMWE0003	Crustacea	Malacostraca	Amphipoda	Paramelitidae	Paramelitidae sp. '2 (DEC)'	1	
2010	JIMWE0003	Crustacea	Ostracoda	Podocopida	Candonidae	<i>Areacandona triangulum</i>	1	
2010	JIMWE0003	Protazoa	-	-	-	Protozoa sp. 'indet'	1	Indeterminate Species
2010	JW021	Crustacea	Copepoda	Calanoida	Ridgewayiidae	<i>Stygoridgewayia trispinosa</i>	4	
2010	JW021	Crustacea	Copepoda	Calanoida	Ridgewayiidae	<i>Stygoridgewayia trispinosa</i>	3	
2010	JW021	Crustacea	Copepoda	Cyclopoida	Cyclopiidae	<i>Diacyclops cockingi</i>	1	
2010	JW021	Crustacea	Malacostraca	Amphipoda	Bogidiellidae	Bogidiellidae sp. 'indet'	1	Indeterminate Species
2010	JW021	Crustacea	Malacostraca	Amphipoda	Bogidiellidae	Bogidiellidae sp. 'indet'	9	Indeterminate Species
2010	JW021	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Eriopisidae sp. '1 (PSS)'	1	Widespread
2010	JW021	Crustacea	Malacostraca	Amphipoda	Eriopisidae	<i>Nedsia hurlberti</i>	21	
2010	JW021	Crustacea	Malacostraca	Amphipoda	Eriopisidae	<i>Nedsia sculptilis</i> group	50	
2010	JW021	Crustacea	Malacostraca	Amphipoda	Neoniphargidae	Neoniphargidae sp. 'B2'	3	
2010	JW021	Crustacea	Malacostraca	Isopoda	Cirolanidae	<i>Kagalana tonde</i>	1	
2010	JW021	Crustacea	Malacostraca	Thermosbaenacea	Halosbaenidae	<i>Halosbaena tulki</i>	8	
2010	JW021	Crustacea	Malacostraca	Thermosbaenacea	Halosbaenidae	<i>Halosbaena tulki</i>	7	
2010	JW021	Crustacea	Ostracoda	Podocopida	Candonidae	<i>Humphreyscandona fovea</i>	2	
2010	JW021	Crustacea	Ostracoda	Podocopida	Candonidae	Pierrecandona sp. 'indet'	1	Indeterminate Species

Year	Site	Phylum	Class	Order	Family	Species	#	Notes
2010	PSS040	Crustacea	Malacostraca	Amphipoda	Eriopisidae	<i>Nedsia hurlberti</i>	2	
2010	PZ10BUN033	Crustacea	Copepoda	Cyclopoida	Cyclopiidae	<i>Halicyclops rochai</i>	2	
2010	PZ10BUN033	Crustacea	Ostracoda	Podocopida	Candonidae	<i>Areacandona brookantha</i>	1	
2011	BC1473	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Diacyclops cockingi</i>	49	
2011	BC1473	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Diacyclops humphreysi humphreysi</i>	10	
2011	BC1473	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Halicyclops rochai</i>	1	
2011	BC1473	Crustacea	Copepoda	Harpacticoida	Canthocamptidae	<i>Elaphoidella humphreysi</i>	1	
2011	BC1473	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Eriopisidae sp. '1 (PSS)'	1	Widespread
2011	BC1473	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Eriopisidae sp. '1 (PSS)'	1	Widespread
2011	BC1473	Crustacea	Malacostraca	Amphipoda	Eriopisidae	<i>Nedsia sculptilis</i> group	5	
2011	BC1473	Crustacea	Malacostraca	Amphipoda	Paramelitidae	Paramelitidae sp. '2 (DEC)'	1	
2011	BC150	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Diacyclops humphreysi humphreysi</i>	3	
2011	BC150	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Halicyclops rochai</i>	10	
2011	BC150	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Halicyclops rochai</i>	7	
2011	BC150	Crustacea	Malacostraca	Amphipoda	Eriopisidae	<i>Nedsia hurlberti</i>	1	
2011	BC150	Crustacea	Malacostraca	Amphipoda	Paramelitidae	Paramelitidae sp. '2 (DEC)'	1	
2011	BC150	Crustacea	Malacostraca	Themosbaenacea	Halosbaenidae	<i>Halosbaena tulki</i>	1	
2011	BC150	Crustacea	Ostracoda	Podocopida	Candonidae	<i>Areacandona brookantha</i>	3	
2011	BC150	Platyhelminthes	Turbellaria	-	-	Turbellaria sp. 'indet'	10	Indeterminate Species
2011	BC150	Platyhelminthes	Turbellaria	-	-	Turbellaria sp. 'indet'	17	Indeterminate Species
2011	BC186	Annelida	Oligochaeta	Tubificida	Enchytraeidae	Enchytraeidae sp. '1 (PSS)'	4	
2011	BC186	Crustacea	Copepoda	Calanoida	Ridgewayiidae	<i>Stygoridgewaya trispinosa</i>	15	
2011	BC186	Crustacea	Copepoda	Calanoida	Ridgewayiidae	<i>Stygoridgewaya trispinosa</i>	22	
2011	BC186	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Diacyclops humphreysi humphreysi</i>	26	
2011	BC186	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Halicyclops rochai</i>	2	
2011	BC186	Crustacea	Malacostraca	Amphipoda	Eriopisidae	<i>Nedsia hurlberti</i>	3	
2011	BC186	Crustacea	Malacostraca	Amphipoda	Eriopisidae	<i>Nedsia hurlberti</i>	1	
2011	BC186	Crustacea	Malacostraca	Themosbaenacea	Halosbaenidae	<i>Halosbaena tulki</i>	12	
2011	BC186	Crustacea	Malacostraca	Themosbaenacea	Halosbaenidae	<i>Halosbaena tulki</i>	24	
2011	BC186	Crustacea	Ostracoda	Podocopida	Candonidae	<i>Areacandona brookantha</i>	1	
2011	BC210	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Microcyclops varicans</i>	16	Widespread
2011	BC225	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Diacyclops humphreysi humphreysi</i>	14	
2011	BC225	Crustacea	Malacostraca	Amphipoda	Eriopisidae	<i>Nedsia sculptilis</i> group	3	
2011	BC225	Crustacea	Ostracoda	Podocopida	Candonidae	<i>Areacandona triangulum</i>	1	
2011	BC401	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Diacyclops humphreysi humphreysi</i>	15	
2011	BC401	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Metacyclops pilbaricus</i>	1	Widespread
2011	BC401	Crustacea	Malacostraca	Amphipoda	Eriopisidae	<i>Nedsia sculptilis</i> group	1	
2011	BC401	Crustacea	Malacostraca	Amphipoda	Eriopisidae	<i>Nedsia sculptilis</i> group	1	
2011	BC434	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Diacyclops humphreysi humphreysi</i>	2	
2011	BC434	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Diacyclops humphreysi humphreysi</i>	6	
2011	BC434	Crustacea	Malacostraca	Bathynellacea	Parabathynellidae	<i>Hexabathynella</i> sp. 'indet'	1	Indeterminate Species
2011	BUNWB13	Crustacea	Malacostraca	Amphipoda	Eriopisidae	<i>Nedsia sculptilis</i> group	6	

Year	Site	Phylum	Class	Order	Family	Species	#	Notes
2011	BUNWB13	Mollusca	Gastropoda	Sorbeoconcha	Hydrobiidae	Hydrobiidae sp. '1'	60	
2011	BUNWO0773	Crustacea	Copepoda	Cyclopoida	Cyclopidae	Diacyclops sp. 'indet'	2	Indeterminate Species
2011	BUNWO1104	Crustacea	Copepoda	Cyclopoida	Cyclopidae	Diacyclops humphreysi humphreysi	6	
2011	BUNWO1104	Crustacea	Malacostraca	Bathynellacea	Parabathynellidae	Bilobathynella sp. 'B05'	2	
2011	D08BU021	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Nedsia sculptilis group	2	
2011	JIMDD080	Crustacea	Copepoda	Cyclopoida	Cyclopidae	Diacyclops cockingi	2	
2011	JIMWE0003	Crustacea	Copepoda	Cyclopoida	Cyclopidae	Diacyclops humphreysi humphreysi	1	
2011	JIMWE0003	Crustacea	Copepoda	Cyclopoida	Cyclopidae	Diacyclops humphreysi humphreysi	11	
2011	JIMWE0003	Crustacea	Copepoda	Cyclopoida	Cyclopidae	Halicyclops rochae	2	
2011	JIMWE0003	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Nedsia hurlberti	17	
2011	JIMWE0003	Crustacea	Ostracoda	Podocopida	Candonidae	Areacandonia triangulum	9	
2011	JW021	Crustacea	Copepoda	Calanoida	Ridgewayiidae	Stygoridgewayia trispinosa	1	
2011	JW021	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Nedsia hurlberti	3	
2011	JW021	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Nedsia sculptilis group	2	
2011	JW021	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Nedsia sculptilis group	18	
2011	JW021	Crustacea	Malacostraca	Thermosbaenacea	Halosbaenidae	Halosbaena tulki	20	
2011	JW021	Crustacea	Malacostraca	Thermosbaenacea	Halosbaenidae	Halosbaena tulki	50	
2011	JW021	Platyhelminthes	Turbellaria	-	-	Turbellaria sp. 'indet'	1	Indeterminate Species
2011	PZ10BUN022	Crustacea	Copepoda	Cyclopoida	Cyclopidae	Diacyclops humphreysi humphreysi	15	
2011	PZ10BUN022	Crustacea	Copepoda	Harpacticoida	Ameridae	Inermipes sp. 'indet'	4	Indeterminate Species
2011	PZ10BUN022	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Nedsia hurlberti	1	
2011	PZ10BUN022	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Nedsia hurlberti	5	
2011	PZ10BUN041	Crustacea	Copepoda	Cyclopoida	Cyclopidae	Diacyclops humphreysi humphreysi	2	
2013	BC186	Crustacea	Copepoda	Harpacticoida	Canthocamptidae	Elaphoidella humphreysi	4	
2013	BC225	Crustacea	Ostracoda	Podocopida	Candonidae	Areacandonia triangulum	1	
2013	BUNWB13	Crustacea	Copepoda	Cyclopoida	Cyclopidae	Diacyclops sp. 'indet'	1	Indeterminate Species
2013	BUNWB13	Crustacea	Copepoda	Harpacticoida	Canthocamptidae	Elaphoidella humphreysi	1	
2013	BUNWB13	Mollusca	Gastropoda	Sorbeoconcha	Hydrobiidae	Hydrobiidae sp. '1'	17	
2013	JIMWE003	Crustacea	Copepoda	Cyclopoida	Cyclopidae	Diacyclops sp. 'indet'	1	Indeterminate Species
2013	JIMWE003	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Nedsia hurlberti	1	
2013	JIMWE003	Crustacea	Ostracoda	Podocopida	Candonidae	Areacandonia triangulum	4	
2013	JW024	Arthropoda	Arachnida	Trombidiformes	Mideopsidae	Tiramideopsis sp. 'indet'	1	Indeterminate Species
2013	JW024	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Nedsia hurlberti	2	
2014	BC156	Crustacea	Copepoda	Calanoida	Ridgewayiidae	Stygoridgewayia trispinosa	29	
2014	BC156	Crustacea	Copepoda	Cyclopoida	-	Cyclopoida sp. 'indet'	7	Indeterminate Species
2014	BC156	Crustacea	Copepoda	Cyclopoida	Cyclopidae	Diacyclops humphreysi humphreysi	12	
2014	BC156	Crustacea	Copepoda	Cyclopoida	Cyclopidae	Halicyclops rochae	15	
2014	BC156	Crustacea	Copepoda	Harpacticoida	Canthocamptidae	Elaphoidella humphreysi	1	
2014	BC156	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Nedsia sculptilis group	1	
2014	BC156	Crustacea	Malacostraca	Bathynellacea	-	Bathynellacea sp. 'indet'	3	Indeterminate Species
2014	BC186	Annelida	Oligochaeta	Tubificida	Enchytraeidae	Enchytraeidae sp. '1 (PSS)'	1	

