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ENVIRONMENTAL SCIENCES

Subterranean fauna survey of the Mulga Downs Project

Prepared for Hancock Prospecting Pty Ltd

January 2013

Final Report

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EXECUTIVE SUMMARY

The Mulga Downs Project, owned by Hancock Prospecting Pty Ltd (Hancock), is located on the Mulga Downs Pastoral Station near Wittenoom. Tenement M47/206 forms the boundary of the study area, located in the Fortescue Plain subregion of the Pilbara Bioregion. The Project is an open cut iron ore mine and the resource, Marra Mamba formation, is situated both above and below the standing water table. The proposed mine was initially planned to go below the water table, but revised plans now restrict mining operations to above the water table.

Hancock commissioned Phoenix Environmental Sciences Pty Ltd (Phoenix) to undertake a two phase stygofauna survey and a single phase troglofauna survey (collectively known as subterranean fauna). The key aims of these surveys were to:

- search for additional specimens of three previously-recorded troglomorphic species
- determine the presence of subterranean SRE fauna and important habitats in the study area
- survey representative impact and reference sites to provide local and regional context for species records and habitats
- map the location of any recorded conservation significant species and habitats
- assess and summarise the potential impacts of the mining project on subterranean species and habitats, then make recommendations for mitigation of impacts.

This report describes the three subterranean fauna surveys undertaken in October 2011, December 2011 and January 2012 at Murrays Hill, representing two seasons.

The sampling intensity of the survey exceeded the minimum requirements of Guidance Statement 54a for stygofauna and troglofauna surveys, and augmented the results of two previous studies of subterranean fauna in the area. Rainfall records for November (2011) and January (2012) were above average, which is ideal for sampling subterranean fauna.

The surveys produced a diverse sample of subterranean invertebrates including 24 target stygofauna species (stygobites and or stygophiles), and 27 troglofauna species (troglobites or troglophiles). Four troglobitic species groups remain unresolved owing to absence of expertise in these groups.

Subterranean fauna with limited range (known as short-range endemics or SRE's) are of most significance, because they have highly specific habitat requirements and are generally restricted in distribution. In many cases, SRE status is assigned, following the 'precautionary principal', to groups where there is limited taxonomic expertise and/or limited numbers of species recorded in the bioregion. In this study, genetic analysis has helped to delineate new species, but it cannot make up for the lack of records.

The limited number of previous subterranean fauna surveys in the study area indicates a high likelihood of recording new species, including SRE's. New species in this study are indicated by a suffix of 'MH'.

The three subterranean species previously sampled by Ecologia, *Nocticola*, Polyxenid and Parajapygid species, appear to be conspecific with *Nocticola* 'MH1', Polyxenidae 'PXD1' and Parajapygidae 'MH1' respectively from this study. These results expand the distribution of both *Nocticola* and the polyxenid found by Ecologia beyond the proposed impact area at Murray's Hill. The only Parajapygidae collected in our survey were restricted to the proposed impact area, as was the single record from Ecologia's survey.

Twenty four troglofauna species and 13 stygofauna species were found to represent likely or potential SRE species. All 24 troglofauna and eight of the stygofauna were considered new species.

Thirteen SRE species from this study were collected in both impact and reference areas, potentially indicating that these SRE species are regionally represented. Six potential SRE troglofauna species and one potential SRE stygofauna species were recorded only from within the proposed impact area (* indicates genetic analysis):

- troglofauna
    - *Cryptops* 'MH1'* – one specimen found at one impact site
    - *Palpigradi* 'MH1'* – one specimen found at one impact site
    - Parajapygidae 'MH1'*– two specimens found at two impact sites
    - Pauropoda 'MH1'* – three specimens found at one impact site
    - Schizomida 'MH2'*– one specimen found at one impact site
    - Troglarmadillo 'MH1' – one specimen found at one impact site
- stygofauna
    - Parabathynellidae 'MH3' – four specimens found at one impact site.

Several indicators point to the need for more survey work:

- For both troglofauna and stygofauna, the observed species richness relative to extrapolated species richness (troglofauna, 74%–87%; stygofauna, 62%–92%) was below level recommended by Guidance Statement 54a, of 95%.
- The species accumulation curves (combined sampling methods) did not reach a plateau, further indicating the need for additional sampling in the study area to adequately represent the species richness for the area.
- The high percentage of new troglofauna species (88%) found only in the Mulga Downs study area indicates the presence of a unique and diverse troglofauna community. The stygofaunal species richness was dominated by widespread copepod species known from other parts of the Pilbara. A smaller endemic component to the stygofauna community was represented by new species (25%) and represented by larger crustaceans: amphipods, syncarids and an isopod.

The troglofauna results indicated higher species richness in one of the surface geologies of the study area (haematite-geothite), suggesting this geology is the primary habitat of the troglofauna. Records of more widely distributed species suggested some connectivity between several surface geologies in the study area (alluvial, alluvial-colluvial and hematite-geothite strata).

While it is possible the six troglofauna species known only from the proposed impact area have broader distributions – similar to the more widespread species – this cannot be confirmed based on current knowledge. The survey results are complicated by:

- a high proportion of single and double records (51.8%)
- a high proportion of new species (88.8%)
- the indication of restricted gene flow, within three species, from troglofauna sampled within the impact and reference areas.

Based on the limited geological and biological data for the study area, the following impacts may affect subterranean fauna:

- direct loss of troglofauna habitat from excavation of the mine pits
- minor sediment compaction and/or vibration on subterranean habitat

- nutrient starvation of subterranean habitat underlying the direct impact area, which may lead to reduction in abundance and diversity.
- spills (e.g. diesel fuel) may lead to minor localised contamination of subterranean habitat.

Data from additional surveys would improve on the following issues:

  - paucity of records (singletons and doubletons)
  - understanding of these species and their distribution in relation to surface geology.

Targeted sequencing of the most widespread taxa would also improve knowledge on the extent of the gene flow restrictions occurring at Mulga Downs and its surrounds and therefore define local endemism more clearly.

The stygofauna results indicate that lateral connectivity and transmissivity of the aquifer is likely, but this cannot be confirmed until hydrological modelling has been completed. As the proposed mine will not go below the water table, no direct impact is likely to occur to stygofauna.

1 INTRODUCTION

In September, 2011, Phoenix Environmental Sciences Pty Ltd (Phoenix) was commissioned by Hancock Prospecting Pty Ltd (Hancock) to undertake a subterranean fauna survey for the Mulga Downs Project (the Project), previously referred to as the Murray's Hill Project. This report describes the subterranean fauna surveys undertaken from October 2011 - February 2012 for the Project.

1.1 BACKGROUND

The Project is situated on the Mulga Downs Pastoral Station and is approximately 22 km north-east of Wittenoom in the Fortescue Plain subregion of the Pilbara Bioregion (Figure 1-1). The study area (Figure 1-1) is bound by tenement E47/1244 and the proposed impact area is bound by tenement M47/206

The proposed development is an open cut iron ore mine and haul road with all processing infrastructure to occur off-site. The resource is situated both above and below the standing water table. Annual tonnage will be approximately 5 mtpa and the proposed disturbance footprint is approximately 580.24 ha: mine footprint, 284.07 ha; waste stockpile, 212.72 ha; plant, 81.2 ha, Sediment pond, 2.25 ha. Hancock requested that a two phase stygofauna survey and a single phase troglofauna survey be undertaken for the purpose of an environmental impact assessment of subterranean fauna for the proposed mine.

Stygofauna surveys have not previously been undertaken within the study area and the two phase stygofauna survey was necessary to meet with the requirements of the Environmental Protection Authority (EPA 2003, 2007).

Two troglofauna surveys were previously undertaken in the study area by Ecologia Environment (Ecologia) (2011). At that time few bores were available for sampling, so those surveys were developed as a pilot study (EPA 2007) for a mining proposal. Ecologia (2011), reported three troglomorphic species from the survey: a pincushion millipede (Polyxenida), a cockroach (*Nocticola* sp.) and a dipluran (Diplura).

The discovery of troglofauna necessitated a full troglofauna survey (EPA 2007). Additionally, the mine was proposed to go below the water table and as no stygofauna surveys had previously been undertaken for the Mulga Downs Project, a full stygofauna survey was also necessary (EPA 2007).

The survey scope was developed to address the environmental impact assessment requirements of both troglofauna and stygofauna; however, subsequent to undertaking the survey, Hancock revised the proposed mine plan to be restricted to resource above water table.

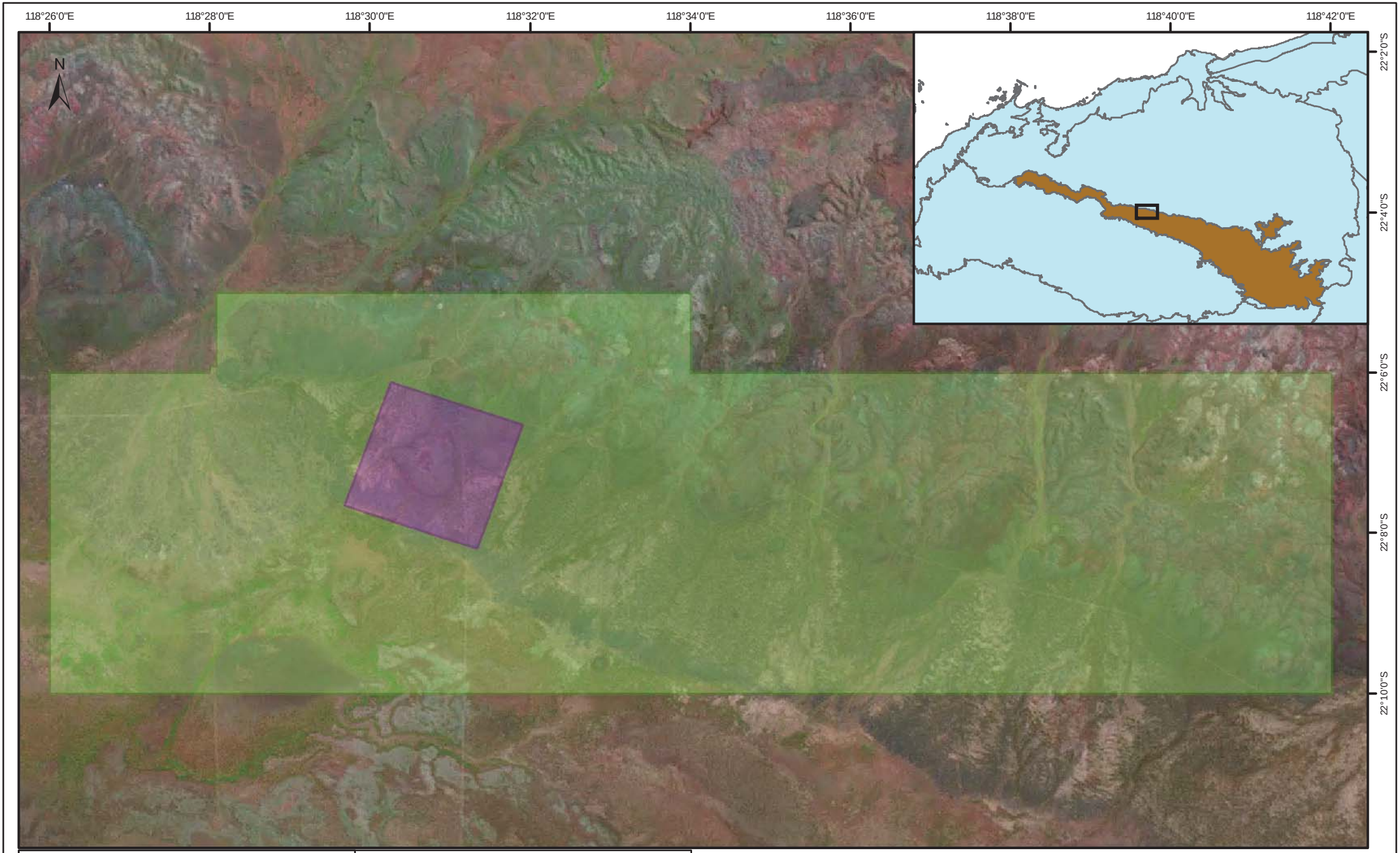

Figure 1-1 Location of the Mulga Downs Project, inset of the Pilbara region of Western Australia, with Fortescue subregion in brown

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AUTHOR: ES Volschenk	**CLIENT:** Hancock Prospecting
DATE: 24 May 2012	**Scale:** 1:111,088
Coordinate System: Projection: Transverse Mercator; DATUM: GDA94	**PROJECT:** Mulga Downs Subterranean Survey

0 0.5 1 2 3 4 5 Kilometres

1.2 SCOPE OF WORK AND SURVEY OBJECTIVES

The objectives of the survey were to:

- search for additional specimens of three previously-recorded troglomorphic species
- determine the presence or absence of subterranean fauna or important habitat in the study area, including both 'impact areas' and reference sites for the Project (Figure 1-1)
- compare any records of potential short-range endemic (SRE) subterranean fauna from within the 'impact area' with records obtained from reference sites to obtain local and regional context for species distributions and habitat extents
- determine the potential impacts of the proposed Project on troglobitic SRE species
- identify management and mitigation measures to avoid or minimise impacts to troglobitic SRE species.

The scope of works undertaken to achieve these objectives was as follows:

- undertake a desktop review of relevant databases, literature and spatial data to assess the potential for presence of subterranean habitats and species in the study area
- undertake surveys for stygofauna and troglofauna within the study area, including both 'impact areas' and reference (non-impact) sites such as regional bores and creek lines to provide regional context for any species found within the proposed impact footprint
- undertake sample processing, species identifications and data analysis of results
- prepare a technical report to assess potential impacts of the Project on troglobitic species and habitats and make recommendations for mitigation of impacts.

The survey methodology complied with the Environmental Protection Authority's (EPA's) requirements for an environmental impact assessment (EIA) of subterranean invertebrates as outlined in:

- *Guidance Statement 54 Consideration of subterranean fauna in groundwater and caves during environmental impact assessment in Western Australia* (EPA 2007)
- *Guidance Statement 54a Sampling methods and survey considerations for subterranean fauna in Western Australia* (Howarth 1983; Humphreys 2000)
- the *Wildlife Conservation Act 1950* (State)
- the *Environment Protection and Biodiversity Conservation Act 1999* (Federal).

The proposed impact area of the proposed pit is bound within tenement M47/206 and is defined in Figure 1-1 and Figure 2-1).

2 EXISTING ENVIRONMENT

Subterranean fauna are organisms (almost exclusively invertebrates) that live beneath the surface of the ground. Surface-dwelling species are generally referred to as epigean (Howarth 1983; Humphreys 2008; Subterranean Ecology 2010) and subterranean species are named to reflect their eco-physiological specialisation to subterranean habitat. Subterranean organisms can exist within a variety of subterranean void networks, including solution cavities within calcrete and karst; fractured rock and course sediments such as cobble or gravel strata (Howarth 1983; Humphreys 2000; Poulson & Lavoie 2000).

The energy and nutrient resources for subterranean habitats are almost exclusively sourced from allochthonous materials. Tree roots and water form the most important transport routes that move energy and nutrients into subterranean network strata (Howarth 1983; Humphreys 2000; Poulson & Lavoie 2000).

2.1 GEOLOGY AND HYDROLOGY

Calcrete and banded iron formation (BIF) are found within the study area. These types of geology are known to support extensive subterranean communities (EPA 2003, 2007).

The hydrology is variable where it intersects the subterranean environment. There are two aquifers present within the study area. A superficial aquifer is likely to be hosted by alluvial strata (Figure 2-1). The study area is low and is frequently subject to inundation after rainfall, therefore the superficial aquifer fluctuates greatly in response to summer rainfall. The 'impact area' is elevated and therefore is less affected by fluctuating water table levels. The deeper and older aquifers are hosted in both calcrete, and within the Marra Mamba formations (Figure 2-1). Connectivity between these aquifers seems likely, but is unconfirmed. The study area hosts four geological features that are well represented in the region: calcrete, Marra Mamba (includes the target resource), alluvial and colluvial deposits (Figure 2-1).

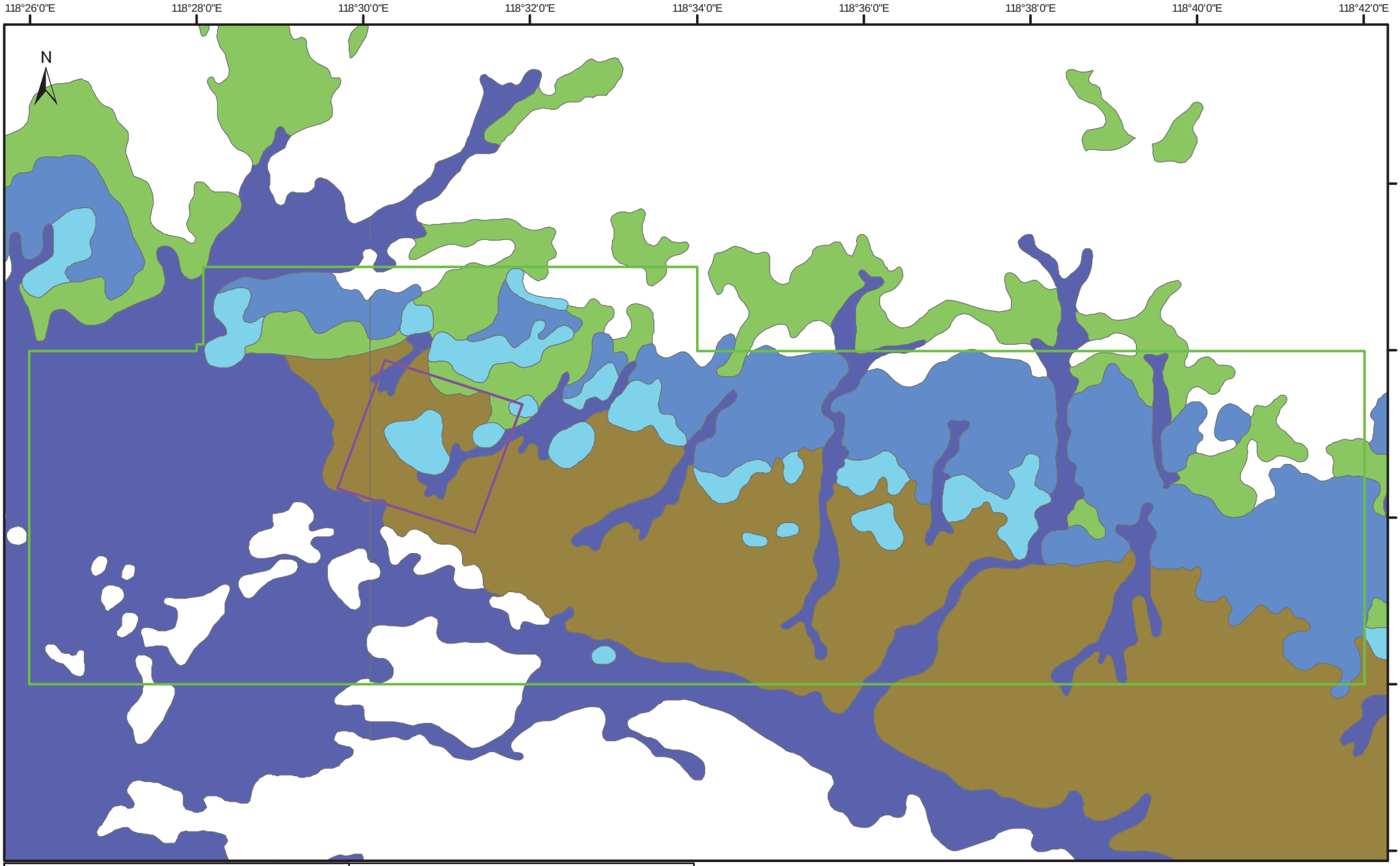

Figure 2-1 Location of the Mulga Downs Project in relation to surface geology.

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AUTHOR: ES Volschenk	CLIENT: Hancock Prospecting
DATE: 24 May 2012	Scale: 1:109,384
Coordinate System: Projection: Transverse Mercator; DATUM: GDA94	PROJECT: Mulga Downs Subterranean Survey

0 0.5 1 2 3 4 5 Kilometres

2.2 CLIMATE AND WEATHER

The Project is located in the Pilbara bioregion which has a semi-arid, tropical climate. McKenzie *et al.* (2009) classified the area in which the Project is situated, as 'hot-persistently dry grassland'. Daily temperatures in summer can exceed 45°C. Thunderstorms and cyclones also occur during the summer months. Rainfall in the region is variable between years and unpredictable throughout the year. Winter is temperate and rainfall is significantly lower than summer.

The nearest Bureau of Meteorology (BOM) weather station is located at Wittenoom, Station 005026, 22.24°S 118.34°E) approximately 27 km south-west of the Project. Wittenoom's highest maximum mean monthly temperature (39.6°C) was recorded in December and January, the lowest maximum mean annual temperature (11.5°C) was recorded in July and the average annual rainfall is 462 mm (BOM 2012; Köhler & Johnson 2012)(Figure 2-2). Leighton (2004) noted substantial variation in annual rainfall in the Pilbara, both locally and regionally.

Rainfall is considered to be an important climatic parameter for troglofauna and stygofauna since both of these groups are dependent on groundwater and are thought to respond to the influx of nutrients carried into the subterranean void networks by rain (Howarth 1983; Humphreys 2000).

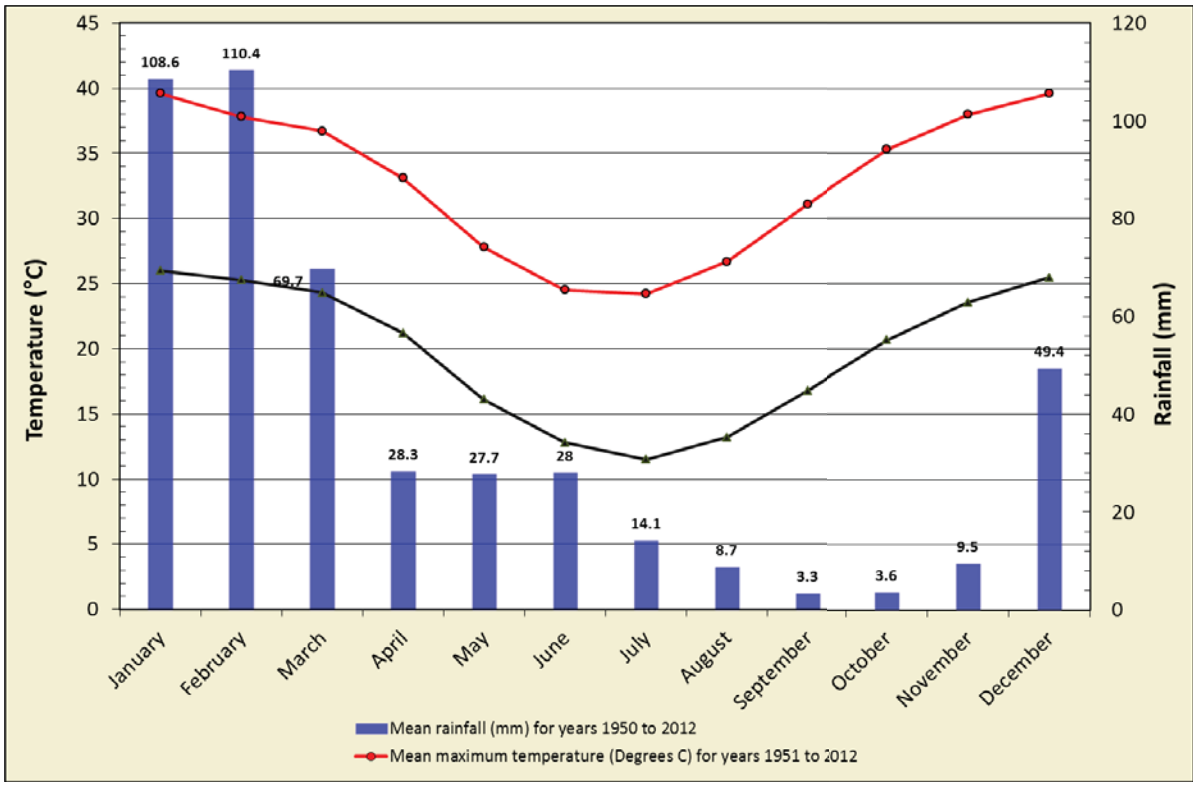

Figure 2-2 **Average monthly temperatures (maximum and minimum) and rainfall records from Wittenoom (BOM Station 005026)**

2.3 BIOLOGICAL CONTEXT

Subterranean fauna live within air or water filled underground networks. They are predominantly invertebrates. Organisms specialised for living in air-filled subterranean networks are referred to as troglofauna, while those inhabiting water-filled subterranean networks are referred to as stygofauna (Howarth 1993).

Subterranean habitats are perpetually dark, extremely constant in temperature and humidity (air-filled networks) and very low in nutrients and energy that are required to support organisms (Harvey 2002b; Holsinger 2000; Howarth 1993; Ponder & Colgan 2002). Evolution under such conditions has resulted in very specialised organisms that are restricted to the void networks in which they have evolved (Harvey 2002b; Ponder & Colgan 2002; Volschenk & Prendini 2008). Such species are obligated to living in subterranean networks and cannot live in epigean (surface) environments. For this reason, organisms specialised to live in subterranean networks are likely to represent short-range endemics (SREs) with extremely limited capabilities of dispersal (Harvey 2002b).

Short-range endemics are species with naturally small distributions; nominally defined by Harvey as less than 10,000 km^2 (Harvey 2002b). Species restricted to subterranean void systems may have considerably smaller distributions and therefore represent extreme SREs (Humphreys 2008). It is these subterranean species that are considered to be of conservation significance because they are at greatest risk of extinction from development projects.

In Western Australia, and particularly in the Pilbara region, there has been a renaissance in the study of subterranean biodiversity (EPA 2003, 2007) driven by the growth of the mineral resources industry and mining environmental impact assessment (Barr 1968; Howarth 1983; Humphreys 2000). Despite the extensive survey work undertaken in the Pilbara, relatively little knowledge on SRE diversity and biology has emerged from the primary literature. The biology, diversity and distributions of most of Western Australia's subterranean fauna are still very poorly understood.

2.3.1 Troglofauna

Troglofauna are typically divided into three categories of specialisation to subterranean life:

- troglobites, that are restricted to subterranean habitats and usually perish on exposure to the surface environment (Barr 1968; Howarth 1983; Humphreys 2000)
- troglophiles, which facultatively use subterranean habitats but are not reliant on them for survival (Howarth 1983, 1993; Humphreys 2000; Poulson & Lavoie 2000)
- trogloxenes, which use subterranean systems for specific purposes, such as roosts for reproduction (Bats and Swiftlets).

Both troglobites and troglophiles may be SRE's and are therefore conservation significant.

Troglobites are organisms that have adapted to exploit the special characteristics of air-filled subterranean networks. They are often characterised by much specialised adaptations to subterranean life, such as:

- lack or reduction of eyes
- lack or reduction of wings (for species that are normally winged)
- lack or reduction of body pigmentation
- heightened chemosensory and mechanosensory systems
- loss of circadian rhythms

- very low metabolic rate.

These adaptations allow troglobites to exploit the dark, humid, nutrient-poor subterranean void networks (Subterranean Ecology 2010). Several soil and litter dwelling groups are also blind and pale, making determination of troglobitic status extremely difficult. In these instances (amongst others), DNA sequencing is used in order to obtain regional context for such finds (Humphreys 2000); that is to determine if any records are conspecific with other previously recorded specimens.

Troglophiles are species that can live and reproduce in subterranean networks, but are not restricted to them. These species are usually very tiny and exist within the soil. Some troglophiles appear to be widespread species, while others, like symphylans and pauropods, are often SREs (Phoenix, unpublished data). This limits any comments regarding species distribution outside of the study area.

2.3.2 Stygofauna

Stygofauna represent the fauna living within subterranean water bodies or aquifers (Humphreys 2008). They typically show similar traits to troglobites in their specialisation to subterranean life, including loss of body pigment, eyes and heightened mechanosensory systems. Stygofauna are similarly termed to troglofauna:

- stygobites, that are restricted to subterranean habitats and usually perish on exposure to the surface environment
- stygophiles, which facultatively use subterranean habitats but are not reliant on them for survival (Humphreys 2000)
- Stygoxenes, which are able to move freely between the underground aquifer and the connected surface water (e.g. springs and permanent pools) (Finston *et al.* 2004; Finston & Johnson 2004; Finston *et al.* 2007). Stygoxenes are non-obligatory stygofauna.

Short-range endemic stygofauna are only represented by stygobitic species.

2.3.3 Identifying troglofauna and stygofauna

Surveys over the last five years have revealed a diverse range of fauna inhabiting the subterranean systems of the Pilbara; however, difficulties arise in assessing the status of fauna collected in subterranean surveys and the effects that mining activities will have on each species and their communities. These difficulties are as follows:

1. Recognising fauna as truly subterranean species

The characterisation of subterranean fauna into troglobites or stygobites is largely based on an understanding of species habitat requirements. The recognition and identification of these species are usually limited to the presence of troglomorphies, such as reduction or loss of eyes or wings etc. Troglomorphies are used to infer a species that have become specialised to subterranean existence over many generations of confinement to subterranean habitats.

The use of troglomorphies may be justified when a species being identified belongs to a genus (or other higher taxonomic rank) in which epigean species do not exhibit troglomorphic characteristics. Some groups, such as diplurans, cryptopid centipedes and atelurine silverfish, are more difficult to assess since all members of these groups, whether subterranean or not, lack eyes and are generally pale.

2. Recognising subterranean fauna as short-range endemics

The classification of subterranean fauna as SREs may be difficult to establish as some subterranean fauna appear to have unexpectedly high dispersal abilities while others are more restricted. Some clearly troglobitic species (such as some species of *Nocticola*) have been found to have wide distributions, well beyond the 10,000 km^2 threshold which limits the recognition of SREs (Helix, unpublished data).

3. Taxonomic resolution

Taxonomic resolution of troglofauna and stygofauna is also difficult to achieve in taxa for which there is no local expertise to provide regional context. The strong evolutionary pressure of subterranean habitats has resulted in highly convergent, morphologically-similar species(Hamilton-Smith & Eberhard 2000) . Molecular techniques such as 'barcoding' (Hebert *et al.* 2003a; Hebert *et al.* 2003b) are routinely employed to overcome these identification problems. Barcoding methods can also resolve specimen identification where specimens represent taxonomically uninformative life stages or sexes.

2.3.4 Threatening processes

Impacts to subterranean fauna can be classed as either:

- primary impacts – impacts that physically destroy the subterranean void networks
- secondary impacts – impacts that change the subterranean habitat without physically destroying the void networks.

Primary impacts are obvious, whereas secondary impacts tend to be cumulative and may affect a far greater area than that being developed (Barr 1968; Humphreys 2000; Humphreys 1991). There are commonly three key threatening processes from mining activities that impact subterranean fauna through the direct loss of habitat:

- Development of mine pits – the most obvious primary impact to subterranean habitats occurs as a result of their physical removal during mining. Troglofauna require air-filled void networks and most of this habitat exists in the overburden, which is typically destroyed during pit construction/excavation. Similarly, direct loss of stygofauna habitat may be caused by the removal of geological formations if any aquifers are associated with these formations, i.e. channel iron or calcrete formations.
- Depletion of an aquifer leading to loss of stygofauna habitat – depletion of an aquifer that is identified as suitable for stygofauna represents a direct loss of stygofauna habitat. The significance of the impact is dependent on the depth of drawdown, the size and extent of the aquifer and the connectivity of the aquifer with adjacent habitat for stygofauna. The DEC has previously considered a lowering of the water table by more than 10 m to be a significant impact .
- Sediment compaction – troglofauna and stygofauna live and move through the interstitial spaces underground. Removal of these spaces can occur from heavy machinery repetitively moving over the surface, or from explosive blasting, resulting in compaction of the ground below.

Secondary impacts are those that affect the physicochemical properties of subterranean habitats. The nature of these changes can be difficult to measure and there is limited empirical evidence to support or refute these putative impacts. There are four secondary impacts that may be relevant to a mining project:

- Depletion of an aquifer leading to altered relative humidity – troglofauna are dependent on high relative humidity (EPA 2003; Howarth 1983; Humphreys 1991). Dewatering may impact

troglofauna habitat in unsaturated strata above the water table by lowering relative humidity.

- Nutrient starvation – surface vegetation is the primary source of nutrients entering subterranean systems. Large-scale clearing of vegetation may result in the localised nutrient starvation of underlying subterranean habitat. Smothering of these nutrient sources on which subterranean systems depend, in the form of waste and overburden stockpiles and tailings ponds, may reduce inflow of nutrients to subterranean systems and lead to nutrient deficient habitats and potential reductions in abundance and diversity (Howarth 1993; Humphreys 2000; Poulson & Lavoie 2000).
- Vibration – propagation of shock waves through subterranean strata from blasting or heavy vehicle traffic may result in the collapse of less-consolidated void spaces and also impact physically on subterranean fauna. There is little data to challenge or corroborate these observations and impacts would generally be localised rather than critically threatening.
- Contamination – contamination of subterranean habitats from spills, such as diesel fuel, may degrade the quality of subterranean habitats. Such impacts would generally be highly localised and minor in scale.

3 METHODS

3.1 DESKTOP REVIEW

Database searches were requested or undertaken to determine if any stygofauna, troglofauna or SRE taxa have previously been recorded in the study area or its vicinity:

WA Museum Arachnology and Myriapodology database, WA Museum Crustacea database and DEC Pilbara Stygofauna Survey (PSS) database – rectangular search grid determined by the proposed maximum range of short-range endemism, i.e. 100 km x 100 km (Harvey 2002b). Therefore, the search grid extended ca. 100 km from the centre of the study area (NE Corner: 21°37'20.67"S 118° 5'17.74"E; SW Corner: 22°37'21.55"S 118°56'36.55"E).

Phoenix's desktop review identified two previous surveys in the study area by Ecologia (2011):

- a pilot survey for troglofauna at Murray's Hill in 2009
- a follow up full troglofauna survey in 2011.

Two subterranean fauna survey reports for Fortescue Metals Group's (FMG's) Public Environmental Review (PER) for the Solomon Project were also investigated (Bennelongia 2010; Subterranean Ecology 2010).

3.2 FIELD METHODS

During this survey, three survey methods were employed at each bore (Appendix 1): troglofauna trapping, bore scraping and stygofauna netting. At each bore, the sampling tasks were carried out in the following succession:

1. depth to water was measured using an electronic dipper (section 3.2.3)
2. a water sample was taken using a disposable bailer and water quality parameters were recorded (section 3.2.3)
3. a bore scrape sample was taken (section 3.2.4)

4. a troglofauna trap was set in the bore (section 3.2.5)
5. a stygofauna netting sample was taken (section 3.2.6).

Karaman-Chappuis sampling was undertaken at creek line locations; this is a method of sampling interstitial sediment fauna (hyporheic fauna) from creeks (section 3.2.7).

3.2.1 Survey effort

Three survey trips were conducted, representing two seasons:

- trip 1 (T1), 20-27 October 2011
- trip 2 (T2), 9-12 December 2011
- trip 3 (T3), 16-24 January 2012.

The survey effort for three trips and each sampling method is summarised (Table 3-1; Appendix 2).

Table 3-1 Summary of survey effort for each survey trip and sampling method

Trip number	Number of samples collected				
	Bore scraping	Stygofauna netting	Troglofauna trapping (litter)	Troglofauna trapping (banana)	Karaman-Chappuis samples
Impact area					
T1	26	25	0	4	n/a
T2	0	0	25	0	n/a
T3	25	25	25	0	n/a
TOTAL	51	50	50	4	n/a
Reference					
T1	36	25	0	0	n/a
T2	0	5 (windmill bores)*	35	0	n/a
T3	35	25	35	0	7*
TOTAL	71	50 bores, 5 regional	70	0	7*

*- regional samples taken from sites other than survey bores

3.2.2 Site selection

Bores were selected from a list provided by Hancock. All bores sampled were greater than six months old and their location encompassed the full extent of the study area to maximise coverage and habitat representation (Appendix 1).

The final site selection included:

- 25 bores selected within the impact area for both the stygofauna and troglofauna survey.
- 35 bores selected as reference sites outside of the impact area for both the troglofauna and stygofauna survey.
- an additional 10 bores selected for the troglofauna survey only (i.e. no stygofauna haul samples taken or water quality measured).
- additional opportunistic sampling of regional bores (cattle watering bores) and creek lines (Karaman-Chappuis) when favourable conditions allowed accessibility. Karaman-Chappuis sampling in creek lines requires the water table to be close to the surface; therefore the wet season is best time for sampling if no permanent springs occur in the area.
- 26 bores selected for scraping from within the impact area and 36 bores selected for scraping from the reference area.

3.2.3 Water quality sampling

Water quality was recorded by lowering a disposable bailer into the bore to obtain a water sample. Bailers were rinsed with clean water between bores and a new bailer was used at approximately every 5th bore. The following water quality records were obtained from each bore: temperature, pH, salinity (ppt), conductivity (ms/cm), oxygen (as both percentage and parts per million), and oxygen reduction potential (ORP) (mV) (see Appendix 3 for data). Water quality was recorded using a YSI Pro Plus Water Quality Meter.

3.2.4 Bore scraping

While Guidance Statement 45a (EPA 2003) does not provide specific guidance on this survey method, its use is strongly encouraged by the Department of Environment and Conservation (DEC) and was therefore employed during this survey. The significance of this survey method was demonstrated by Subterranean Ecology (Subterranean Ecology 2010), who found that it complements troglofauna trapping by sampling more specimens and collecting additional species than troglofauna trapping alone. Scraping has historically been used for troglofauna surveys; however, more recently, it has also been demonstrated that this method is valuable for the collection of stygofauna (2010).

Scrapes were taken from both stygofauna and troglofauna bores in the reference area (Figure 3-1; Figure 3-2 and Figure 3-3). Samples were collected using a 150 µm plankton net, with a 'tickler device' positioned approximately 40 cm above the net. The assembly of net and 'tickler' is referred to as a 'scraper'. The tickler device was comprised of numerous strands of heavy gauge nylon fishing line, and this design closely follows that used by Subterranean Ecology (2007). The effect of the 'tickler' was to gently agitate the sides of the bore and dislodge any fauna present. Dislodged troglofauna are likely to drop into the net on either lowering or retrieval of the scraper.

Scrape samples were obtained using the following methodology:

- Each bore was scraped four times, once along each of the four sides: north, south, east and west. For the first scrape, the scraper was lowered and retrieved along one side of the bore, but subsequent scrapes were lowered along the side previously scraped and retrieved along the side intended for sampling. This method was used to insure greater scraping coverage on the inside of the bore, rather than scraping the one side repeatedly.
- Where the bore intercepted the water table, the scraper was allowed to sink into the water to a depth of approximately 1 m before being retrieved, in an attempt to net any troglofauna that may have missed the net after being dislodged. In dry bores, the scraper was lowered to the bottom of the bore then retrieved.
- Between each scrape, the sample contents were emptied into a jug of clean water.
- After four scrapes were collected, the combined net samples were elutriated to consolidate fauna and remove sediment. Samples were then cold-fixed. Cold fixing involved the following methodology:
    - Each sample was fixed with cold (~0°C) 95+% ethanol and was maintained at a constant temperature within a cooler bag or cooler box filled with ice.
    - The sample was stored in the same ice bag as the ethanol for the remainder of the day.
    - At the end of the day, samples were transferred and stored in a refrigerator (approximately 2°C) for at least 48 hours prior to transport to the laboratory for processing.