Year	Site	Phylum	Class	Order	Family	Species	#	Notes
2014	BC186	Annelida	Oligochaeta	Tubificida	Enchytraeidae	Enchytraeidae sp. '1 (PSS)'	2	
2014	BC186	Arthropoda	Arachnida	Sacoptiformes	-	Sarcoptiformes group 1 (PSW)	1	
2014	BC186	Arthropoda	Arachnida	Trombidiformes	Mideopsidae	Tiramideopsis sp. 'indet'	2	Indeterminate Species
2014	BC186	Crustacea	Copepoda	Cyclopoida	Cyclopidae	Diacyclops cockingi	4	
2014	BC186	Crustacea	Copepoda	Cyclopoida	Cyclopidae	Diacyclops humphreysi humphreysi	1	
2014	BC186	Crustacea	Copepoda	Cyclopoida	Cyclopidae	Halicyclops rochai	4	
2014	BC186	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Nedsia sp. 'indet'	1	Indeterminate Species
2014	BC186	Crustacea	Malacostraca	Thermosbaenacea	Halosbaenidae	Halosbaena tulki	3	
2014	BC186	Crustacea	Malacostraca	Thermosbaenacea	Halosbaenidae	Halosbaena tulki	1	
2014	BC186	Crustacea	Malacostraca	Thermosbaenacea	Halosbaenidae	Halosbaena tulki	1	
2014	BC186	Crustacea	Malacostraca	Thermosbaenacea	Halosbaenidae	Halosbaena tulki	1	
2014	BC186	Crustacea	Malacostraca	Thermosbaenacea	Halosbaenidae	Halosbaena tulki	1	
2014	BC186	Crustacea	Malacostraca	Thermosbaenacea	Halosbaenidae	Halosbaena tulki	2	
2014	BC225	Crustacea	Copepoda	Cyclopoida	Cyclopidae	Diacyclops humphreysi humphreysi	9	
2014	BC225	Crustacea	Ostracoda	Podocopida	Candonidae	Areacandona triangulum	1	
2014	BC292	Crustacea	Copepoda	Cyclopoida	Cyclopidae	Diacyclops humphreysi humphreysi	24	
2014	BC292	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Eriopisidae sp. '1 (PSS)'	1	Widespread
2014	BC292	Crustacea	Malacostraca	Bathynellacea	Parabathynelliidae	Brevisomabathynella sp. 'indet'	3	Indeterminate Species
2014	BC434	Crustacea	Copepoda	Cyclopoida	Cyclopidae	Diacyclops humphreysi humphreysi	3	
2014	BUNWB09	Crustacea	Copepoda	Cyclopoida	Cyclopidae	Halicyclops rochai	39	
2014	BUNWB09	Crustacea	Copepoda	Cyclopoida	Cyclopidae	Halicyclops rochai	31	
2014	BUNWB09	Crustacea	Copepoda	Harpacticoida	Canthocamptidae	Elaphoidella humphreysi	3	
2014	BUNWB09	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Nedsia sp. 'indet'	2	Indeterminate Species
2014	BUNWB09	Crustacea	Malacostraca	Bathynellacea	Parabathynelliidae	Bilobathynella sp. 'B05'	1	
2014	BUNWB09	Mollusca	Gastropoda	Sorbeoconcha	Hydrobiidae	Hydrobiidae sp. '1'	5	
2014	BUNWB13	Crustacea	Copepoda	Cyclopoida	Cyclopidae	Diacyclops humphreysi humphreysi	3	
2014	BUNWB13	Crustacea	Copepoda	Cyclopoida	Cyclopidae	Diacyclops humphreysi humphreysi	1	
2014	BUNWB13	Crustacea	Copepoda	Cyclopoida	Cyclopidae	Metacyclops pilbaricus	3	Widespread
2014	BUNWB13	Crustacea	Copepoda	Cyclopoida	Cyclopidae	Metacyclops pilbaricus	1	Widespread
2014	BUNWB13	Crustacea	Copepoda	Harpacticoida	Canthocamptidae	Elaphoidella humphreysi	1	
2014	BUNWB13	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Nedsia sculptilis group	1	
2014	BUNWB13	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Nedsia sculptilis group	11	
2014	BUNWB13	Mollusca	Gastropoda	Sorbeoconcha	Hydrobiidae	Hydrobiidae sp. '1'	17	
2014	BUNWB13	Mollusca	Gastropoda	Sorbeoconcha	Hydrobiidae	Hydrobiidae sp. '1'	27	
2014	BUNWP006	Crustacea	Copepoda	Cyclopoida	Cyclopidae	Diacyclops humphreysi humphreysi	6	
2014	BUNWP006	Crustacea	Malacostraca	Amphipoda	Paramelitidae	Paramelitidae sp. 'B44'	2	
2014	JIMWE003	Crustacea	Copepoda	Cyclopoida	Cyclopidae	Diacyclops humphreysi humphreysi	1	
2014	JIMWE003	Crustacea	Copepoda	Cyclopoida	Cyclopidae	Halicyclops rochai	1	
2014	JIMWE003	Crustacea	Ostracoda	Podocopida	Candonidae	Areacandona triangulum	11	
2014	JIMWE004	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Nedsia hurlberti	4	
2014	JIMWE004	Rotifera	Bdelloidea	-	-	Bdelloidea sp. 'indet'	1	Indeterminate Species
2014	JIMWE004	Rotifera	Bdelloidea	-	-	Bdelloidea sp. 'indet'	2	Indeterminate Species
2014	JW023	Annelida	Oligochaeta	Tubificida	Naididae	Antipodrilus sp. 'nov.'	2	

Year	Site	Phylum	Class	Order	Family	Species	#	Notes
2014	JW023	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Halicyclops rochai</i>	23	
2014	JW023	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Halicyclops rochai</i>	27	
2014	JW023	Crustacea	Copepoda	Harpacticoida	Parastenocarididae	<i>Parastenocaris</i> sp. 'B28'	1	
2014	JW023	Crustacea	Malacostraca	Amphipoda	Eriopisidae	<i>Eriopisidae</i> sp. '1 (PSS)'	2	Widespread
2014	JW023	Crustacea	Malacostraca	Amphipoda	Eriopisidae	<i>Nedsia hurlberti</i>	2	
2014	JW023	Crustacea	Malacostraca	Isopoda	Cirolanidae	<i>Kagalana tonde</i>	1	
2014	JW023	Crustacea	Malacostraca	Isopoda	Cirolanidae	<i>Kagalana tonde</i>	1	
2014	JW023	Crustacea	Ostracoda	Podocopida	Candonidae	<i>Areacandona brookantha</i>	1	
2014	JW023	Mollusca	Gastropoda	Sorbeoconcha	Hydrobiidae	<i>Hydrobiidae</i> sp. '2'	4	
2014	JW024	Crustacea	Copepoda	Calanoida	Ridgewayiidae	<i>Stygoridgewayia trispinosa</i>	6	
2014	JW024	Crustacea	Copepoda	Calanoida	Ridgewayiidae	<i>Stygoridgewayia trispinosa</i>	38	
2014	JW024	Crustacea	Malacostraca	Amphipoda	Bogidiellidae	<i>Bogidiellidae</i> sp. 'indet'	1	Indeterminate Species
2014	JW024	Crustacea	Malacostraca	Amphipoda	Eriopisidae	<i>Nedsia hurlberti</i>	46	
2014	JW024	Crustacea	Malacostraca	Amphipoda	Eriopisidae	<i>Nedsia hurlberti</i>	23	
2014	JW024	Crustacea	Malacostraca	Isopoda	Cirolanidae	<i>Kagalana tonde</i>	1	
2014	JW024	Crustacea	Malacostraca	Isopoda	Cirolanidae	<i>Kagalana tonde</i>	1	
2014	JW024	Crustacea	Malacostraca	Thermosbaenacea	Halosbaenidae	<i>Halosbaena tulki</i>	13	
2014	JW024	Crustacea	Malacostraca	Thermosbaenacea	Halosbaenidae	<i>Halosbaena tulki</i>	39	
2015	BC186	Annelida	Oligochaeta	-	-	<i>Oligochaeta</i> sp. 'indet'	1	Indeterminate Species
2015	BC186	Crustacea	Copepoda	Calanoida	-	<i>Calanoida</i> sp. 'indet'	1	Indeterminate Species
2015	BC186	Crustacea	Copepoda	Calanoida	Ridgewayiidae	<i>Stygoridgewayia trispinosa</i>	8	
2015	BC186	Crustacea	Copepoda	Calanoida	Ridgewayiidae	<i>Stygoridgewayia trispinosa</i>	2	
2015	BC186	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Diacyclops cockingi</i>	2	
2015	BC186	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Halicyclops rochai</i>	5	
2015	BC186	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Halicyclops rochai</i>	2	
2015	BC186	Crustacea	Copepoda	Harpacticoida	Canthocamptidae	<i>Elaphoidella humphreysi</i>	1	
2015	BC186	Crustacea	Malacostraca	Amphipoda	Eriopisidae	<i>Nedsia hurlberti</i>	1	
2015	BC186	Crustacea	Malacostraca	Amphipoda	Eriopisidae	<i>Nedsia hurlberti</i>	1	
2015	BC186	Crustacea	Malacostraca	Amphipoda	Paramelitidae	<i>Paramelitidae</i> sp. '2 (DEC)'	2	
2015	BC225	Crustacea	Copepoda	Cyclopoida	-	<i>Cyclopoida</i> sp. 'indet'	1	Indeterminate Species
2015	BC225	Crustacea	Copepoda	Cyclopoida	-	<i>Cyclopoida</i> sp. 'indet'	1	Indeterminate Species
2015	BC225	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Diacyclops humphreysi humphreysi</i>	1	
2015	BC225	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Diacyclops humphreysi humphreysi</i>	1	
2015	BC225	Crustacea	Malacostraca	Amphipoda	-	<i>Amphipoda</i> sp. 'indet'	1	Indeterminate Species
2015	BC225	Crustacea	Malacostraca	Amphipoda	-	<i>Amphipoda</i> sp. 'indet'	1	Indeterminate Species
2015	BC225	Crustacea	Malacostraca	Amphipoda	Eriopisidae	<i>Nedsia hurlberti</i>	1	
2015	BC225	Crustacea	Malacostraca	Amphipoda	Eriopisidae	<i>Nedsia hurlberti</i>	1	
2015	BC292	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Diacyclops humphreysi humphreysi</i>	7	
2015	BC292	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Diacyclops humphreysi humphreysi</i>	7	
2015	BC360	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Diacyclops cockingi</i>	20	
2015	BC401	Annelida	Oligochaeta	Tubificida	Phreodrilidae	<i>Phreodrilidae</i> sp. 'dissimilar ventral'	1	Widespread

Year	Site	Phylum	Class	Order	Family	Species	#	Notes
						chaetae'		
2015	BC401	Crustacea	Malacostraca	Amphipoda	Eriopisidae	<i>Nedsia sculptilis</i> group	1	
2015	BC434	Crustacea	Copepoda	Cyclopoida	-	<i>Cyclopoida</i> sp. 'indet'	1	Indeterminate Species
2015	BC434	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Diacyclops humphreysi humphreysi</i>	3	
2015	BC667	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Eriopisidae sp. '1 (PSS)'	1	Widespread
2015	BC667	Crustacea	Malacostraca	Amphipoda	Eriopisidae	<i>Nedsia sculptilis</i> group	1	
2015	BC690	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Diacyclops humphreysi humphreysi</i>	1	
2015	BUNWB09	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Diacyclops humphreysi humphreysi</i>	50	
2015	BUNWB09	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Halicyclops rochai</i>	44	
2015	BUNWB09	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Halicyclops rochai</i>	6	
2015	BUNWB09	Crustacea	Copepoda	Harpacticoida	Ameiridae	<i>Lucionitocrella yalleenensis</i>	1	
2015	BUNWB09	Crustacea	Copepoda	Harpacticoida	Canthocamptidae	<i>Elaphoidella humphreysi</i>	7	
2015	BUNWB09	Crustacea	Malacostraca	Amphipoda	Eriopisidae	<i>Nedsia sculptilis</i> group	3	
2015	BUNWB09	Crustacea	Malacostraca	Amphipoda	Eriopisidae	<i>Nedsia</i> sp. 'indet'	1	Indeterminate Species
2015	BUNWB09	Mollusca	Gastropoda	Sorbeoconcha	Hydrobiidae	Hydrobiidae sp. '1'	82	
2015	BUNWB13	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Pescecylops pilbaricus</i>	2	
2015	BUNWB13	Crustacea	Malacostraca	Amphipoda	Eriopisidae	<i>Nedsia hurlberti</i>	1	
2015	BUNWB13	Crustacea	Malacostraca	Amphipoda	Eriopisidae	<i>Nedsia sculptilis</i> group	1	
2015	BUNWB13	Crustacea	Malacostraca	Amphipoda	Eriopisidae	<i>Nedsia sculptilis</i> group	1	
2015	BUNWB13	Crustacea	Malacostraca	Amphipoda	Eriopisidae	<i>Nedsia sculptilis</i> group	2	
2015	BUNWB13	Mollusca	Gastropoda	Sorbeoconcha	Hydrobiidae	Hydrobiidae sp. '1'	17	
2015	BUNWB13	Mollusca	Gastropoda	Sorbeoconcha	Hydrobiidae	Hydrobiidae sp. '1'	400	
2015	BUNWO1105	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Diacyclops humphreysi humphreysi</i>	1	
2015	BUNWO1108	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Diacyclops cockingi</i>	2	
2015	BUNWO1108	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Diacyclops humphreysi humphreysi</i>	4	
2015	BUNWO1108	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Halicyclops rochai</i>	2	
2015	BUNWO1108	Crustacea	Malacostraca	Amphipoda	Eriopisidae	<i>Nedsia sculptilis</i> group	2	
2015	BUNWP0006	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Diacyclops humphreysi humphreysi</i>	38	
2015	BUNWP0006	Crustacea	Copepoda	Harpacticoida	Canthocamptidae	<i>Elaphoidella humphreysi</i>	3	
2015	BUNWP0006	Crustacea	Malacostraca	Bathynellacea	Parabathynellidae	<i>Billibathynella</i> sp. 'indet'	2	Indeterminate Species
2015	BUNWP0006	Crustacea	Ostracoda	Podocopida	Candoninae	<i>Areacandona triangulum</i>	7	
2015	DD13MEH0007	Crustacea	Copepoda	Calanoida	Ridgewayiidae	<i>Stygoridgewayia trispinosa</i>	10	
2015	DD13MEH0007	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Diacyclops humphreysi humphreysi</i>	10	
2015	DD13MEH0007	Crustacea	Malacostraca	Amphipoda	Eriopisidae	<i>Nedsia</i> sp. 'AMM001/029/030'	1	
2015	DD13MEH0007	Crustacea	Malacostraca	Amphipoda	Eriopisidae	<i>Nedsia</i> sp. 'AMM001/029/030'	1	
2015	DD13MEH0007	Crustacea	Malacostraca	Amphipoda	Eriopisidae	<i>Nedsia</i> sp. 'AMM001/029/030'	1	
2015	DD13MEH0007	Crustacea	Malacostraca	Amphipoda	Eriopisidae	<i>Nedsia</i> sp. 'AMM001/029/030'	1	
2015	DD13MEH0007	Crustacea	Malacostraca	Amphipoda	Eriopisidae	<i>Nedsia</i> sp. 'AMM001/029/030'	1	
2015	JIMWE003	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Diacyclops humphreysi humphreysi</i>	3	
2015	JIMWE003	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Diacyclops humphreysi humphreysi</i>	3	
2015	JIMWE003	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Diacyclops humphreysi humphreysi</i>	3	
2015	JIMWE003	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Diacyclops humphreysi humphreysi</i>	3	

Year	Site	Phylum	Class	Order	Family	Species	#	Notes
2015	JIMWE003	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Halicyclops rochai</i>	1	
2015	JIMWE003	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Halicyclops rochai</i>	1	
2015	JIMWE003	Crustacea	Malacostraca	Amphipoda	Eriopisidae	<i>Nedsia hurlberti</i>	1	
2015	JIMWE003	Crustacea	Malacostraca	Amphipoda	Eriopisidae	<i>Nedsia hurlberti</i>	1	
2015	JIMWE003	Crustacea	Ostracoda	Podocopida	Candoninae	<i>Areacandona triangulum</i>	3	
2015	JIMWE003	Crustacea	Ostracoda	Podocopida	Candoninae	<i>Areacandona triangulum</i>	3	
2015	JIMWE004	Crustacea	Copepoda	Calanoida	Ridgewayiidae	<i>Stygoridgewayia trispinosa</i>	1	
2015	JIMWE004	Crustacea	Copepoda	Calanoida	Ridgewayiidae	<i>Stygoridgewayia trispinosa</i>	1	
2015	JIMWE004	Crustacea	Copepoda	Calanoida	Ridgewayiidae	<i>Stygoridgewayia trispinosa</i>	1	
2015	JIMWE004	Crustacea	Copepoda	Calanoida	Ridgewayiidae	<i>Stygoridgewayia trispinosa</i>	1	
2015	JIMWE004	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Diacyclops humphreysi humphreysi</i>	2	
2015	JIMWE004	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Diacyclops humphreysi humphreysi</i>	2	
2015	JIMWE004	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Diacyclops humphreysi humphreysi</i>	33	
2015	JIMWE004	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Diacyclops humphreysi humphreysi</i>	2	
2015	JIMWE004	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Diacyclops humphreysi humphreysi</i>	33	
2015	JIMWE004	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Diacyclops humphreysi humphreysi</i>	2	
2015	JIMWE004	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Diacyclops humphreysi humphreysi</i>	2	
2015	JIMWE004	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Diacyclops humphreysi humphreysi</i>	1	
2015	JIMWE004	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Halicyclops rochai</i>	1	
2015	JIMWE004	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Halicyclops rochai</i>	1	
2015	JIMWE004	Crustacea	Copepoda	Harpacticoida	Parastenocarididae	<i>Parastenocaris sp. 'indet'</i>	1	Indeterminate Species
2015	JIMWE004	Crustacea	Copepoda	Harpacticoida	Parastenocarididae	<i>Parastenocaris sp. 'indet'</i>	1	Indeterminate Species
2015	JW023	Crustacea	Copepoda	Cyclopoida	-	<i>Cyclopoida sp. 'indet'</i>	1	Indeterminate Species
2015	JW023	Crustacea	Copepoda	Cyclopoida	-	<i>Cyclopoida sp. 'indet'</i>	1	Indeterminate Species
2015	JW023	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Halicyclops rochai</i>	6	
2015	JW023	Crustacea	Malacostraca	Amphipoda	Eriopisidae	<i>Eriopisidae sp. '1 (PSS)'</i>	1	Widespread
2015	JW023	Crustacea	Malacostraca	Amphipoda	Eriopisidae	<i>Eriopisidae sp. '1 (PSS)'</i>	1	Widespread
2015	JW023	Crustacea	Malacostraca	Amphipoda	Eriopisidae	<i>Nedsia hurlberti</i>	1	
2015	JW023	Crustacea	Malacostraca	Amphipoda	Eriopisidae	<i>Nedsia hurlberti</i>	1	
2015	JW023	Crustacea	Malacostraca	Amphipoda	Eriopisidae	<i>Nedsia sp. 'indet'</i>	1	Indeterminate Species
2015	JW023	Crustacea	Malacostraca	Amphipoda	Eriopisidae	<i>Nedsia sp. 'indet'</i>	1	Indeterminate Species
2015	JW023	Crustacea	Malacostraca	Isopoda	Cirolanidae	<i>Kagalana tonde</i>	2	
2015	JW023	Crustacea	Malacostraca	Isopoda	Tainisopidae	<i>Pygolabis sp. 'indet'</i>	1	Indeterminate Species
2015	JW023	Crustacea	Malacostraca	Isopoda	Tainisopidae	<i>Pygolabis sp. 'indet'</i>	1	Indeterminate Species
2015	JW024	Crustacea	Copepoda	Calanoida	Ridgewayiidae	<i>Stygoridgewayia trispinosa</i>	5	
2015	JW024	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Diacyclops sp. 'indet'</i>	1	Indeterminate Species
2015	JW024	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Diacyclops sp. 'indet'</i>	1	Indeterminate Species
2015	JW024	Crustacea	Malacostraca	Amphipoda	-	<i>Amphipoda sp. 'indet'</i>	3	Indeterminate Species
2015	JW024	Crustacea	Malacostraca	Amphipoda	Bogidiellidae	<i>Bogidiellidae sp. 'indet'</i>	2	Indeterminate Species
2015	JW024	Crustacea	Malacostraca	Amphipoda	Bogidiellidae	<i>Bogidiellidae sp. 'indet'</i>	2	Indeterminate Species
2015	JW024	Crustacea	Malacostraca	Amphipoda	Eriopisidae	<i>Nedsia hurlberti</i>	2	
2015	JW024	Crustacea	Malacostraca	Amphipoda	Eriopisidae	<i>Nedsia hurlberti</i>	7	
2015	JW024	Crustacea	Malacostraca	Amphipoda	Eriopisidae	<i>Nedsia sp. 'indet'</i>	1	Indeterminate Species