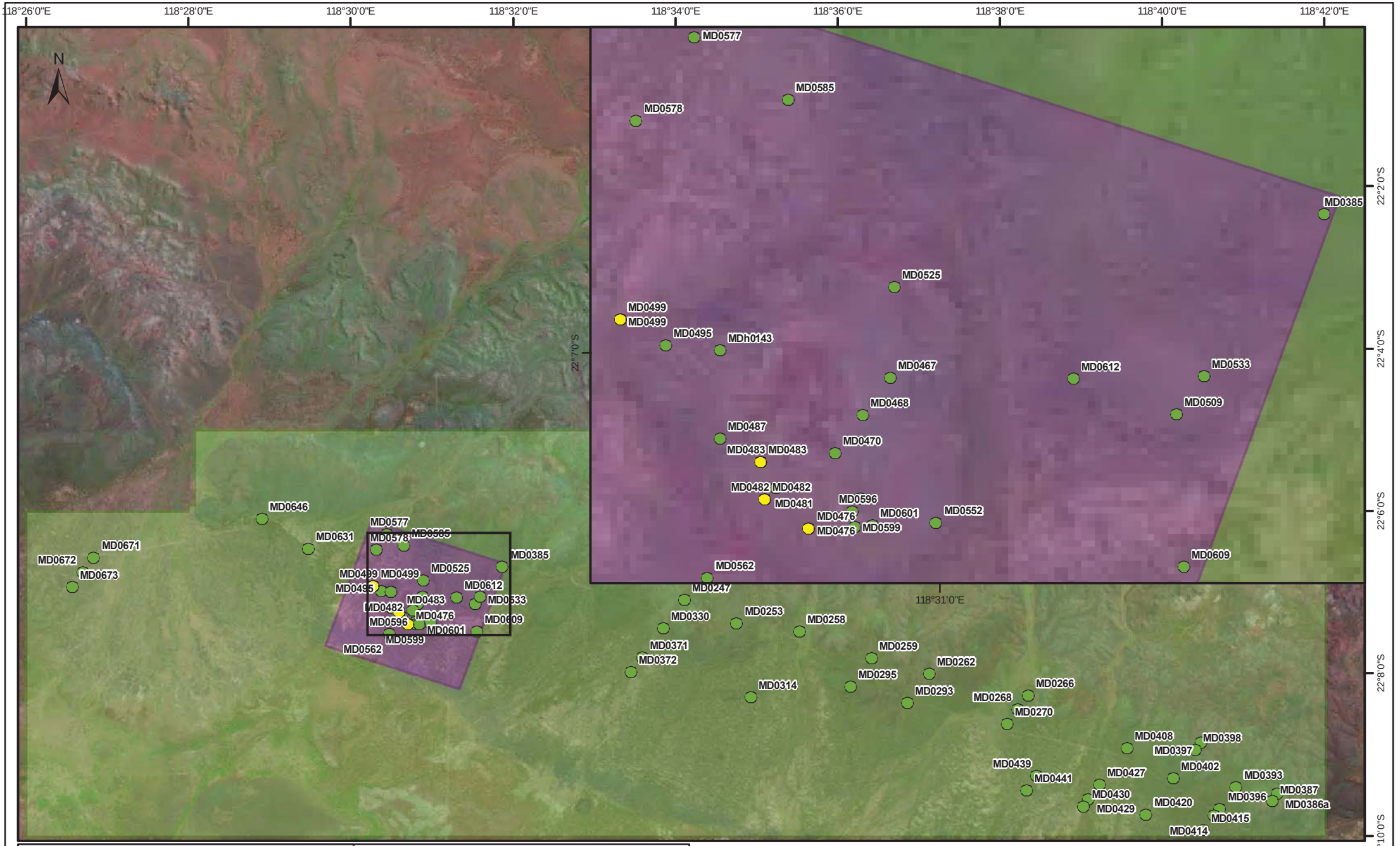

Figure 3-1 Locations of troglofauna trapping sites

AUTHOR: ES Volschenk	CLIENT: Hancock Prospecting
DATE 24 May 2012:	Scale: 1:109,384
Coordinate System: Projection: Transverse Mercator; DATUM: GDA94	PROJECT: Mulga Downs Subterranean Survey

PHOENIX ENVIRONMENTAL SCIENCES

0 0.05 0.1 0.2 0.3 0.4 0.5 Kilometres

Troglofauna Trap: Banana Bait

Troglofauna Trap: Leaflitter

Proposed Impact Area

Study Area

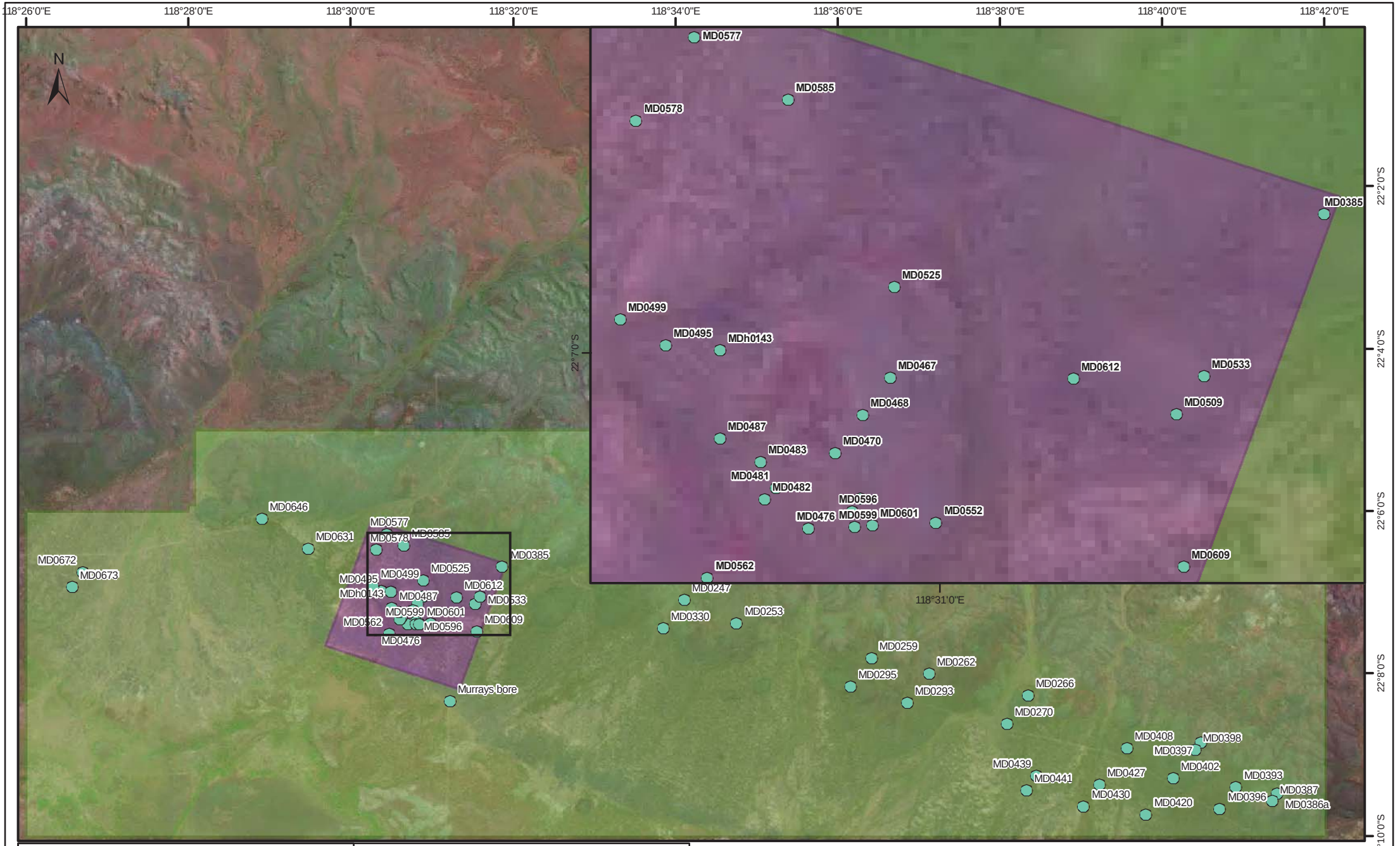

Figure 3-2 Locations of stygofauna survey bores

AUTHOR: ES Volschenk	**CLIENT:** Hancock Prospecting
DATE 24 May 2012:	**Scale:** 1:109,384
Coordinate System: Projection: Transverse Mercator; DATUM: GDA94	0 0.05 0.1 0.2 0.3 0.4 0.5 Kilometres

PHOENIX ENVIRONMENTAL SCIENCES

PROJECT: Mulga Downs Subterranean Survey

Stygofauna Haul | Proposed Disturbance Area | Study Area

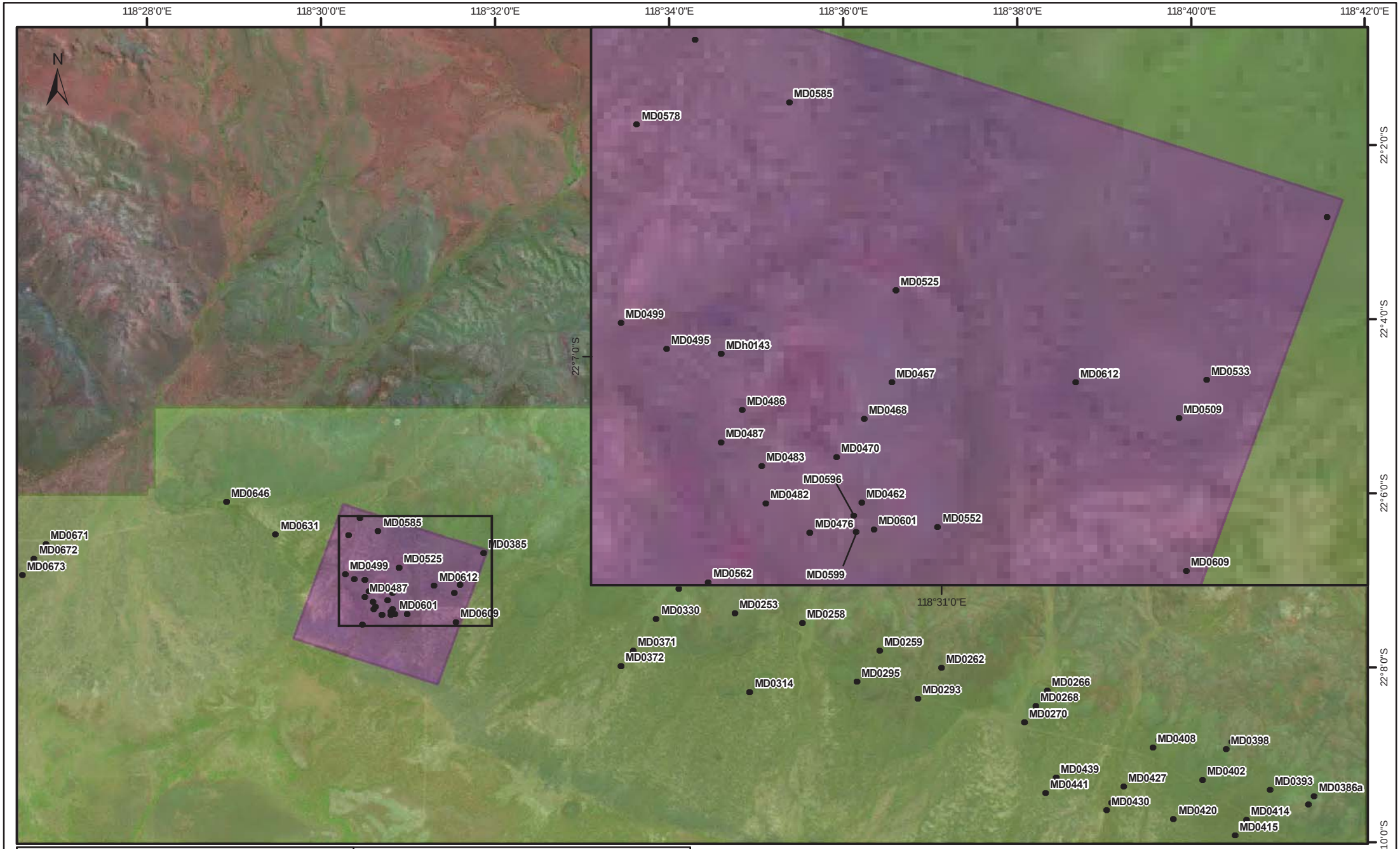

Figure 3-3 Locations of bore scraping sites

AUTHOR: ES Volschenk	CLIENT: Hancock Prospecting
DATE 24 May 2012:	Scale: 1:102,395
Coordinate System: Projection: Transverse Mercator; DATUM: GDA94	PROJECT: Mulga Downs Subterranean Survey

PHOENIX ENVIRONMENTAL SCIENCES

0 0.05 0.1 0.2 0.3 0.4 0.5 Kilometres

• Bore Scrape Samples Proposed Impact Area Study Area

3.2.5 Troglofauna trapping

The methodology employed for troglofauna trapping closely followed the EPA's (2007) recommendations for the surveying of troglofauna. Troglofauna trapping was conducted in the study area (Figure 3-1).

Traps were comprised of PVC cylinders of dimensions 20 cm long and 5 cm diameter. The top end of each trap was left open to allow access by troglobites. The bottom of each trap was capped with a PVC end-cap, with a small drain hole to allow water to drain out.

Traps were filled with aged and wetted spinifex litter. Approximately three days prior to deployment, the 'litter loaded' traps were flooded with boiling water, and left in the water until cooled (approximately 3 hours), in order to kill any potentially-contaminating arthropods, and to saturate the samples. After cooling, the traps drained and packed for shipping.

At deployment, each trap was lowered into its bore until it reached the bottom of the bore, or the water table. The trap was then lifted and tied off at approximately 2-3 m above the water table or bottom of the bore.

Traps deployed on trip 1 were retrieved seven weeks later on trip 2. Traps redeployed on trip 2 were retrieved ten weeks later on trip 3. Each trap was placed directly into a brown paper bag, and then sealed in plastic snap lock bags prior to being placed into cooler boxes which were subsequently transported to Perth. Traps were placed into Phoenix's custom Tullgren extractors with a programmed temperature ramp-up from 25°C to 50°C over 12 hours and were then maintained at 50°C for an additional 12 hours.

Four banana traps were deployed on trip 1. Banana traps are the same as litter traps but have a small piece of banana placed in the trap to attract troglofauna. These traps were deployed in bore holes where troglofauna had been collected on previous surveys and are only left in the bore hole for two to three days.

3.2.6 Stygofauna netting

The methodology employed for stygofauna netting closely followed the EPA's (1983b) recommendations for the surveying of stygofauna. Stygofauna netting was conducted at all study areas (Figure 3-2) and at five regional bores (Figure 3-4).

Six net hauls were collected from each bore using a 150 µm plankton net (three hauls), followed by a 50 µm plankton net (three hauls). Each netting assembly was fitted with a tickler device (section 3.2.4) placed approximately 40 cm above the sampling net to dislodge crawling taxa from the sides of the bore. Each haul sampled the entire water column of the bore.

The six samples were elutriated in a 2 L jug to consolidate fauna and to remove excess sediments, producing a single sample for each bore. Excess water was removed from the sample and samples were cold-fixed (section 3.2.4) to maximize DNA yields from tissues, should sequencing be required.

The five regional bores were windmill cattle watering bores. These were sampled by trawling a 150 µm and/or a 50 µm net through the trough, occasionally stirring up the bottom.

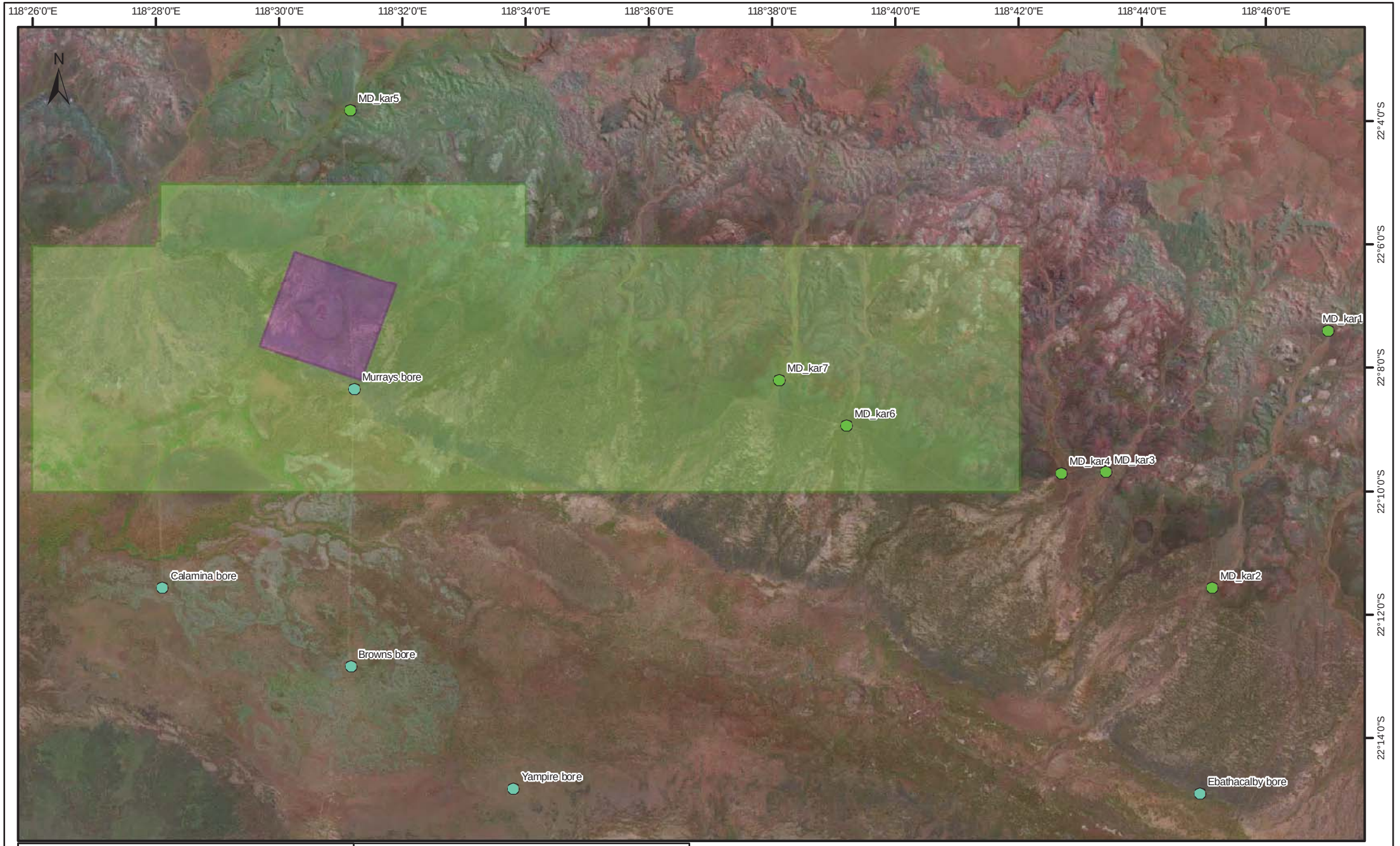

Figure 3-4 Locations of regional survey sites

AUTHOR: ES Volschenk	**CLIENT:** Hancock Prospecting
DATE 24 May 2012:	**Scale:** 1:143,964
Coordinate System: Projection: Transverse Mercator; DATUM: GDA94	

PHOENIX ENVIRONMENTAL SCIENCES

PROJECT: Mulga Downs Subterranean Survey

0 0.1 0.2 0.4 0.6 0.8 1 Kilometres

- Karaman-Chappuis Samples
- Windmill Bores
- Study Area
- Proposed Impact Area

3.2.7 Karaman-Chappuis sampling

The Karaman-Chappuis sampling method was used to provide regional data for interstitial fauna in accessible creeks. These samples help to evaluate the habitat constraints of fauna that were collected from bores in the 'impact area', and therefore provide regional context. The method targets interstitial fauna beneath gravel banks of rivers and streams. Some of these fauna are also likely to be present within the superficial aquifer and therefore appear in bore samples.

Karaman-Chappuis sampling was conducted along seven creeks within the study area (Figure 3-4). A hole was dug into the gravel bank of a creek until the water table was reached. Then, as water flowed into the hole, it was scooped out and filtered through a 50 µm stygofauna net. Approximately 60 L of water was sampled per site. After filtering through the stygofauna net, the samples were elutriated and preserved following the cold fixing method (section 3.2.4).

3.3 TAXONOMY

Phoenix applies a phylogenetic species approach to taxonomy, whereby morphospecies are defined by the presence of consistent morphological characteristics, following Cracraft (1982, 1983a). Specialist taxonomists were consulted for groups that were targeted in the survey (Table 3-2).

Table 3-2 Taxonomic specialists

Personnel	Taxonomic group/s
Dr Erich S. Volschenk[1]	Arachnida (non-spiders), Syncarida, Myriapoda, Diplura, Pseudoscorpiones, Polyxenida
Ms Anna Leung[1]	Pseudoscorpiones, Myriapoda, Diplura
Dr Mark Harvey[2]	Arachnida, Myriapoda
Mr Mike Scanlon[3]	Oligochaeta
Ms Jane McRae[3]	Copepoda

[1] Phoenix Environmental Sciences; [2] Western Australian Museum; [3] Bennelongia Environmental Consultants.

3.4 GENOMIC ANALYSES

The WA fauna collection licence (Regulation 17 *Licence to take fauna for scientific purposes*, under the WC Act) requires lodgement of voucher specimens with the WA Museum. Some environmental consultancies do not lodge voucher specimens and the data remain inaccessible to the remainder of the industry. In some cases however, these taxa are sequenced for their DNA and their sequences can be accessed through Helix Molecular Solutions to obtain regional context for species by DNA sequence analyses. Genomic analyses were used in this survey for specimens that were suspected to be SREs.

Sequencing usually targets the gene COXI (Cytochrome C Oxidase Subunit 1), also referred to as the 'barcoding gene' (Hebert *et al.* 2003b). Hebert *et al.* (1994) found sequence differences of 10.1% or more between 1400 different arthropod species, and more than 50% of these comparisons showed more than 8% sequence divergence. Species within groups for which morphological taxonomy is not available, can be assessed by comparing the pairwise COXI sequence divergences. Species with COXI sequence divergences of 8%, or greater, are likely to represent different species and those with less than 8% divergence are likely to be members of the same species. In instances where COXI

sequences could not be obtained, the ribosomal genes 12S and 18S were targeted and used in a similar way. Helix Molecular Solutions methodologies are presented in attached reports (Appendix 4).

3.5 STATISTICAL ANALYSES

The efficiency of the survey effort was evaluated by comparing the observed species richness of both troglofauna and stygofauna against the predicted species richness of seven widely used species richness estimators. Species accumulation curves and richness estimation were made with EstimateS (v8.2.0) using the default settings, with the following exceptions:

- species accumulation curves were smoothed using 10,000 repetitions rather than the default setting of 50 to provide greater accuracy to extrapolations
- the coverage estimator value was set to two rather than 10, so as to more reliably treat 'rare' taxa, since troglobites are often sampled in very low numbers.

A variety of richness estimators were used: ACE, ICE, Chao 1, Chao 2, Jack 1, Jack 2, and Bootstrap. The methods used by Colwell and Coddington (2009) and Moir *et al*. (2009) were followed to examine the complementarity of sample methods. Extrapolations were performed on the abundance data from defined morphospecies.

Taxon selection conformed to the following requirements:

- ambiguous identifications (designated with "sp. indet.") were not included in the analyses since the number of species involved was unknown
- species were only included if they were sampled from survey bores since species only recorded from Karaman-Chappuis and or Windmill bores may be representatives of independent communities.

3.6 SURVEY PERSONNEL AND ACKNOWLEDGEMENTS

The survey personnel involved in the Project are presented (Table 3-3).

Table 3-3 Project team

Name	Role/s
Dr Erich S. Volschenk	Project Manager, field surveys, taxonomy, GIS, report writing
Ms Anna Leung	Field surveys, taxonomy, GIS, report writing, lab Work
Mr Conor O'Neill	Field surveys, project administration, lab work
Ms Kate Penwarden	Field surveys, lab work
Mrs Melanie White	Report review
Ms Karen Crews	Report review
Mr Xavier Leenders	Lab work

3.7 GEOLOGICAL AND SPATIAL DATA

Mapping was undertaken using geological core data logs (Appendix 5) and project-specific shapefiles provided by Hancock. Surface geology data were obtained from the Geological Survey of Western Australia (GSWA) (http://geodownloads.dmp.wa.gov.au/seriesmapping/digitalgeology_enh2.asp):

"1:250,000 geological map - MOUNT BRUCE (SF50-11), second edition"

4 RESULTS

4.1 ENVIRONMENTAL PARAMETERS

Records from the Bureau of Meteorology Wittenoom weather station (Station 005026) during the period between September 2011 and February 2012 show erratic rainfall relative to the long term average. This was mainly attributed to a below average rainfall in September, October December and February, but well above average rainfall for November and January (Figure 4-1). During the survey period, mean daily maximum and minimum temperatures tracked close to the long term monthly averages, but in February both maximum and minimum temperatures were below the long term averages (Figure 4-1).

The rainfall data suggest that November (2011) and January (2012) received above average rainfall while the remaining months received less than average rainfall, representing ideal (above average) conditions for subterranean fauna; however, it should be noted that these conditions are an approximate indication of weather in the region and are not indicative of exact conditions on site. Temperature is thought to be less influential than rainfall on subterranean fauna sampling outcomes.

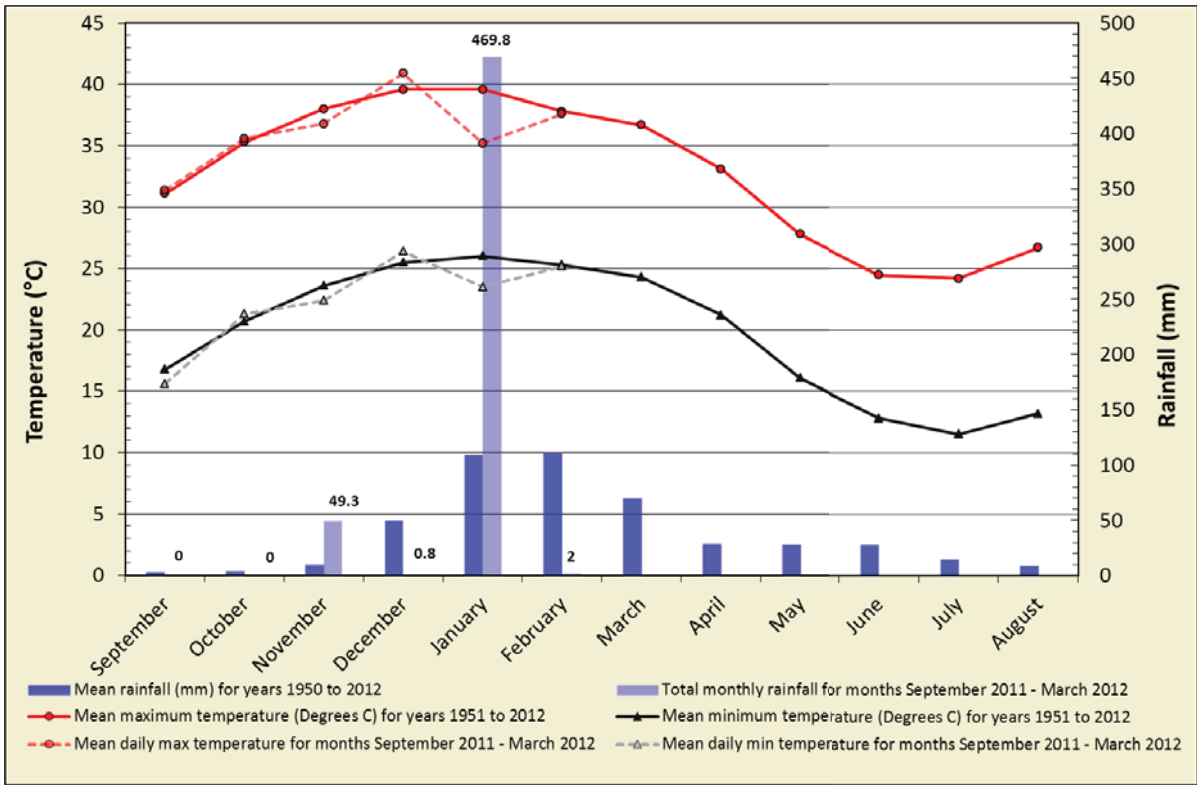

Figure 4-1 Temperature and rainfall variables collected during the field survey period

4.2 DESKTOP REVIEW

A review of the WA Museum database revealed a single undescribed species of Polyxenid millipede WA Museum registration number T100180. This specimen is a voucher of the Polyxenid sampled by Ecologia at Mulga Downs in 2010. Ecologia sampled 'Murrays Hill' in 2010 and recorded three putative morphospecies: *Nocticola* sp., Polyxenida sp., Parajapygidae sp. No genomic studies were undertaken on these specimens.

Two subterranean surveys (Bennelongia 2010; Subterranean Ecology 2010) were undertaken for FMG (Fortescue Metals Group) for the Solomon Project PER. These reports document a very rich subterranean fauna comprising nearly all of the known troglofauna and stygofauna groups known from the Pilbara. The Solomon surveys were conducted approximately 85 km SW of the study area, in the Hamersley Range. The geology of Solomon is very different to that of the study area, being dominated by channel iron deposit (CID) and Brockman formation. Both the disparate geology and the placement of these sites on opposite sides of the Fortescue Plain suggest there is a low likelihood of conspecific species between these locations.

4.3 OVERVIEW OF SAMPLING RESULTS

This survey produced a diverse sample of subterranean invertebrates including several new species, indicated by the suffix 'MH'. Thirty one groups of troglofauna were recorded (Table 4-1). Four species groups remain unresolved owing to absence of expertise in these groups:

- Palpigradi sp. indet.
- Japygidae sp. indet.
- Meenoplidae sp. indet.
- *Trinemura* sp. indet.

Twenty seven troglofauna species were recorded from the bore samples (Table 4-1) and of these, 11 species were recorded from both impact and reference bores (Table 4-2). Six troglofauna species were only collected from the impact area:

- *Cryptops* 'MH1'
- *Palpigradi* 'MH1'
- Parajapygidae 'MH1'
- Pauropoda 'MH1'
- Schizomida 'MH2'
- *Troglarmadillo* 'MH1'.

Twenty four stygofauna species were recorded from the bore samples (Table 4-1) and of these, 10 species were collected in both impact and reference bores (Table 4-2). A single stygofauna species was only collected from the impact area:

- Parabathynellidae 'MH3'.

Table 4-1 Subterranean fauna classification and sample abundance from which records were obtained for impact and reference areas

Class	Order	Family	Species name	Ecotype	SRE status	Impact area samples	Reference area samples
Arachnida	Araneae	Symphytognathidae	*Anapistula* 'MH1'	Troglobite	Likely SRE	1	3
	Palpigradi	-	Palpigradi 'MH1'	Troglophile	Likely SRE	1	0
			Palpigradi 'MH2'	Troglophile	Likely SRE	0	1
			Palpigradi sp. indet.	Troglophile	**Undetermined**	4	2
	Pseudoscorpiones	Chthoniidae	*Tyrannochthonius* 'MH1'	Troglobite	Likely SRE	0	1
		Hyidae	*Indohya* 'MH1'	Troglobite	Likely SRE	0	1
	Schizomida		Schizomida 'MH1'	Troglobite	Likely SRE	0	1
			Schizomida 'MH2'	Troglobite	Likely SRE	1	0
Chilopoda	Scolopendromorpha	Cryptopidae	*Cryptops* 'MH1'	Troglobite	Likely SRE	1	0
			Cryptops 'MH2'	Troglophile	Likely SRE	0	4
		Scolopendridae	*Cormocephalus* 'MH1'	Troglobite	Likely SRE	0	1
Diplopoda	Polyxenida	Polyxenidae	Polyxenidae PXD1'	Troglophile	Not SRE	1	5
Entognatha	Diplura	Japygidae	Japygidae 'MH1'	Troglobite	Likely SRE	1	1
			Japygidae 'MH2'	Troglobite	Likely SRE	0	2
			Japygidae sp. indet.	Troglobite	**Undetermined**	0	1
		Parajapygidae	Parajapygidae 'MH1'	Troglophile	Likely SRE	2	0
		Projapygidae	Projapygidae 'MH1'	Troglophile	Likely SRE	1	2

Class	Order	Family	Species name	Ecotype	SRE status	Impact area samples	Reference area samples
Insecta	Blattaria	Nocticolidae	*Nocticola* 'MH1'	Troglobite	SRE	9	8
	Coleoptera	Carabidae	Anillini 'MH1'	Troglophile	Likely SRE	4	4
	Hemiptera	Meenoplidae	Meenoplidae sp. indet.	Troglophile	**Undetermined**	2	4
			Meenoplidae 'USF'	Troglophile	Not SRE	1	0
			Meenoplidae 'widespread'	Troglophile	Not SRE	0	1
	Thysanura	Nicoletiidae	Atelurinae 'MH1'	Probable troglophile	Likely SRE	1	1
			Trinemura 'MH1'	Troglobite	Likely SRE	5	3
			Trinemura 'MH2'	Troglobite	Likely SRE	5	2
			Trinemura sp. indet.	Unknown	**Undetermined**	1	3
Malacostraca	Isopoda	Armadillidae	*Troglarmadillo* 'MH1'	Troglobite	Likely SRE	1	0
Pauropoda	-	-	Pauropoda 'MH1'	Probable troglophile	Likely SRE	1	0
			Pauropoda 'MH2'	Probable troglophile	Likely SRE	1	2
			Pauropoda 'MH3'	Probable troglophile	Likely SRE	1	1
Symphyla	-	-	Symphyla 'MH1'	Probable troglophile	Likely SRE	0	4

Class	Order	Family	Species name	Ecotype	SRE status	Impact area samples	Reference area samples
Stygofauna							
Arachnida	Acari	Mideopsidae	*Guineaxonopsis* sp. S1 (PSS)	Stygobite	Not SRE	0	1
Clitellata	Haplotaxida	Enchytraeidae	**Enchytraeidae sp. indet.**	**Undetermined**	**Undetermined**	2	0
			Enchytraeus 'Pilbara 1 (PSS)'	Stygobite	Not SRE	8	25
			Enchytraeus sp. indet.	**Undetermined**	**Undetermined**	0	1
		Naididae	*Pristina longiseta*	Stygophile	Not SRE	0	2
		Phreodrilidae	Phreodrilid 'with dissimilar ventral chaetae'	Stygophile	Not SRE	3	2
			Phreodrilus peniculus	Stygobite	Not SRE	0	1
Malacostraca	Amphipoda	Paramelitidae	Paramelitidae 'MH1'	Stygobite	Likely SRE	40	5
	Bathynellacea	Bathynellidae	Bathynellidae 'MH1'	Stygobite	Likely SRE	2	1
			Bathynellidae 'MH2'	Stygobite	Likely SRE	0	3
			Bathynellidae sp. indet.	**Undetermined**	**Undetermined**	0	1
		Parabathynellidae	Parabathynellidae 'MH1'	Stygobite	Likely SRE	0	2
			Parabathynellidae 'MH2'	Stygobite	Likely SRE	3	2
			Parabathynellidae 'MH3'	Stygobite	Likely SRE	2	0
	Isopoda	Tainisopidae	*Pygolabis* 'MH1'	Stygophile	SRE	0	1
Maxillopoda	Cyclopoida	Cyclopidae	*Australocyclops* cf *similis*	Stygophile	Not SRE	0	5
			Diacyclops humphreysi humphreysi	Stygophile	Not SRE	30	3

Class	Order	Family	Species name	Ecotype	SRE status	Impact area samples	Reference area samples
			Fierscyclops sp. B3 (nr *frustratio*)	Stygobite	Not SRE	0	1
			Goniocyclops sp. B08 (cf *mortoni*)	Stygophile	Not SRE	0	2
			Mesocyclops cf *brooksi*	Stygophile	Not SRE	2	9
			Metacyclops pilbaricus	Stygophile	Not SRE	3	0
			***Mesocyclops* sp. indet.**	**Undetermined**	**Undetermined**	**0**	**1**
			Microcyclops varicans	Stygophile	Not SRE	0	8
			Thermocyclops B04	Stygophile	Not SRE	0	1
	Harpacticoida	Canthocamptidae	Canthocamptidae B3	Stygophile	Not SRE	5	0
			Dussartstenocaris sp. B01	Stygophile	SRE	0	1
			***Dussartstenocaris* sp. indet.**	**Undetermined**	**Undetermined**	**0**	**1**
			Elaphoidella sp. B2	Stygophile	Not SRE	0	3
		Parastenocarididae	*Parastenocaris* B18	Stygophile	Likely SRE	1	1
Ostracoda	Podocopida	Candonidae	*Areacandona brookanthana*	Stygobite	SRE	1	1
			Areacandona cf *clementia*	Stygobite	Not SRE	1	0
			Candonopsis cf *dedeckkeri*	Stygobite	Likely SRE	0	1
			Candonopsis tenuis	Stygophile	Not SRE	0	2
			Deminutiocandona cf *quasimica*	Stygophile	Likely SRE	1	1
			Meridiescandona sp. BOS297	Stygobite	SRE	0	1

Class	Order	Family	Species name	Ecotype	SRE status	Impact area samples	Reference area samples
		Cyprididae	*Sarscypridopsis* sp.	Surface	Not SRE	0	1
			Strandesia 466	Stygophile	Not SRE	0	2
			Cypridopsis BOS301	Surface	Not SRE	0	1
			Cyprididae sp. indet.	**Undetermined**	**Undetermined**	**0**	**1**
		Limnocytheridae	*Limnocythere dorsosicula*	Stygophile	Not SRE	0	1
Polychaeta	Scolecida	Aelosomatidae	*Aelosomatidae* sp. indet.	Stygobite	Not SRE	0	1

Table 4-2 Summary of distribution records and ecotype for target species

Species name	Valid morphospecies	Valid taxa from bores	Likely SRE or SRE	SRE species restricted to impact area bores	SRE morphospecies in impact and reference bores	SRE morphospecies from reference bores only
Troglofauna						
Anapistula 'MH1'	X	X	X	-	X	-
Palpigradi 'MH1'	X	X	X	X	-	-
Palpigradi 'MH2'	X	X	X	-	-	X
Palpigradi sp. indet.	-	-	-	-	-	-
Tyrannochthonius 'MH1'	X	X	X	-	-	X
Indohya 'MH1'	X	X	X	-	-	X
Schizomida 'MH1'	X	X	X	-	-	X
Schizomida 'MH2'	X	X	X	X	-	-
Cryptops 'MH1'	X	X	X	X	-	-
Cryptops 'MH2'	X	X	X	-	-	X
Cormocephalus 'MH1'	X	X	X	-	-	X
Polyxenidae PXD1'	X	X	-	-	X	-
Japygidae 'MH1'	X	X	X	-	X	-
Japygidae 'MH2'	X	X	X	-	-	X
Japygidae sp. indet.	-	-	-	-	-	-
Parajapygidae 'MH1'	X	X	X	X	-	-
Projapygidae 'MH1'	X	X	X	-	X	-
Nocticola 'MH1'	X	X	X	-	X	-
Anillini 'MH1'	X	X	X	-	X	-
Meenoplidae sp. indet.	-	-	-	-	-	-
Meenoplidae 'USF'	X	X	-	-	-	-
Meenoplidae 'widespread'	X	X	-	-	-	-
Atelurinae 'MH1'	X	X	X	-	X	-
Trinemura 'MH1'	X	X	X	-	X	-
Trinemura 'MH2'	X	X	X	-	X	-

Species name	Valid morphospecies	Valid taxa from bores	Likely SRE or SRE	SRE species restricted to impact area bores	SRE morphospecies in impact and reference bores	SRE morphospecies from reference bores only
Trinemura sp. indet.	-	-	-	-	-	-
Troglarmadillo 'MH1'	X	X	X	X	-	-
Pauropoda 'MH1'	X	X	X	X	-	-
Pauropoda 'MH2'	X	X	X	-	X	-
Pauropoda 'MH3'	X	X	X	-	X	-
Symphyla 'MH1'	X	X	X	-	-	X
Stygofauna						
Guineaxonopsis sp. S1 (PSS)	X	-	-	-	-	-
Enchytraeidae sp. indet.	-	-	-	-	-	-
Enchytraeus 'Pilbara 1 (PSS)'	X	X	-	-	X	
***Enchytraeus* sp. indet.**	-	-	-	-	-	**X**
Pristina longiseta	X	-	-	-	-	-
Phreodrilid 'with dissimilar ventral chaetae'	X	X	-	-	X	-
Phreodrilus peniculus	X	X	-	-	-	-
Paramelitidae 'MH1'	X	X	X	-	X	-
Bathynellidae 'MH1'	X	X	X	-	X	-
Bathynellidae 'MH2'	X	X	X	-	-	X
Bathynellidae sp. indet.	-	-	-	-	-	-
Parabathynellidae 'MH1'	X	X	X	-	-	X
Parabathynellidae 'MH2'	X	X	X	-	X	-
Parabathynellidae 'MH3'	X	X	X	X	-	-
Pygolabis 'MH1'	X	-	X	-	-	X
Australocyclops cf *similis*	X	X	-	-	-	X
Diacyclops humphreysi humphreysi	X	X	-	-	X	-
Fierscyclops sp. B3 (nr *frustratio*)	X	X	-	-	-	-

Species name	Valid morphospecies	Valid taxa from bores	Likely SRE or SRE	SRE species restricted to impact area bores	SRE morphospecies in impact and reference bores	SRE morphospecies from reference bores only
Goniocyclops sp. B08 (cf *mortoni*)	X	X	-	-	-	-
Mesocyclops cf *brooksi*	X	X	-	-	X	-
Metacyclops pilbaricus	X	X	-	-	-	-
***Mesocyclops* sp. indet.**	-	-	-	-	-	-
Microcyclops varicans	X	X	-	-	-	-
Thermocyclops B04	X	-	-	-	-	-
Canthocamptidae B3	X	X	-	-	-	-
Dussartstenocaris sp. B01	X	-	X	-	-	X
***Dussartstenocaris* sp. indet.**	-	-	-	-	-	-
Elaphoidella sp. B2	X	X	-	-	-	-
Parastenocaris B18	X	X	X	-	X	-
Areacandona brookanthana	X	X	X	-	X	-
Areacandona cf *clementia*	X	X	-	-	-	-
Candonopsis cf *dedeckkeri*	**X**	-	**X**	-	-	**X**
Candonopsis tenuis	X	-	-	-	-	-
Deminutiocandona cf *quasimica*	X	X	X	-	X	
Meridiescandona sp. BOS297	X	X	X	-	-	X
Sarscypridopsis sp.	X	-	-	-	-	-
Strandesia 466	X	-	-	-	-	-
Cypridopsis BOS301	X	-	-	-	-	-
Cyprididae sp. indet.	-	-	-	-	-	-
Limnocythere dorsosicula	X	-	-	-	-	-
Aelosomatidae sp.	X	X	-	-	-	-

4.4 ASSESSMENT OF SPECIES RICHNESS

4.4.1 Troglofauna richness estimation and evaluation of survey results

The species accumulation curves for each sampling method (and combined methods) indicate that the species richness was relatively well sampled because the combined effort of all samples resulted in a plateauing curve. The species accumulation rate was highest for scraping and lowest for troglofauna trapping (Figure 4-2).