Year	Site	Phylum	Class	Order	Family	Species	#	Notes
2015	JW024	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Nedsia sp. 'indet'	1	Indeterminate Species
2015	JW024	Crustacea	Malacostraca	Amphipoda	Paramelitidae	Paramelitidae Genus 2 sp. 'Indet'	1	Indeterminate Species
2015	JW024	Crustacea	Malacostraca	Amphipoda	Paramelitidae	Paramelitidae Genus 2 sp. 'Indet'	1	Indeterminate Species
2015	JW024	Crustacea	Malacostraca	Isopoda	Cirolanidae	Haptolana sp. 'B01'	1	
2015	JW024	Crustacea	Malacostraca	Isopoda	Cirolanidae	Haptolana sp. 'B01'	1	
2015	JW024	Crustacea	Malacostraca	Themosbaenacea	Halosbaenidae	Halosbaena tulki	92	
2015	JW024	Crustacea	Ostracoda	Podocopida	Candoninae	Candoninae sp. 'BOS541'	1	
2015	PZ10BUN004	Crustacea	Copepoda	Cyclopoida	Cyclopidae	Diacyclops humphreysi humphreysi	2	
2015	PZ11BUN003	Crustacea	Copepoda	Cyclopoida	Cyclopidae	Halicyclops rochai	6	
2015	PZ11BUN008	Crustacea	Malacostraca	Amphipoda	Paramelitidae	Paramelitidae Genus 2 sp. 'Indet'	1	Indeterminate Species
2015	RC13MEH0007	Crustacea	Copepoda	Calanoida	Ridgewayiidae	Stygoridgewayia trispinosa	14	
2015	RC13MEH0007	Crustacea	Copepoda	Cyclopoida	Cyclopidae	Diacyclops humphreysi humphreysi	10	
2015	RC13MEH0007	Crustacea	Malacostraca	Amphipoda	Paramelitidae	Paramelitidae sp. 'Mesa H A'	1	
2015	RC13MEH0041	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Nedsia sp. 'AMM001/029/030'	1	
2015	RC13MEH0097	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Nedsia sp. 'AMM001/029/030'	1	
2015	RC13MEH0097	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Nedsia sp. 'AMM001/029/030'	1	
2015	RC13MEH0097	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Nedsia sp. 'AMM001/029/030'	1	
2015	RC14MEH0018	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Nedsia sp. 'AMM001/029/030'	1	
2015	RC14MEH0053	Crustacea	Copepoda	Calanoida	Ridgewayiidae	Stygoridgewayia trispinosa	9	
2015	RC14MEH0053	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Nedsia sp. 'AMM001/029/030'	1	
2015	RC14MEH0053	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Nedsia sp. 'AMM001/029/030'	1	
2016	25	Crustacea	Copepoda	Cyclopoida	-	Cyclopoida sp. 'indet'	1	Indeterminate Species
2016	25	Crustacea	Malacostraca	Amphipoda	-	Amphipoda sp. 'indet'	3	Indeterminate Species
2016	25	Crustacea	Malacostraca	Bathynellacea	-	Bathynellacea sp. 'indet'	1	Indeterminate Species
2016	31	Crustacea	Copepoda	Calanoida	Ridgewayiidae	Stygoridgewayia trispinosa	4	
2016	31	Crustacea	Copepoda	Cyclopoida	-	Cyclopoida sp. 'indet'	20	Indeterminate Species
2016	31	Crustacea	Copepoda	Cyclopoida	Cyclopidae	Halicyclops rochai	2	
2016	31	Crustacea	Malacostraca	Amphipoda	-	Amphipoda sp. 'indet'	32	Indeterminate Species
2016	31	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Nedsia sp. 'AMM001/029/030'	1	
2016	31	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Nedsia sp. 'AMM001/029/030'	1	
2016	31	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Nedsia sp. 'AMM001/029/030'	1	
2016	31	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Nedsia sp. 'Mesa H A'	1	
2016	31	Crustacea	Malacostraca	Themosbaenacea	-	Themosbaenacea sp. 'indet'	16	Indeterminate Species
2016	31	Platyhelminthes	Turbellaria	-	-	Turbellaria sp. 'indet'	8	Indeterminate Species
2016	32	Crustacea	Copepoda	Cyclopoida	-	Cyclopoida sp. 'indet'	5	Indeterminate Species
2016	32	Crustacea	Malacostraca	Amphipoda	-	Amphipoda sp. 'indet'	4	Indeterminate Species
2016	32	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Nedsia sp. 'AMM001/029/030'	1	
2016	32	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Nedsia sp. 'AMM001/029/030'	1	
2016	32	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Nedsia sp. 'AMM001/029/030'	1	
2016	32	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Nedsia sp. 'AMM001/029/030'	1	
2016	32	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Nedsia sp. 'AMM001/029/030'	1	
2016	32	Crustacea	Malacostraca	Amphipoda	Neoniphargidae	Neoniphargidae sp. 'B1'	1	

Year	Site	Phylum	Class	Order	Family	Species	#	Notes
2016	32	Platyhelminthes	Turbellaria	-	-	Turbellaria sp. 'indet'	1	Indeterminate Species
2016	34	Crustacea	Copepoda	Cyclopoida	-	Cyclopoida sp. 'indet'	3	Indeterminate Species
2016	34	Crustacea	Malacostraca	Amphipoda	-	Amphipoda sp. 'indet'	3	Indeterminate Species
2016	34	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Nedsia sp. 'AMM001/029/030'	1	
2016	87	Crustacea	Copepoda	Cyclopoida	-	Cyclopoida sp. 'indet'	11	Indeterminate Species
2016	87	Crustacea	Malacostraca	Amphipoda	-	Amphipoda sp. 'indet'	19	Indeterminate Species
2016	87	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Nedsia sp. 'AMM004'	1	
2016	87	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Nedsia sp. 'AMM004'	1	
2016	87	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Nedsia sp. 'AMM004'	1	
2016	87	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Nedsia sp. 'AMM004'	1	
2016	87	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Nedsia sp. 'AMM004'	1	
2016	87	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Nedsia sp. 'AMM004'	1	
2016	87	Crustacea	Ostracoda	-	-	Ostracoda sp. 'indet'	2	Indeterminate Species
2016	87	Crustacea	Ostracoda	Podocopida	Candonidae	Humphreyscandona imperfecta	1	
2016	200	Crustacea	Malacostraca	Amphipoda	-	Amphipoda sp. 'indet'	4	Indeterminate Species
2016	200	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Nedsia sp. 'AMM004'	1	
2016	200	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Nedsia sp. 'AMM004'	1	
2016	200	Crustacea	Malacostraca	Amphipoda	Niphargidae	Niphargidae sp. 'AMN008'	1	
2016	200	Crustacea	Malacostraca	Amphipoda	Niphargidae	Niphargidae sp. 'AMN008'	1	
2016	200	Crustacea	Malacostraca	Amphipoda	Niphargidae	Niphargidae sp. 'AMN008'	1	
2016	200	Crustacea	Ostracoda	-	-	Ostracoda sp. 'indet'	1	Indeterminate Species
2016	200	Crustacea	Ostracoda	Podocopida	Candonidae	Pilbaracandona sp. 'BOS526'	1	
2016	BC186	Annelida	Oligochaeta	Tubificida	Enchytraeidae	Enchytraeidae sp. '1 (PSS)'	1	
2016	BC186	Crustacea	Copepoda	Calanoida	Ridgewayiidae	Stygoridgewayia trispinosa	70	
2016	BC186	Crustacea	Copepoda	Calanoida	Ridgewayiidae	Stygoridgewayia trispinosa	35	
2016	BC186	Crustacea	Copepoda	Cyclopoida	Cyclopidae	Halicyclops rochai	2	
2016	BC186	Crustacea	Copepoda	Cyclopoida	Cyclopidae	Halicyclops rochai	2	
2016	BC186	Crustacea	Malacostraca	Amphipoda	-	Amphipoda sp. 'indet'	1	Indeterminate Species
2016	BC186	Crustacea	Malacostraca	Amphipoda	-	Amphipoda sp. 'indet'	2	Indeterminate Species
2016	BC186	Crustacea	Malacostraca	Thermosbaenacea	Halosbaenidae	Halosbaena tulki	18	
2016	BC186	Crustacea	Malacostraca	Thermosbaenacea	Halosbaenidae	Halosbaena tulki	3	
2016	BC225	Crustacea	Malacostraca	Amphipoda	-	Amphipoda sp. 'indet'	1	Indeterminate Species
2016	BC225	Crustacea	Ostracoda	-	-	Ostracoda sp. 'BOS661'	1	
2016	BC292	Crustacea	Copepoda	Cyclopoida	Cyclopidae	Diacyclops humphreysi humphreysi	1	
2016	BC292	Crustacea	Malacostraca	Bathynellacea	Parabathynellidae	Brevisomabathynella sp. 'indet'	1	Indeterminate Species
2016	BC401	Crustacea	Malacostraca	Amphipoda	-	Amphipoda sp. 'indet'	1	Indeterminate Species
2016	BC401	Crustacea	Malacostraca	Bathynellacea	Parabathynellidae	Hexabathynella sp. B06	2	
2016	BC405	Annelida	Oligochaeta	Tubificida	Tubificidae	Tubificidae sp. 'group B'	1	
2016	BC405	Crustacea	Copepoda	Cyclopoida	Cyclopidae	Halicyclops rochai	11	
2016	BC405	Crustacea	Malacostraca	Amphipoda	-	Amphipoda sp. 'indet'	5	Indeterminate Species
2016	BC405	Platyhelminthes	-	-	-	Platyhelminthes sp. 'indet'	50	Indeterminate Species
2016	BC434	Annelida	Oligochaeta	Tubificida	Phreodrilidae	Phreodrilidae sp. 'dissimilar ventral'	1	Widespread

Year	Site	Phylum	Class	Order	Family	Species	#	Notes
						chaetae'		
2016	BC434	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Diacyclops humphreysi humphreysi</i>	1	
2016	BC434	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Diacyclops humphreysi humphreysi</i>	1	
2016	BC434	Crustacea	Malacostraca	Bathynellacea	Parabathynellidae	<i>Hexabathynella</i> sp. B06	1	
2016	BUNUNK01	Crustacea	Malacostraca	Amphipoda	-	Amphipoda sp. "indet"	1	Indeterminate Species
2016	BUNWB09	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Halicyclops rochai</i>	41	
2016	BUNWB09	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Halicyclops rochai</i>	9	
2016	BUNWB09	Crustacea	Diplostraca	Cladocera	-	Cladocera sp. "indet"	1	Indeterminate Species
2016	BUNWB09	Crustacea	Malacostraca	Amphipoda	-	Amphipoda sp. "indet"	1	Indeterminate Species
2016	BUNWB09	Crustacea	Malacostraca	Amphipoda	-	Amphipoda sp. "indet"	4	Indeterminate Species
2016	BUNWB09	Crustacea	Malacostraca	Isopoda	Microcerberidae	Microcerberidae sp. 'B13'	1	
2016	BUNWB09	Mollusca	Gastropoda	Sorbeoconcha	Hydrobiidae	Hydrobiidae sp. '1'	45	
2016	BUNWB13	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Diacyclops humphreysi humphreysi</i>	3	
2016	BUNWB13	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Halicyclops rochai</i>	1	
2016	BUNWB13	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Pescecylops pilbaricus</i>	1	
2016	BUNWB13	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Pescecylops pilbaricus</i>	1	
2016	BUNWB13	Crustacea	Copepoda	Harpacticoida	Canthocamptidae	Canthocamptidae sp. "indet"	1	Indeterminate Species
2016	BUNWB13	Crustacea	Malacostraca	Amphipoda	-	Amphipoda sp. "indet"	3	Indeterminate Species
2016	BUNWB13	Crustacea	Malacostraca	Amphipoda	-	Amphipoda sp. "indet"	1	Indeterminate Species
2016	BUNWB13	Crustacea	Malacostraca	Bathynellacea	Parabathynellidae	<i>Bilobathynella</i> sp. 'B10'	1	
2016	BUNWB13	Crustacea	Malacostraca	Bathynellacea	Parabathynellidae	<i>Bilobathynella</i> sp. 'B10'	1	
2016	BUNWB13	Crustacea	Malacostraca	Bathynellacea	Parabathynellidae	<i>Hexabathynella</i> sp. B11	1	
2016	BUNWB13	Mollusca	Gastropoda	Sorbeoconcha	Hydrobiidae	Hydrobiidae sp. '1'	127	
2016	BUNWO1108	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Diacyclops humphreysi humphreysi</i>	1	
2016	BUNWO1108	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Halicyclops rochai</i>	6	
2016	BUNWO1108	Crustacea	Malacostraca	Amphipoda	-	Amphipoda sp. "indet"	1	Indeterminate Species
2016	BUNWP0005	Crustacea	Copepoda	Calanoida	Ridgewayiidae	<i>Stygoridgewaya trispinosa</i>	4	
2016	BUNWP0005	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Diacyclops humphreysi humphreysi</i>	1	
2016	BUNWP0005	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Halicyclops rochai</i>	23	
2016	BUNWP0005	Crustacea	Copepoda	Harpacticoida	Canthocamptidae	<i>Elaphoidella humphreysi</i>	1	
2016	BUNWP0005	Crustacea	Malacostraca	Amphipoda	-	Amphipoda sp. "indet"	1	Indeterminate Species
2016	BUNWP0005	Platyhelminthes	Turbellaria	-	-	Platyhelminthes sp. "indet"	6	Indeterminate Species
2016	BUNWP0006	Crustacea	Copepoda	Cyclopoida	Cyclopidae	<i>Diacyclops humphreysi humphreysi</i>	10	
2016	BUNWP0006	Crustacea	Copepoda	Harpacticoida	Canthocamptidae	<i>Elaphoidella humphreysi</i>	1	
2016	BUNWP0006	Crustacea	Diplostraca	Cladocera	-	Cladocera sp. "indet"	1	Indeterminate Species
2016	BUNWP0006	Crustacea	Ostracoda	Podocopida	Candonidae	<i>Areacandona triangulum</i>	1	
2016	BUNWP0006	Crustacea	Ostracoda	Podocopida	Candonidae	<i>Areacandona triangulum</i>	2	
2016	DD13MEH0007	Crustacea	Copepoda	Cyclopoida	-	Cyclopoida sp. "indet"	8	Indeterminate Species
2016	DD13MEH0007	Crustacea	Malacostraca	Amphipoda	-	Amphipoda sp. "indet"	7	Indeterminate Species
2016	DD13MEH0007	Crustacea	Malacostraca	Amphipoda	Eriopisidae	<i>Nedsia</i> sp. 'AMM001/029/030'	1	
2016	DD13MEH0007	Crustacea	Malacostraca	Amphipoda	Eriopisidae	<i>Nedsia</i> sp. 'AMM001/029/030'	1	
2016	DD13MEH0007	Crustacea	Malacostraca	Amphipoda	Eriopisidae	<i>Nedsia</i> sp. 'AMM001/029/030'	1	