The troglofauna richness estimation indicates that between 32 and 38 species were predicted to occur within the study area (Table 4-3, Figure 4-3). With 27 troglofauna species recorded from this survey, the percentage of species sampled relative to extrapolated species richness ranges from 74% to 87% (Figure 4-3).

Table 4-3 Estimation of troglofauna richness using seven commonly used richness estimators

	Observed species richness	ACE mean	ICE mean	Chao 1 mean	Chao 2 mean	Jack 1 mean	Jack 2 mean	Bootstrap mean
Combined (355)	27	37.33	37.33	33.33	33.33	35.98	37.98	32.04

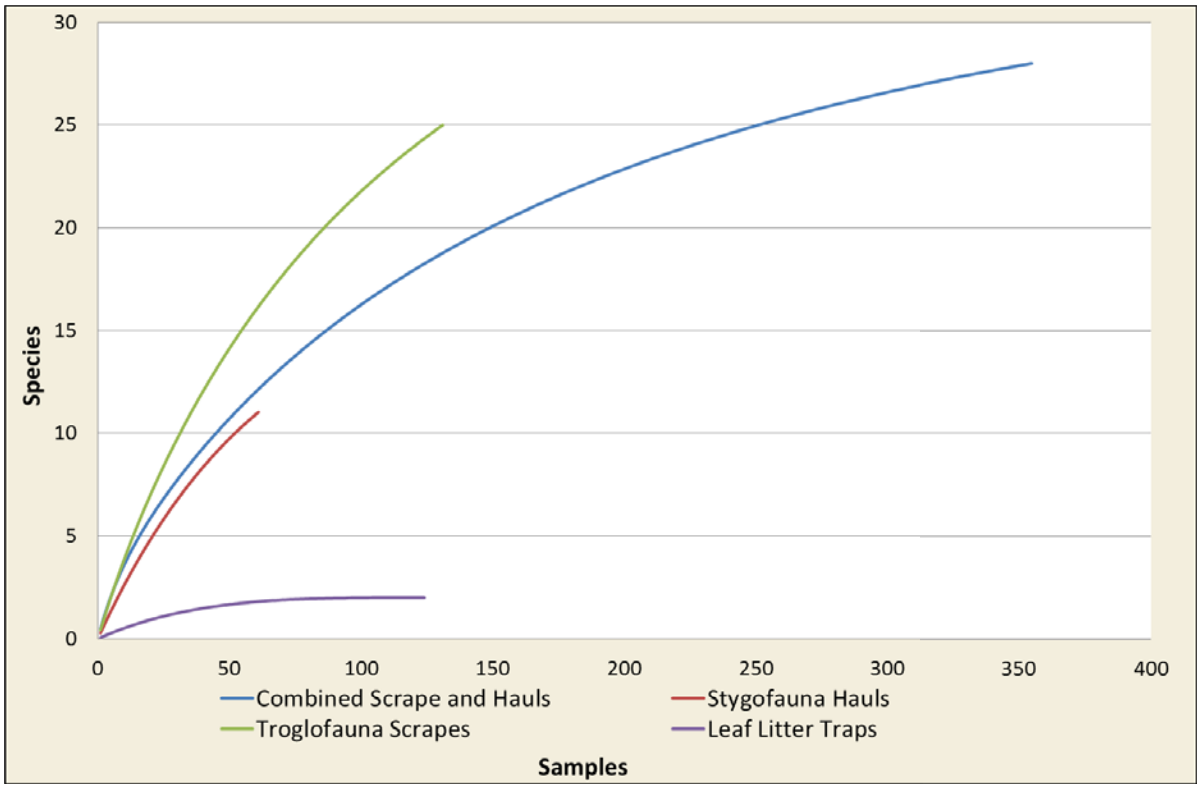

Figure 4-2 Species accumulation curves for troglofauna sampling

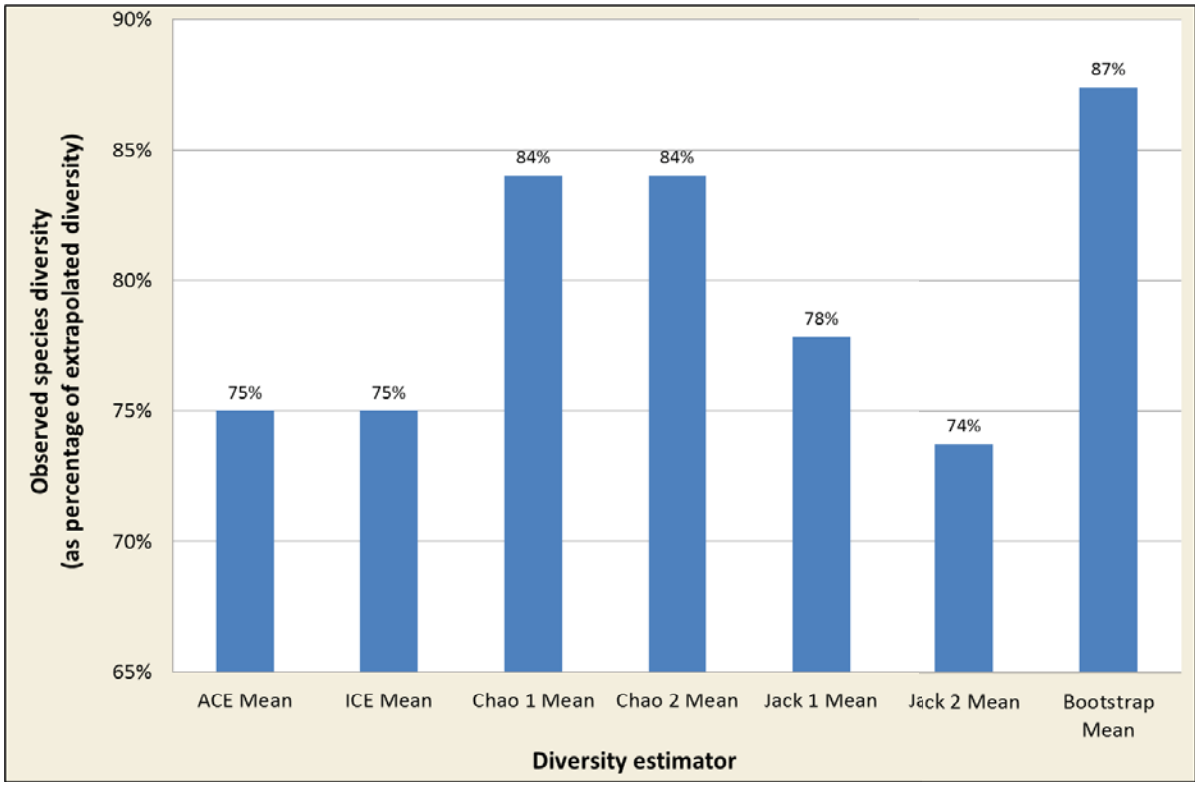

Figure 4-3 **Observed troglofauna species richness as a percentage of extrapolated species richness**

4.4.2 Stygofauna species richness estimation and evaluation of survey results

Richness estimations that were calculated using seven common richness estimators, extrapolated the presence of between 26 and 38 species (Table 4-4). The recorded species richness of 24 species represents between 62% and 92% of the extrapolated species richness (Figure 4-4).

The species accumulation curves for each sampling method (and combined methods) indicate that the species richness was moderately well surveyed. The species accumulation rates for both scraping and stygofauna netting were almost identical, indicating that sampling rates for stygofauna was nearly the same for both methods (Figure 4-5).

Table 4-4 **Extrapolated stygofauna richness using seven commonly used richness estimators**

	Observed species richness	ACE mean	ICE mean	Chao 1 mean	Chao 2 mean	Jack 1 mean	Jack 2 mean	Bootstrap mean
Combined (355)	24	28	38.63	26	34.13	32.96	37.93	28.08

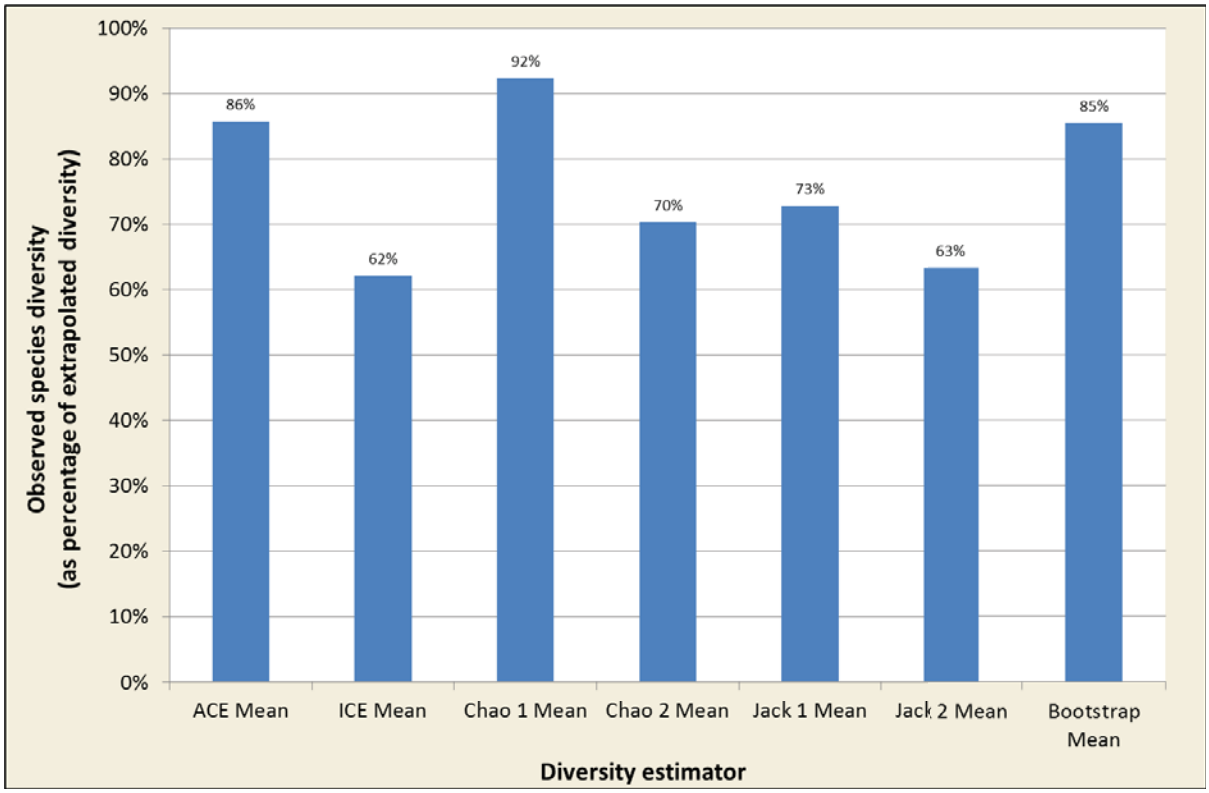

Figure 4-4 **Observed stygofauna species richness as a percentage of extrapolated species richness**

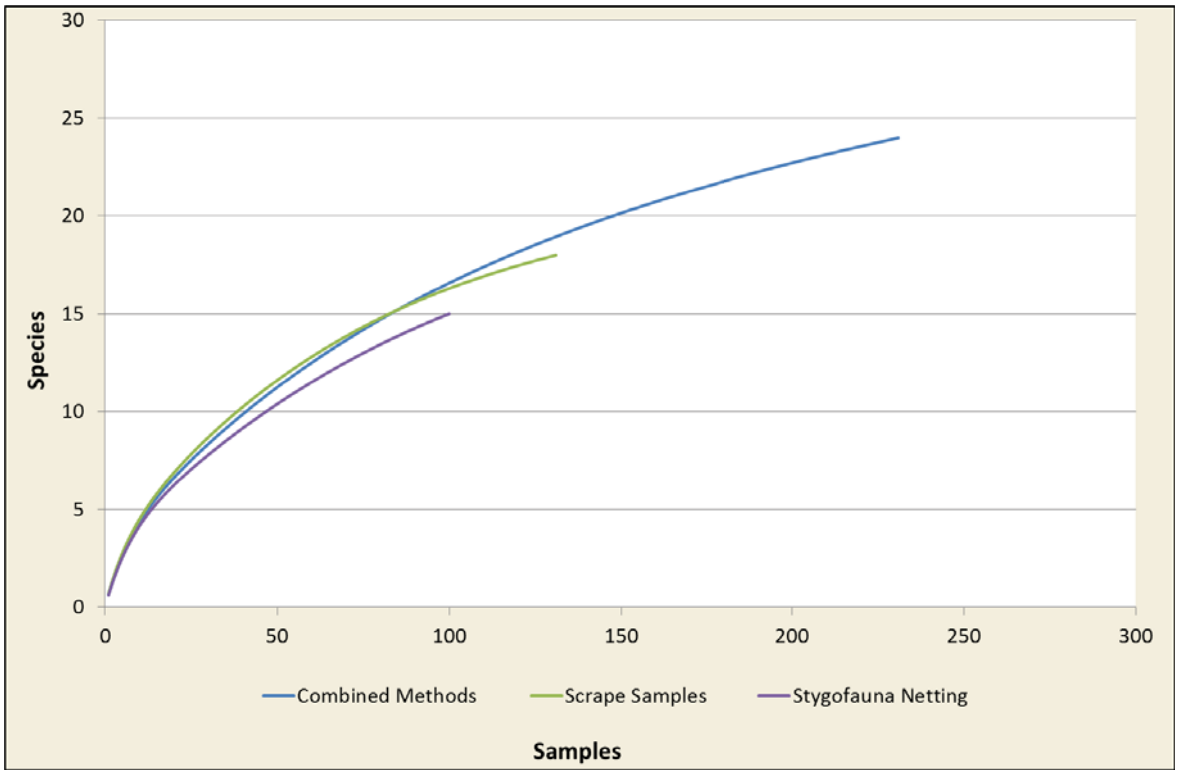

Figure 4-5 **Species accumulation curves for stygofauna sampling methods**

4.5 TROGLOFAUNA RECORDS

Twenty seven putative troglobitic or troglophilic species were recorded from this survey. A total of 179 individuals were collected from a total sample effort of 355 samples. Of the species sampled, 14 were represented by only one or two specimens (Figure 4-6).

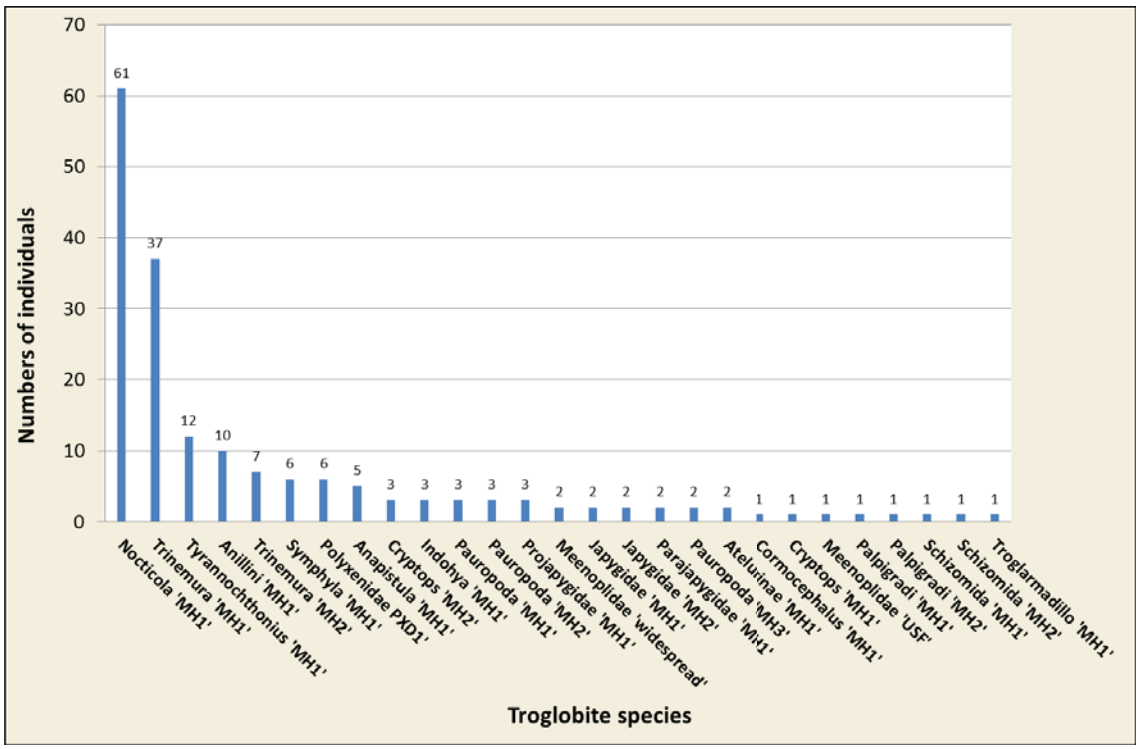

Figure 4-6 Abundance records for troglobitic species

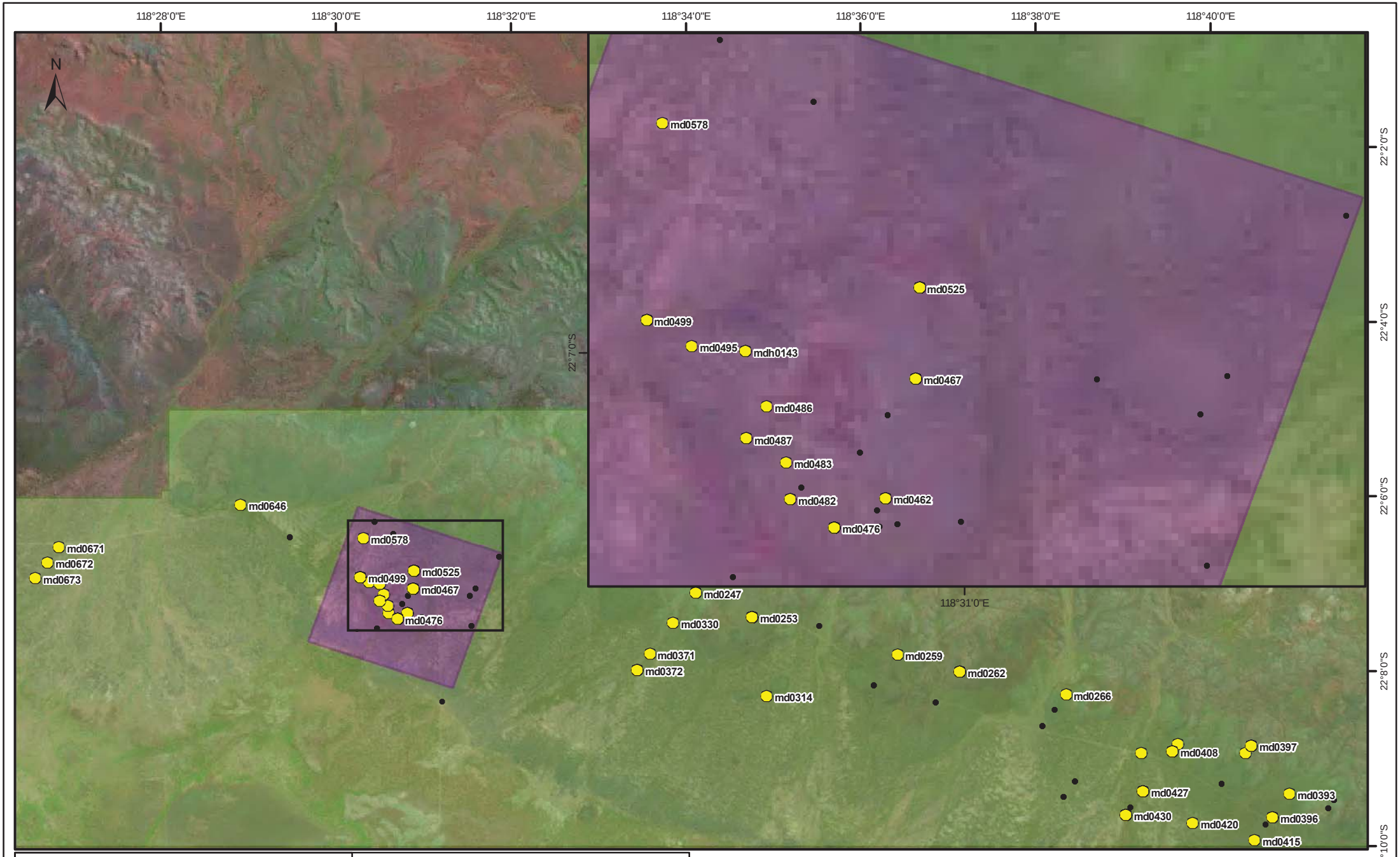

Figure 4-7 Troglofauna site records from the survey

AUTHOR: ES Volschenk	CLIENT: Hancock Prospecting
DATE 24 May 2012:	Scale: 1:101,991
Coordinate System: Projection: Transverse Mercator; DATUM: GDA94	PROJECT: Mulga Downs Subterranean Survey

PHOENIX ENVIRONMENTAL SCIENCES

0 0.5 1 2 3 4 5 Kilometres

4.5.1 Arthropoda: Arachnida: Araneae

4.5.1.1 *Anapistula* 'MH1'

Taxonomic resolution: little is known about the Australian subterranean spiders. Specimens of this species all lack palps, a distinctive feature of the family Symphytognathidae (M. Harvey pers comm. May 2011). The only known subterranean symphytognathids in WA belong to the genus *Anapistula*. Two other species of *Anapistula* (also undescribed) has been previously recorded from the Pilbara (Harvey & Yen 1989); however, specimens of those species were not available for direct comparison since they have not been lodged at the WA Museum.

Genomic taxonomy: tissues of one specimen of this species were sequenced in order to obtain genomic comparisons with other WA species. The only inside impact specimen was in too poor condition to warrant sequencing. *Anapistula* 'MH1' differed from the reference specimens by between 19.0 and 25.5% sequence divergence indicating that it a different species (Appendix 4).

SRE status: *Anapistula* 'MH1' (Figure 4-8) is likely to be an SRE.

Known distribution: the distribution of this species is restricted to the records obtained from this survey (Figure 4-9).

Survey records: *Anapistula* 'MH1' was recorded from the following localities:

- impact area: number of sites, 1; number of samples, 1: md0467
- reference area: number of sites, 2; number of samples, 4: md0253, md0430[DNA].

[DNA] - site from which DNA sequenced specimen was obtained.

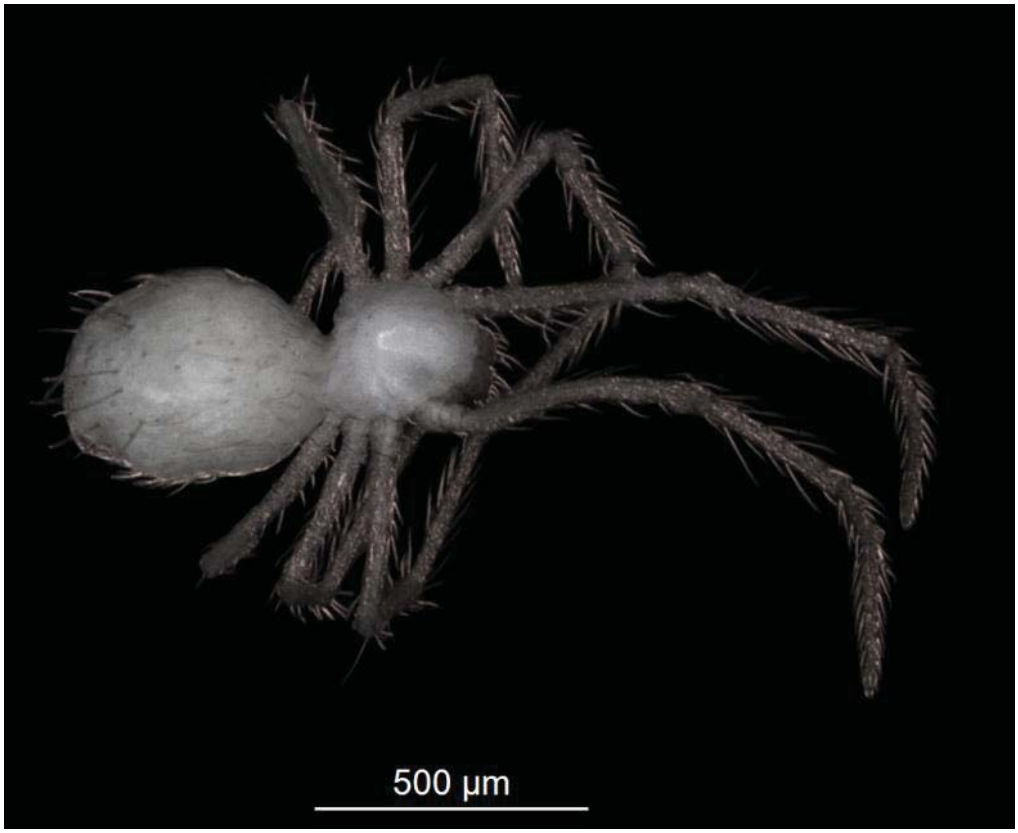

Figure 4-8 Image of *Anapistula* 'MH1'

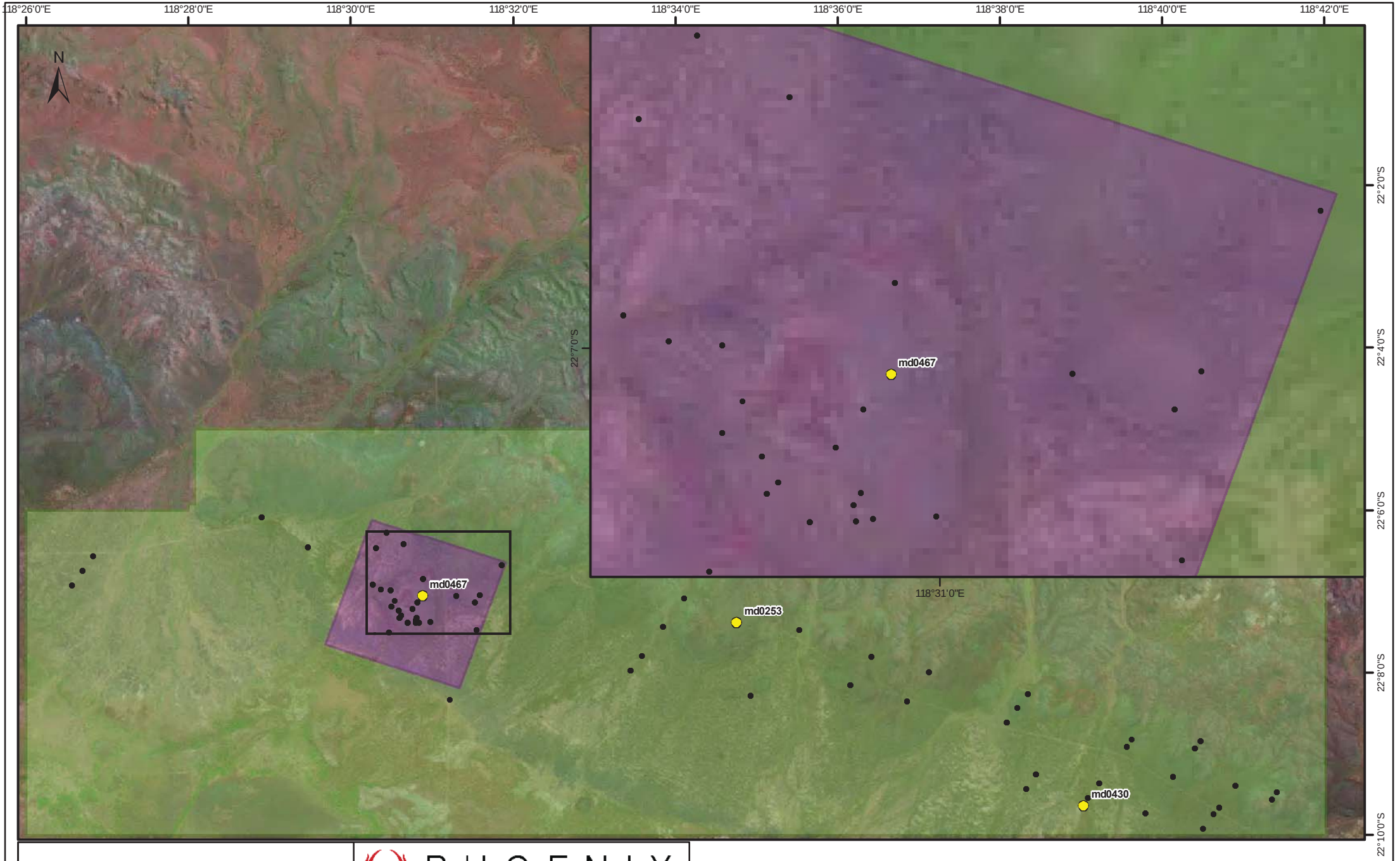

Figure 4-9 *Anapistula* 'MH1' site records

AUTHOR: ES Volschenk	CLIENT: Hancock Prospecting
DATE 24 May 2012:	Scale: 1:109,384
Coordinate System: Projection: Transverse Mercator; DATUM: GDA94	PROJECT: Mulga Downs Subterranean Survey

PHOENIX ENVIRONMENTAL SCIENCES

0 0.5 1 2 3 4 5 Kilometres

Anapistula 'MH1'
Survey Bores
Proposed Disturbance Area
Study Area

4.5.2 Arthropoda: Arachnida: Palpigradi

Palpigrades, commonly known as micro-whip scorpions, are an order of arachnid and are therefore related to spiders and scorpions. They are very small (usually only a few millimetres), pale and possess a distinctively long articulated tail. The tail is very fragile and typically broken off during the sampling process. Palpigrades inhabit moist soils and leaf litter (Barranco & Harvey 2008). Palpigrades are distributed worldwide including Australia; however few Australian species have been described. For a long time, it was thought that only two introduced species occurred is Australia; however in recent years, several endemic species have been discovered from the Yilgarn, Pilbara and Kimberly bioregions of Western Australia (Harvey & Yen 1989) Phoenix (unpublished data).

4.5.2.1 Palpigradi 'MH1' and Palpigradi 'MH2'

Taxonomic resolution: Very little is known about the subterranean Palpigradi of WA, and there are no palpigrade experts in WA; therefore, the only reliable species level identifications depend on genomic assessment. Unpublished studies by Helix Molecular Solutions indicate that species of palpigrades are often locally endemic.

Genomic taxonomy: tissues from two specimens were sequenced for genomic comparisons. These specimens differed from each other by 33.4%, indicating that they are different species, here referred to as Palpigradi 'MH1'and Palpigradi 'MH2'. Morphological characters were investigated for these species; however no reliable features could be found and so the remaining specimens are referred to as Palpigradi sp. indet. It is probable that Palpigradi sp. indet comprises more than one species, including the species identified by the genomic study, since no discernible features could be found to separate Palpigradi MH1 from Palpigradi MH2.

SRE status: both Palpigradi 'MH1' (Figure 4-10) and Palpigradi 'MH2' appear to be SREs.

Known distribution: The records obtained for these species represent their known distributions.

Survey records: Palpigradi specimens were recorded from the following localities (Figure 4-11):

- Palpigradi ‘MH1’,
    - impact area: number of sites, 1; number of samples, 1: md0467 [DNA]
- Palpigradi ‘MH2’
    - reference area: number of sites, 1; number of samples, 1: md0398 [DNA]
- Palpigradi sp. indet.,
    - impact area: number of sites, 4; number of samples, 4: md0462, md0495, md0525 and mdh0143
    - reference area: number of sites, 2; number of samples, 2: md0253 and md0408.

[DNA] sites from which sequenced specimens were obtained.

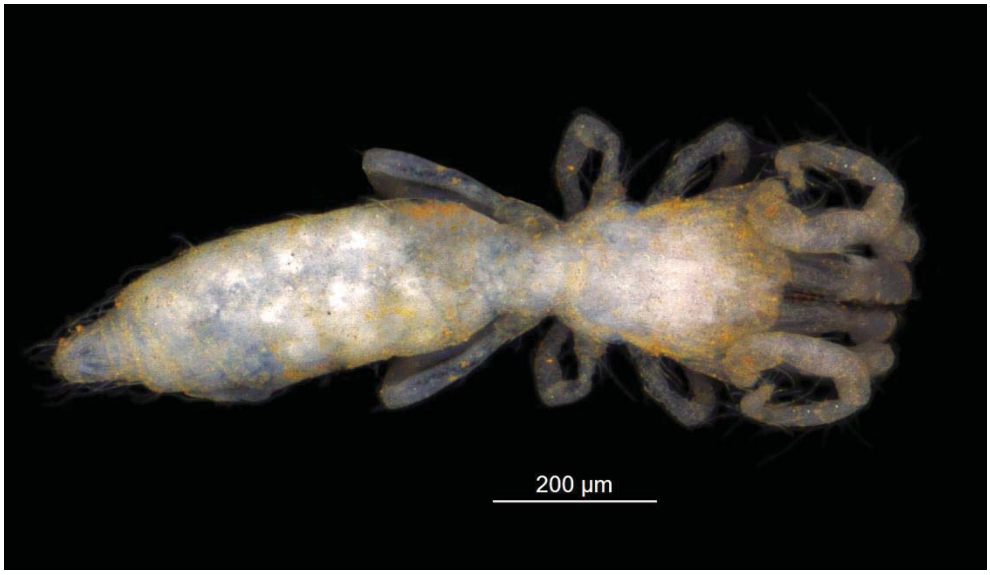

Figure 4-10 Image of Palpigradi 'MH1'

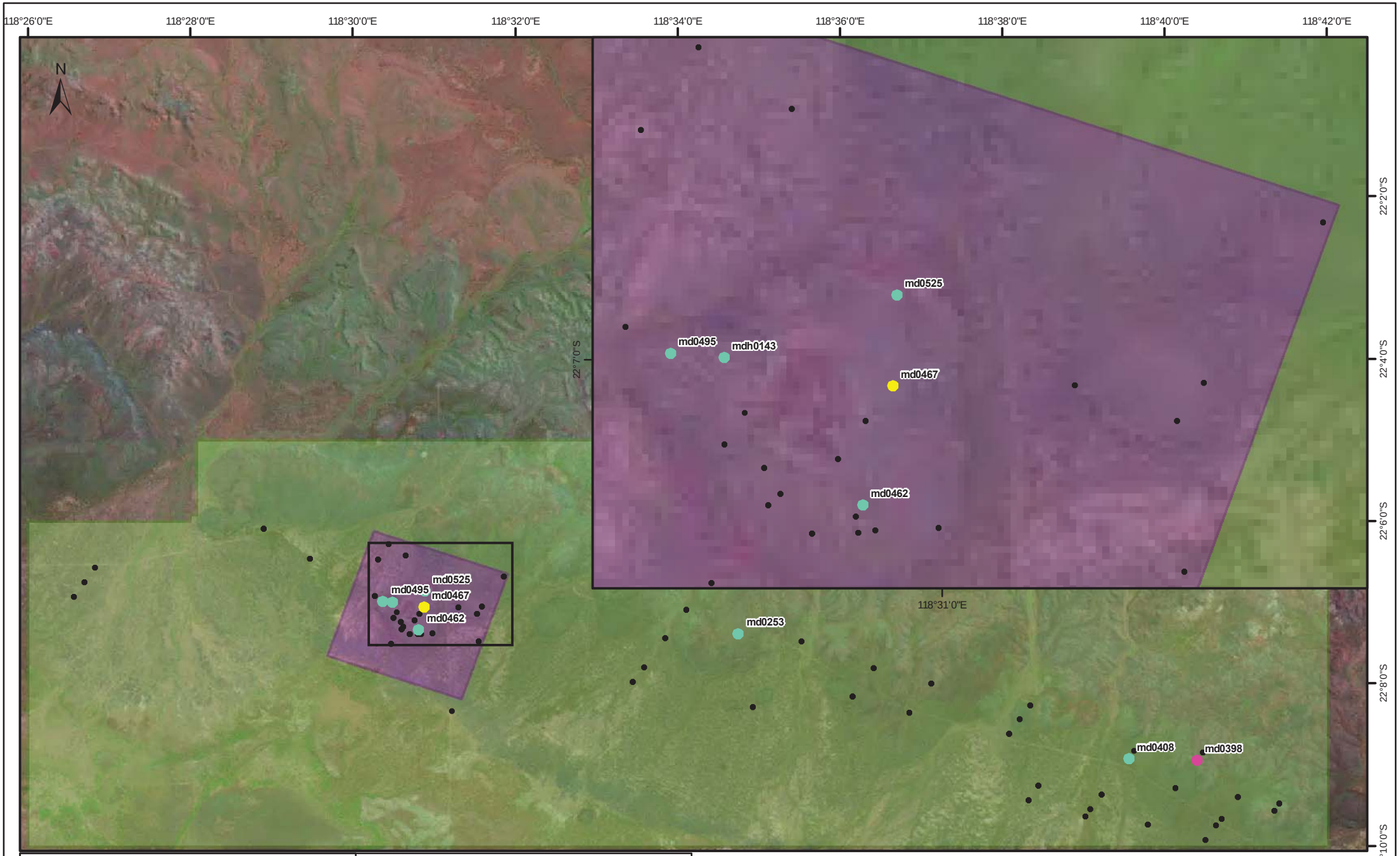

Figure 4-11 Palpigradi record sites

AUTHOR: ES Volschenk	CLIENT: Hancock Prospecting
DATE 24 May 2012:	Scale: 1:109,384
Coordinate System: Projection: Transverse Mercator; DATUM: GDA94	PROJECT: Mulga Downs Subterranean Survey

PHOENIX ENVIRONMENTAL SCIENCES

Kilometres
0 0.5 1 2 3 4 5

- Palpigradi 'MH1'
- Palpigradi 'MH2'
- Palpigradi sp. indet.
- Survey Bores
- Study Area
- Proposed Impact Area

4.5.3 Arthropoda: Arachnida: Pseudoscorpiones

Pseudoscorpiones resemble scorpions in that they possess a pair of long pedipalps with pincers which are directed anteriorly of the body; however, they do not possess the tail or a sting of scorpions. Most species are small to very small in size (most species are less than 1cm long) (Harvey & Yen 1989; Main 1985; Rupert & Barnes 1994). Pseudoscorpions can be found inhabiting a wide variety of habitats including leaf litter, soil, under the bark of trees, under stones, and in rock crevices (Harvey 2011). In Western Australian, 17 families of pseudoscorpions have been recorded to date (M. Harvey pers. Comm.). The group contains several SRE species, for example species in the genus *Synsphyronus* (family Garypidae) are often habitat specific SREs on rocky outcrops (Harvey & Volschenk 2007b). Pseudoscorpions from the families Hyidae (Harvey & Leng 2008), Olpiidae (Harvey & Volschenk 2007a), Chernetidae (Edward & Harvey 2008) and Chthoniidae (Harvey 2002b; Harvey *et al.* 2011), are also often encountered in subterranean surveys were they are usually SRE's (2008).

4.5.3.1 *Tyrannochthonius* 'MH1'

Taxonomic resolution: Edward and Harvey (Edward & Harvey) described several subterranean *Tyrannochthonius* from WA and many more undescribed species are known (Harvey, pers. comm.). This species did not conform with any of the species described by Edward and Harvey (Harvey 1993; Harvey & Volschenk 2007b). We consider this to be a new species. This species was not found within the proposed impact area and so no further investigations of this were undertake.

Genomic taxonomy: no genomic investigations of this species were undertaken.

SRE status: *Tyrannochthonius* 'MH1' (Figure 4-12) is likely to be an SRE.

Known distribution: the records obtained for this species represent its known distribution.

Survey records: *Tyrannochthonius* 'MH1' was recorded from the following localities (Figure 4-14):

- reference area: number of sites, 4; number of samples, 12: md0247, md0253, md0262, md0408.

4.5.3.2 *Indohya* 'MH1'

Taxonomic resolution: very little is known about the hyid pseudoscorpions of WA. In the Pilbara, only the genus *Indohya* is known and all but one species are subterranean (Harvey 2002a; Harvey 2001; Harvey 1992; Harvey *et al.* 2008; Harvey & Humphreys 1995). This species is not like any of the other known *Indohya* from the Pilbara (Harvey, pers. Comm.) and it is therefore consider it to be a new species. This species was not found within the proposed impact area and so no further investigations of this were undertake.

Genomic taxonomy: no genomic investigations of this species were undertaken.

SRE status: *Indohya* 'MH1' (Figure 4-13) is likely to be an SRE.

Known distribution: the records from this survey represent the known distribution of this species.

Survey records: *Indohya* 'MH1' was recorded from the following localities (Figure 4-14):

- reference area: number of sites, 1; number of samples, 3: md0253.

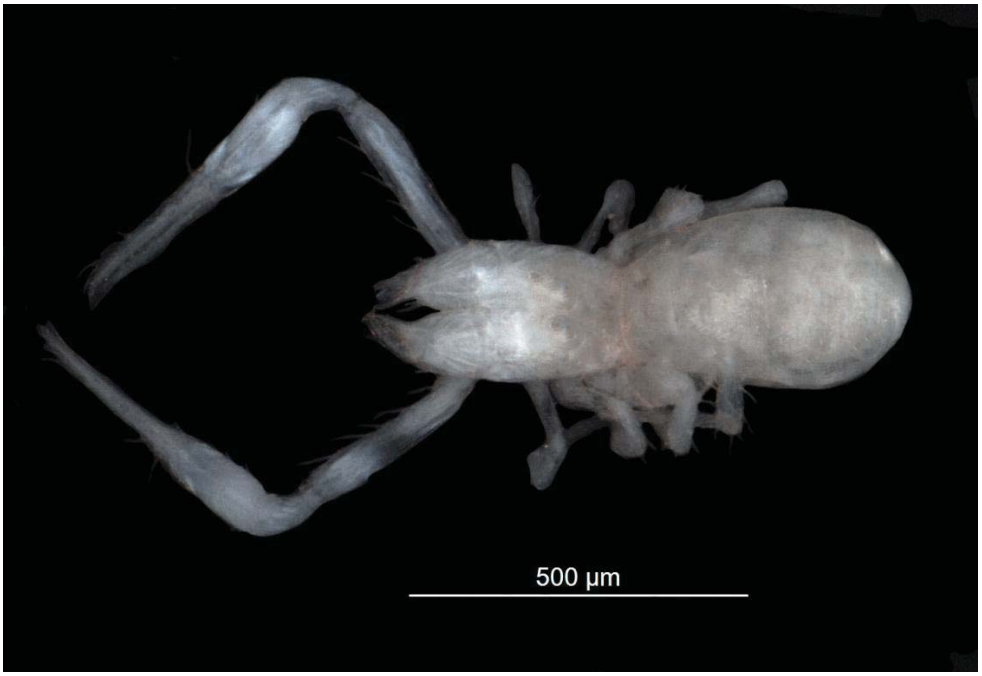

Figure 4-12 Image of *Tyrannochthonius* 'MH1'

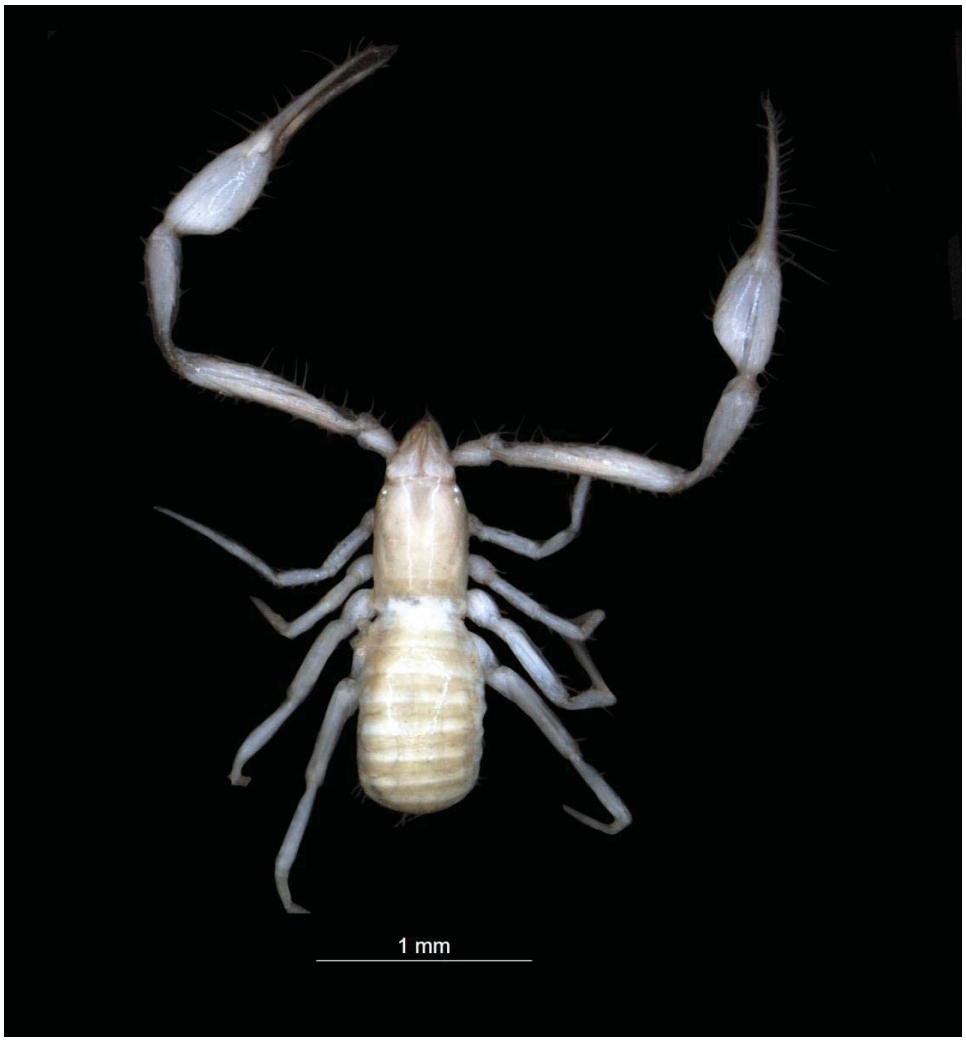

Figure 4-13 Image of *Indohya* 'MH1'

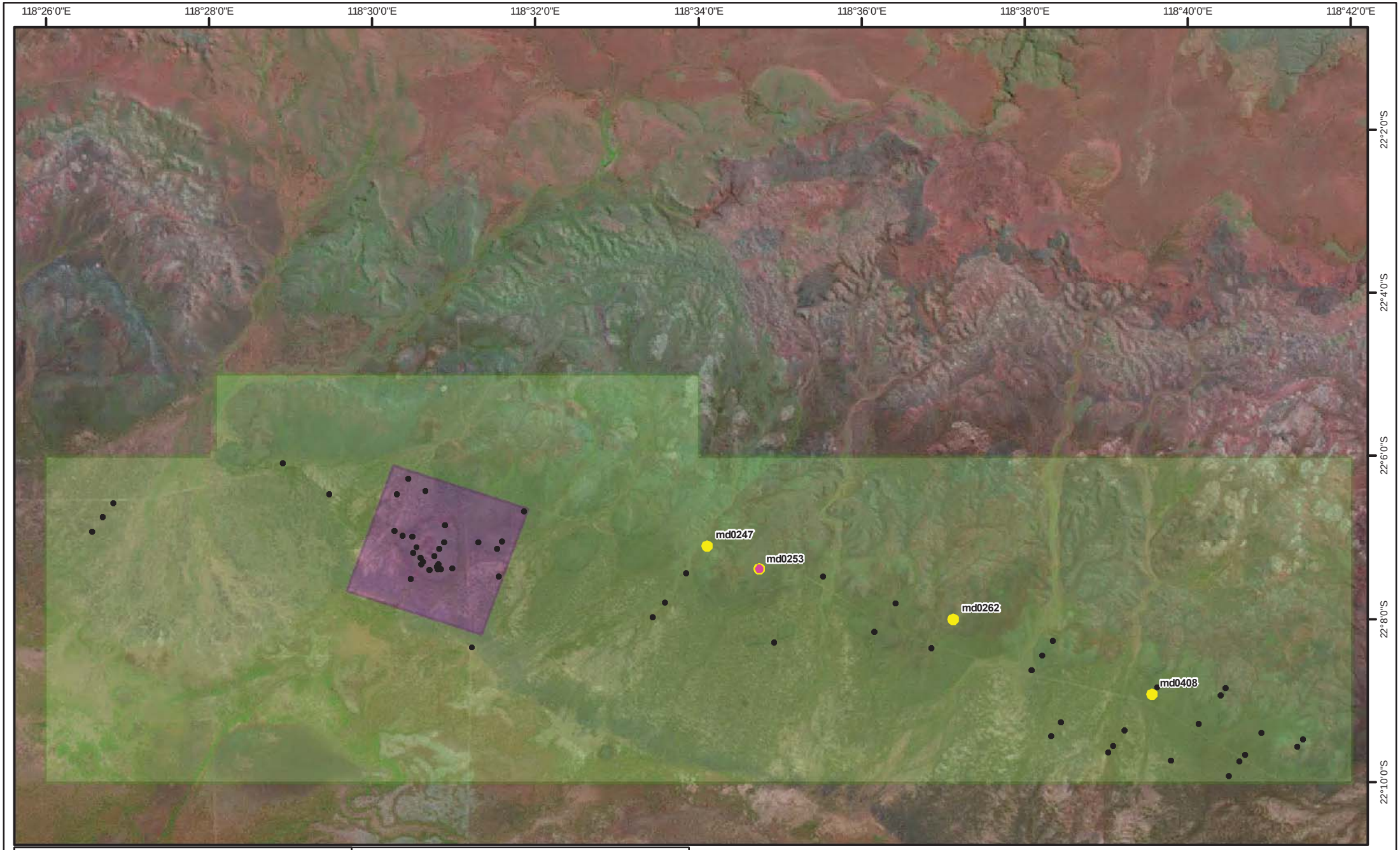

Figure 4-14 Pseudoscorpion site records

AUTHOR: ES Volschenk	**CLIENT:** Hancock Prospecting
DATE 24 May 2012:	**Scale:** 1:109,384
Coordinate System: Projection: Transverse Mercator; DATUM: GDA94	

PHOENIX ENVIRONMENTAL SCIENCES

PROJECT: Mulga Downs Subterranean Survey

0 0.5 1 2 3 4 5 Kilometres

- *Indohya* 'MH1'
- *Tyrannochthonius* 'MH1'
- Survey Bores
- Proposed Disturbance Area
- Study Area

4.5.4 Arthropoda: Arachnida: Schizomida

4.5.4.1 Schizomida 'MH1' and Schizomida 'MH2'

Taxonomic resolution: The schizomids of WA are relatively well studied and numerous species are known from WA, both described and undescribed (Bennelongia 2010; Subterranean Ecology 2010). Assessment of species boundaries is largely dependent on characteristics of the adult male, and since specimens collected were female and sub-adult, the species could not be accurately determined. Murrays Hill is also not near any previously recorded localities (M. Harvey, pers. comm).

Genomic taxonomy: Two specimens of what was thought to be one species of schizomid were sequenced for genomic comparisons. These analyses revealed that these are two separate species, differing from each other by 13.3% and from other reference specimens by 11.8 - 19.2% sequence divergence. These two specimens therefore appear to represent two distinct and new species and are here referred to as Schizomida 'MH1' and Schizomida 'MH2' .

SRE status: Schizomida 'MH1' (Figure 4-15) and Schizomida 'MH2' are both likely to represent SRE's.

Known distribution: The samples obtained during this study represent the known distribution of these two species.

Survey records: schizomid specimens were recorded from the following localities (Figure 4-16):

- Schizomida 'MH1'
    - reference area: number of sites, 1; number of samples, 1: 991-md0408[DNA]
- Schizomida 'MH2'
    - impact area: number of sites, 1; number of samples, 1: 991-md0525 [DNA].

[DNA] - sites from which sequenced specimens were obtained.

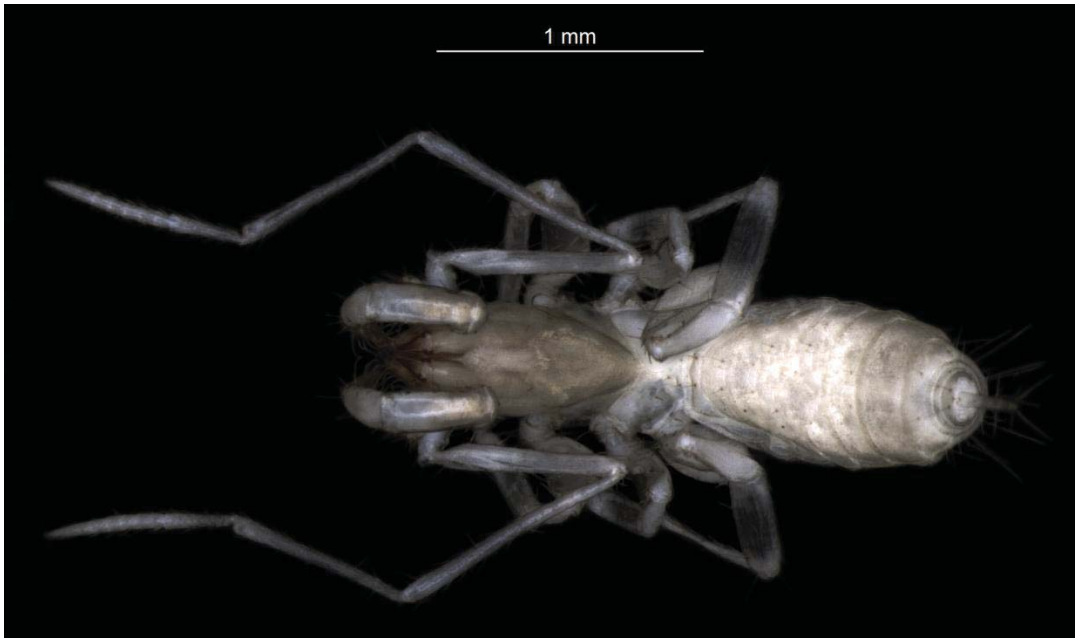

Figure 4-15 Image of Schizomida 'MH1'

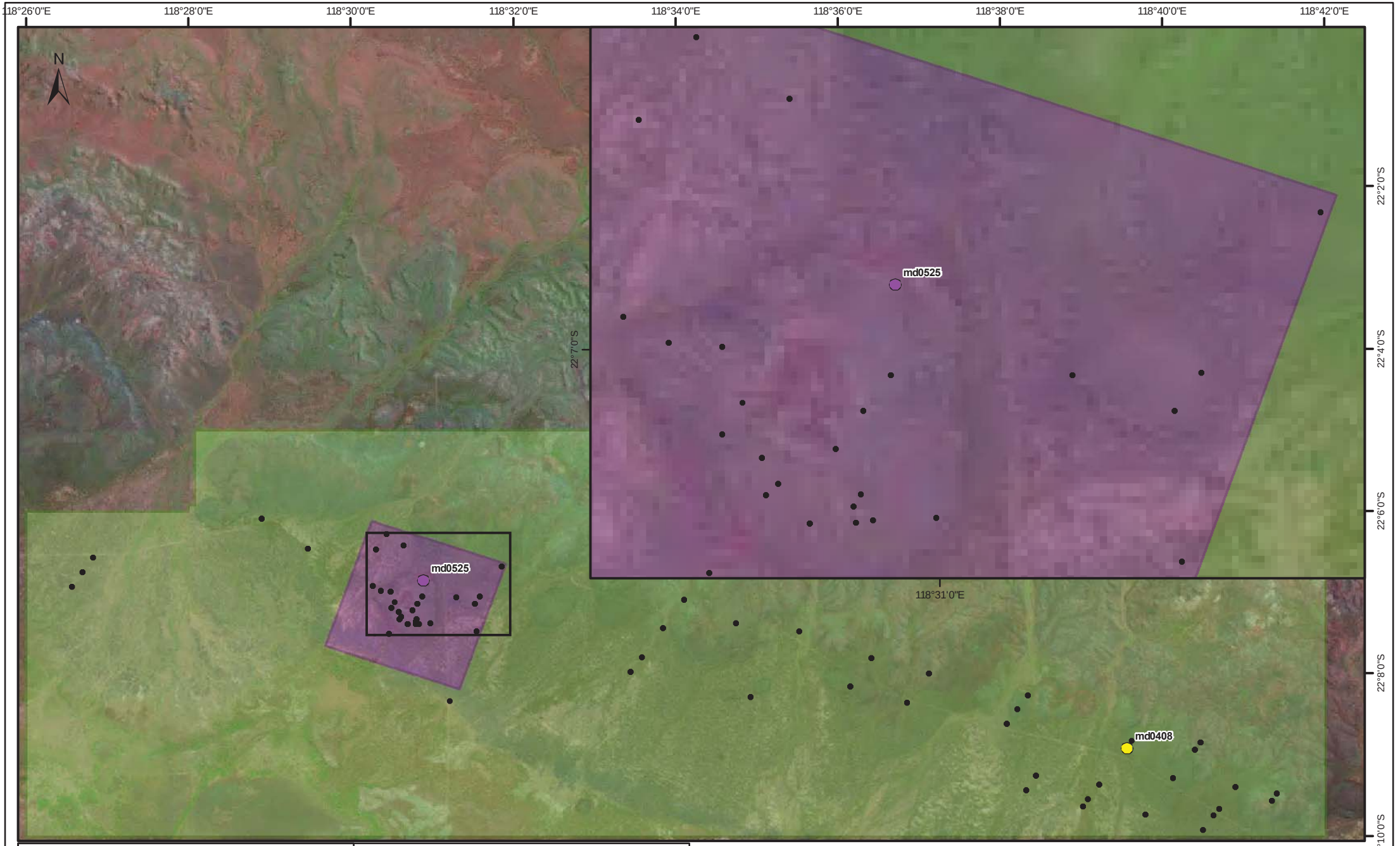

Figure 4-16 Schizomida record sites

AUTHOR: ES Volschenk	CLIENT: Hancock Prospecting
DATE 24 May 2012:	Scale: 1:109,384
Coordinate System: Projection: Transverse Mercator; DATUM: GDA94	PROJECT: Mulga Downs Subterranean Survey

PHOENIX ENVIRONMENTAL SCIENCES

0 0.5 1 2 3 4 5 Kilometres

4.5.5 Arthropoda: Chilopoda: Scolopendromorpha

4.5.5.1 *Cryptops* 'MH1' and *Cryptops* 'MH2'

Taxonomic resolution: Very little is known about the cryptopid centipedes of WA and there are here are also no cryptopid experts in WA; therefore, the only reliable species level identifications depend on genomic assessment. Genomic studies by Helix Molecular Solutions (unpublished) have demonstrated the highly endemic nature of the Pilbara subterranean cryptopid species.

Genomic taxonomy: Three specimens from this survey were sequenced for DNA comparisons. Two distinct species were detected which differed from each other by 17.4%. These species did not group with any of the reference species (which included two epigean species) indicating that they are likely to be new species and are here referred to as *Cryptops* 'MH1' and *Cryptops* 'MH2'.

SRE status: *Cryptops* 'MH1' (Figure 4-17) and *Cryptops* 'MH2' are both likely to be SREs.

Known distribution: Records of these species obtained during this survey represent their known distributions.

Survey records: these species were recorded from the following localities:

- *Cryptops* 'MH1':
    - impact area: number of sites, 1; number of samples, 1: md0525 [DNA]
- *Cryptops* 'MH2'
    - reference area: number of sites, 4; number of samples, 4: md_kar3, md0253, md0420[DNA], md0427.

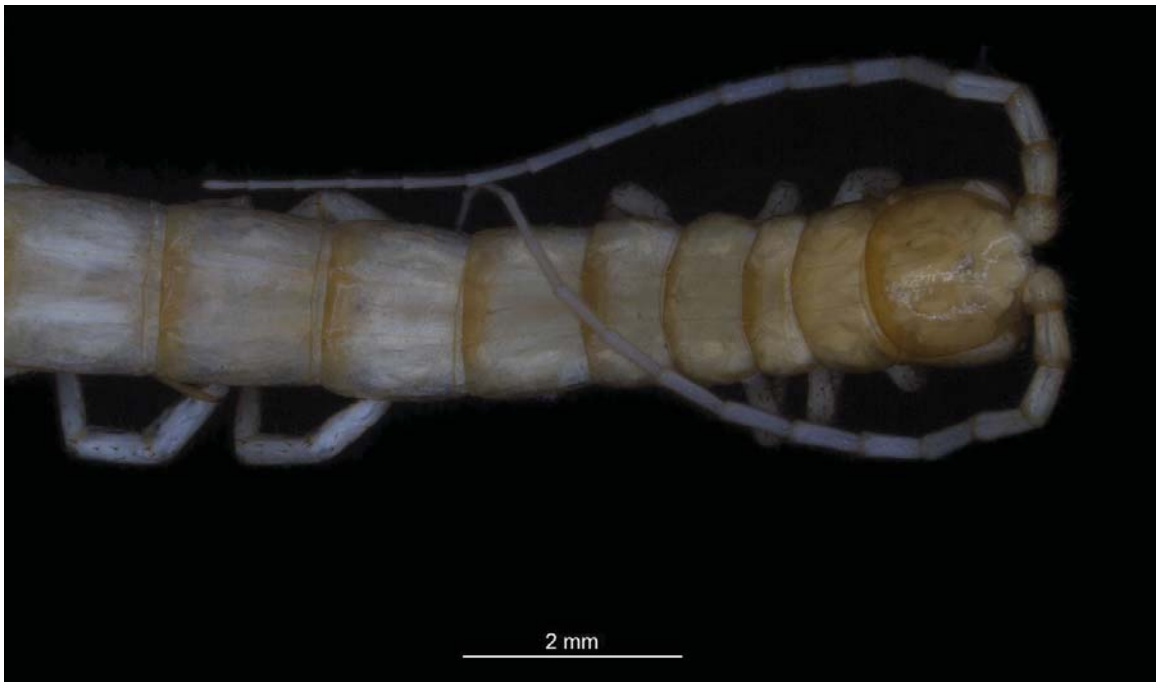

Figure 4-17 Image of *Cryptops* 'MH1'

4.5.5.2 *Cormocephalus* 'MH1'

Taxonomic resolution: Very little is known about the subterranean centipedes of the family Scolopendridae. Currently all species level identifications rely on genomic assessment. Only one other species (also undescribed) appears to have been collected previously, from FMG's Solomon Project (Harvey & Yen 1989); however, specimens of that species were not available for direct comparison since they have not been lodged with the WAM. This species was not found within the proposed impact area and so no further investigations were undertake.

Genomic taxonomy: No genomic investigations of this species were undertaken.

SRE status: *Cormocephalus* 'MH1' (Figure 4-18) is a likely SRE.

Known distribution: In the absence of morphological or genomic data to ascertain species boundaries with the species from Solomon, the regional context of this morphospecies remains unclear. On the basis of unpublished studies by Helix Molecular Solutions, and the absence of subterranean studies in the near vicinity of Murrays Hill, it seems likely that this morphospecies will be a new species.

Survey records: *Cormocephalus* 'MH1' was recorded from the following localities (Figure 4-19):

- reference area: number of sites, 1; number of samples, 1: md0430.

Figure 4-18 Image of *Cormocephalus* 'MH1'

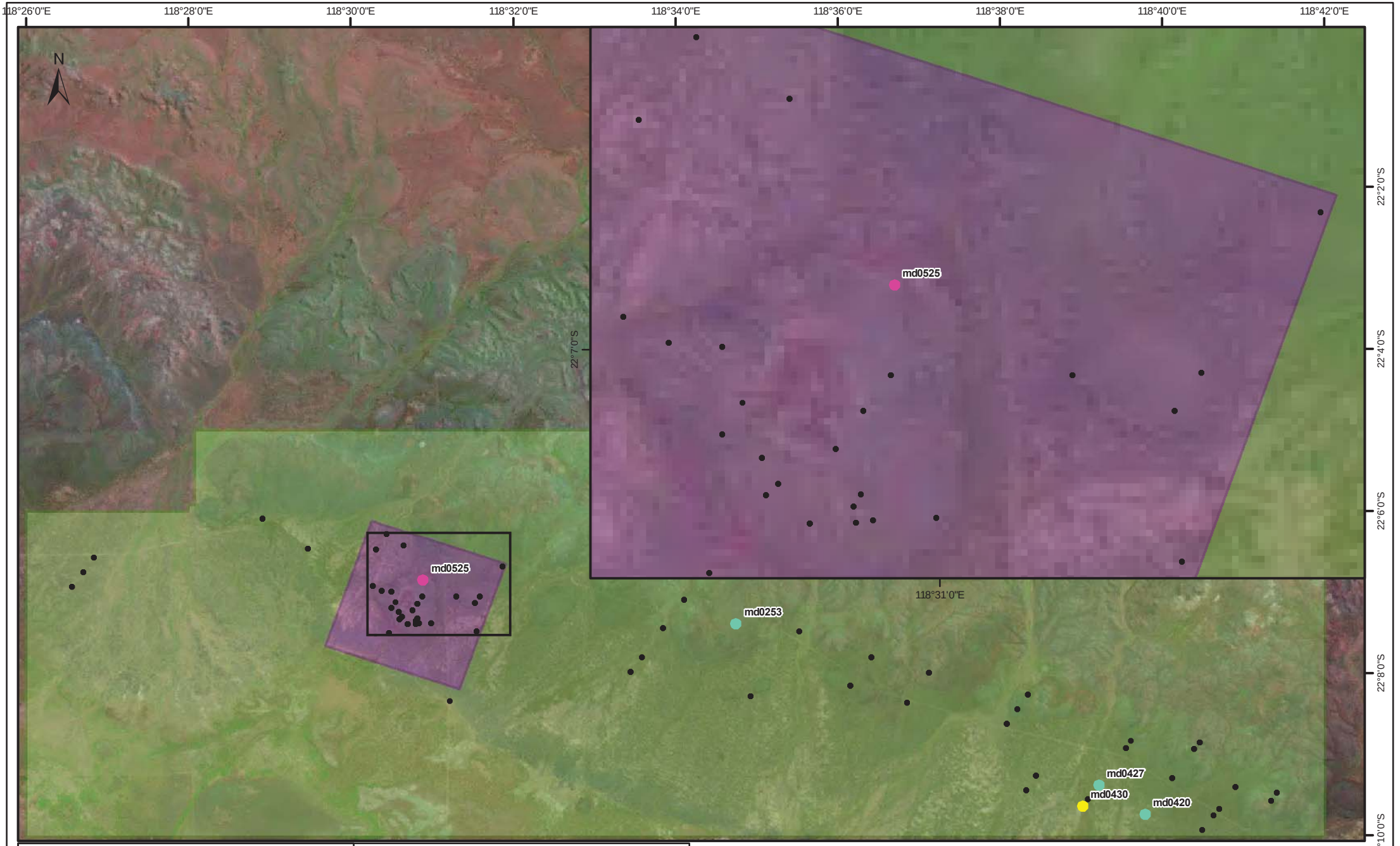

Figure 4-19 Centipede site records

AUTHOR: ES Volschenk	CLIENT: Hancock Prospecting
DATE 24 May 2012:	Scale: 1:109,384
Coordinate System: Projection: Transverse Mercator; DATUM: GDA94	PROJECT: Mulga Downs Subterranean Survey

PHOENIX ENVIRONMENTAL SCIENCES

0 0.5 1 2 3 4 5 Kilometres

4.5.6 Arthropoda: Diplopoda: Polyxenida

4.5.6.1 Polyxenidae 'PXD1'

Taxonomic resolution: The subterranean Polyxenida of the Pilbara have been relatively well studied in unpublished studies by Helix Molecular Solutions. There are no polyxenid experts in WA; therefore, the only reliable species level identifications depend on genomic assessment. Unpublished studies by Helix Molecular Solutions indicate that one species of polyxenid is very widespread throughout the Pilbara; however, there are also several locally endemic species.

Genomic taxonomy: two specimens of Polyxenidae 'PXD1' were sequenced for the COI gene in order to make genomic level comparisons. Specimens were found to be very similar, differing by only 0.5% and therefore represent the same species. These species also grouped with a clade of polyxenids that are widespread in the Pilbara, therefore demonstrating that this species is not an SRE.

SRE status: Polyxenidae 'PXD1' (Figure 4-20) is not an SRE.

Known distribution: This species has been widely collected in the Pilbara (Appendix 4).

Survey records: Polyxenidae 'PXD1' was recorded from the following localities (Figure 4-21):

- impact area: number of sites, 1; number of samples, 1: md0483^{DNA},
- reference area: number of sites, 5; number of samples, 5: md0314, md0427^{DNA}, md0671, md0672, md0673.

^{DNA} - sites from which sequenced specimens were obtained.

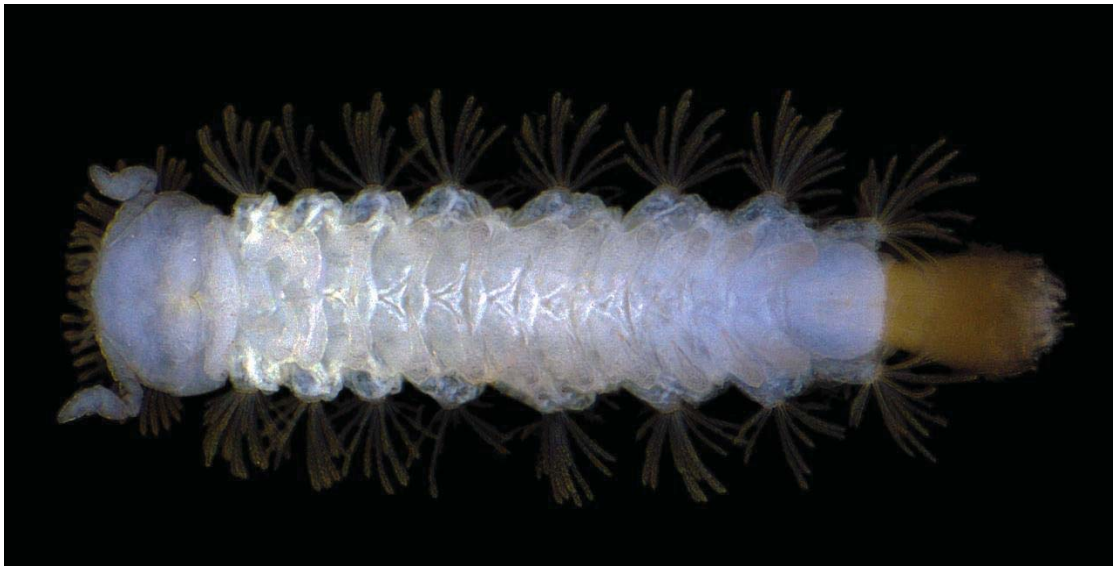

Figure 4-20 Image of Polyxenidae 'PXD1'

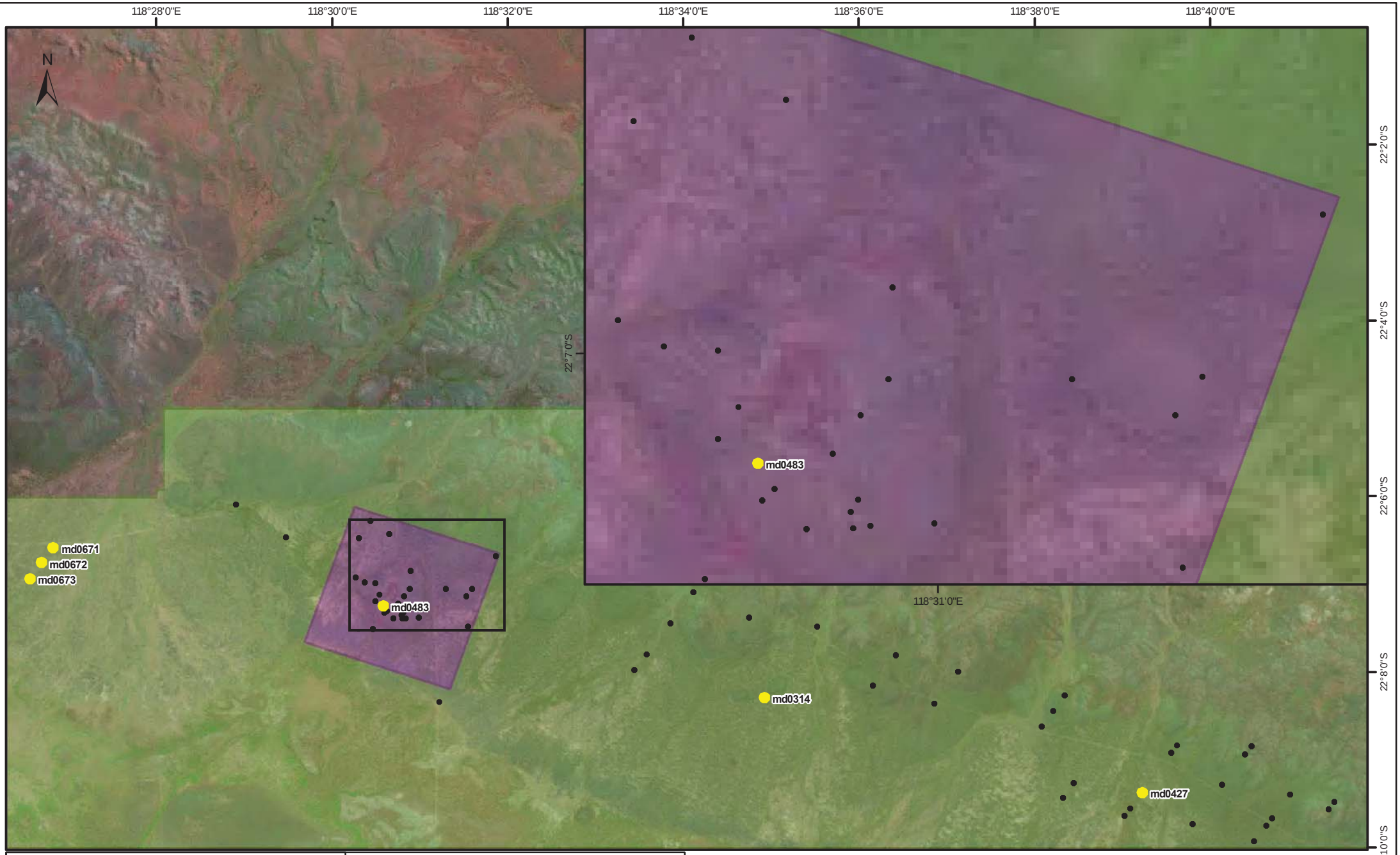

Figure 4-21 Polyxenid site records

AUTHOR: ES Volschenk	CLIENT: Hancock Prospecting
DATE 24 May 2012:	Scale: 1:102,183
Coordinate System: Projection: Transverse Mercator; DATUM: GDA94	PROJECT: Mulga Downs Subterranean Survey

PHOENIX ENVIRONMENTAL SCIENCES

0 0.45 0.9 1.8 2.7 3.6 4.5 Kilometres

Polyxenidae 'PXD1'
Survey Bores
Proposed Impact Area
Study Area

4.5.7 Arthropoda: Entognatha: Diplura

4.5.7.1 Japygidae 'MH1' and Japygidae 'MH2'

Taxonomic resolution: Very little is known about the subterranean Japygidae of WA, and there are no Japygidae experts in WA; therefore, the only reliable species level identifications depend on genomic assessment. Unpublished studies by Helix Molecular Solutions indicate that japygid species are often locally endemic.

Genomic taxonomy: two specimens of what was thought to be a single species were sequenced for genomic comparisons. The specimens differed from each other by 13.0% sequence divergence indicating that they are likely to represent two separate species: Japygidae 'MH1' and Japygidae 'MH2'. Both of these species did not group with any other reference specimens indicating that they are likely to represent new species (Appendix 4). The morphology of the genetically resolved specimens was reviewed and characters were found that permitted the assignment of the remaining japygid specimens to the two species.

SRE status: both Japygidae 'MH1' (Figure 4-22) and Japygidae 'MH2' are likely to be SREs.

Known distribution: the records obtained for these species represent their known distribution.

Survey records: these species were recorded from the following localities:

- Japygidae 'MH1'
    - impact area: number of sites, 1; number of samples, 1: md0486^{DNA};
    - reference area: number of sites, 1; number of samples, 1: md0266;
- Japygidae 'MH2'
    - reference area: number of sites, 2; number of samples, 2: md0253, md0396^{DNA}
- Japygidae sp. indet.,
    - impact area: number of sites, 4; number of samples, 4: md0462, md0495, md0525 and mdh0143
    - reference area: number of sites, 2; number of samples, 2: md0253 and md0408.
- ^{DNA} - sites from which sequenced specimens were obtained.

Figure 4-22 Image of Japygidae 'MH1'

4.5.7.2 Parajapygidae 'MH1'

Taxonomic resolution: very little is known about the subterranean Parajapygidae of WA, and there are no parajapygid experts in WA; therefore, the only reliable species level identifications depend on genomic assessment. Unpublished studies by Helix Molecular Solutions indicate that parajapygid species are often locally endemic.

Genomic taxonomy: two specimens of what was thought to be a single species were sequenced for genomic comparisons. The specimens differed from each other by 3.0% sequence divergence indicating that they are likely to represent the same species here referred to as Parajapygidae 'MH1. This species did not group with any other reference specimens in the analysis, therefore indicating that it is likely to represent a new species (Appendix 4).

SRE status: Parajapygidae 'MH1' is a likely SRE.

Known distribution: the records obtained for this species represent its known distribution.

Survey records: Parajapygidae 'MH1' was recorded from the following localities:

- impact area: number of sites, 2; number of samples, 2: 991-md0462^{DNA}, 991-md0578^{DNA}.

^{DNA} - sites from which sequenced specimens were obtained.

4.5.7.3 Projapygidae 'MH1'

Taxonomic resolution: very little is known about the subterranean Projapygidae of WA, and there are no projapygid experts in WA; therefore, the only reliable species level identifications depend on genomic assessment. Unpublished studies by Helix Molecular Solutions indicate that projapygid species are often locally endemic.

Genomic taxonomy: two specimens were submitted for sequencing; however, only one specimen yielded sequences for genomic comparisons. This species differed from the reference sequences by 14.3% - 18.7% sequence divergence, indicating that it is likely to represent a new species (Appendix 4) and is here referred to as Projapygidae 'MH1'. The specimens all appeared very similar and all of the remaining projapygid specimens were assigned to this species.