Year	Site	Phylum	Class	Order	Family	Species	#	Notes
2016	DD13MEH0007	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Nedsia sp. 'AMM001/029/030'	1	
2016	DD13MEH0007	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Nedsia sp. 'AMM001/029/030'	1	
2016	DD13MEH0007	Platyhelminthes	Turbellaria	-	-	Platyhelminthes sp. 'indet'	1	Indeterminate Species
2016	J154	Crustacea	Copepoda	Cyclopoida	Cyclopidae	Diacyclops humphreysi humphreysi	1	
2016	J154	Crustacea	Malacostraca	Amphipoda	-	Amphipoda sp. 'indet'	1	Indeterminate Species
2016	JIMWE003	Crustacea	Copepoda	Cyclopoida	Cyclopidae	Diacyclops humphreysi humphreysi	6	
2016	JIMWE003	Crustacea	Copepoda	Harpacticoida	Ameiridae	Inermipes sp. 'B01'	1	
2016	JIMWE003	Crustacea	Ostracoda	Podocopida	Candonidae	Areacandona triangulum	1	
2016	JIMWE004	Crustacea	Copepoda	Cyclopoida	Cyclopidae	Diacyclops humphreysi humphreysi	2	
2016	JIMWE004	Crustacea	Copepoda	Cyclopoida	Cyclopidae	Halicyclops rochai	3	
2016	JIMWE004	Crustacea	Malacostraca	Amphipoda	-	Amphipoda sp. 'indet'	14	Indeterminate Species
2016	JW023	Annelida	Oligochaeta	Tubificida	Phreodrilidae	Phreodrilidae sp. 'dissimilar ventral chaetae'	3	Widespread
2016	JW023	Annelida	Oligochaeta	Tubificida	Tubificidae	Tubificidae sp. 'group B'	5	
2016	JW023	Chordata	Actinopterygii	Synbranchiformes	Synbranchidae	Ophisternon candidum	1	
2016	JW023	Crustacea	Copepoda	Cyclopoida	Cyclopidae	Diacyclops humphreysi humphreysi	1	
2016	JW023	Crustacea	Copepoda	Cyclopoida	Cyclopidae	Halicyclops rochai	10	
2016	JW023	Crustacea	Malacostraca	Amphipoda	-	Amphipoda sp. 'indet'	1	Indeterminate Species
2016	JW023	Crustacea	Malacostraca	Amphipoda	-	Amphipoda sp. 'indet'	6	Indeterminate Species
2016	JW023	Crustacea	Malacostraca	Isopoda	Cirolanidae	Kagalana tonde	1	
2016	JW024	Crustacea	Copepoda	Calanoida	Ridgewayiidae	Stygoridgewaya trispinosa	16	
2016	JW024	Crustacea	Malacostraca	Amphipoda	-	Amphipoda sp. 'indet'	11	Indeterminate Species
2016	JW024	Crustacea	Malacostraca	Amphipoda	-	Amphipoda sp. 'indet'	19	Indeterminate Species
2016	JW024	Crustacea	Malacostraca	Thermosbaenacea	Halosbaenidae	Halosbaena tulki	22	
2016	JW024	Platyhelminthes	Turbellaria	-	-	Platyhelminthes sp. 'indet'	1	Indeterminate Species
2016	MCPE5	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Nedsia sp. 'AMM001/029/030'	1	
2016	MCPE5	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Nedsia sp. 'AMM001/029/030'	1	
2016	MCPE5	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Nedsia sp. 'Indet'	12	Indeterminate Species
2016	MCPE5	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Nedsia sp. 'Indet'	1	Indeterminate Species
2016	MCPE6	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Nedsia sp. 'Indet'	20	Indeterminate Species
2016	MCR2	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Nedsia sp. 'Indet'	1	Indeterminate Species
2016	MCR3*	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Nedsia sp. 'AMM001/029/030'	1	
2016	MCR3*	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Nedsia sp. 'AMP-Eri-001A'	1	
2016	MCR3*	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Nedsia sp. 'Indet'	4	Indeterminate Species
2016	MCR3*	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Nedsia sp. 'Indet'	29	Indeterminate Species
2016	PZ10BUN004	Crustacea	Copepoda	Cyclopoida	Cyclopidae	Diacyclops humphreysi humphreysi	2	
2016	RC12JIM0019	Crustacea	Malacostraca	Amphipoda	-	Amphipoda sp. 'indet'	1	Indeterminate Species
2016	RC12JIM0019	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Nedsia sp. 'AMM001/029/030'	1	
2016	RC12JIM0019	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Nedsia sp. 'AMM001/029/030'	1	
2016	RC12JIM0019	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Nedsia sp. 'AMM001/029/030'	1	
2016	RC12JIM0019	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Nedsia sp. 'AMM001/029/030'	1	

Year	Site	Phylum	Class	Order	Family	Species	#	Notes
2016	RC12JIM0019	Platyhelminthes	Turbellaria	-	-	Platyhelminthes sp. 'indet'	1	Indeterminate Species
2016	RC13MEH0007	Crustacea	Copepoda	Cyclopoida	-	Cyclopoida sp. 'indet'	24	Indeterminate Species
2016	RC13MEH0040	Crustacea	Copepoda	Cyclopoida	-	Cyclopoida sp. 'indet'	1	Indeterminate Species
2016	RC13MEH0040	Crustacea	Malacostraca	Amphipoda	-	Amphipoda sp. 'indet'	3	Indeterminate Species
2016	RC13MEH0040	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Nedsia sp. 'AMM001/029/030'	1	
2016	RC13MEH0040	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Nedsia sp. 'AMM001/029/030'	1	
2016	RC13MEH0041	Crustacea	Malacostraca	Amphipoda	Paramelitidae	Paramelitidae sp. 'Mesa H A'	1	
2016	RC14MEH0018	Crustacea	Copepoda	Calanoida	Ridgewayiidae	Stygoridgewayia trispinosa	1	
2016	RC14MEH0018	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Nedsia sp. 'AMM001/029/030'	1	
2016	RC14MEH0018	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Nedsia sp. 'AMM001/029/030'	1	
2016	RC14MEH0018	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Nedsia sp. 'AMM001/029/030'	1	
2016	RC14MEH0018	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Nedsia sp. 'AMM001/029/030'	1	
2016	RC14MEH0018	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Nedsia sp. 'AMM001/029/030'	1	
2016	RC14MEH0053	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Nedsia sp. 'AMM001/029/030'	1	
2016	RC14MEH0053	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Nedsia sp. 'AMM001/029/030'	1	
2016	RC14MEH0053	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Nedsia sp. 'AMM001/029/030'	1	
2016	RC14MEH0053	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Nedsia sp. 'AMM001/029/030'	1	
2016	RC14MEH0053	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Nedsia sp. 'AMM001/029/030'	1	
2016	RC16JIM0019	Crustacea	Malacostraca	Amphipoda	-	Amphipoda sp. 'indet'	19	Indeterminate Species
2016	RR1	Crustacea	Copepoda	Calanoida	Ridgewayiidae	Stygoridgewayia trispinosa	10	
2016	RR1	Crustacea	Copepoda	Cyclopoida	Cyclopidae	Diacyclops cockingi	1	
2016	RR1	Crustacea	Copepoda	Cyclopoida	Cyclopidae	Halicyclops rochai	2	
2016	RR1	Crustacea	Malacostraca	Amphipoda	-	Amphipoda sp. 'indet'	1	Indeterminate Species
2016	RR1	Crustacea	Malacostraca	Amphipoda	-	Amphipoda sp. 'indet'	1	Indeterminate Species
2016	RR1	Crustacea	Malacostraca	Amphipoda	-	Amphipoda sp. 'indet'	9	Indeterminate Species
2016	RR1	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Nedsia sp. 'AMM001/029/030'	1	
2016	RR1	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Nedsia sp. 'AMM001/029/030'	1	
2016	RR1	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Nedsia sp. 'AMM001/029/030'	1	
2016	RR1	Crustacea	Malacostraca	Isopoda	Cirolanidae	Haptolana yarraloola	1	
2016	RR1	Crustacea	Malacostraca	Isopoda	Cirolanidae	Kagalana tonde	1	
2016	RR1	Crustacea	Ostracoda	-	-	Ostracoda sp. 'indet'	7	Indeterminate Species
2016	RR1	Crustacea	Ostracoda	Podocopida	Candonidae	Candoninae n. gen sp. 'BOS577'	3	
2016	RR1	Crustacea	Ostracoda	Podocopida	Candonidae	Pierrecandona sp. 'BOS576'	1	
2016	RRD1	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Nedsia sp. 'Indet'	24	Indeterminate Species
2016	RRD2	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Nedsia sp. 'Indet'	12	Indeterminate Species
2016	RRD3	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Nedsia sp. 'Indet'	15	Indeterminate Species
2016	RRD3	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Nedsia sp. 'Indet'	9	Indeterminate Species
2016	RRD3	Crustacea	Malacostraca	Amphipoda	Paramelitidae	Chydaekata sp. 'AMP-Par-001'	1	
2016	RRD4	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Nedsia sp. 'AMM001/029/030'	1	
2016	RRD4	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Nedsia sp. 'AMM001/029/030'	1	
2016	RRD4	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Nedsia sp. 'AMM001/029/030'	1	
2016	RRD4	Crustacea	Malacostraca	Amphipoda	Eriopisidae	Nedsia sp. 'AMM001/029/030'	1	

Year	Site	Phylum	Class	Order	Family	Species	#	Notes
2016	RRD4	Crustacea	Malacostraca	Amphipoda	Eriopisidae	<i>Nedsia</i> sp. 'AMP-Eri-001A'	1	
2016	RRD4	Crustacea	Malacostraca	Amphipoda	Eriopisidae	<i>Nedsia</i> sp. 'Indet'	6	Indeterminate Species
2016	RRU1	Crustacea	Malacostraca	Amphipoda	Eriopisidae	<i>Nedsia</i> sp. 'Indet'	1	Indeterminate Species
2016	RRU3	Crustacea	Malacostraca	Amphipoda	Eriopisidae	<i>Nedsia</i> sp. 'AMM001/029/030'	1	
2016	RRU3	Crustacea	Malacostraca	Amphipoda	Eriopisidae	<i>Nedsia</i> sp. 'AMM001/029/030'	1	
2016	RRU3	Crustacea	Malacostraca	Amphipoda	Eriopisidae	<i>Nedsia</i> sp. 'Indet'	6	Indeterminate Species
2016	RRU4	Crustacea	Malacostraca	Amphipoda	Eriopisidae	<i>Nedsia</i> sp. 'Indet'	1	Indeterminate Species
2016	RRU5	Crustacea	Malacostraca	Amphipoda	Eriopisidae	<i>Nedsia</i> sp. 'Indet'	4	Indeterminate Species
2016	RRU6	Crustacea	Malacostraca	Amphipoda	Eriopisidae	<i>Nedsia</i> sp. 'AMM001/029/030'	1	
2016	RRU6	Crustacea	Malacostraca	Amphipoda	Eriopisidae	<i>Nedsia</i> sp. 'AMM001/029/030'	1	
2016	RRU6	Crustacea	Malacostraca	Amphipoda	Eriopisidae	<i>Nedsia</i> sp. 'Indet'	28	Indeterminate Species