SRE status: Projapygidae 'MH1' (Figure 4-23) is likely to be an SRE.

Known distribution: the records obtained for this species represent its known distribution.

Survey records: Projapygidae 'MH1' was recorded from the following localities (Figure 4-24):

- impact area: number of sites, 1; number of samples, 1: md0467[DNA],
- reference area: number of sites, 2; number of samples, 2: md0259, md0397[DNA].

[DNA] - sites from which sequenced specimens were obtained.

Figure 4-23 Image of Projapygidae 'MH1'

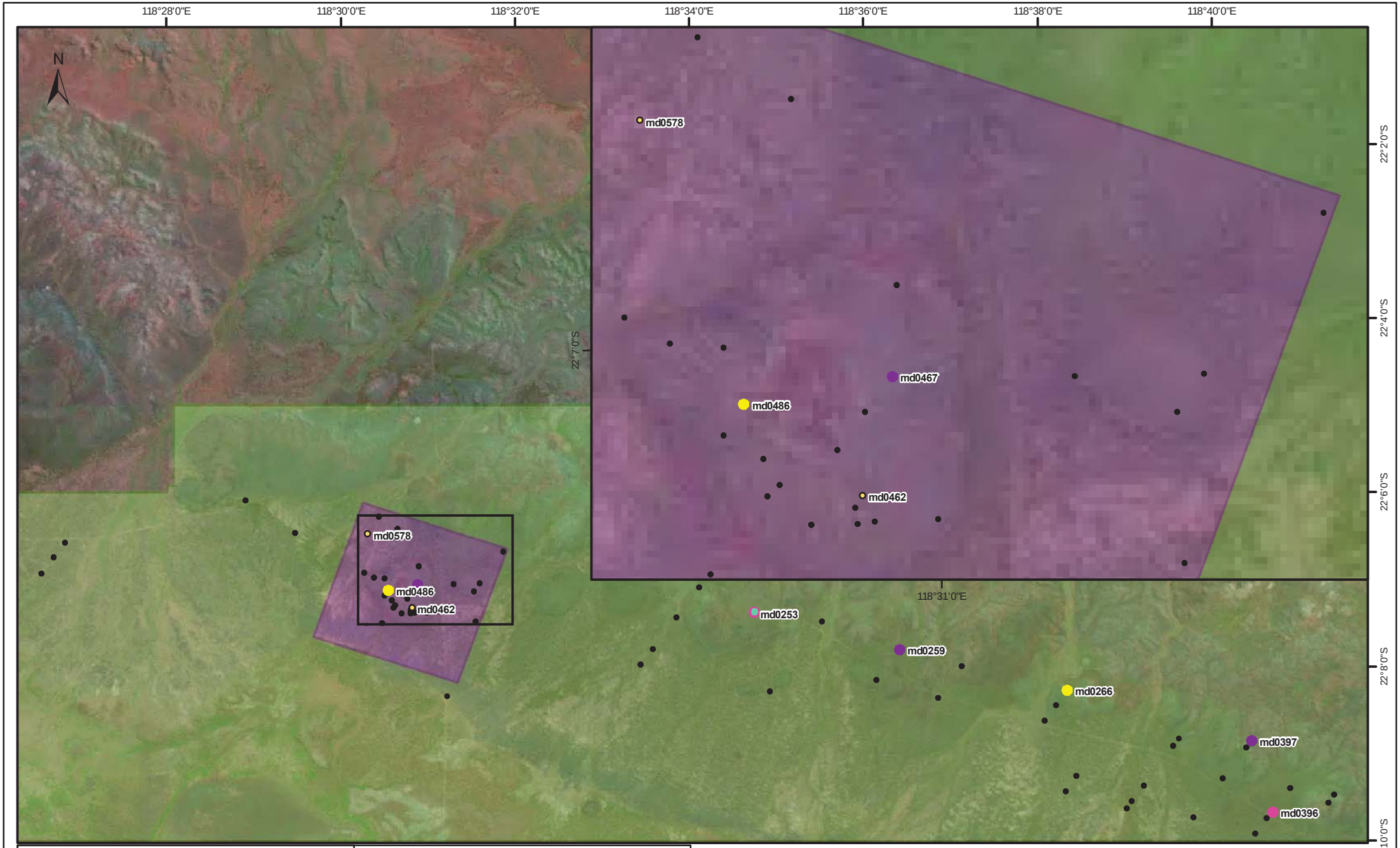

Figure 4-24 Dipluran site records

AUTHOR: ES Volschenk	CLIENT: Hancock Prospecting
DATE 24 May 2012:	Scale: 1:102,183
Coordinate System: Projection: Transverse Mercator; DATUM: GDA94	PROJECT: Mulga Downs Subterranean Survey

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4.5.8 Arthropoda: Insecta: Blattaria

4.5.8.1 *Nocticola* 'MH1'

Taxonomic resolution: little is known about the *Nocticola* of WA, and there are no *Nocticola* experts in WA; therefore, the only reliable species level identifications depend on genomic assessment. Unpublished studies by Helix Molecular Solutions indicate that species of *Nocticola* are often locally endemic, but at least two widespread species are also known to exist.

Genomic taxonomy: four specimens were sequenced for genomic comparisons. Specimens differed from each other by 2.8% - 4.6% sequence divergence, therefore indicating that they are the same species (Appendix 4). Divergence within this group was, however, greater than is usually seen and indicates that the population from site md0262 may be isolated from the remaining three localities. These specimens also failed to group with any reference species, therefore indicating it is likely to represent a new species, here referred to as *Nocticola* 'MH1'.

SRE status: *Nocticola* 'MH1' (Figure 4-25) is likely to be an SRE.

Known distribution: the records obtained for this species represent its known distribution.

Survey records: *Nocticola* 'MH1' was re-recorded from the following localities (Figure 4-26):

- impact area: number of sites, 3; number of samples, 20: md0476^{DNA}, md0482, md0525,
- reference area: number of sites, 7; number of samples, 41: 991-east_reference, md0247^{DNA}, md0253, md0262^{DNA}, md0330, md0405, md0430^{DNA}.

^{DNA} - sites from which sequenced specimens were obtained.

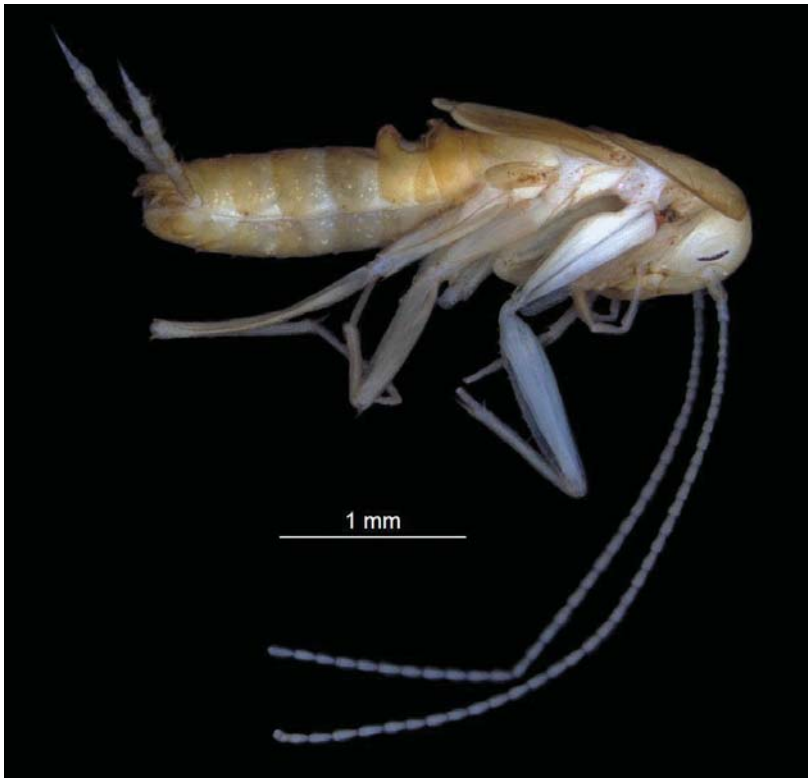

Figure 4-25 Image of *Nocticola* 'MH1'

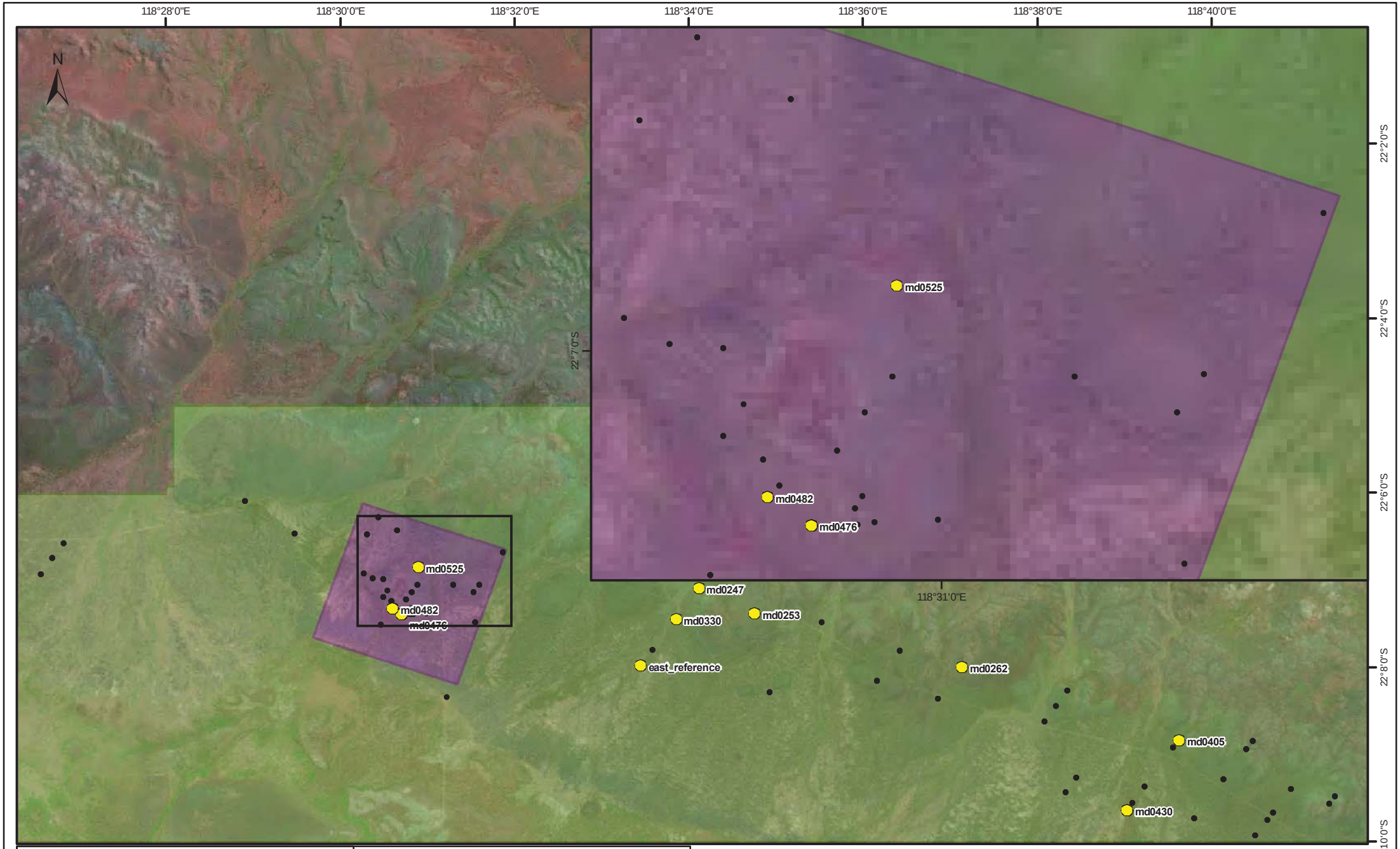

Figure 4-2 *Nocticola* 'MH1' site records

AUTHOR: ES Volschenk	CLIENT: Hancock Prospecting
DATE 24 May 2012:	Scale: 1:102,183
Coordinate System: Projection: Transverse Mercator; DATUM: GDA94	PROJECT: Mulga Downs Subterranean Survey

PHOENIX ENVIRONMENTAL SCIENCES

0 0.45 0.9 1.8 2.7 3.6 4.5 Kilometres

Nocticola 'MH1'
Survey Bores
Study Area
Proposed Impact Area

4.5.9 Arthropoda: Insecta: Coleoptera

4.5.9.1 Anillini 'MH1'

Taxonomic resolution: very little is known about the subterranean Carabidae of WA and there are no experts on subterranean carabids in WA; therefore, the only reliable species level identifications depend on genomic assessment. Genomic studies on *Bembidion*-like carabids have been undertaken by Helix Molecular Solutions (unpublished) indicate that members of this group of beetles show high levels of local endemism.

Genomic taxonomy: two specimens (initially identified as *Benbidion*) were sequenced for genomic comparisons. The two specimens were found to be 3.1% divergent, and therefore are representatives of the same species. This species did not group with any of the reference sequences and therefore indicate that this is a new species. This species did however group with several species of Anillini, indicating that it belongs to that tribe of carabid beetles; therefore this taxon is referred to as Anillini 'MH1'.

SRE status: Anillini 'MH1' (Figure 4-27) is likely to be an SRE.

Known distribution: the distribution of this species is limited to the records resulting from this survey.

Survey records: Anillini 'MH1' was recorded from the following localities (Figure 4-28):

- impact area: number of sites, 3; number of samples, 4: md0462, md0476, md0499[DNA],
- reference area: number of sites, 3; number of samples, 6: md0253[DNA], md0371, md0396.

[DNA] - sites from which sequenced specimens were obtained.

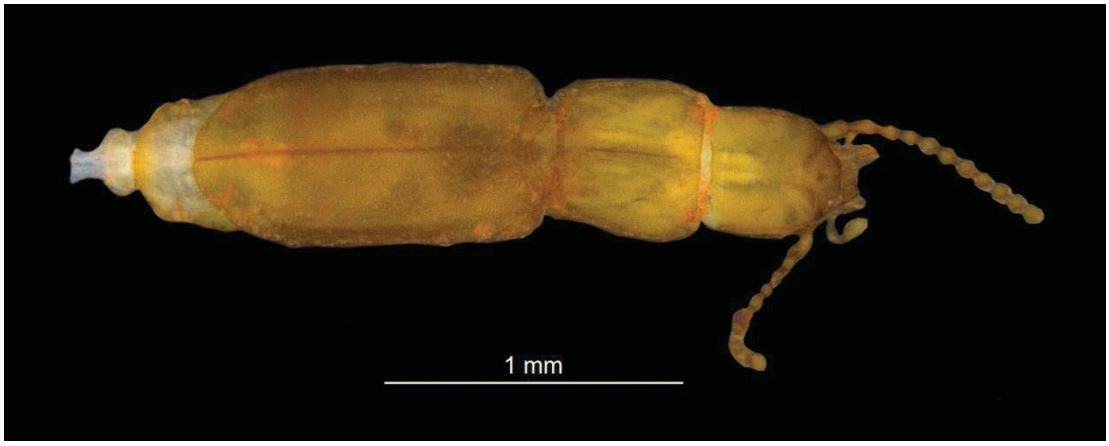

Figure 4-27 Image of Anillini 'MH1'

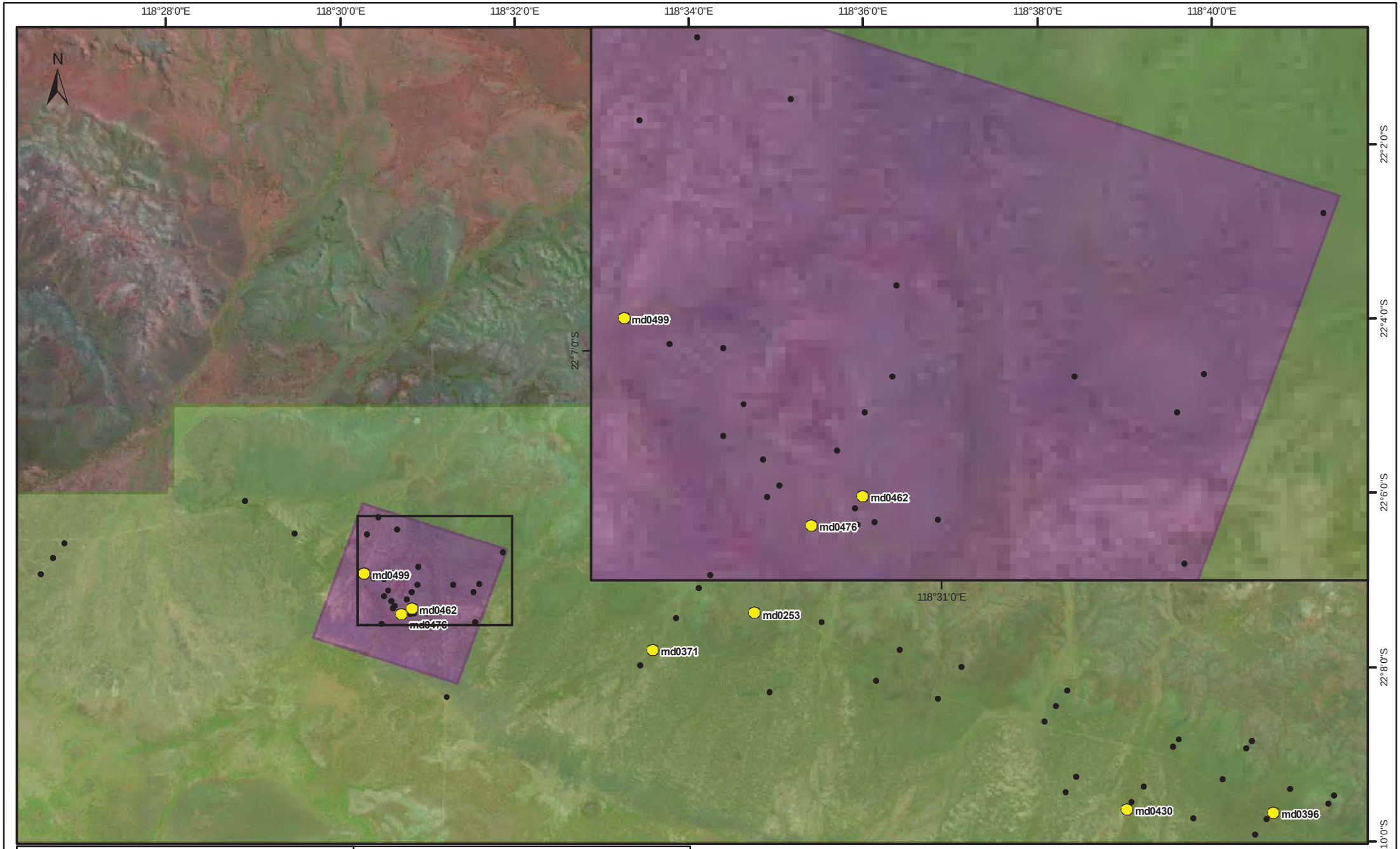

Figure 4-28 Anillini 'MH1' site records

AUTHOR: ES Volschenk	CLIENT: Hancock Prospecting
DATE 24 May 2012:	Scale: 1:102,183
Coordinate System: Projection: Transverse Mercator; DATUM: GDA94	0 0.45 0.9 1.8 2.7 3.6 4.5 Kilometres

PHOENIX ENVIRONMENTAL SCIENCES

PROJECT: Mulga Downs Subterranean Survey

Anillini 'MH1'
Survey Bores
Study Area
Proposed Impact Area

4.5.10 Arthropoda: Insecta: Hemiptera

4.5.10.1 Meenoplidae 'USF' and Meenoplidae 'Widespread'

Taxonomic resolution: very little is known about the subterranean Meenoplidae of WA, and there are no meenoplid experts in WA; therefore, the only reliable species level identifications depend on genomic assessment. Unpublished studies by Helix Molecular Solutions indicate that species of Meenoplidae are often locally endemic.

Genomic taxonomy: two specimens of what was thought to be a single species were sequenced for genomic comparisons. These two species differed from each other by 15.1% sequence divergence (appendix 4), thus indicating that they are different species. Genomic comparisons with reference specimens found that one of the species grouped with a species known from upper south Fortescue with 0.9% sequence divergence (Appendix 4), and is here referred to as Meenoplidae 'USF' (Figure 4-29). The second specimen grouped (0.3% sequence divergence (Appendix 4) with a species known to be widespread in the Pilbara and is here referred to as Meenoplidae 'widespread'. Attempts were made to find suitable diagnostic features on the sequenced specimens, but none could be found, so the remaining specimens are collectively referred to as Meenoplidae sp. indet.

SRE status: is a likely SRE.

Known distribution: The records obtained for this species represent its known distribution.

Survey records: these species were recorded from the following localities (Figure 4-30):

- Meenoplidae 'USF'
    - impact area: number of sites, 1; number of samples, 1: md0499^{DNA}
- Meenoplidae 'Widespread'
    - reference area: number of sites, 1; number of samples, 2: 991-md0262^{DNA},
- Meenoplidae sp. indet.:
    - impact area: number of sites, 1; number of samples, 2: md0476,
    - reference area: number of sites, 2; number of samples, 13: md0247, md0253.

^{DNA} - sites from which sequenced specimens were obtained.

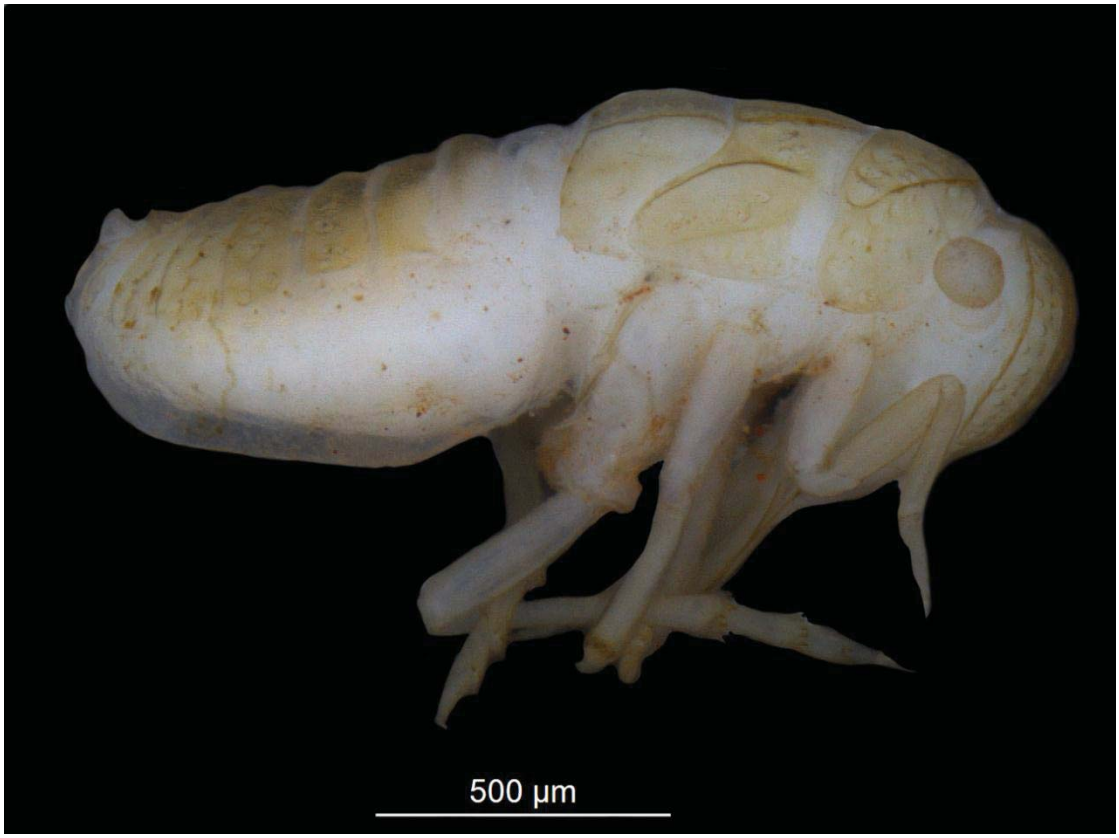

Figure 4-29 Image of Meenoplidae 'widespread'

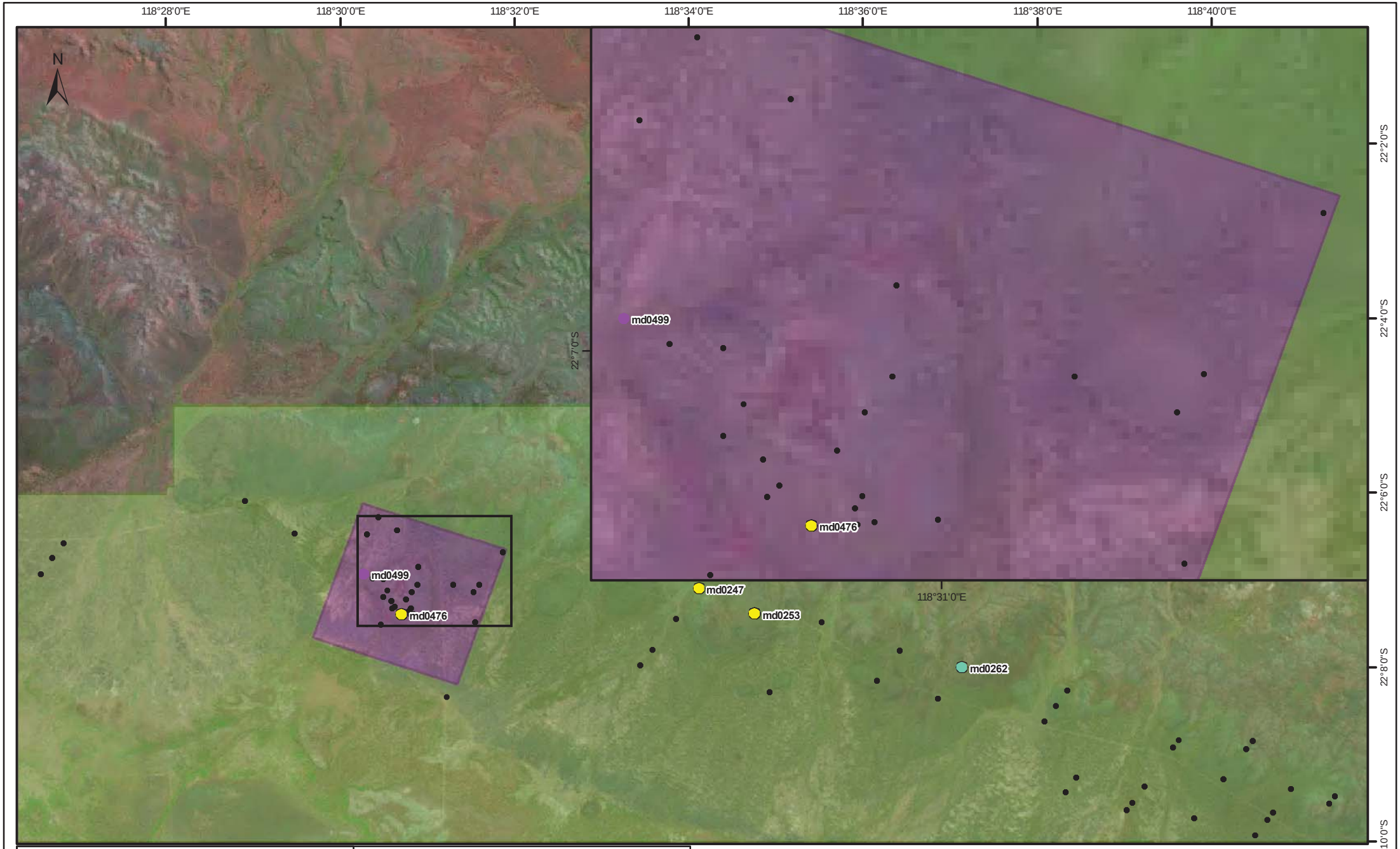

Figure 4-30 Meenoplid site records

AUTHOR: ES Volschenk	CLIENT: Hancock Prospecting
DATE 24 May 2012:	Scale: 1:102,183
Coordinate System: Projection: Transverse Mercator; DATUM: GDA94	PROJECT: Mulga Downs Subterranean Survey

PHOENIX ENVIRONMENTAL SCIENCES

0 0.45 0.9 1.8 2.7 3.6 4.5 Kilometres

4.5.11 Arthropoda: Insecta: Thysanura

4.5.11.1 Atelurinae 'MH1'

Taxonomic resolution: very little is known about the subterranean Atelurinae and there are no atelurid experts in WA; therefore, the only reliable species level identifications depend on genomic assessment. Genomic studies undertaken by Helix Molecular Solutions (unpublished) indicate that species of atelurids often appear to represent SRE's.

Genomic taxonomy: two specimens were submitted for genomic comparisons, of which one specimen failed to yield DNA sequenced. The successfully sequenced specimen failed to group with any of the reference species (Appendix 4), indicating that it is likely to represent a new species; here referred to as Atelurinae 'MH1'. The close morphological similarity between the sequenced specimens and the remaining Atelurid specimen lead to both specimens being considered the same species.

SRE status: Atelurinae 'MH1' (Figure 4-31) is likely to be an SRE.

Known distribution: the records obtained during this survey represent the known locality records of Atelurinae 'MH1' (Figure 4-33).

Survey records: Atelurinae 'MH1' was recorded from the following localities:

- impact area: number of sites, 1; number of samples, 1: md0499,
- reference area: number of sites, 1; number of samples, 1: md0262[DNA].

[DNA] - sites from which sequenced specimens were obtained.

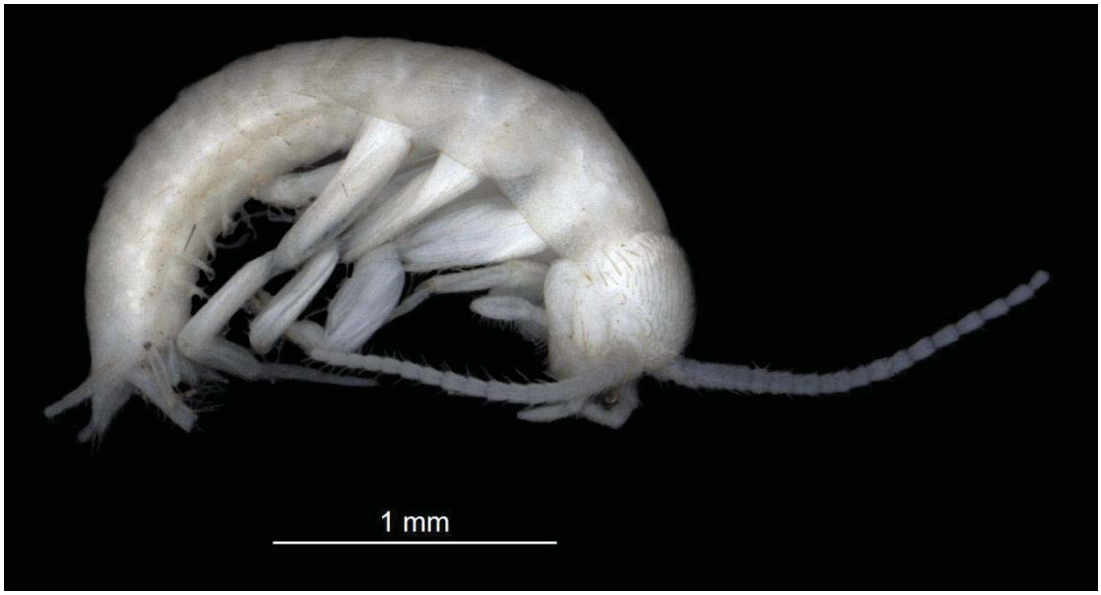

Figure 4-31 Image of Atelurinae 'MH1'

4.5.11.2 *Trinemura* 'MH1' and *Trinemura* 'MH2'

Taxonomic resolution: very little is known about the subterranean *Trinemura* of WA, and there are no *Trinemura* experts in WA; therefore, the only reliable species level identifications depend on genomic assessment. Unpublished studies by Helix Molecular Solutions indicate that this genus is moderately diverse in WA and often locally endemic.

Genomic taxonomy: two specimens, of what was thought to represent a single species, were sequenced for genomic comparisons. Their sequences differed from one another by 12.6% indicating that they belong to different species. Neither of these species grouped with any of the reference sequences, therefore indicating that these are both likely to represent new species and are here referred to as *Trinemura* 'MH1' and *Trinemura* 'MH2'. On the basis of morphological differences observed between these genomic species identified to be diff the remaining specimens were separated into

SRE status: both species are likely to be SREs.

Known distribution: the records obtained for this species represent its known distribution.

Survey records: these species were recorded from the following localities (Figure 4-33):

- *Trinemura* 'MH1' (Figure 4-32)
    - impact area: number of sites, 3; number of samples, 9: md0476, md0487, md0525
    - reference area: number of sites, 3; number of samples, 28: md0253, md0427[DNA], md0430
- *Trinemura* 'MH2'
    - impact area: number of sites, 3; number of samples, 5: md0467[DNA], md0499, md0525,
    - reference area: number of sites, 2; number of samples, 2: md0372, md0646
- *Trinemura sp. indet.*
    - impact area: number of sites, 1; number of samples, 1: md0476
    - reference area: number of sites, 3; number of samples, 3: 991-east_reference, 991-md0253, md0427.

[DNA] - sites from which sequenced specimens were obtained.

Figure 4-32 Image of *Trinemura* 'MH1'

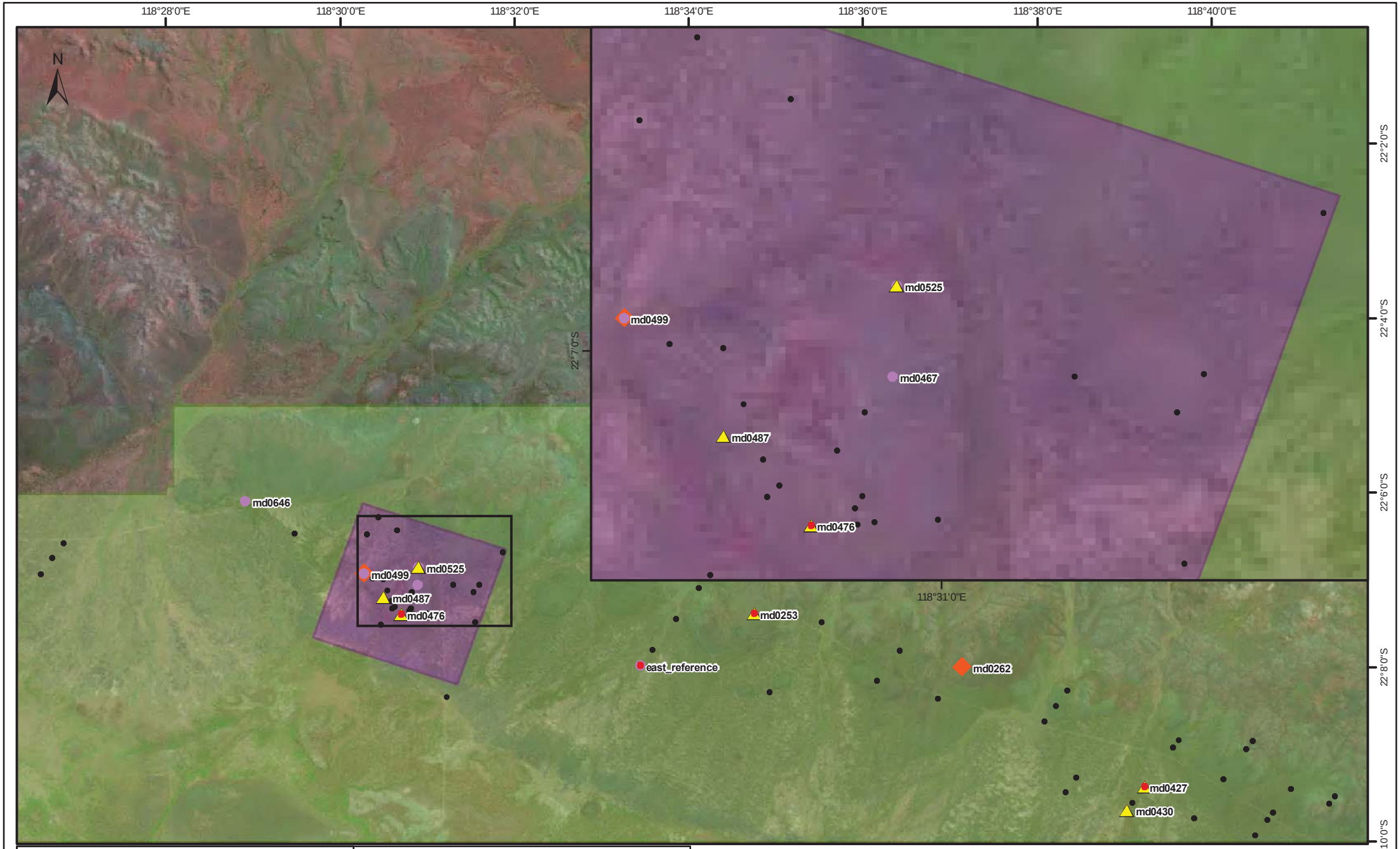

Figure 4-33 Thysanuran site records

AUTHOR: ES Volschenk	CLIENT: Hancock Prospecting
DATE 24 May 2012:	Scale: 1:102,183
Coordinate System: Projection: Transverse Mercator; DATUM: GDA94	PROJECT: Mulga Downs Subterranean Survey

PHOENIX ENVIRONMENTAL SCIENCES

4.5.12 Arthropoda: Malacostraca: Isopoda

4.5.12.1 *Troglarmadillo* 'MH1'

Taxonomic resolution: very little is known about *Troglarmadillo*, despite the fact that they are frequently sampled during subterranean surveys. There are no experts on this genus in WA therefore; the only reliable species level identifications depend on genomic assessment. Unpublished studies by Helix Molecular Solutions indicate that *Troglarmadillo* is very diverse and shows high levels of local endemism. In the absence of genomic comparisons, we consider this species to be new and undescribed, owing to the absence of specimens from previous surveys in the area.

Genomic taxonomy: a single specimen (the only specimen sampled) was submitted for DNA sequencing; however, the sample failed to yield sequences (Appendix 4).

SRE status: *Troglarmadillo* 'MH1' (Figure 4-34) is likely to be an SRE.

Known distribution: the record obtained for this species represents its known distribution (Figure 4-35).

Survey records: the specimen was recorded from the following locality:

- impact area: number of sites, 1; number of samples, 1: md0467**.**

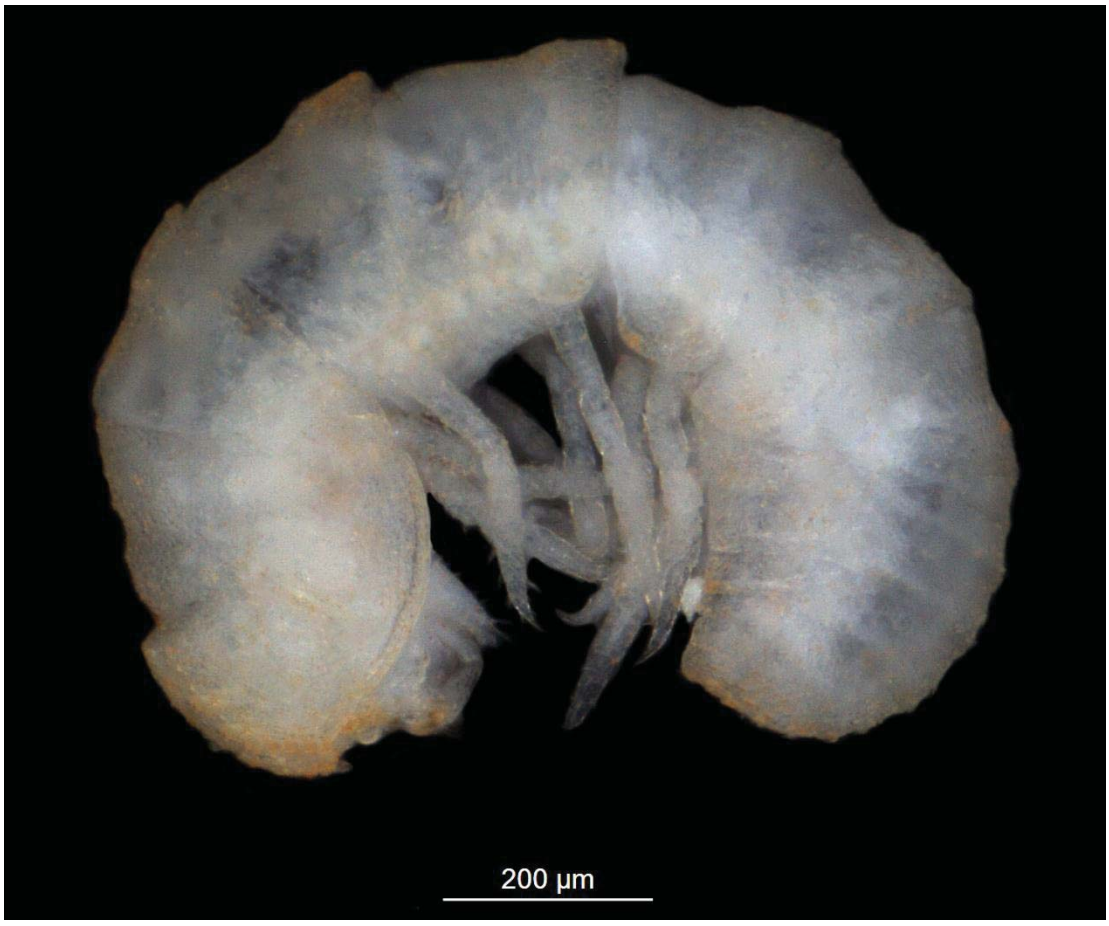

Figure 4-34 Image of *Troglarmadillo* 'MH1'

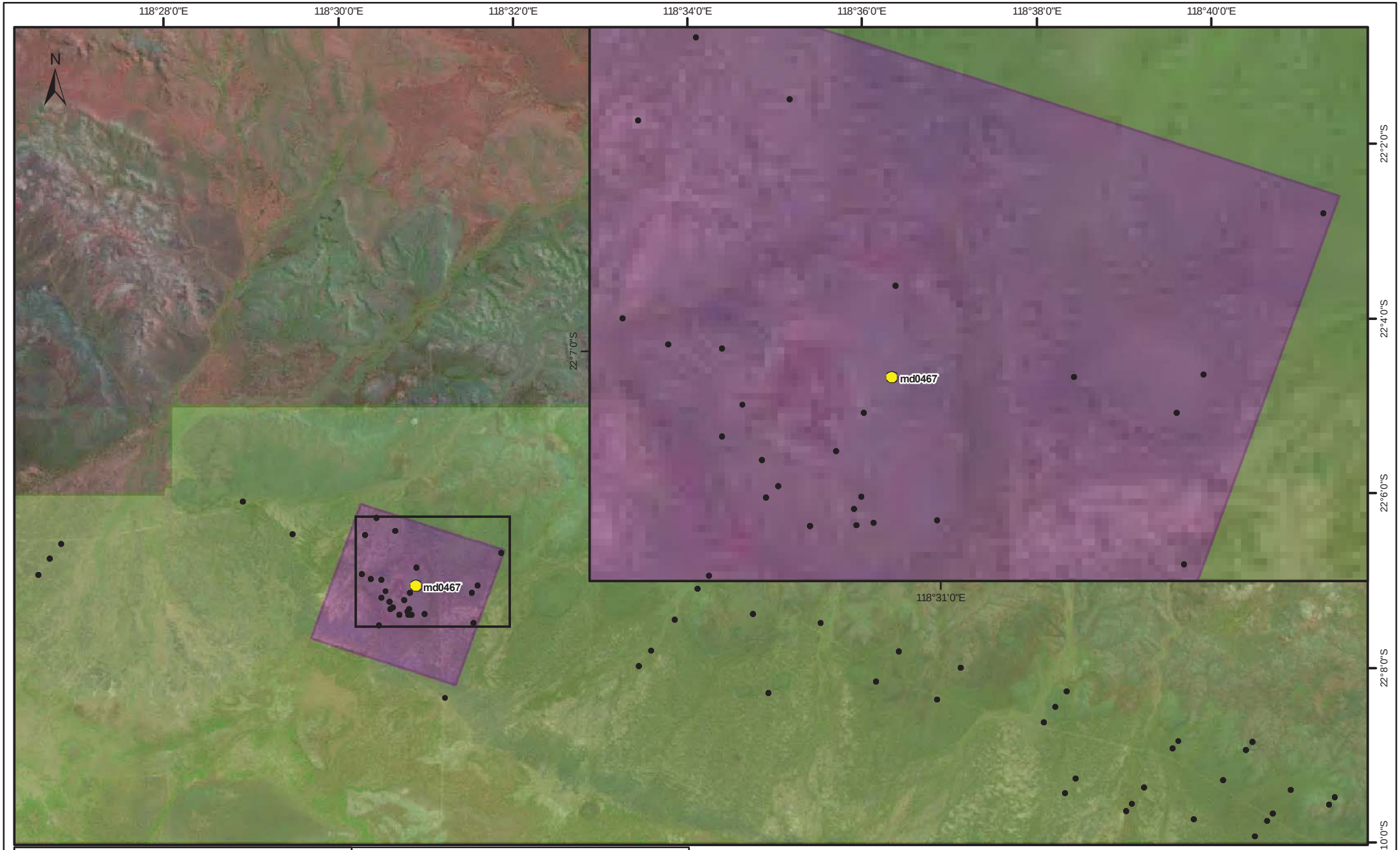

Figure 4-35 *Troglarmadillo* 'MH1' site record

AUTHOR: ES Volschenk	CLIENT: Hancock Prospecting
DATE 24 May 2012:	Scale: 1:102,183
Coordinate System: Projection: Transverse Mercator; DATUM: GDA94	PROJECT: Mulga Downs Subterranean Survey

PHOENIX ENVIRONMENTAL SCIENCES

0 0.45 0.9 1.8 2.7 3.6 4.5 Kilometres

4.5.13 Arthropoda: Pauropoda

4.5.13.1 Pauropoda 'MH1', Pauropoda 'MH2' and Pauropoda 'MH3'

Taxonomic resolution: very little is known about the subterranean Pauropoda of WA, and there are no pauropod experts in WA; therefore, the only reliable species level identifications depend on genomic assessment. Unpublished studies by Helix Molecular Solutions indicate that species of pauropods are often locally endemic.

Genomic taxonomy: two specimens, thought to be the same species, were sequenced for genomic comparisons. These specimens were found to have highly divergent sequences (30% sequence divergence Appendix 4) and therefore represent two distinct species: Pauropoda 'MH1' and Pauropoda 'MH2'. These species did not group with any of the reference sequences, indicating that both species are also new (Appendix 4).

The morphology of the two species was reviewed and several consistent morphological characters were discovered. Using these new characters, the remaining pauropod specimens were reviewed. An additional morphospecies (Pauropoda 'MH3') was found using these characters, and the remaining specimens were identified to either Pauropoda 'MH1' or Pauropoda 'MH2'.

SRE status: Pauropoda 'MH1', Pauropoda 'MH2' (Figure 4-36) and Pauropoda 'MH3' are likely to be SREs.

Known distribution: the records obtained for these species represent their known distribution (Figure 4-37).

Survey records: these species were recorded from the following localities:

- Pauropoda 'MH1':
    - impact area: number of sites, 1; number of samples, 3: md0487^{DNA}
- Pauropoda 'MH2':
    - impact area: number of sites, 1; number of samples, 1: mdh0143
    - reference area: number of sites, 2; number of samples, 2: md0396^{DNA}, md0415
- Pauropoda 'MH3':
    - impact area: number of sites, 1; number of samples, 1: md0467
    - reference area: number of sites, 1; number of samples, 1: md0427.

^{DNA} - sites from which sequenced specimens were obtained.

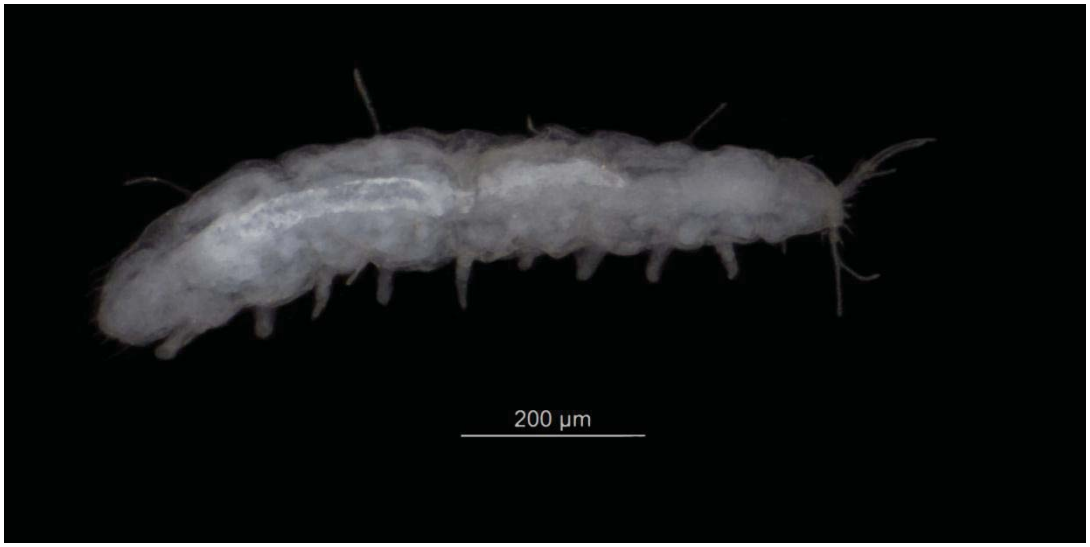

Figure 4-36 Image of Pauropoda 'MH2'

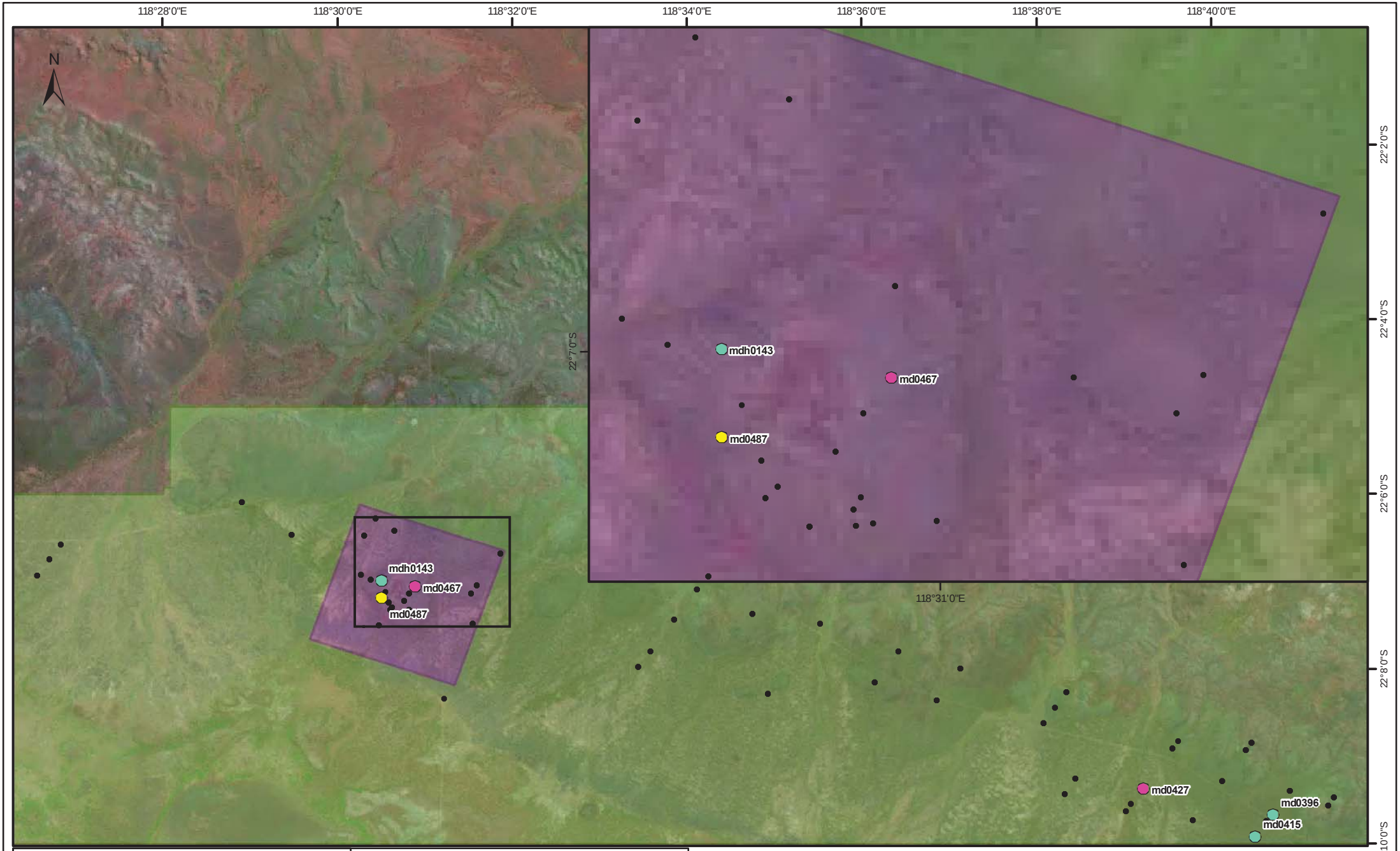

Figure 4-37 Pauropoda site records

AUTHOR: ES Volschenk	CLIENT: Hancock Prospecting
DATE 24 May 2012:	Scale: 1:102,183
Coordinate System: Projection: Transverse Mercator; DATUM: GDA94	PROJECT: Mulga Downs Subterranean Survey

PHOENIX ENVIRONMENTAL SCIENCES

0 0.45 0.9 1.8 2.7 3.6 4.5 Kilometres

4.5.14 Arthropoda: Symphyla

Symphylans are a small group of animals resembling centipedes in that they have a multi-segmented body which bears 1 pair of legs per segment. All Symphylans are blind and pale, possess 12 pairs of legs and a pair of long antennae and are usually less than 1 cm in length. Symphylans can be found in the soil, leaf litter and under rocks (Finston *et al.* 2009; Keable & Wilson 2006; Wilson 2003). This group is poorly known and literature on the Australian species is very limited. In Western Australia the diversity of still very poorly known, but data suggests that they are diverse.

Species level identification of symphylans relies on genomic analysis. Genomic studies undertaken by Helix Molecular Solutions (unpublished) indicate that numerous undescribed species exist in the Pilbara and that most appear to be SRE's. Helix's studies focussed on specimens collected from subterranean surveys; however, since some symphylans may be soil fauna, some species may represent functional troglophiles. Regardless of whether these species are considered to be troglofauna or epigean fauna, many symphylans appear to be SRE's and are therefore of conservation significance.

4.5.14.1 Symphyla 'MH1'.

Taxonomic resolution: very little is known about the subterranean Symphyla of WA, and there are no symphylan experts in WA; therefore, the only reliable species level identifications depend on genomic assessment. Unpublished studies by Helix Molecular Solutions indicate that symphylan species show high levels of diversity and local endemism; therefore, we consider this species to be new. None of these specimens were found within the proposed impact area and so no further investigations were undertake.

Genomic taxonomy: no genomic investigations of this species were undertaken.

SRE status: Symphyla 'MH1' (Figure 4-38) is likely to be an SRE.

Known distribution: the records obtained for this species represent its known distribution.

Survey records: Symphyla 'MH1' was recorded from the following localities (Figure 4-39):

- reference area: number of sites, 3; number of samples, 7: md_kar6, md0393, md0397.

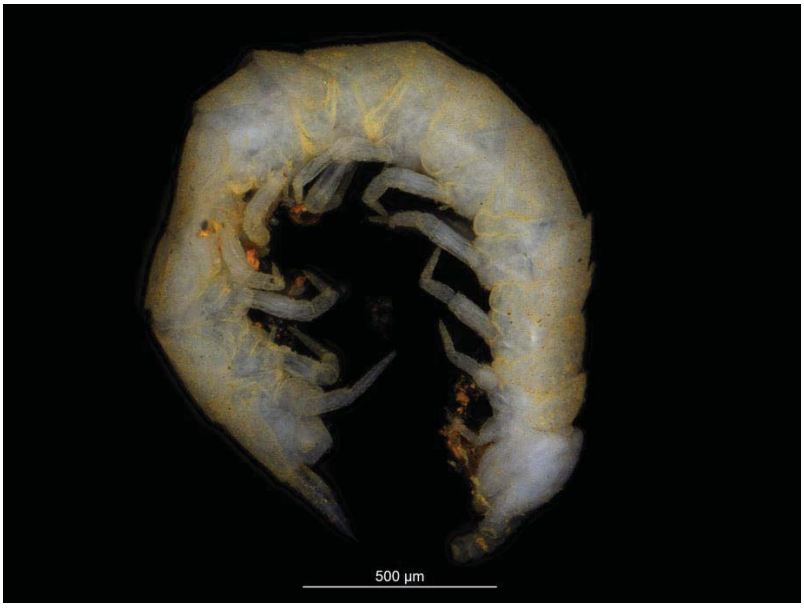

Figure 4-38 Image of Symphyla 'MH1'

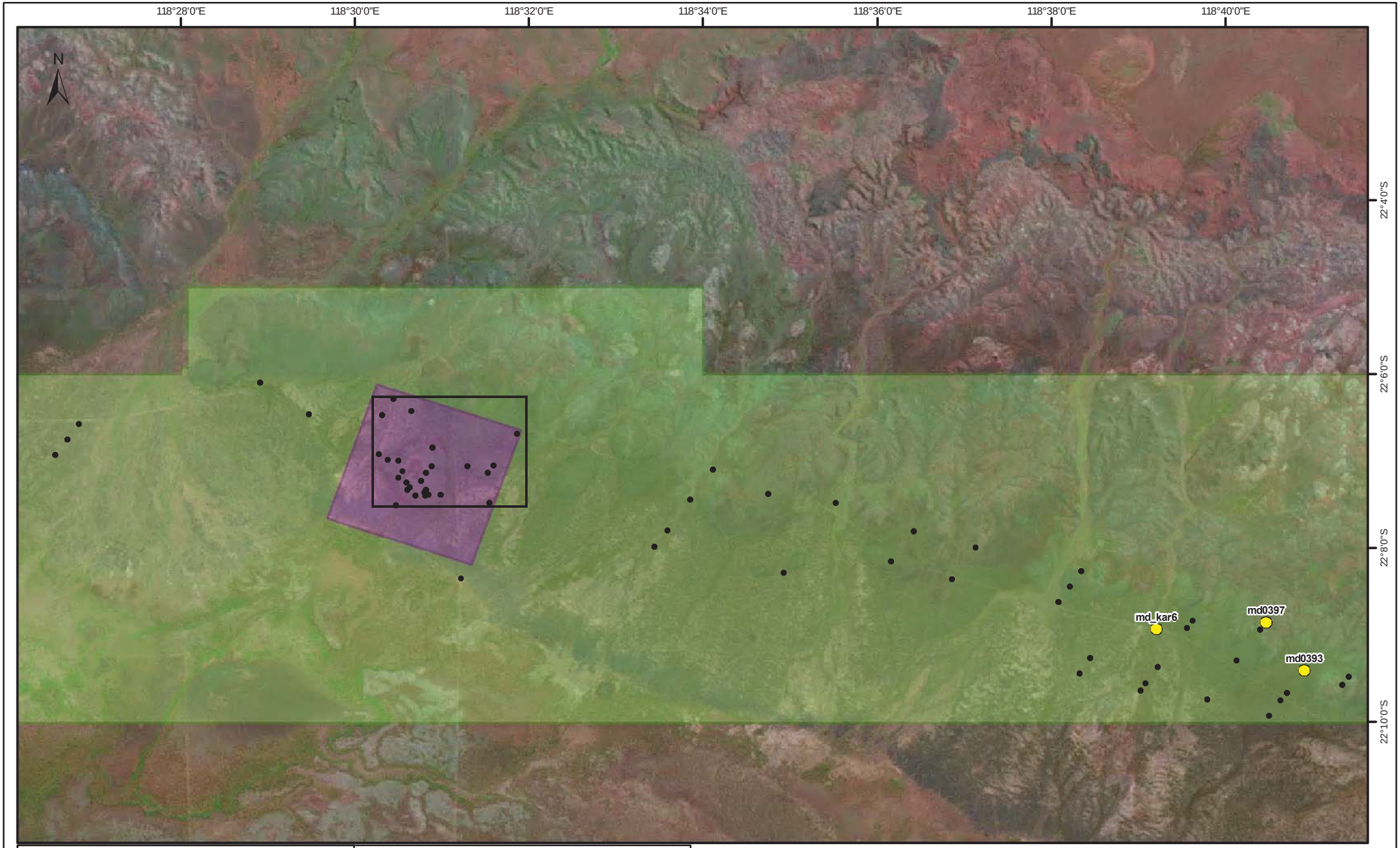

Figure 4-39 Symphylan site records

AUTHOR: ES Volschenk	CLIENT: Hancock Prospecting
DATE 24 May 2012:	Scale: 1:102,183
Coordinate System: Projection: Transverse Mercator; DATUM: GDA94	PROJECT: Mulga Downs Subterranean Survey

PHOENIX ENVIRONMENTAL SCIENCES

0 0.45 0.9 1.8 2.7 3.6 4.5 Kilometres

4.6 STYGOFAUNA RECORDS

Twenty four (24) putative stygofauna species were recorded from survey bores. Eight (8) of these species were represented by only one or two specimens (Figure 4-40). Stygofauna specimens were recorded from 52 sites (Figure 4-41).

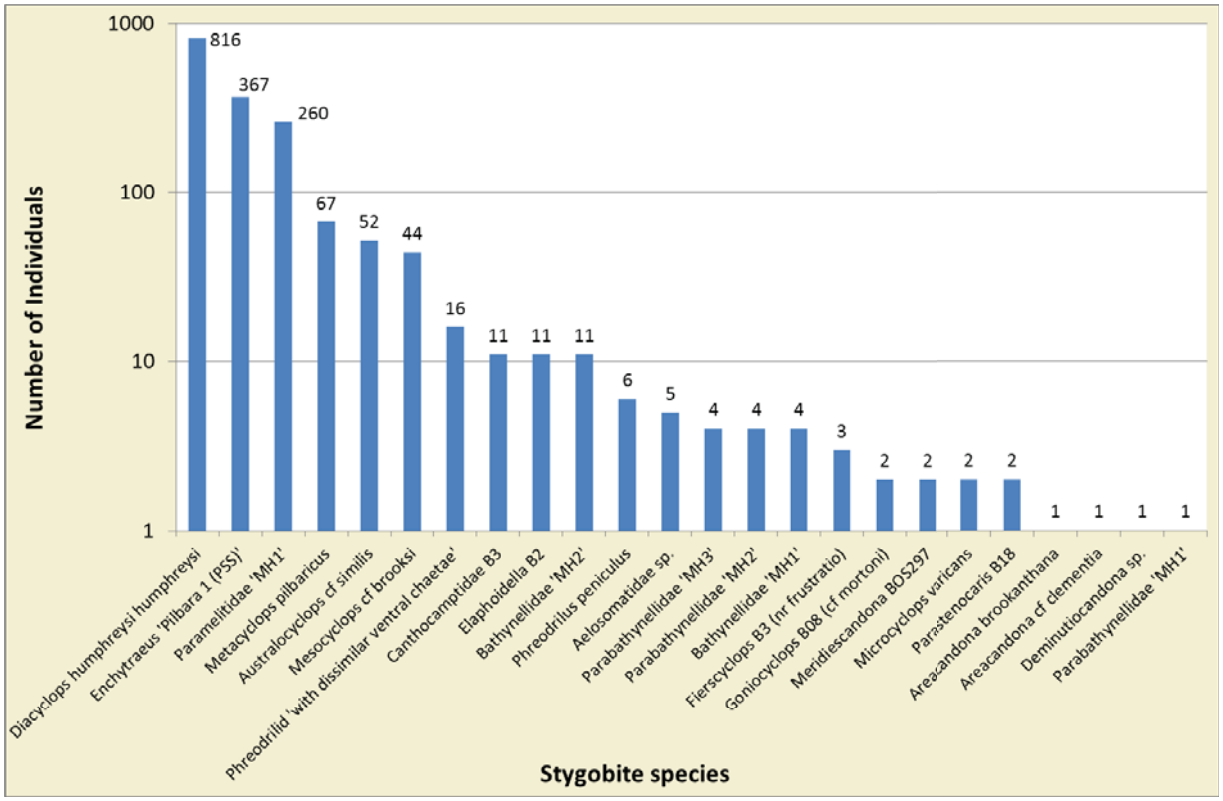

Figure 4-40 Abundance records for stygofauna species

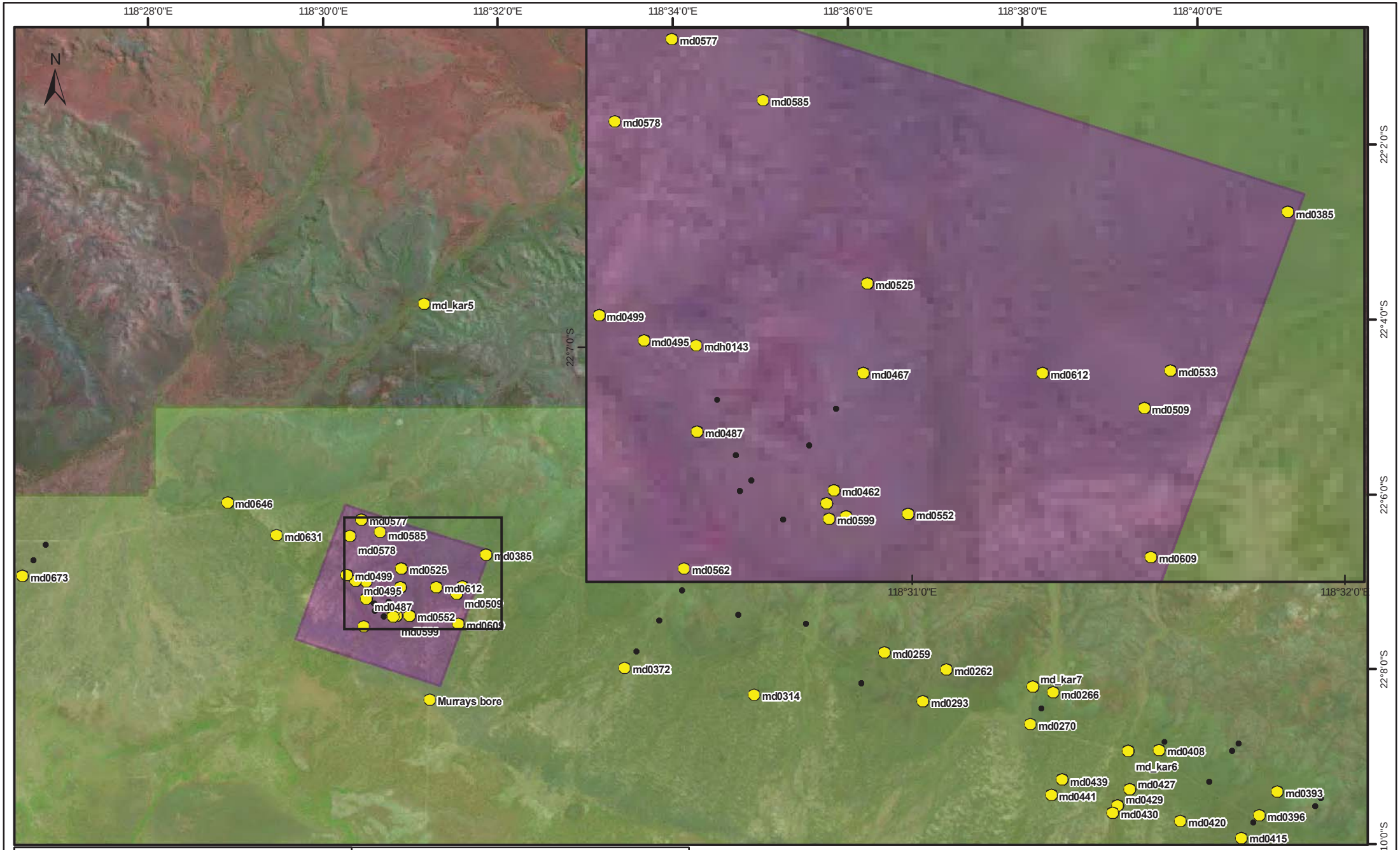

Figure 4-41 Stygoofauna site records from survey

AUTHOR: ES Volschenk	CLIENT: Hancock Prospecting
DATE 24 May 2012:	Scale: 1:101,991
Coordinate System: Projection: Transverse Mercator; DATUM: GDA94	PROJECT: Mulga Downs Subterranean Survey

PHOENIX ENVIRONMENTAL SCIENCES

0 0.5 1 2 3 4 5 Kilometres

4.6.1 Annelida: Haplotaxida: Clitellata

4.6.1.1 Enchytraeidae

Taxonomic resolution: Enchytraeidae is a large and complex family of annelid worms. Specimens were identified by Mr Mike Scanlon (Bennelongia Environmental Consultants). Specimens were identified to *Enchytraeus* 'Pilbara 1 (PSS)'. Additional immature or damaged specimens were also identified to Enchytraeidae sp. indet. or *Enchytraeus* sp. indet.

Genomic taxonomy: specimens were not sequenced, owing to the widespread nature of this species.

SRE status: *Enchytraeus* 'Pilbara 1 (PSS)' is not considered to be an SRE.

Known distribution: *Enchytraeus* 'Pilbara 1 (PSS)' (Figure 4-43) is widely distributed throughout the Pilbara (M. Scanlon pers. comm. March, 2011).

Survey records: Enchytraeid specimens were recorded from the following sites (Figure 4-42):

- Enchytraeus 'Pilbara 1 (PSS)'
    - impact area: number of sites, 4; number of samples, 104: md0499, md0525, md0578, md0596
    - reference area: number of sites, 12; number of samples, 276: md0262, md0266, md0270, md0293, md0396, md0408, md0427, md0439, md0441, md0631, md0646, md0673
- Enchytraeus sp. indet
    - reference area: number of sites, 1; number of samples, 2: md0393
- Enchytraeidae sp. indet.
    - impact area: number of sites, 2; number of samples, 2: md0385, md0601.

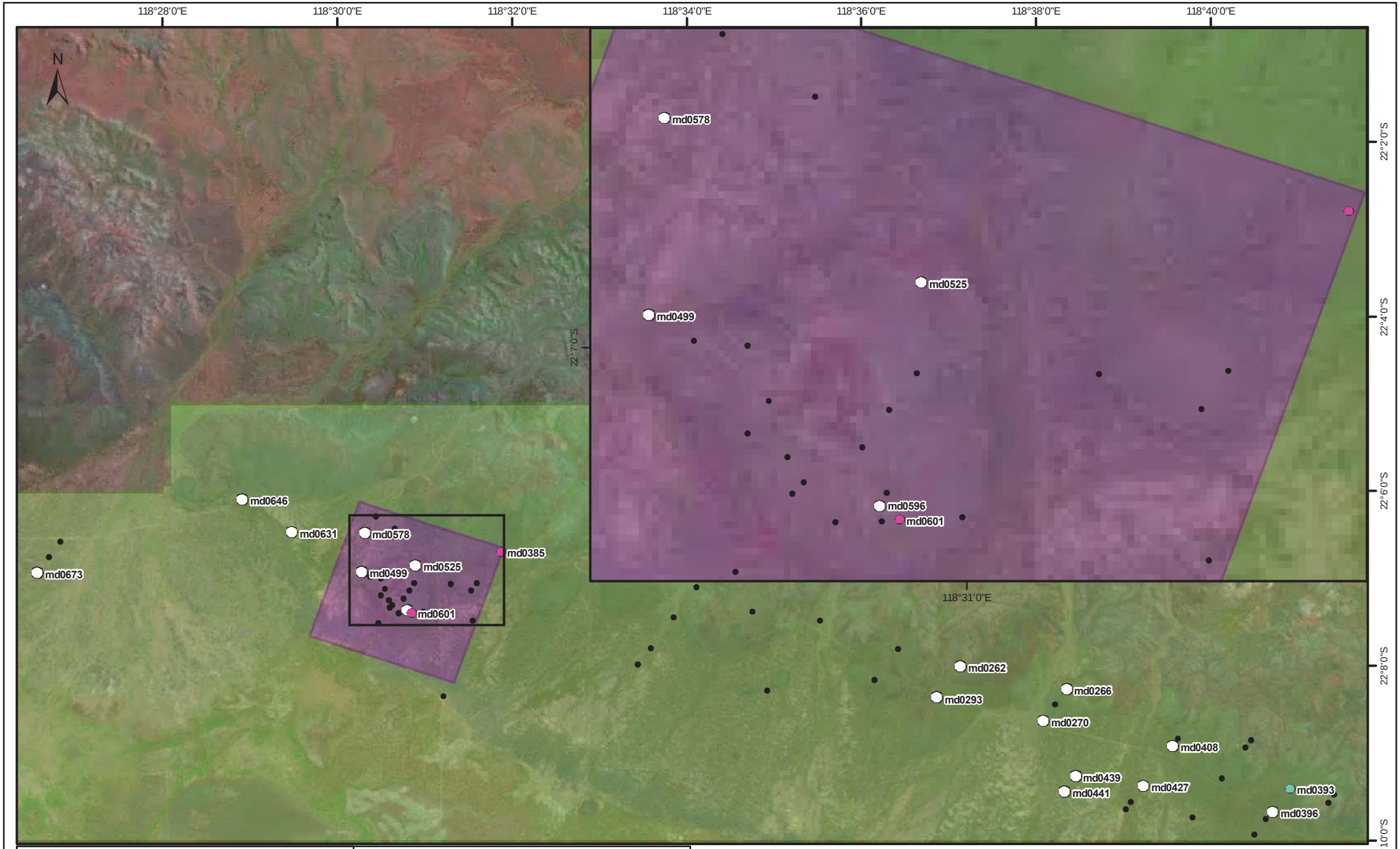

Figure 4-42 Enchytraeid site records

AUTHOR: ES Volschenk	CLIENT: Hancock Prospecting
DATE 24 May 2012:	Scale: 1:101,991
Coordinate System: Projection: Transverse Mercator; DATUM: GDA94	PROJECT: Mulga Downs Subterranean Survey

PHOENIX ENVIRONMENTAL SCIENCES

0 0.5 1 2 3 4 5 Kilometres

- Enchytraeidae sp. indet.
- Enchytraeus sp. indet.
- *Enchytraeus* 'Pilbara 1 (PSS)'
- Survey Bores
- Proposed Impact Area
- Study Area

4.6.1.2 Naididae

Taxonomic resolution: specimens were identified by Mike Scanlon at Bennelongia. Specimens were identified to morphospecies. A single species if Naididae, *Pristina longiseta* was identified from the survey.

Genomic taxonomy: specimens were not sequenced, owing to the widespread nature of this species.

SRE status: *Pristina longiseta* is not an SRE.

Known distribution: this species is widespread in the Pilbara.

Survey records: specimens were recorded from the following sites:

- *Pristina longiseta*:
    - reference area: number of sites, 2; number of samples, 43md_kar2 and md_kar6.

4.6.1.3 Phreodrilidae

Taxonomic resolution: specimens were identified by Mike Scanlon at Bennelongia. Specimens were identified to morphospecies. Two morphospecies were identified: Phreodrilid 'with dissimilar ventral chaetae' and *Phreodrilus peniculus*.

Genomic taxonomy: Specimens were not sequenced, owing to the widespread nature of these species and the resolved state of their taxonomy.

SRE status: Phreodrilid 'with dissimilar ventral chaetae' and *Phreodrilus peniculus* are not SRE species.

Known distribution: Phreodrilid 'with dissimilar ventral chaetae' and *Phreodrilus peniculus* are widespread species.

Survey records: specimens were recorded from the following sites (Figure 4-44):

- Phreodrilid 'with dissimilar ventral chaetae':
    - impact area: number of sites, 1; number of samples, 11: md0525
    - reference area: number of sites, 2; number of samples, 6: md0430, md0646
- *Phreodrilus peniculus* are widespread species:
    - reference area: number of sites, 1; number of samples, 6: md0430.

Figure 4-43 Image of *Phreodrilus peniculus*.

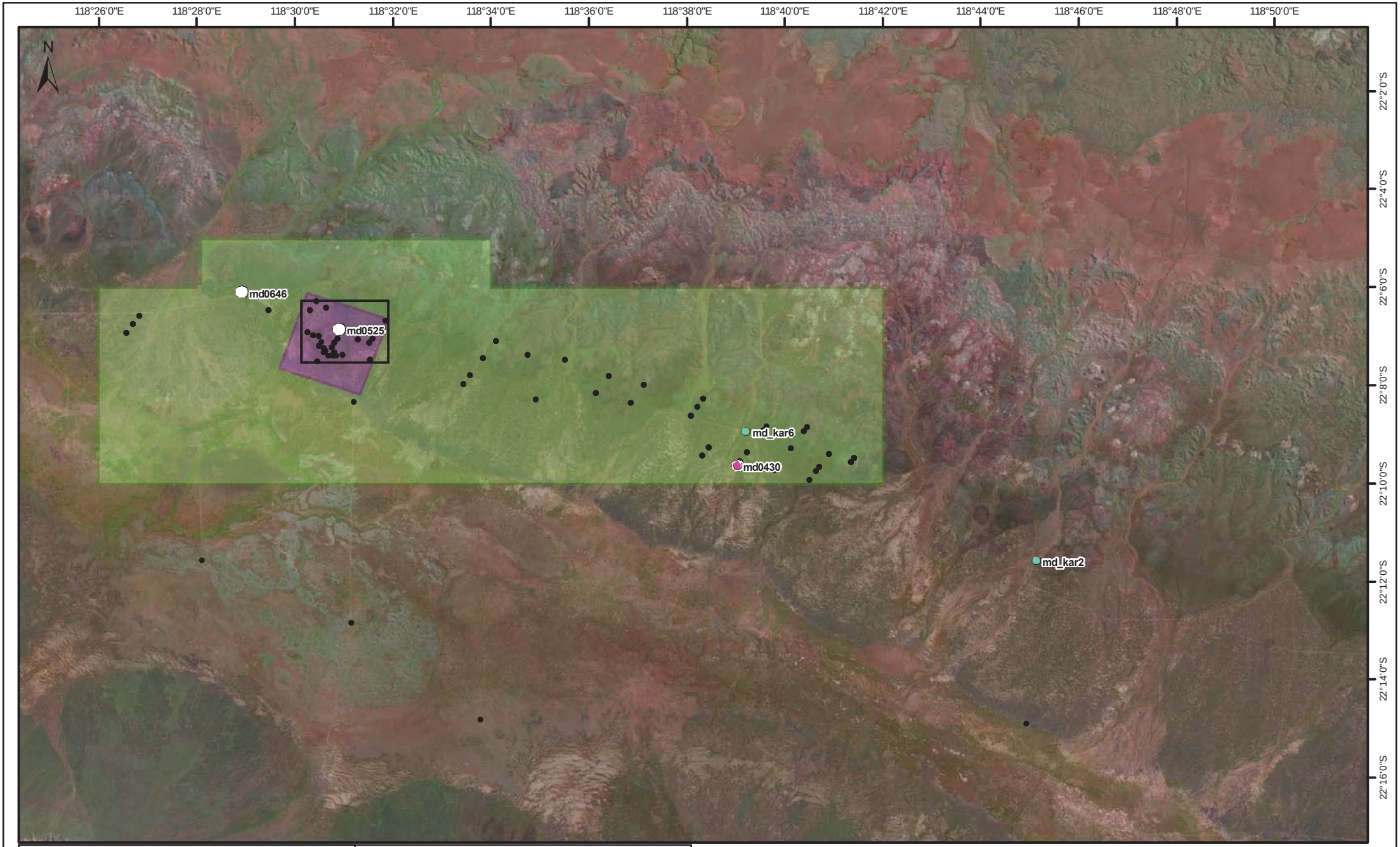

Figure 4-44 Naididae and Phreodrilidae site records

AUTHOR: ES Volschenk	**CLIENT:** Hancock Prospecting
DATE 24 May 2012:	**Scale:** 1:181,317
Coordinate System: Projection: Transverse Mercator; DATUM: GDA94	**PROJECT:** Mulga Downs Subterranean Survey

PHOENIX ENVIRONMENTAL SCIENCES

0 1 2 4 6 8 10 Kilometres

- *Pristina longiseta*
- *Phreodrilus peniculus*
- Phreodrilid 'with dissimilar ventral chaetae'
- Survey Bores
- Proposed Impact Area
- Study Area

4.6.1.4 Annelida: Polychaeta: Scolecida

Taxonomic resolution: specimens were identified by Mike Scanlon at Bennelongia. Specimens were identified to a species of Aelosomatidae; here referred to as Aelosomatidae sp.. Aelosomatids are extremely unusual annelids and are loosely placed in the Order Polychaeta. Aelosomatids are therefore unusual representatives of the order, living in fresh water, since almost all polychaetes are marine (Beesley *et al.* 1998).