## Appendix 6

Raw Sampling Data (Warramboo and  
Mesa C)





Site Name	Easting (m E)	Northing (m N)	Phase	Order	Family	Species	N	WAM Number	ID by	ID Method
<b>Warramboo</b>										
TOBRC0009	380913	7600605	1	Amphipoda	Eriopisidae	Eriopisidae nov. gen. sp. 'AMM006'	1		Helix	
Camp Bore	382763	7612704	1	Amphipoda	Eriopisidae	Nedsia sp. 'AMM001/029/030'	1		Helix	
Camp Bore	381745	7617580	1	Amphipoda	Eriopisidae	Nedsia sp. 'AMM001/029/030'	1		Helix	
Camp Bore	381745	7617580	1	Amphipoda	Eriopisidae	Nedsia sp. 'AMM001/029/030'	1		Helix	
Budgie Bore	382495	7615587	1	Amphipoda	Eriopisidae	Nedsia sp. 'AMM002'	1		Helix	
Budgie Bore	382495	7615587	1	Amphipoda	Eriopisidae	Nedsia sp. 'AMM002'	1		Helix	
Daisy Well	381745	7617580	1	Amphipoda	Eriopisidae	Nedsia sp. 'AMM002'	1		Helix	
MB13WARR010	377109	7605909	1	Amphipoda	Eriopisidae	Nedsia sp. 'AMM005'	1		Helix	Potential SRE species
MB13WARR010	377109	7605909	1	Amphipoda	Eriopisidae	Nedsia sp. 'AMM005'	1		Helix	Potential SRE species
MB13WARR010	377109	7605909	1	Amphipoda	Eriopisidae	Nedsia sp. 'AMM005'	1		Helix	Potential SRE species
MB13WARR001	377532	7604747	1	Amphipoda	Eriopisidae	Nedsia sp. 'AMM005'	1		Helix	Potential SRE species
MB13WARR001	377532	7604747	1	Amphipoda	Eriopisidae	Nedsia sp. 'AMM005'	1		Helix	Potential SRE species
MB13WARR001	377532	7604747	1	Amphipoda	Eriopisidae	Nedsia sp. 'AMM005'	1		Helix	Potential SRE species
MB13WARR001	377532	7604747	1	Amphipoda	Eriopisidae	Nedsia sp. 'AMM005'	1		Helix	Potential SRE species
Budgie Bore	382495	7615587	1	Amphipoda	Eriopisidae	Nedsia sp. 'AMM028'	1		Helix	
Budgie Bore	382495	7615587	1	Amphipoda	Indeterminate	Amphipoda sp. Indet	1		Biota	Failed to yield sequence
Daisy Well	382763	7612704	1	Amphipoda	Indeterminate	Amphipoda sp. Indet	1		Biota	Failed to yield sequence
MB13WARR001	377532	7604747	1	Amphipoda	Indeterminate	Amphipoda sp. Indet	18		Biota	
MB13WARR010	377109	7605909	1	Amphipoda	Indeterminate	Amphipoda sp. Indet	6		Biota	
MB13WARR010	377109	7605909	1	Amphipoda	Indeterminate	Amphipoda sp. Indet	1		Biota	Failed to yield sequence
MB13WARR010	377109	7605909	1	Amphipoda	Indeterminate	Amphipoda sp. Indet	1		Biota	Failed to yield sequence

RC13MEA0279	376781	7605110	1	Amphipoda	Indeterminate	Amphipoda sp. Indet	1		Biota	Failed to yield sequence
TOBRC0009	380913	7600605	1	Amphipoda	Indeterminate	Amphipoda sp. Indet	1		Biota	Failed to yield sequence
Budgie Bore	382495	7615587	1	Amphipoda	Niphargidae	Niphargidae sp. 'AMN008'	1		Helix	
Budgie Bore	382495	7615587	1	Amphipoda	Niphargidae	Niphargidae sp. 'AMN008'	1		Helix	
Budgie Bore	382495	7615587	1	Amphipoda	Paramelitidae	Paramelitidae sp. 'AMP009'	1		Helix	
TOBRC0009	380913	7600605	1	Amphipoda	Paramelitidae	Paramelitidae sp. 'AMP023'	1		Helix	Widespread species
TOBRC0009	380913	7600605	1	Amphipoda	Paramelitidae	Paramelitidae sp. 'AMP023'	1		Helix	Widespread species
TOBRC0009	380913	7600605	1	Amphipoda	Paramelitidae	Paramelitidae sp. 'AMP023'	1		Helix	Widespread species
TOBRC0009	380913	7600605	1	Amphipoda	Paramelitidae	Paramelitidae sp. 'AMP023'	1		Helix	Widespread species
Budgie Bore	382495	7615587	1	Calanoida	Ridgewayiidae	Stygoridgewayia trispinosa	2		Bennelongia	
Camp Bore	382763	7612704	1	Cyclopoida	Cyclopidae	Diacyclops humphreysi humphreysi	15		Bennelongia	
RC13MEA0279	376781	7605110	1	Cyclopoida	Cyclopidae	Diacyclops humphreysi unispinosus	15		Bennelongia	
Budgie Bore	382495	7615587	1	Cyclopoida	Cyclopidae	Microcyclops varicans	19		Bennelongia	Widespread species
Queen Well	374567	7617795	1	Cyclopoida	Cyclopidae	Paracyclops chiltoni	21		Bennelongia	
Queen Well	374567	7617795	1	Haplotaxida	Enchytraeidae	Enchytraeidae sp. Indet	1		Adrian Pinder	
Daisy Well	381745	7617580	1	Haplotaxida	Naididae	Dero furcata	4		Adrian Pinder	
Budgie Bore	382495	7615587	1	Haplotaxida	Naididae	Pristina longiseta	6		Adrian Pinder	
RC13MEA0279	376781	7605110	1	Harpacticoida	Ameiridae	Inermipes humphreysi	4		Bennelongia	Widespread species
Budgie Bore	382495	7615587	1	Indeterminate	Indeterminate	Nematoda sp. Indet	3		Bennelongia	
Budgie Bore	382495	7615587	1	Thermosbaenacea	Halosbaenidae	Halosbaena tulki	27		Bennelongia	
Budgie Bore	382495	7615587	2	Amphipoda	Eriopisidae	Nedsia sp. 'AMM001/029/030'	1		Helix	
Budgie Bore	382495	7615587	2	Amphipoda	Eriopisidae	Nedsia sp. 'AMM001/029/030'	1		Helix	
Budgie Bore	382495	7615587	2	Amphipoda	Eriopisidae	Nedsia sp. 'AMM001/029/030'	1		Helix	
Budgie Bore	382495	7615587	2	Amphipoda	Eriopisidae	Nedsia sp. 'AMM001/029/030'	1		Helix	

Budgie Bore	382495	7615587	2	Amphipoda	Eriopisidae	Nedsia sp. 'AMM001/029/030'	1		Helix	
Budgie Bore	382495	7615587	2	Amphipoda	Eriopisidae	Nedsia sp. 'AMM001/029/030'	1		Helix	
Budgie Bore	382495	7615587	2	Amphipoda	Eriopisidae	Nedsia sp. 'AMM001/029/030'	1		Helix	
Budgie Bore	382495	7615587	2	Amphipoda	Eriopisidae	Nedsia sp. 'AMM001/029/030'	1		Helix	
Budgie Bore	382495	7615587	2	Amphipoda	Eriopisidae	Nedsia sp. 'AMM001/029/030'	1		Helix	
Budgie Bore	382495	7615587	2	Amphipoda	Eriopisidae	Nedsia sp. 'AMM001/029/030'	1		Helix	
Camp Bore	382763	7612704	2	Amphipoda	Eriopisidae	Nedsia sp. 'AMM001/029/030'	1		Helix	
MB13WARR001	377532	7604747	2	Amphipoda	Eriopisidae	Nedsia sp. 'AMM005'	1		Helix	Potential SRE species
Budgie Bore	382495	7615587	2	Amphipoda	Eriopisidae	Nedsia sp. 'AMM027'	1		Helix	
Budgie Bore	382495	7615587	2	Amphipoda	Eriopisidae	Nedsia sp. 'AMM031'	1		Helix	
Budgie Bore	382495	7615587	2	Amphipoda	Eriopisidae	Nedsia sp. 'AMM031'	1		Helix	
Budgie Bore	382495	7615587	2	Amphipoda	Indeterminate	Amphipoda sp. Indet	1		Biota	Failed to yield sequence
Budgie Bore	382495	7615587	2	Amphipoda	Indeterminate	Amphipoda sp. Indet	1		Biota	Failed to yield sequence
TOBRC0009	380913	7600605	2	Amphipoda	Indeterminate	Amphipoda sp. Indet	1		Biota	Failed to yield sequence
TOBRC0009	380913	7600605	2	Amphipoda	Indeterminate	Amphipoda sp. Indet	1		Biota	Failed to yield sequence
TOBRC0009	380913	7600605	2	Amphipoda	Indeterminate	Amphipoda sp. Indet	1		Biota	Failed to yield sequence
TOBRC0009	380913	7600605	2	Amphipoda	Indeterminate	Amphipoda sp. Indet	1		Biota	Failed to yield sequence
Budgie Bore	382495	7615587	2	Amphipoda	Niphargidae	Niphargidae sp. 'AMN001'	1		Helix	
Budgie Bore	382495	7615587	2	Amphipoda	Niphargidae	Niphargidae sp. 'AMN008'	1		Helix	
Budgie Bore	382495	7615587	2	Amphipoda	Niphargidae	Niphargidae sp. 'AMN008'	1		Helix	
Budgie Bore	382495	7615587	2	Amphipoda	Niphargidae	Niphargidae sp. 'AMN008'	1		Helix	
Budgie Bore	382495	7615587	2	Amphipoda	Niphargidae	Niphargidae sp. 'AMN008'	1		Helix	
Budgie Bore	382495	7615587	2	Amphipoda	Niphargidae	Niphargidae sp. 'AMN008'	1		Helix	
Budgie Bore	382495	7615587	2	Amphipoda	Niphargidae	Niphargidae sp. 'AMN008'	1		Helix	