Genomic taxonomy: specimens were not sequenced, owing to the time constraints in receiving identified specimens from Bennelongia. The species was also restricted to a reference site.

SRE status: Aelosomatidae sp. may an accidental by-catch since all specimens (5) only came from a single bore. Little is known about the Aelosomatids of the Pilbara but they are thought to be widespread stygophiles and are probably not SRE's.

Known distribution: Aelosomatids have been collected widely from the Pilbara; however, they never appear to be abundant.

Survey records: specimens were recorded from the following site (Figure 4-45):

- reference area: number of sites, 1; number of samples, 5: md0430.

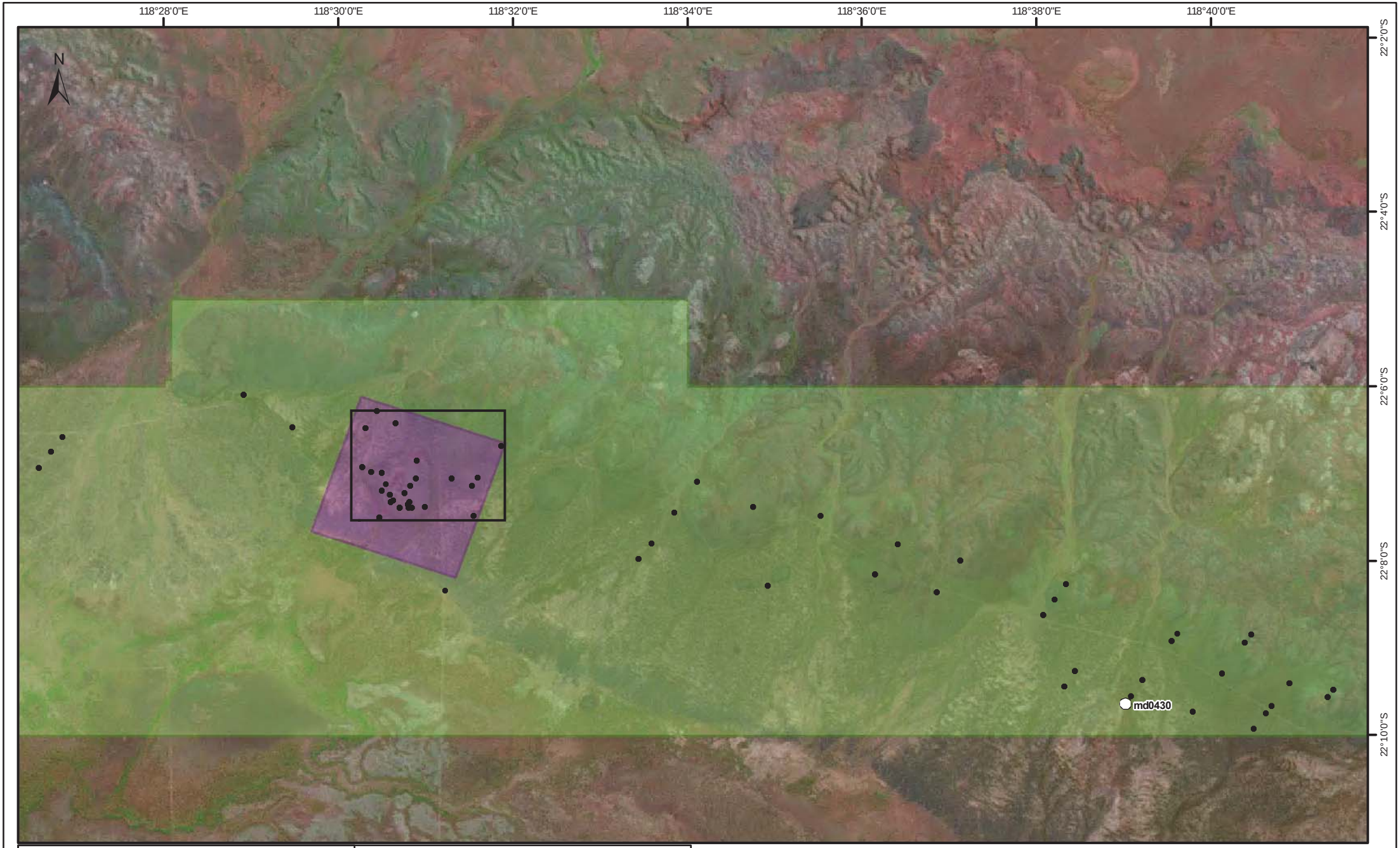

Figure 4-45 Aelosomatidae site records

AUTHOR: ES Volschenk	CLIENT: Hancock Prospecting
DATE 24 May 2012:	Scale: 1:101,991
Coordinate System: Projection: Transverse Mercator; DATUM: GDA94	0 0.5 1 2 3 4 5 Kilometres

PHOENIX ENVIRONMENTAL SCIENCES

PROJECT: Mulga Downs Subterranean Survey

Aelosomatidae sp.
Survey Bores
Proposed Impact Area
Study Area

4.6.2 Arthropoda: Malacostraca: Amphipoda

4.6.2.1 Paramelitidae 'MH1'

Taxonomic resolution: stygobitic Paramelitidae from the Pilbara are relatively well studied (Finston et al. 2004; Finston and Johnson 2004; Finston et al. 2007). These studies clearly indicate both, the high levels of endemicity that exist within paramelitid amphipods, and the inconsistency between morphology and genomic information in obtaining reliable species level identifications. Morphological features can be misleading in Pilbara Paramelitidae and species level identifications are heavily reliant on genomic assessment. Current knowledge of Paramelitidae indicates that they are typically endemic to aquifers and that their distributions reflect an interaction of modern geological events and paleodrainage systems. They are frequently SRE's.

Genomic taxonomy: five specimens were submitted for sequencing in order to make genomic comparisons: one specimen from Wittenoom and the remainder from Murrays Hill survey bores. All were tentatively identified to the same species: Paramelitidae 'MH1'. The Wittenoom specimen and one of the Murrays Hill survey specimens failed to yield sequences (Appendix 4). The three Murrays Hill specimens that yielded DNA sequences were found to have an average sequence divergence of 1.6%; therefore confirming that they are the same species, here referred to as Paramelitidae 'MH1'. Sequences from this species did not group with any of the reference sequences, indicating that this is a new species (Appendix 4).

SRE status: Paramelitidae 'MH1' is a likely SRE (Figure 4-46).

Known distribution: the records obtained for this species represent its known distribution (Figure 4-47).

Survey records: Specimens were recorded from the following localities:

- impact area: number of sites, 18; number of samples, 239: md0385, md0462, md0467^{DNA}, md0467, md0487, md0495, md0499, md0509, md0525, md0533, md0552, md0577, md0596, md0599, md0601, md0609, md0612, mdh0143
- reference area: number of sites, 5; number of samples, 21: md0314^{DNA}, md0415, md0415DNA, md0420, md0420^{DNA}.

^{DNA} - sites from which sequenced specimens were obtained.

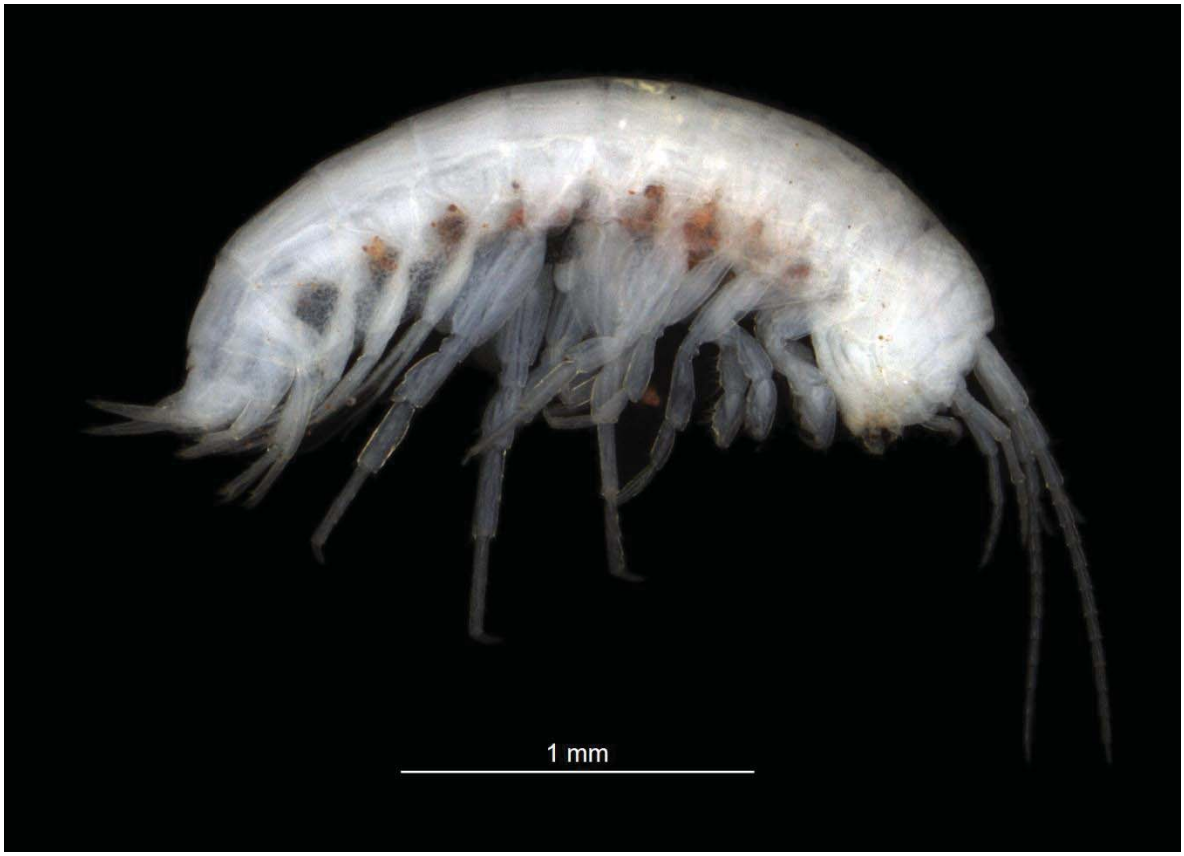

Figure 4-46 Image of Paramelitidae 'MH1'

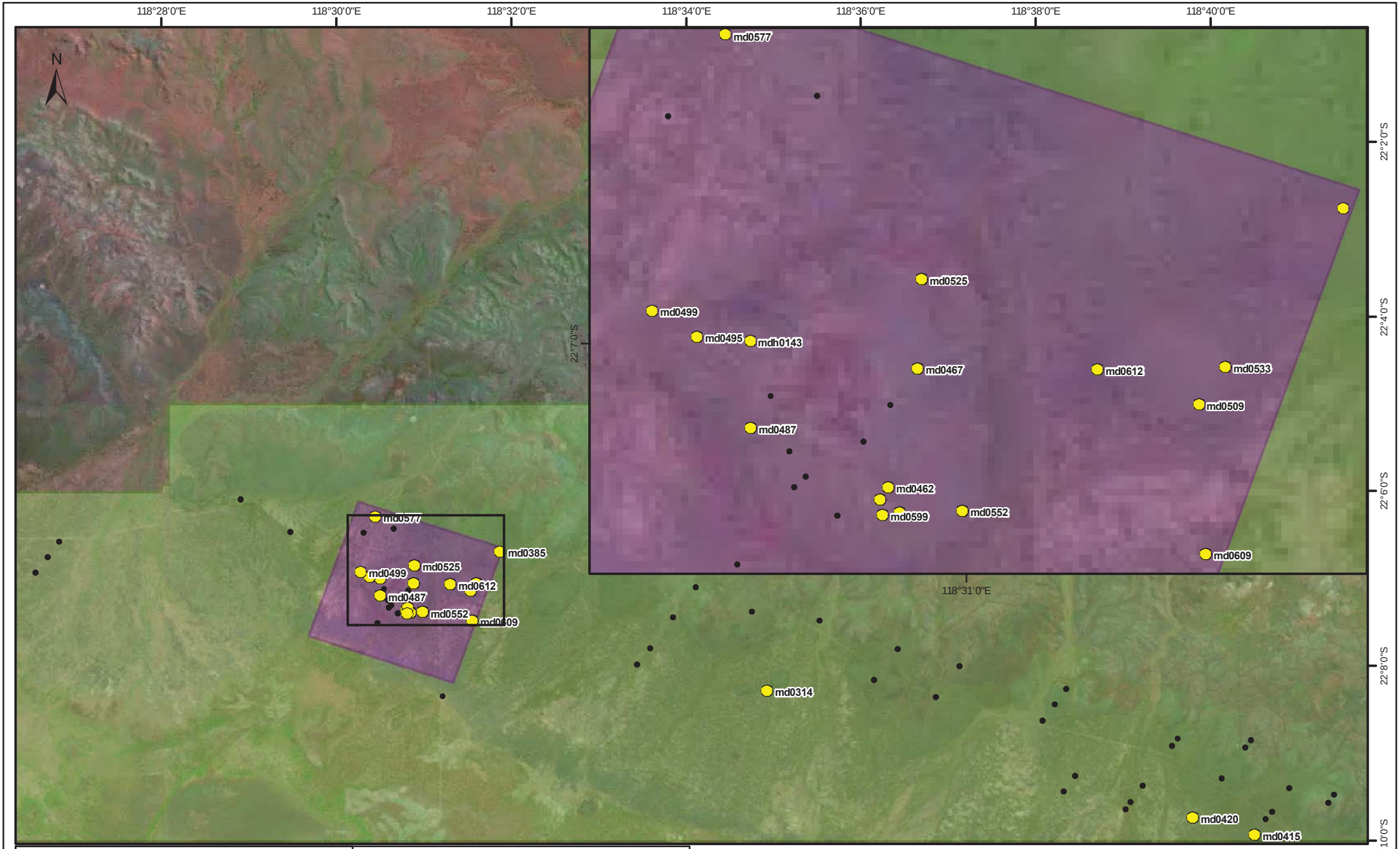

Figure 4-47 Paramelitidae 'MH1' site records

AUTHOR: ES Volschenk	CLIENT: Hancock Prospecting
DATE 24 May 2012:	Scale: 1:101,991
Coordinate System: Projection: Transverse Mercator; DATUM: GDA94	0 0.5 1 2 3 4 5 Kilometres

PHOENIX ENVIRONMENTAL SCIENCES

PROJECT: Mulga Downs Subterranean Survey

Paramelitidae 'MH1'
Survey Bores
Proposed Impact Area
Study Area

4.6.3 Arthropoda: Malacostraca: Isopoda

4.6.3.1 *Pygolabis* 'MH1'

Taxonomic resolution: studies undertaken on the systematics and distribution of *Pygolabus* demonstrate high levels of endemism (2006). This species could not be attributed to any described species using Keable & Wilson (Bennelongia 2007; Biota 2008; Pesce & De Laurentiis 1996). We therefore consider this to be a new species.

Genomic taxonomy: this species was not found within the proposed area of development and so no genetic investigation was warranted.

SRE status: this species is very likely to be an SRE.

Known distribution: the records obtained for *Pygolabis* 'MH1' during this survey represent its known distribution.

Survey records: species were recorded from the following localities:

- reference area: number of sites, 1; number of samples, 12: Browns bore.

4.6.4 Arthropoda: Malacostraca: Syncarida

4.6.4.1 Bathynellidae

Taxonomic resolution: very little is known about the bathynellids of WA and there are no bathynellid experts in WA; therefore, reliable species level identifications depend on genomic assessment. Genomic studies by Helix Molecular solutions (unpublished) have demonstrated the highly endemic nature of stygobitic bathynellids.

Genomic taxonomy: a single species was initially identified and two specimens were chosen for DNA sequencing. These specimens were found to be divergent from each other by 18% sequence divergence, demonstrating that they are two different species, here referred to as Bathynellidae 'MH1' and Bathynellidae 'MH2'. These species also failed to group with any of the reference species indicating that they are both likely to be new species (Appendix 4). The morphology of the sequenced specimens was reviewed, revealing characters that appear to support species delineation. Using these characters, the remaining species were assigned to either species. In several samples, damaged specimens could not be attributed to either species and are referred to as Bathynellidae sp. indet.

SRE status: Bathynellidae 'MH1' and Bathynellidae 'MH2' are likely SREs.

Known distribution: the records of Bathynellidae 'MH1' (Figure 4-48) and Bathynellidae 'MH2' obtained in this survey represent the known distribution of this species.

Survey records: Bathynellid specimens were recorded from the following localities (Figure 4-49):

- Bathynellidae 'MH1'
    - impact area: number of sites, 2; Number of Samples, 4: md0499^{DNA}, md0577
    - reference area: number of sites, 1; number of samples, 6: kar6
- Bathynellidae 'MH2'
    - reference area: number of sites, 2; number of samples, 11: md0429^{DNA}, md0429

- Bathynellidae sp. indet.
    - impact area: number of sites, 4; number of samples, 4: md0462, md0495, md0525 and mdh0143
    - reference area: number of sites, 2; number of samples, 2: md0253 and md0408.

[DNA] - sites from which sequenced specimens were obtained.

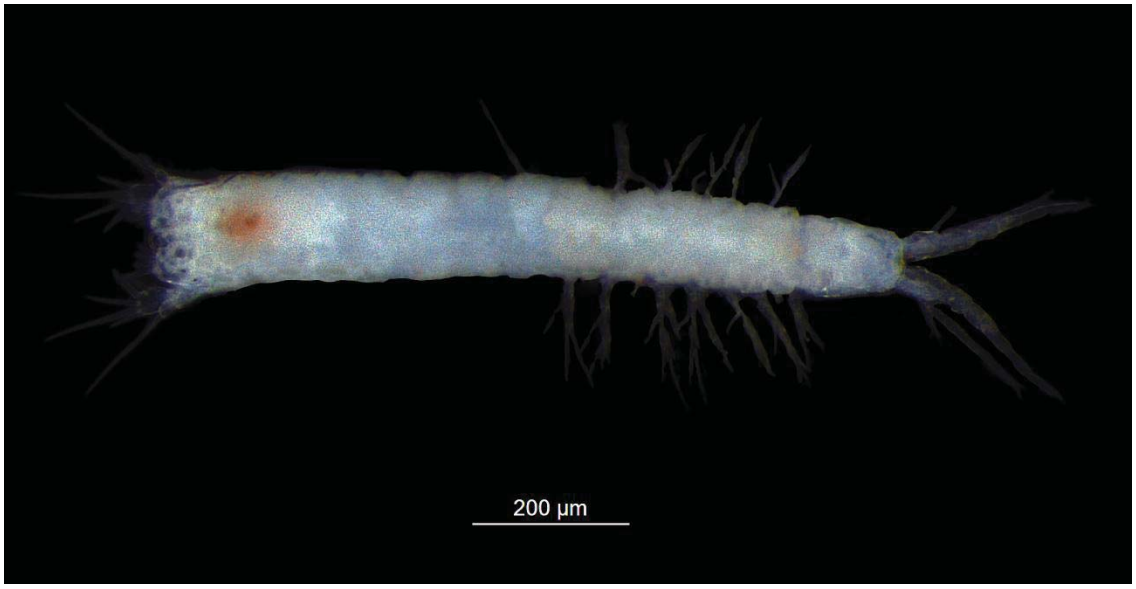

Figure 4-48 Image of Bathynellidae 'MH1'

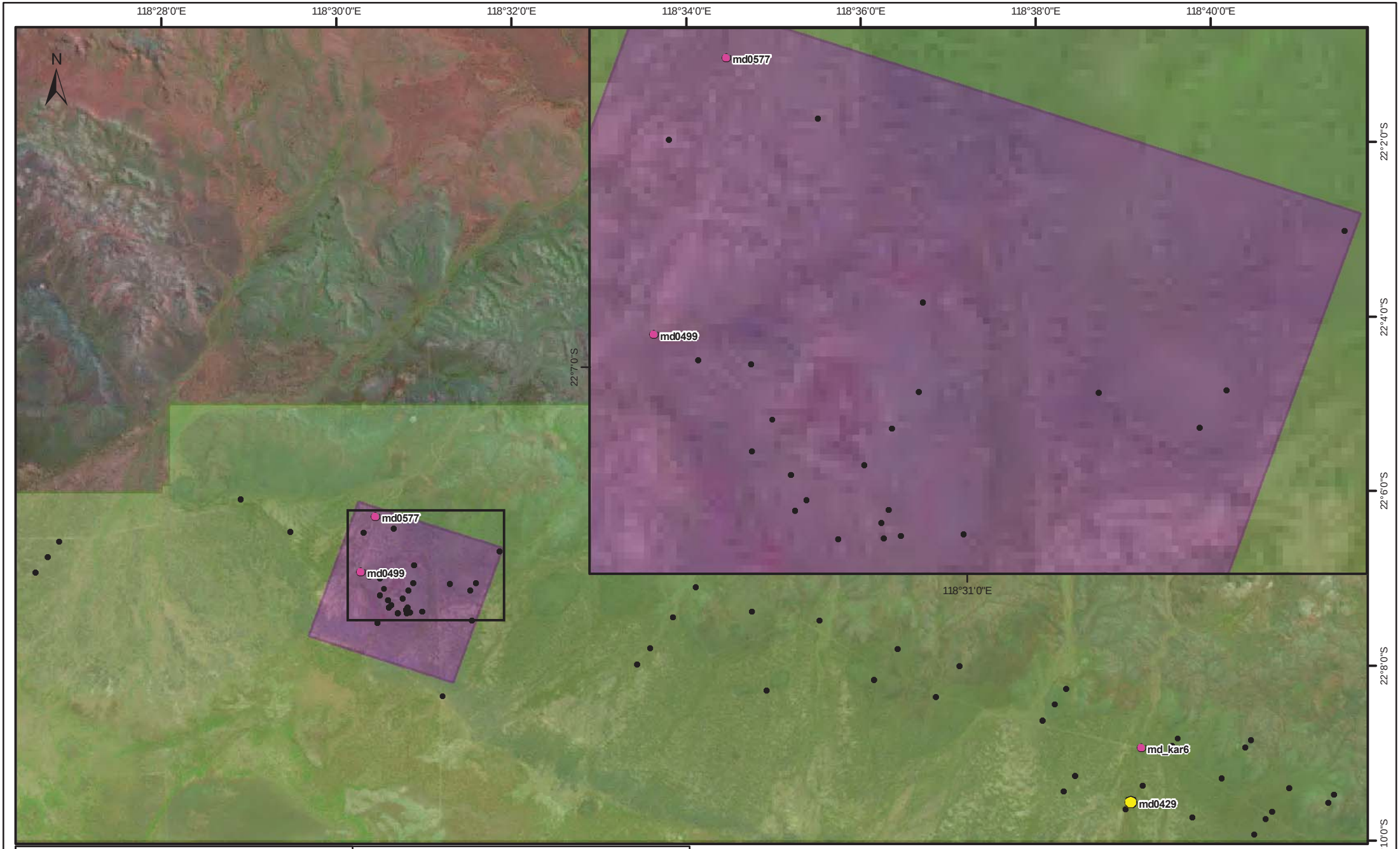

Figure 4-49 Bathynellid site records

AUTHOR: ES Volschenk	CLIENT: Hancock Prospecting
DATE 24 May 2012:	Scale: 1:101,991
Coordinate System: Projection: Transverse Mercator; DATUM: GDA94	0 0.5 1 2 3 4 5 Kilometres

PHOENIX ENVIRONMENTAL SCIENCES

PROJECT: Mulga Downs Subterranean Survey

4.6.4.2 Parabathynellidae

Taxonomic resolution: very little is known about the stygobitic Parabathynellidae of WA, and there are no parabathynellid experts in WA; therefore, the only reliable species level identifications depend on genomic assessment. Unpublished studies by Helix Molecular Solutions indicate that parabathynellid species are often locally endemic.

Genomic taxonomy: a single species was initially identified and three specimens were chosen for DNA sequencing. Only two of these specimens yielded DNA sequences and they were found to be divergent from each other by 21.6% sequence divergence, demonstrating that they are two different species. These two species are here referred to as Parabathynellidae 'MH1' and Parabathynellidae 'MH2'. These species also failed to group with any of the reference species indicating that they are both likely to be new species (Appendix 4). The morphology of the sequenced specimens was reviewed and characters were found that appear to support species delineation by sequence divergence. Using these characters, the remaining species were assigned to either species as well as a third species, Parabathynellidae 'MH3'.

SRE status: Parabathynellidae 'MH1' (Figure 4-50), Parabathynellidae 'MH2' and Parabathynellidae 'MH3' are likely to be SRE's.

Known distribution: the records obtained for these species represent their known distributions.

Survey records: Parabathynellid specimens were recorded from the following localities (Figure 4-51):

- Parabathynellidae 'MH1'
    - reference area: number of sites, 2; number of samples, 5: md_kar7[DNA], md0429
- Parabathynellidae 'MH2'
    - impact area: number of sites, 3; number of samples, 3: md0509, md0533, md0562[DNA]
    - reference area: number of sites, 2; number of samples, 7: kar6, md0396
- Parabathynellidae 'MH3'
    - impact area: number of sites, 1; number of samples, 4: md0525

[DNA] - sites from which sequenced specimens were obtained.

Figure 4-50 Image of Parabathynellidae 'MH3'

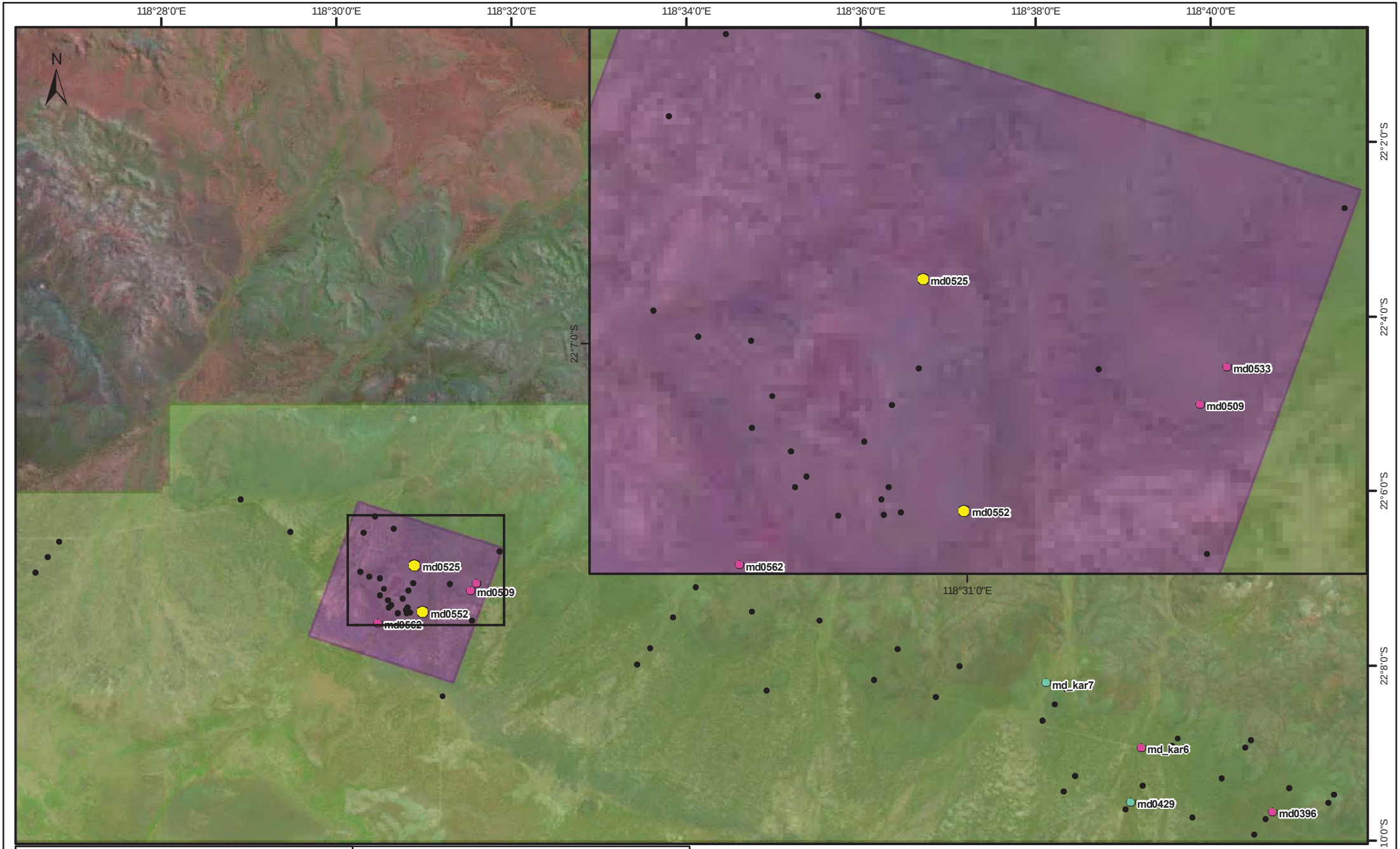

Figure 4-51 Parabathynellid site records

AUTHOR: ES Volschenk	CLIENT: Hancock Prospecting
DATE 24 May 2012:	Scale: 1:101,991
Coordinate System: Projection: Transverse Mercator; DATUM: GDA94	PROJECT: Mulga Downs Subterranean Survey

PHOENIX ENVIRONMENTAL SCIENCES

0 0.5 1 2 3 4 5 Kilometres

- Parabathynellidae 'MH1'
- Parabathynellidae 'MH2'
- Parabathynellidae 'MH3'
- Survey Bores
- Proposed Impact Area
- Study Area

4.6.5 Arthropoda: Maxillopoda: Copepoda

4.6.5.1 *Cyclopoida*

Taxonomic resolution: Cyclopoid copepods are very diverse and often abundant freshwater crustaceans. Stygomorphic species were identified by the absence, or major reduction, of eyes or eyes pots. Specimens were identified to species level by Ms Jane McRae (Bennelongia Environmental services). Specimens were identified to morphospecies level. Seven (7) morphospecies were identified from bore samples: *Australocyclops* cf *similis*, *Diacyclops humphreysi humphreysi* (Figure 4-52), *Fierscyclops* B3 (cf *frustratio*), *Goniocyclops* B08 (cf *mortoni*), *Mesocyclops* cf *brooksi*, *Metacyclops pilbaricus* and *Microcyclops varicans*, and two (2) morphospecies were only recoded from the regional sampling (Karaman-Chappuis and Windmill Bore sites): *Thermocyclops* B04, *Mesocyclops* sp. indet.

Genomic taxonomy: all of the cyclopoids were identified to morphospecies level from morphology; therefore, genomic investigation was not deemed necessary.

SRE status: None of the cyclopoid copepods identified from this survey are recognised as SRE's.

Known distribution: all of these species are widespread in the Pilbara (EPA 2007).

Survey records: specimens were recorded from the following localities (Figure 4-53):

- *Australocyclops* cf *similis*
    - reference area: number of sites, 4; number of samples, 103: kar4, kar7, md0393, md0429
- *Diacyclops humphreysi humphreysi*
    - impact area: number of sites, 12; number of samples, 813: md0385, md0462, md0467, md0487, md0495, md0509 md0525, md0552, md0596, md0599, md0601, md0612
    - reference area: number of sites, 2; number of samples, 3: md0259, md0408
- *Fierscyclops* B3 (cf *frustratio*)
    - reference area: number of sites, 1; number of samples, 3: md0427
- *Goniocyclops* B08 (cf *mortoni*)
    - reference area: number of sites, 1; number of samples, 2: md0393
- *Mesocyclops* cf *brooksi*
    - impact area: number of sites, 2; number of samples, 6: md0585, md0599
    - reference area: number of sites, 9; number of samples, 80: kar1, kar4, kar6, md0427, md0646, Yampire bore
- *Metacyclops pilbaricus*
    - impact area: number of sites, 2; number of samples, 67: md0499, md0577
- *Microcyclops varicans*
    - reference area: number of sites, 8; number of samples, 73: Browns bore, Calamina bore, kar1, kar2, kar3, kar4, kar6, md0430
- *Thermocyclops* B04

- reference area: number of sites, 1; number of samples, 50: kar5

- *Mesocyclops* sp. indet.
  - reference area: number of sites, 1; number of samples, 50: kar7.

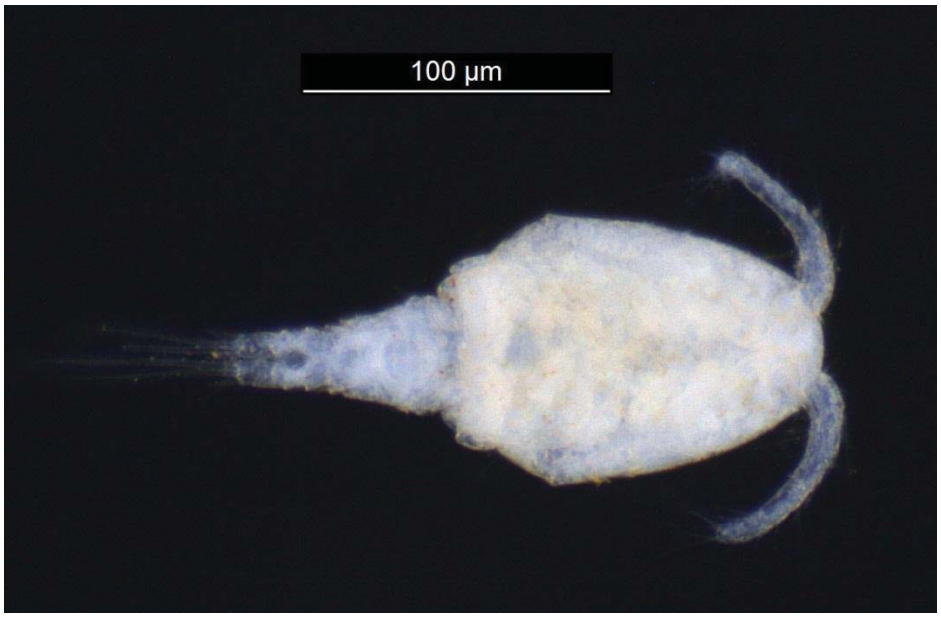

Figure 4-52 Image of *Diacyclops humphreysi humphreysi*

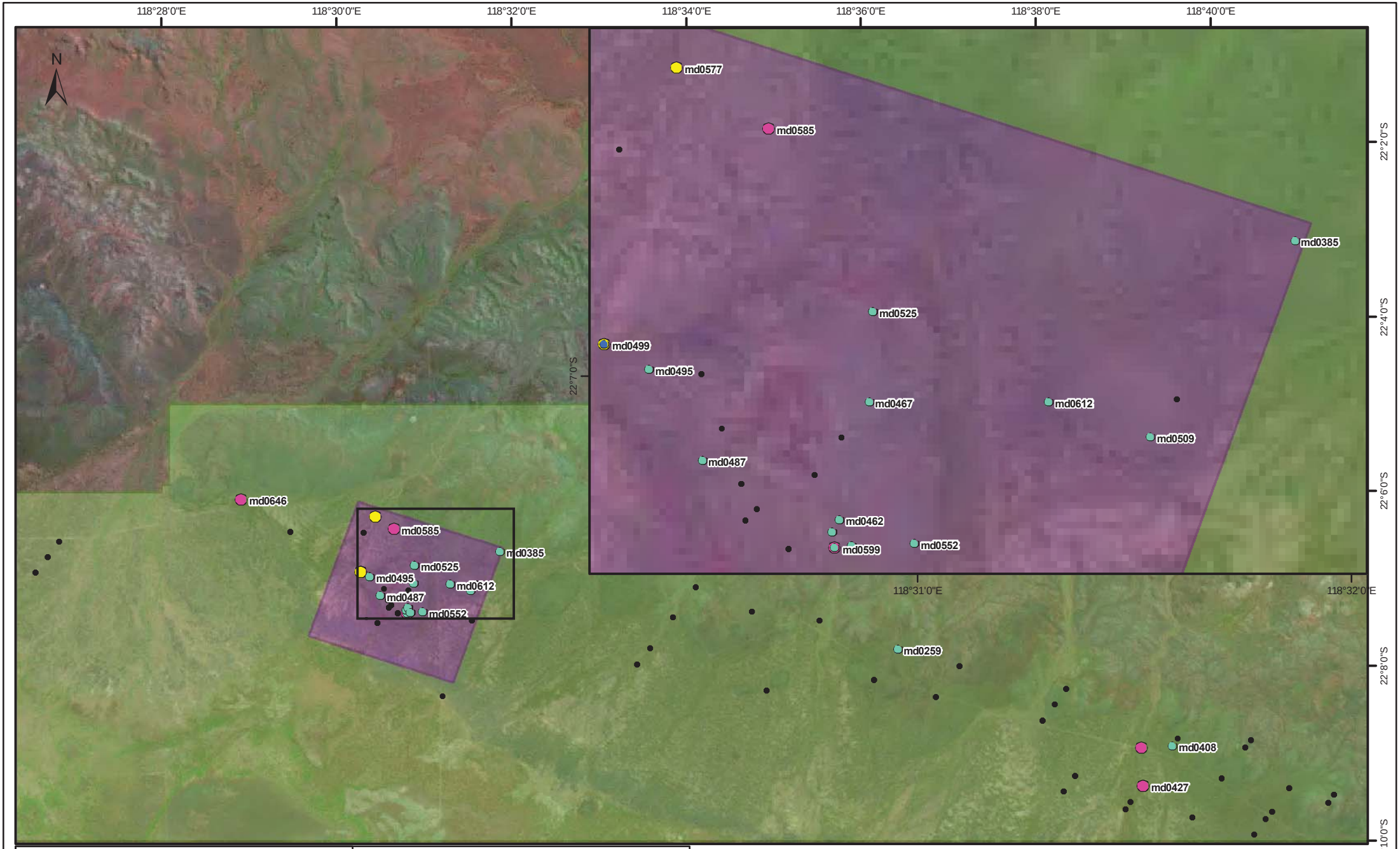

Figure 4-53 Copepod site record for species occuring within the impact area

AUTHOR: ES Volschenk	CLIENT: Hancock Prospecting
DATE 24 May 2012:	Scale: 1:101,991
Coordinate System: Projection: Transverse Mercator; DATUM: GDA94	PROJECT: Mulga Downs Subterranean Survey

PHOENIX ENVIRONMENTAL SCIENCES

0 0.5 1 2 3 4 5 Kilometres

- *Parastenocaris* B18
- *Diacyclops humphreysi humphreysi*
- *Mesocyclops cf brooksi*
- *Metacyclops pilbaricus*
- Survey Bores
- Proposed Impact Area
- Study Area

4.6.5.2 Harpacticoida

Taxonomic resolution: Harpacticoid copepods are very diverse and abundant freshwater crustaceans that are frequently represented in subterranean systems. Stygomorphic species were identified by the absence, or major reduction, of eyes or eye spots. Specimens were identified to species level by Ms Jane McRae (Bennelongia Environmental services). Specimens were identified to morphospecies level. Four (4) species of harpacticoid copepod were identified: *Canthocamptidae* B3 (Figure 4-54), *Dussartstenocaris* sp., *Elaphoidella* B2 and *Parastenocaris* B18.

Genomic taxonomy: all of the harpacticoids were identified to morphospecies level from morphology; therefore, genomic investigation was not deemed necessary.

SRE status: of the four species collected only one *Parastenocaris* B18 is considered to be a potential SRE.

Known distribution: with the exception of *Parastenocaris* B18, the remaining species are known to be widespread in the Pilbara. *Parastenocaris* B18 is currently known only from the study area.