TOBRC0009	380913	7600605	2	Amphipoda	Paramelitidae	Paramelitidae sp. 'AMP023'	1		Helix	Widespread species
TOBRC0009	380913	7600605	2	Amphipoda	Paramelitidae	Paramelitidae sp. 'AMP023'	1		Helix	Widespread species
TOBRC0009	380913	7600605	2	Amphipoda	Paramelitidae	Paramelitidae sp. 'AMP023'	1		Helix	Widespread species
TOBRC0009	380913	7600605	2	Amphipoda	Paramelitidae	Paramelitidae sp. 'AMP023'	1		Helix	Widespread species
TOBRC0009	380913	7600605	2	Amphipoda	Paramelitidae	Paramelitidae sp. 'AMP023'	1		Helix	Widespread species
TOBRC0009	380913	7600605	2	Amphipoda	Paramelitidae	Paramelitidae sp. 'AMP023'	1		Helix	Widespread species
TOBRC0009	380913	7600605	2	Amphipoda	Paramelitidae	Paramelitidae sp. 'AMP023'	1		Helix	Widespread species
TOBRC0009	380913	7600605	2	Amphipoda	Paramelitidae	Paramelitidae sp. 'AMP023'	1		Helix	Widespread species
TOBRC0009	380913	7600605	2	Amphipoda	Paramelitidae	Paramelitidae sp. 'AMP023'	1		Helix	Widespread species
Budgie Bore	382495	7615587	2	Cyclopoida	Cyclopidae	Diacyclops humphreysi unispinosus	1		Bennelongia	
Camp Bore	382763	7612704	2	Cyclopoida	Cyclopidae	Diacyclops humphreysi unispinosus	45		Bennelongia	
RC13MEA0279	376781	7605110	2	Cyclopoida	Cyclopidae	Diacyclops humphreysi unispinosus	19		Bennelongia	
TOBRC0009	380913	7600605	2	Cyclopoida	Cyclopidae	Diacyclops humphreysi unispinosus	13		Bennelongia	
Budgie Bore	382495	7615587	2	Cyclopoida	Cyclopidae	Microcyclops varicans	2		Bennelongia	Widespread species
Budgie Bore	382495	7615587	2	Thermosbaenacea	Halosbaenidae	Halosbaena tulki	12		Bennelongia	
RC13TOB0023	376172	7597836	3	Amphipoda	Eriopisidae	Eriopisidae nov. gen. sp. 'AMM006'	1		Helix	
Budgie Bore	382495	7615587	3	Amphipoda	Eriopisidae	Nedsia sp. 'AMM001/029/030'	1		Helix	
Budgie Bore	382495	7615587	3	Amphipoda	Eriopisidae	Nedsia sp. 'AMM002'	1		Helix	
Budgie Bore	382495	7615587	3	Amphipoda	Eriopisidae	Nedsia sp. 'AMM002'	1		Helix	
Budgie Bore	382495	7615587	3	Amphipoda	Eriopisidae	Nedsia sp. 'AMM028'	1		Helix	
Budgie Bore	382495	7615587	3	Amphipoda	Eriopisidae	Nedsia sp. 'AMM028'	1		Helix	
Budgie Bore	382495	7615587	3	Amphipoda	Eriopisidae	Nedsia sp. 'AMM031'	1		Helix	
Budgie Bore	382495	7615587	3	Amphipoda	Eriopisidae	Nedsia sp. 'AMM031'	1		Helix	
Budgie Bore	382495	7615587	3	Amphipoda	Eriopisidae	Nedsia sp. 'AMM031'	1		Helix	

Budgie Bore	382495	7615587	3	Amphipoda	Indeterminate	Amphipoda sp. Indet	1		Biota	Failed to yield sequence
Budgie Bore	382495	7615587	3	Amphipoda	Indeterminate	Amphipoda sp. Indet	1		Biota	Failed to yield sequence
Budgie Bore	382495	7615587	3	Amphipoda	Indeterminate	Amphipoda sp. Indet	1		Biota	Failed to yield sequence
Budgie Bore	382495	7615587	3	Amphipoda	Indeterminate	Amphipoda sp. Indet	1		Biota	Failed to yield sequence
Budgie Bore	382495	7615587	3	Amphipoda	Indeterminate	Amphipoda sp. Indet	1		Biota	Failed to yield sequence
Budgie Bore	382495	7615587	3	Amphipoda	Indeterminate	Amphipoda sp. Indet	1		Biota	Failed to yield sequence
MB16WARR0009	374358	7600324	3	Amphipoda	Indeterminate	Amphipoda sp. Indet	1		Biota	Failed to yield sequence
MB16WARR0009	374358	7600324	3	Amphipoda	Indeterminate	Amphipoda sp. Indet	1		Biota	Failed to yield sequence
MB16WARR0009	374358	7600324	3	Amphipoda	Indeterminate	Amphipoda sp. Indet	1		Biota	Failed to yield sequence
MB16WARR0009	374358	7600324	3	Amphipoda	Indeterminate	Amphipoda sp. Indet	1		Biota	Failed to yield sequence
MB16WARR0009	374358	7600324	3	Amphipoda	Indeterminate	Amphipoda sp. Indet	1		Biota	Failed to yield sequence
MB16WARR0009	374358	7600324	3	Amphipoda	Indeterminate	Amphipoda sp. Indet	1		Biota	Failed to yield sequence
Budgie Bore	382495	7615587	3	Amphipoda	Niphargidae	Niphargidae sp. 'AMN008'	1		Helix	
MB16WARR0009	374358	7600324	3	Amphipoda	Paramelitidae	Paramelitidae sp. 'AMP023'	1		Helix	Widespread species
MB16WARR0009	374358	7600324	3	Amphipoda	Paramelitidae	Paramelitidae sp. 'AMP023'	1		Helix	Widespread species
MB16WARR0009	374358	7600324	3	Amphipoda	Paramelitidae	Paramelitidae sp. 'AMP023'	1		Helix	Widespread species
MB16WARR0009	374358	7600324	3	Amphipoda	Paramelitidae	Paramelitidae sp. 'AMP023'	1		Helix	Widespread species
MB16WARR0009	374358	7600324	3	Amphipoda	Paramelitidae	Paramelitidae sp. 'AMP023'	1		Helix	Widespread species
MB16WARR0009	374358	7600324	3	Amphipoda	Paramelitidae	Paramelitidae sp. 'AMP023'	1		Helix	Widespread species
MB16WARR0009	374358	7600324	3	Amphipoda	Paramelitidae	Paramelitidae sp. 'AMP023'	1		Helix	Widespread species

MB16WARR0009	374358	7600324	3	Amphipoda	Paramelitidae	Paramelitidae sp. 'AMP023'	1		Helix	Widespread species
MB16WARR0009	374358	7600324	3	Amphipoda	Paramelitidae	Paramelitidae sp. 'AMP023'	1		Helix	Widespread species
MB16WARR0009	374358	7600324	3	Amphipoda	Paramelitidae	Paramelitidae sp. 'AMP023'	1		Helix	Widespread species
MB16WARR0009	374358	7600324	3	Amphipoda	Paramelitidae	Paramelitidae sp. 'AMP023'	1		Helix	Widespread species
MB16WARR0009	374358	7600324	3	Amphipoda	Paramelitidae	Paramelitidae sp. 'AMP023'	1		Helix	Widespread species
MB16WARR0009	374358	7600324	3	Amphipoda	Paramelitidae	Paramelitidae sp. 'AMP023'	1		Helix	Widespread species
MB16WARR0009	374358	7600324	3	Amphipoda	Paramelitidae	Paramelitidae sp. 'AMP023'	1		Helix	Widespread species
MB16WARR0009	374358	7600324	3	Amphipoda	Paramelitidae	Paramelitidae sp. 'AMP023'	1		Helix	Widespread species
MB16WARR0009	374358	7600324	3	Amphipoda	Paramelitidae	Paramelitidae sp. 'AMP023'	1		Helix	Widespread species
MB16WARR0009	374358	7600324	3	Amphipoda	Paramelitidae	Paramelitidae sp. 'AMP023'	1		Helix	Widespread species
MB16WARR0009	374358	7600324	3	Amphipoda	Paramelitidae	Paramelitidae sp. 'AMP023'	1		Helix	Widespread species
MB16WARR0009	374358	7600324	3	Amphipoda	Paramelitidae	Paramelitidae sp. 'AMP023'	1		Helix	Widespread species
MB16WARR0009	374358	7600324	3	Amphipoda	Paramelitidae	Paramelitidae sp. 'AMP023'	1		Helix	Widespread species
MB16WARR0009	374358	7600324	3	Amphipoda	Paramelitidae	Paramelitidae sp. 'AMP023'	1		Helix	Widespread species
MB16WARR0009	374358	7600324	3	Amphipoda	Paramelitidae	Paramelitidae sp. 'AMP023'	1		Helix	Widespread species
MB16WARR0009	374358	7600324	3	Amphipoda	Paramelitidae	Paramelitidae sp. 'AMP023'	1		Helix	Widespread species
MB16WARR0009	374358	7600324	3	Amphipoda	Paramelitidae	Paramelitidae sp. 'AMP023'	1		Helix	Widespread species
MB16WARR0009	374358	7600324	3	Amphipoda	Paramelitidae	Paramelitidae sp. 'AMP023'	1		Helix	Widespread species
MB16WARR0009	374358	7600324	3	Amphipoda	Paramelitidae	Paramelitidae sp. 'AMP023'	1		Helix	Widespread species

MB16WARR0009	374358	7600324	3	Amphipoda	Paramelitidae	Paramelitidae sp. 'AMP023'	1		Helix	Widespread species
MB16WARR0009	374358	7600324	3	Amphipoda	Paramelitidae	Paramelitidae sp. 'AMP023'	1		Helix	Widespread species
MB16WARR0009	374358	7600324	3	Amphipoda	Paramelitidae	Paramelitidae sp. 'AMP023'	1		Helix	Widespread species
MB16WARR0009	374358	7600324	3	Amphipoda	Paramelitidae	Paramelitidae sp. 'AMP023'	1		Helix	Widespread species
MB16WARR0009	374358	7600324	3	Amphipoda	Paramelitidae	Paramelitidae sp. 'AMP023'	1		Helix	Widespread species
MB16WARR0009	374358	7600324	3	Amphipoda	Paramelitidae	Paramelitidae sp. 'AMP023'	1		Helix	Widespread species
MB16WARR0009	374358	7600324	3	Amphipoda	Paramelitidae	Paramelitidae sp. 'AMP023'	1		Helix	Widespread species
MB16WARR0009	374358	7600324	3	Amphipoda	Paramelitidae	Paramelitidae sp. 'AMP023'	1		Helix	Widespread species
MB16WARR0009	374358	7600324	3	Amphipoda	Paramelitidae	Paramelitidae sp. 'AMP023'	1		Helix	Widespread species
MB16WARR0009	374358	7600324	3	Amphipoda	Paramelitidae	Paramelitidae sp. 'AMP023'	1		Helix	Widespread species
MB16WARR0009	374358	7600324	3	Amphipoda	Paramelitidae	Paramelitidae sp. 'AMP023'	1		Helix	Widespread species
MB16WARR0009	374358	7600324	3	Amphipoda	Paramelitidae	Paramelitidae sp. 'AMP023'	1		Helix	Widespread species
MB16WARR0009	374358	7600324	3	Amphipoda	Paramelitidae	Paramelitidae sp. 'AMP023'	1		Helix	Widespread species
MB16WARR0009	374358	7600324	3	Amphipoda	Paramelitidae	Paramelitidae sp. 'AMP023'	1		Helix	Widespread species
MB16WARR0009	374358	7600324	3	Amphipoda	Paramelitidae	Paramelitidae sp. 'AMP023'	1		Helix	Widespread species
MB16WARR0009	374358	7600324	3	Amphipoda	Paramelitidae	Paramelitidae sp. 'AMP023'	1		Helix	Widespread species
MB16WARR0009	374358	7600324	3	Amphipoda	Paramelitidae	Paramelitidae sp. 'AMP023'	1		Helix	Widespread species
MB16WARR0009	374358	7600324	3	Amphipoda	Paramelitidae	Paramelitidae sp. 'AMP023'	1		Helix	Widespread species
MB16WARR0009	374358	7600324	3	Amphipoda	Paramelitidae	Paramelitidae sp. 'AMP023'	1		Helix	Widespread species

MB16WARR0009	374358	7600324	3	Amphipoda	Paramelitidae	Paramelitidae sp. 'AMP023'	1		Helix	Widespread species
MB16WARR0009	374358	7600324	3	Amphipoda	Paramelitidae	Paramelitidae sp. 'AMP023'	1		Helix	Widespread species
MB16WARR0009	374358	7600324	3	Amphipoda	Paramelitidae	Paramelitidae sp. 'AMP023'	1		Helix	Widespread species
MB16WARR0009	374358	7600324	3	Amphipoda	Paramelitidae	Paramelitidae sp. 'AMP023'	1		Helix	Widespread species
MB16WARR0009	374358	7600324	3	Amphipoda	Paramelitidae	Paramelitidae sp. 'AMP023'	1		Helix	Widespread species
MB16WARR0009	374358	7600324	3	Amphipoda	Paramelitidae	Paramelitidae sp. 'AMP023'	1		Helix	Widespread species
MB16WARR0009	374358	7600324	3	Amphipoda	Paramelitidae	Paramelitidae sp. 'AMP023'	1		Helix	Widespread species
MB16WARR0009	374358	7600324	3	Amphipoda	Paramelitidae	Paramelitidae sp. 'AMP023'	1		Helix	Widespread species
MB16WARR0009	374358	7600324	3	Bathynellacea	Parabathynellid ae	Atopobathynella sp. B25	1		Bennelongia	Potential SRE species
Budgie Bore	382495	7615587	3	Calanoida	Ridgewayiidae	Stygoridgewayia trispinosa	1		Bennelongia	
Budgie Bore	382495	7615587	3	Cyclopoida	Cyclopidae	Microcyclops varicans	4		Bennelongia	Widespread species
Budgie Bore	382495	7615587	3	Haplotaxida	Naididae	Pristina longiseta	1		Adrian Pinder	
MB16WARR0009	374358	7600324	3	Indeterminate	Indeterminate	Platyhelminthes sp. Indet	1		Bennelongia	
Budgie Bore	382495	7615587	3	Isopoda	Cirolanidae	Haptolana yarraloola	2		Bennelongia	
Budgie Bore	382495	7615587	3	Thermosbaenacea	Halosbaenidae	Halosbaena tulki	30		Bennelongia	
<b>Mesa C</b>										
Dave Bore	392512	7607436	1	Amphipoda	Eriopisidae	Nedsia sp. 'AMM004'	1		Helix	Potential SRE species
Dave Bore	392512	7607436	1	Amphipoda	Eriopisidae	Nedsia sp. 'AMM004'	1		Helix	Potential SRE species
Dave Bore	392512	7607436	1	Amphipoda	Eriopisidae	Nedsia sp. 'AMM031'	1		Helix	Potential SRE species
Dave Bore	392512	7607436	1	Amphipoda	Eriopisidae	Nedsia sp. 'AMM031'	1		Helix	Potential SRE species
Dave Bore	392512	7607436	1	Amphipoda	Indeterminate	Amphipoda sp. Indet	1		Biota	Failed to yield a sequence
Dave Bore	392512	7607436	1	Amphipoda	Indeterminate	Amphipoda sp. Indet	1		Biota	Failed to yield a sequence
Dave Bore	392512	7607436	1	Amphipoda	Indeterminate	Amphipoda sp. Indet	1		Biota	Failed to yield a sequence

Dave Bore	392512	7607436	1	Amphipoda	Indeterminate	Amphipoda sp. Indet	1		Biota	Failed to yield a sequence
Dave Bore	392512	7607436	1	Amphipoda	Indeterminate	Amphipoda sp. Indet	1		Biota	Failed to yield a sequence
Dave Bore	392512	7607436	1	Amphipoda	Niphargidae	Niphargidae sp. 'AMN007'	1		Helix	
Dave Bore	392512	7607436	1	Amphipoda	Niphargidae	Niphargidae sp. 'AMN008'	1		Helix	
Dave Bore	392512	7607436	1	Amphipoda	Niphargidae	Niphargidae sp. 'AMN008'	1		Helix	
Dave Bore	392512	7607436	1	Amphipoda	Niphargidae	Niphargidae sp. 'AMN008'	1		Helix	
Dave Bore	392512	7607436	1	Amphipoda	Niphargidae	Niphargidae sp. 'AMN008'	1		Helix	
Dave Bore	392512	7607436	1	Calanoida	Ridgewayiidae	Stygoridgewayia trispinosa	9		Bennelongia	
Dave Bore	392512	7607436	1	Calanoida	Ridgewayiidae	Stygoridgewayia trispinosa	9		Bennelongia	
MEAWO4086	386829	7605287	1	Calanoida	Ridgewayiidae	Stygoridgewayia trispinosa	5		Bennelongia	
Dave Bore	392512	7607436	1	Cyclopoida	Cyclopidae	Cyclopoida sp. Indet	1		Bennelongia	
Dave Bore	392512	7607436	1	Cyclopoida	Cyclopidae	Diacyclops humphreysi unispinosus	31		Bennelongia	
Dave Bore	392512	7607436	1	Isopoda	Cirolanidae	Haptolana yarraloola	1		Bennelongia	
Dave Bore	392512	7607436	1	Podocopida	Candonidae	Pilbaracandona sp. BOSS26	3		Bennelongia	
Dave Bore	392512	7607436	1	Podocopida	Candonidae	Pilbaracandona sp. BOSS26	5		Bennelongia	
Dave Bore	392512	7607436	1	Podocopida	Candonidae	Pilbaracandona sp. BOSS26	1		Bennelongia	
Dave Bore	392512	7607436	1	Sorbeoconcha	Hydrobiidae	Hydrobiidae sp. Indet	9		Bennelongia	
Dave Bore	392512	7607436	1	Sorbeoconcha	Hydrobiidae	Hydrobiidae sp. Indet	1		Bennelongia	
Dave Bore	392512	7607436	1	Thermosbaenacea	Halosbaenidae	Halosbaena tulki	4		Bennelongia	
Dave Bore	392512	7607436	1	Thermosbaenacea	Halosbaenidae	Halosbaena tulki	14		Bennelongia	
Dave Bore	392512	7607436	1	Thermosbaenacea	Halosbaenidae	Halosbaena tulki	1		Bennelongia	
MB16MEC0009	393590	7601145	2	Amphipoda	Eriopisidae	Eriopisidae sp. 'AMM026'	1		Helix	
MB16MEC0009	393590	7601145	2	Amphipoda	Eriopisidae	Eriopisidae sp. 'AMM026'	1		Helix	
MB16MEC0009	393590	7601145	2	Amphipoda	Eriopisidae	Eriopisidae sp. 'AMM026'	1		Helix	
MB16MEC0009	393590	7601145	2	Amphipoda	Eriopisidae	Eriopisidae sp. 'AMM026'	1		Helix	
MB16MEC0009	393590	7601145	2	Amphipoda	Eriopisidae	Eriopisidae sp. 'AMM026'	1		Helix	
MB16MEC0009	393590	7601145	2	Amphipoda	Eriopisidae	Eriopisidae sp. 'AMM026'	1		Helix	
MB16MEC0007	392713	7601954	2	Amphipoda	Eriopisidae	Nedsia sp. 'AMM004'	1		Helix	Potential SRE species
MB16MEC0007	392713	7601954	2	Amphipoda	Eriopisidae	Nedsia sp. 'AMM004'	1		Helix	Potential SRE species
MB16MEC0009	393590	7601145	2	Amphipoda	Eriopisidae	Nedsia sp. 'AMM004'	1		Helix	Potential SRE species

MB16MEC0009	393590	7601145	2	Amphipoda	Eriopisidae	Nedsia sp. 'AMM004'	1		Helix	Potential SRE species
MB16MEC0009	393590	7601145	2	Amphipoda	Eriopisidae	Nedsia sp. 'AMM004'	1		Helix	Potential SRE species
MB16MEC0009	393590	7601145	2	Amphipoda	Eriopisidae	Nedsia sp. 'AMM004'	1		Helix	Potential SRE species
MB16MEC0009	393590	7601145	2	Amphipoda	Eriopisidae	Nedsia sp. 'AMM004'	1		Helix	Potential SRE species
RC15MEC0027	392792	7600255	2	Amphipoda	Eriopisidae	Nedsia sp. 'AMM004'	1		Helix	Potential SRE species
RC16MEC0102	392790	7601511	2	Amphipoda	Eriopisidae	Nedsia sp. 'AMM004'	1		Helix	Potential SRE species
WB16MEC0002	392973	7600507	2	Amphipoda	Eriopisidae	Nedsia sp. 'AMM004'	1		Helix	Potential SRE species
MEAWO4086	386829	7605287	2	Amphipoda	Eriopisidae	Nedsia sp. 'AMM031'	1		Helix	Potential SRE species
RC15MEC0200	392746	7602204	2	Amphipoda	Eriopisidae	Nedsia sp. 'AMM031'	1		Helix	Potential SRE species
RC15MEC0200	392746	7602204	2	Amphipoda	Eriopisidae	Nedsia sp. 'AMM031'	1		Helix	Potential SRE species
RC15MEC0200	392746	7602204	2	Amphipoda	Eriopisidae	Nedsia sp. 'AMM031'	1		Helix	Potential SRE species
MB16MEC0008	393565	7600580	2	Amphipoda	Indeterminate	Amphipoda sp. 'Indet'	1		Biota	Failed to yield a sequence
MB16MEC0008	393565	7600580	2	Amphipoda	Indeterminate	Amphipoda sp. 'Indet'	1		Biota	Failed to yield a sequence
MB16MEC0009	393590	7601145	2	Amphipoda	Indeterminate	Amphipoda sp. 'Indet'	1		Biota	Failed to yield a sequence
MB16MEC0009	393590	7601145	2	Amphipoda	Indeterminate	Amphipoda sp. 'Indet'	1		Biota	Failed to yield a sequence
MEAWO4086	386829	7605287	2	Amphipoda	Niphargidae	Niphargidae sp. 'AMN008'	1		Helix	
MEAWO4086	386829	7605287	2	Amphipoda	Niphargidae	Niphargidae sp. 'AMN008'	1		Helix	
MEAWO4086	386829	7605287	2	Amphipoda	Niphargidae	Niphargidae sp. 'AMN008'	1		Helix	
MB16MEC0008	393565	7600580	2	Calanoida	Ridgewayiidae	Stygoridgewayia trispinosa	1		Bennelongia	
MEAWO4086	386829	7605287	2	Calanoida	Ridgewayiidae	Stygoridgewayia trispinosa	20		Bennelongia	
MB16MEC0009	393590	7601145	2	Cyclopoida	Cyclopidae	Diacyclops humphreysi humphreysi	1		Bennelongia	
MB16MEC0009	393590	7601145	2	Cyclopoida	Cyclopidae	Diacyclops humphreysi unispinosus	25		Bennelongia	

MB16MEC0008	393565	7600580	2	Cyclopoida	Cyclopidae	Dussartcyclops uniarticulatus	15		Bennelongia	
MB16MEC0009	393590	7601145	2	Harpacticoida	Ameiridae	Lucionitocrella yalleenensis	3		Bennelongia	
MB16MEC0008	393565	7600580	2	Harpacticoida	Ameiridae	Megastygonitocrella unispinosa	5		Bennelongia	
MB16MEC0009	393590	7601145	2	Harpacticoida	Ameiridae	Megastygonitocrella unispinosa	29		Bennelongia	
MB16MEC0008	393565	7600580	2	Harpacticoida	Canthocamptidae	Elaphoidella nr humphreysi	10		Bennelongia	
MB16MEC0008	393565	7600580	2	Harpacticoida	Miraciidae	Schizopera roberiverensis	4		Bennelongia	
MB16MEC0008	393565	7600580	2	Podocopida	Candonidae	Areacandona sp. BOS818	1		Bennelongia	
MEAWO4086	386829	7605287	2	Podocopida	Candonidae	Humphreyscandona fovea	1		Bennelongia	
Dave Bore	392512	7607436	2	Podocopida	Candonidae	Pilbaracandona sp. BOS526	3		Bennelongia	
Dave Bore	392512	7607436	2	Sorbeoconcha	Hydrobiidae	Hydrobiidae sp. Indet	8		Bennelongia	
Dave Bore	392512	7607436	2	Thermosbaenacea	Halosbaeniidae	Halosbaena tulki	19		Bennelongia	
MB16MEC0009	393590	7601145	2	Thermosbaenacea	Halosbaeniidae	Halosbaena tulki	5		Bennelongia	