Survey records: specimens were recorded from the following localities:

- *Canthocamptidae* sp. B3
    - impact area: number of sites, 3; number of samples, 11: md0385, md0467, md0525
- *Dussartstenocaris* sp.
    - reference area: number of sites, 1; number of samples, 50: kar6
- *Elaphoidella* B2
    - reference area: number of sites, 1; number of samples, 11: md0429
- *Parastenocaris* B18
    - impact area: number of sites, 1; number of samples, 1: md0499
    - reference area: number of sites, 1; number of samples, 1: md0372.

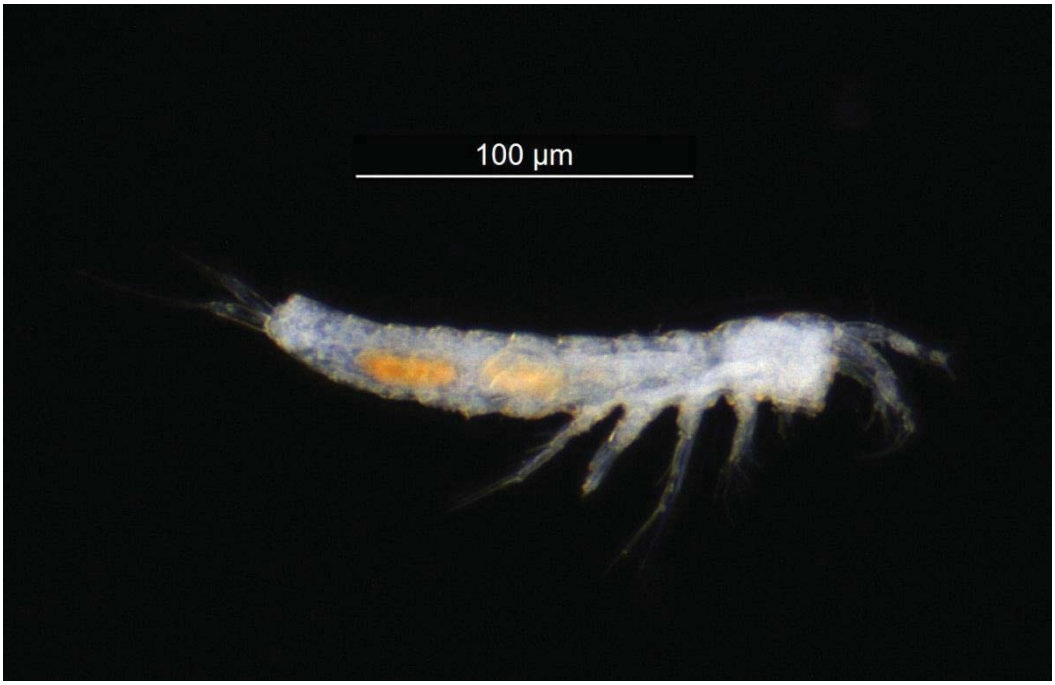

Figure 4-54 Image of *Parastenocaris* sp.

4.6.6 Arthropoda: Ostracoda

4.6.6.1 *Podocopida*

Taxonomic resolution: Ostracods are small bivalve crustaceans that are commonly referred to as seed shrimps (Williams 1981). The ostracod fauna of the Pilbara is very diverse, with numerous epigean and subterranean species known (Eberhard *et al.* 2005; Karanovic 2006). Species level identifications were provided by S. Halse (Bennelongia Environmental Consultants).

Five (5) morphospecies were identified from the family Candonidae: *Areacandona brookanthana, Areacandona* cf *clementia* (Figure 4-55)*, Candonopsis* cf *dedeckkeri, Candonopsis tenuis, Deminutiocandona* sp.,

Six (6) morphospecies from three (3) families were only sampled from regional sites: Candonidae: *Meridiescandona* sp. BOS297; Cyprididae: *Cypridopsis* BOS301, *Sarscypridopsis* sp., *Strandesia* 466; Limnocytheridae: *Limnocythere dorsosicula*.

Genomic taxonomy: specimen identifications were not received in time to enable sequencing to be undertaken on the ostracods.

SRE status: the following species are considered to be likely SRE's on the basis that 70% of Pilbara stygobitic ostracods are SRE's (Eberhard *et al.* 2009): *Candonopsis* cf *dedeckkeri, Deminutiocandona* cf *quasimica.*

Distribution: with the exception of the SRE species noted above, these ostracods are widespread in the Pilbara.

Survey records: specimens were recorded from the following localities (Figure 4-56):

Candonidae

- *Areacandona brookanthana*
    - impact area: number of sites, 1; number of samples, 1: md0495
    - reference area: number of sites, 1; number of samples, 5: kar6
- *Areacandona* cf *clementia*
    - impact area: number of sites, 1; number of samples, 1: md0462
- *Candonopsis* cf *dedeckkeri*:
    - reference area: number of sites, 1; number of samples, 50: Yampire bore
- *Candonopsis tenuis*
    - reference area: number of sites, 2; number of samples, 14: kar5, kar7
- *Deminutiocandona* cf *quasimica*
    - impact area: number of sites, 1; number of samples, 1: md0495
    - reference area: number of sites, 1; number of samples, 1: kar3
- *Meridiescandona* sp. BOS297
    - reference area: number of sites, 1; number of samples, 2: md0429

Cyprididae

- Cyprididae sp. indet.

- reference area: number of sites, 1; number of samples, 1: kar6

- *Cypridopsis* BOS301
  - reference area: number of sites, 1; number of samples, 1: Yampire bore
- *Sarscypridopsis* sp.
  - reference area: number of sites, 1; number of samples, 20: Calamina bore
- *Strandesia* 466
  - reference area: number of sites, 2; number of samples, 2: Calamina bore, Yampire bore

Limnocytheridae

- *Limnocythere dorsosicula*
  - reference area: number of sites, 1; number of samples, 1: Yampire bore.

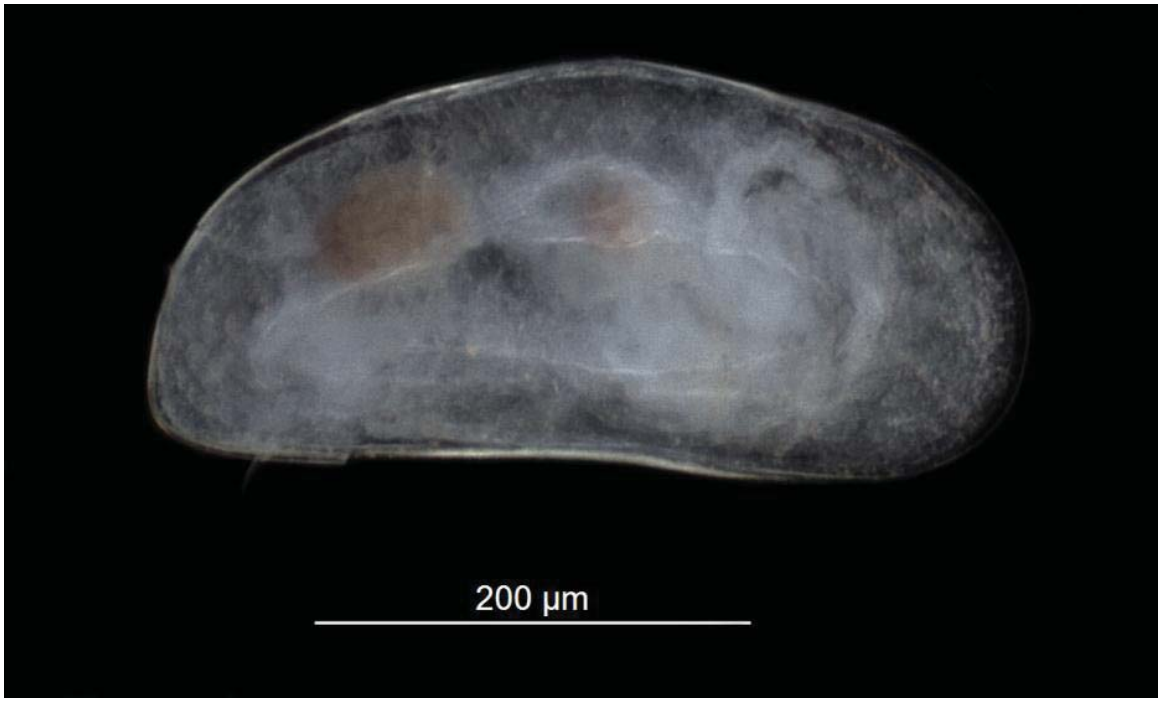

Figure 4-55 Image of *Areacandona* sp.

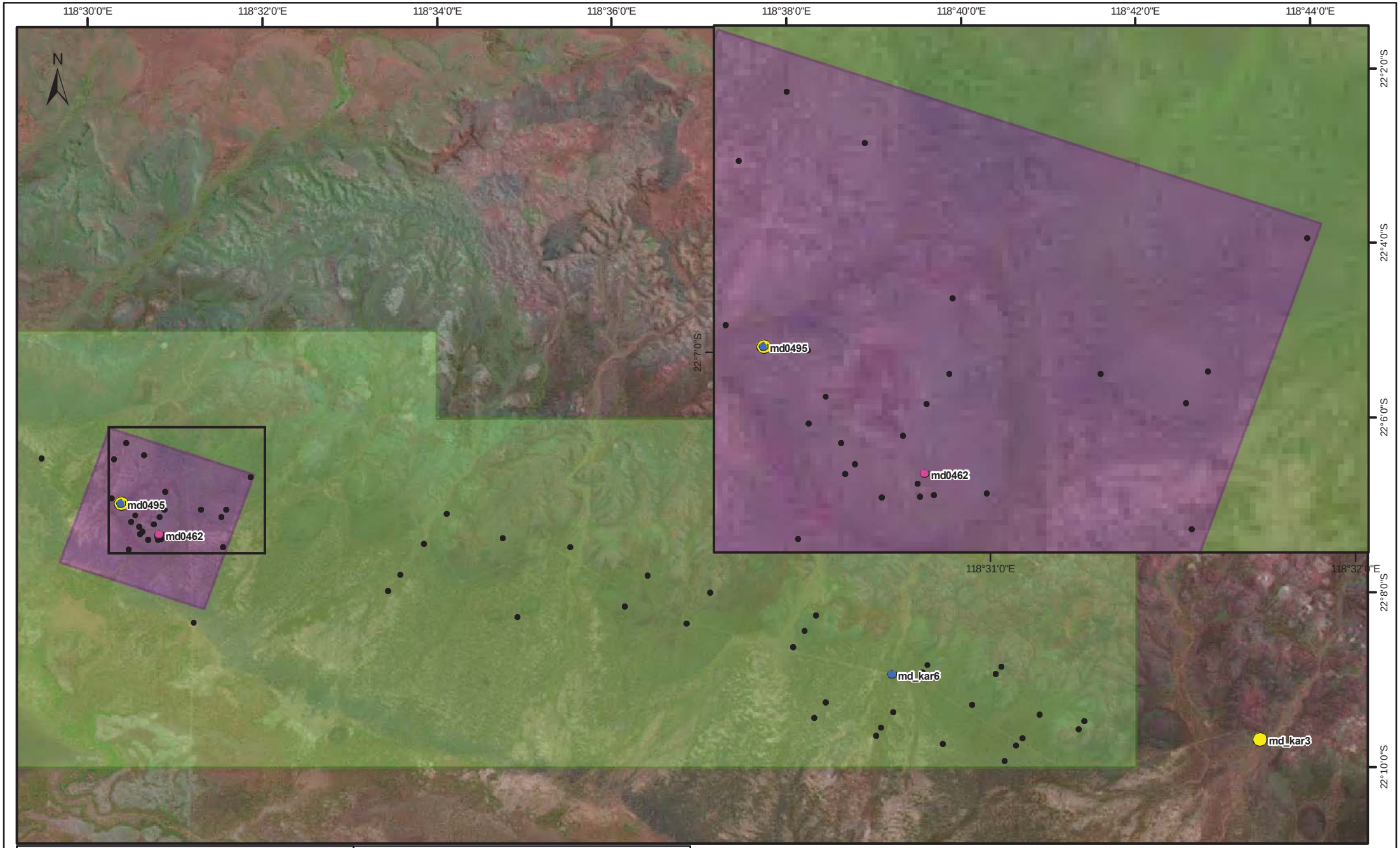

Figure 4-56 Ostracod site record for species occuring within the impact area

AUTHOR: ES Volschenk	CLIENT: Hancock Prospecting
DATE 24 May 2012:	Scale: 1:101,991
Coordinate System: Projection: Transverse Mercator; DATUM: GDA94	PROJECT: Mulga Downs Subterranean Survey

PHOENIX ENVIRONMENTAL SCIENCES

0 0.5 1 2 3 4 5 Kilometres

- *Areacandona brookanthana*
- *Areacandona* cf *clementia*
- *Deminutiocandona* cf *squasimica*
- Survey Bores
- Proposed Impact Area
- Study Area

4.7 CHARACTERISATION OF SUBTERRANEAN HABITAT

Most geologies in the Pilbara are very highly likely to support rich stygofauna and troglofauna assemblages (EPA 2003, 2007). The surface geology of the survey area (impact and reference sites) is dominated by alluvial fans and lateritic outcroppings. In order to examine possible correlation between species and geologies, the exploration bore logs were related to troglobitic species richness and distribution.

4.7.1 Geological strata and troglobite distribution

Drill log data were provided by Hancock and indicate a fairly homogeneous spread of geologies, with almost all bores containing the same geological strata types above the standing water table. An assessment of species richness and geology (Table 4-5; Figure 4-57) showed no obvious support for an association between any specific geological formations identified in the drill records and troglobite species distributions.

Table 4-5 Cross tabulation of troglobitic species and geologies (<25 m deep) present in the bores that the species were sampled from

Troglobite species	BIF/shale - nammuldi	Geothetic zone	Tertiary alluvial	Jerrina	Calcrete
Anapistula 'MH1'	X	X	X		
Anillini 'MH1'	X	X	X	X	
Atelurinae 'MH1'	X	X		X	
Cormocephalus 'MH1'			X		
Cryptops 'MH1'	X	X			
Cryptops 'MH2'	X	X	X		
Indohya 'MH1'	X				
Japygidae 'MH1'			X	X	
Japygidae 'MH2'	X		X		
Meenoplidae 'USF'	X	X		X	
Meenoplidae 'widespread'	X				
Nocticola 'MH1'	X	X	X		
Palpigradi 'MH1'		X			
Palpigradi 'MH2'	X				
Parajapygidae 'MH1'	X	X	X		

Troglobite species	BIF/shale - nammuldi	Geothetic zone	Tertiary alluvial	Jerrina	Calcrete
Pauropoda 'MH1'	X	X		X	
Pauropoda 'MH2'	X	X	X	X	
Pauropoda 'MH3'		X	X		
Polyxenidae PXD1'	X	X	X	X	X
Projapygidae 'MH1'	X	X	X		
Schizomida 'MH1'	X	X	X		
Schizomida 'MH2'	X	X			
Symphyla 'MH1'	X		X		
Trinemura 'MH1'	X	X	X	X	
Trinemura 'MH2'	X	X	X	X	
Troglarmadillo 'MH1'		X			
Tyrannochthonius 'MH1'	X	X	X		

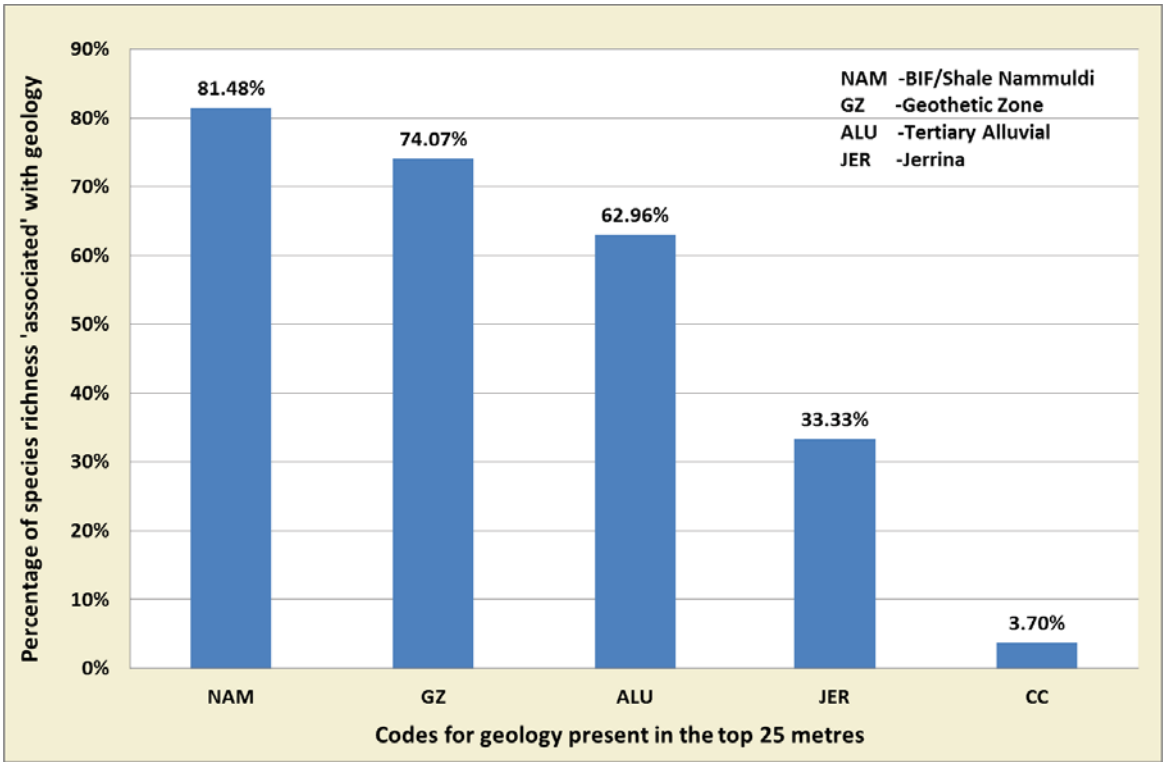

Figure 4-57 Histogram of percentage of troglobite species richness associated with each geology (<25 m)

4.7.2 Distribution of 'widespread' species

In order to try and understand connectivity between habitats, the distributions of species that were sampled from five or more different sites were examined. Of the 27 troglofauna species identified, five species were identified from five or more sites (Figure 4-58; Figure 4-59). The distribution of these 'widespread' species was related to surface geology data from the Geological Survey of Western Australia (GSWA). All of these species were found in association with multiple surface geologies, indicating that no clear affinity with any one surface geology type (Figure 4-59). This pattern indicates one of the following hypotheses:

- these species are either highly mobile and can move through the geologies, but a preferred geology may exist; or
- that they have no preference for any particular geology and are resident in all of them.

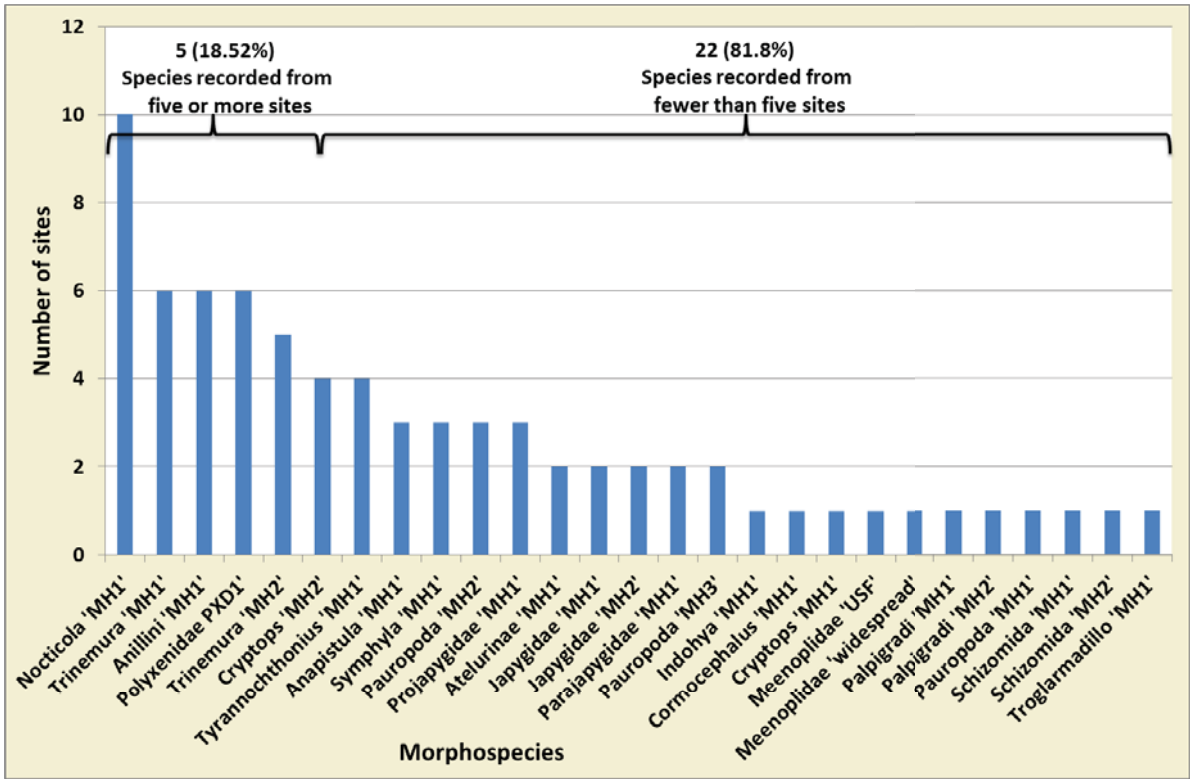

Figure 4-58 Histogram of troglobite species and the number of sites (bores) from which these were sampled

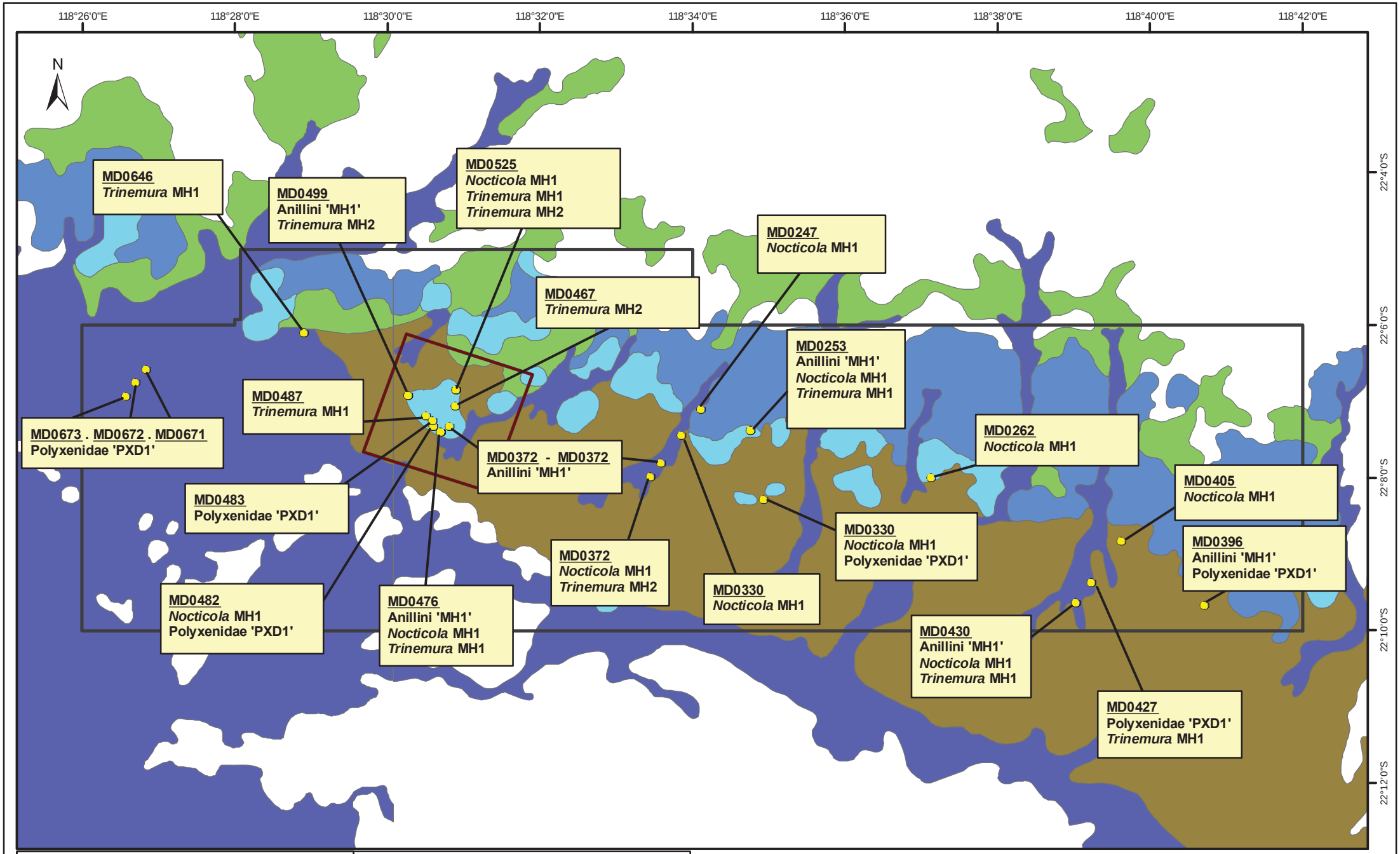

Figure 4-59 Distribution of species found within area of development that are also found in five or more sites.

AUTHOR: ES Volschenk	CLIENT: Hancock Prospecting
DATE: 21 September 2012	Scale: 1:116,788
Coordinate System: Projection: Transverse Mercator; DATUM: GDA94	PROJECT: Mulga Downs Subterranean Survey

PHOENIX ENVIRONMENTAL SCIENCES

0 0.5 1 2 3 4 5 Kilometres

4.7.3 Distribution and composition of troglofauna communities

The distribution and richness (species richness) of troglobite communities (sites where three or more species were recorded) was examined in relation to the surface geology. Troglobite 'communities' were categorised into 3 types:

- comprising 1-2 species
- comprising 3-9 species
- comprising more than 10 species.

Surface geology data were graphed with the three community richness categories (Figure 4-60). Troglobite communities of two or less species were most frequent (11) in alluvial strata, while six (6) communities were associated with alluvium-colluvium, five (5) were associated with hematite-geothite, and two (2) with Marra Mamba iron (Figure 4-61). Troglobite communities comprising three or more species were most frequent (7) in hematite-geothite, while the remaining geologies had two (2) in each (Figure 4-61). Both communities that were comprised of more than 10 species were associated with hematite-geothite.

In order to better understand the distribution of troglobite species the distributions of species found at three or more sites were examined in relation to surface geology (Figure 4-60). All of these species were found in multiple surface geologies, indicating no specific association with surface geology.

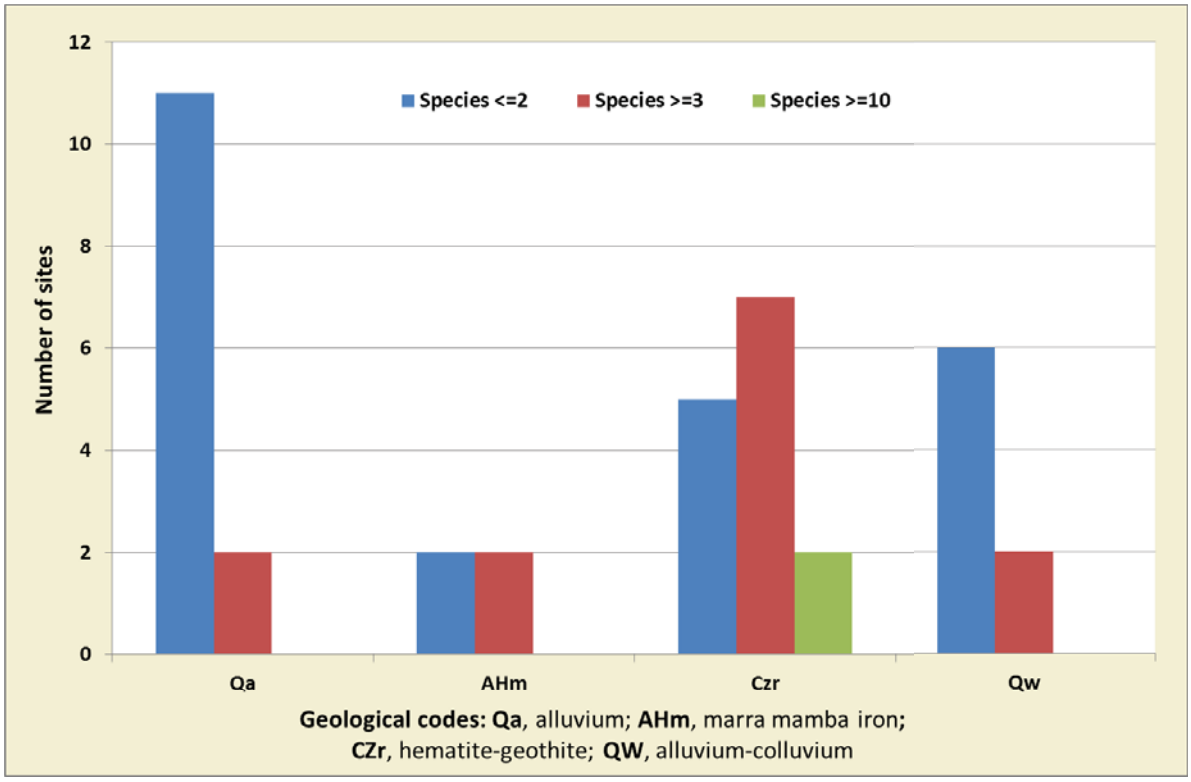

Figure 4-60 Histogram of the number troglobite communities recorded from each of the present surface geologies.

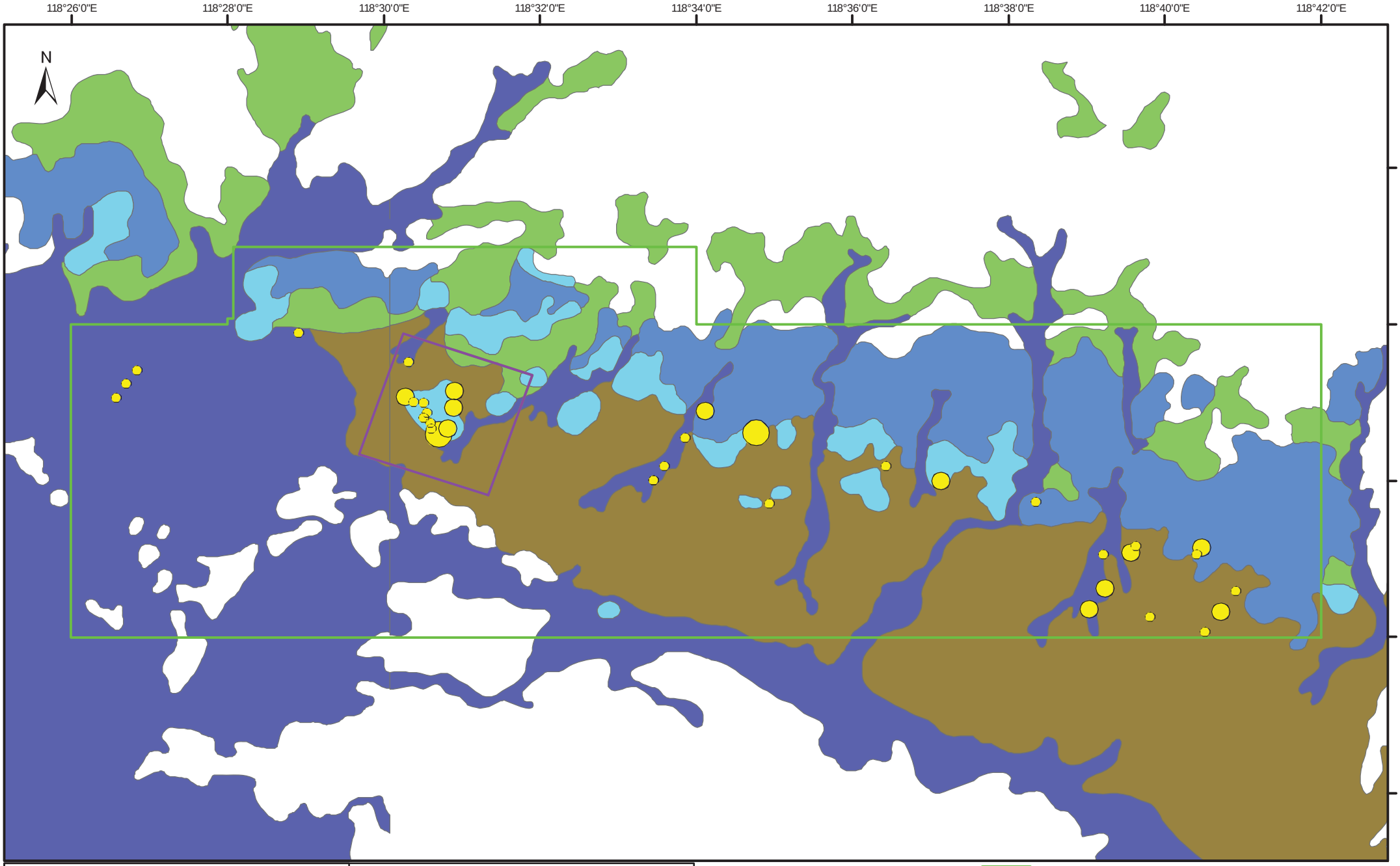

Figure 4-61 Map of troglofauna community richness relative to surface geology.

AUTHOR: ES Volschenk	CLIENT: Hancock Prospecting
DATE: 27 September 2012	Scale: 1:116,788
Coordinate System: Projection: Transverse Mercator; DATUM: GDA94	0 0.5 1 2 3 4 5 Kilometres

PHOENIX ENVIRONMENTAL SCIENCES

PROJECT: Mulga Downs Subterranean Survey

4.8 SURVEY LIMITATIONS

4.8.1 Survey intensity

The intensity of this survey exceeded the minimum intensity outlined in Guidance Statement 54a for troglobite surveys: 50 troglofauna trap samples were collected within the impact area to augment the survey previously undertaken by Ecologia (61 samples); an additional 50 stygofauna netting samples and 51 bore scrape samples yielded numerous stygofauna records to increase the subterranean fauna survey effort and coverage (Appendix 2 shows a detailed list of samples and types taken from each survey bore).

Despite sampling subterranean fauna above the minimum recommended target in Guidance Statement 54a (95% of extrapolated species richness):

- Observed troglofauna species richness ranged between 74%-87% of extrapolated species richness (Figure 4-3)
- Observed stygofauna species richness ranged between 62%-92% of extrapolated species richness (Figure 4-4).

With the exception of one diversity estimation (Figure 4-4: stygofauna bootstrap), all of the extrapolations indicated that less than 90% of the species richness was achieved. This result is typical for subterranean fauna studies in the Pilbara and indicates the need for further surveys to reach appropriate sampling intensity (Subterranean Ecology 2010).

The species accumulation curves support the diversity estimation data (Figure 4-2). The combined accumulation curves depict a trend of increasing numbers of species with increased sampling effort (as expected), but the curves do not plateau which indicates that further sampling is required.

4.8.2 Bore hole condition

Guidance Statement 54a (EPA 2007) includes a requirement for all bores sampled for stygofauna to be at least six months old to allow for colonisation. All of the stygofauna bore samples in this survey were greater than six months in age. All bores found to contain anaerobic water or oil were excluded from sampling.

4.8.3 Taxonomic resolution and regional context

Guidance Statement 54a (EPA 2007) includes a requirement for specimens to be identified to species or morphospecies level. In the absence of specialists to undertake morphological identifications, species boundaries need to be assessed on genetic data. All target species were assessed using genomic analyses, therefore fully meeting the requirements of the EPA.

4.8.4 Seasonality

Guidance Statement 54a (EPA 2007) advises a seasonal survey approach; however if a single season of surveying is implemented, it must occur over the ‘wet’ season. This survey was undertaken over the wet season (from October 2011 to January 2012) thereby meeting this requirement of the guidance. Rainfall well above average was received during January (Figure 4-1). Such high rainfalls often impact negatively on troglofauna trapping, however they appear to work more favourably for scrape sampling. We do not believe that the survey was compromised by the high levels of rainfall observed in January.

5 DISCUSSION

5.1 TROGLOFAUNA SPECIES RECORDED WITHIN IMPACT AREAS

A total of 27 target species were sampled (Table 4-1 and Figure 4-6). Of these, 14 (51.8% of the species recorded) of the target species appear to be rare, i.e. single or double records (Figure 4-6); these are significant since distributions cannot be interpreted from them. Twenty four (24) of the species, representing 88.9% of the troglofauna species richness, appear to be new species (indicated by the suffix 'MH').

Six SRE troglofauna species were only recorded in the proposed impact area. All of these are represented by single or double records and all appear to be new species:

- Palpigradi 'MH1' (single record)
- Schizomida 'MH2' (single record)
- *Cryptops* 'MH1' (single record)
- Parajapygidae 'MH1' (double records)
- *Troglarmadillo* 'MH1' (single record).

Eleven morphospecies were recorded from both inside and outside the impact area, and five of these species were recorded from five or more sites. The records suggest that these species are distributed across the study area. In several of species targeted for genomic investigation, genetic diversity was higher than would be expected within a population, suggesting that the troglofauna populations may have been recently fragmented and undergoing speciation (Appendix 4): *Nocticola* MH1; Anillini MH1; Parajapygidae MH1. This is an indication that there may be geological barriers to dispersal for some species within the study area, and that some populations may be in the process of speciation (Appendix 4).

5.2 STYGOFAUNA SPECIES RECORDED WITHIN IMPACT AREAS

A total of 24 target taxa were sampled (Table 4-1 and Figure 4-40). Of these, eight (28.5% of the species recorded) of the target species are represented by single and double records (Figure 4-40) and therefore cannot be used to determine species distributions. Six (6) of these species, representing 25% of the species richness, appear to be new species.

One stygofauna species was only recorded within the impact area: Parabathynellidae 'MH3' (from one site). Since the proposed mine will not go below the water table, no direct impact is likely to occur.

The stygofauna results indicate that lateral connectivity and transmissivity of the aquifer is likely, but this cannot be confirmed until hydrological modelling has been completed. The anomalous presence of Parabathynellidae 'MH3' from a single bore hole may represent penetration of that bore onto a deeper aquifer.

5.3 FOLLOW-UP SAMPLING

One of the aims of this survey was to obtain additional specimens of subterranean species previously sampled by Ecologia: polyxenid millipede, *Nocticola* species and a species of Parajapygid dipluran. Ecologia did not sequence any specimen vouchers so genomic comparison is not possible.

It is likely that the Polyxenid, *Nocticola* and Parajapygid species sampled by Ecologia are conspecific with Polyxenidae 'PXD1', *Nocticola* 'MH1' and Parajapygidae 'MH1' respectively, since no other similar taxa resulted from our survey.

The results of this survey expand the distribution of both *Nocticola* and the polyxenid found by Ecologia beyond the impact area at Mulga Downs. The only Parajapygidae collected in our survey were restricted to the impact area, as was the single record from Ecologia's survey.

5.4 SUBTERRANEAN HABITATS AND TROGLOFAUNA DISTRIBUTION PATTERNS

Geological data provided by Hancock identified three geological strata present within most of the survey bores from which troglofauna were sampled: BIF/Shale nammuldi, geothetic zone and Tertiary alluvial (Figure 4-57). No clear association between any of these strata can be made with troglofauna because the troglofauna survey methods employed do not discriminate between geological strata within a survey bore. Each survey bore functions as a vertical corridor through which troglofauna can travel, so even if troglofauna were sampled from a particular depth, there can be no assurances that they did not migrate through the bore from above or below the survey point in the bore. Troglofauna could therefore be associated with any one (or more) strata recorded from each bore.

The surface geology data from GSWA provide an overall description of the dominant surface geology and may represent a more accurate means of interpreting troglofauna distribution patterns. When the relationship between troglofauna community richness, and surface geology was examined, bores containing higher diversities of troglofauna were most frequently found in hematite-geothite deposits (Figure 4-60). Bores with only one or two troglofauna species records were most frequently associated with alluvial deposits, but these species were also well represented in alluvial-colluvial and hematite-geothite deposits (Figure 4-60).

The distribution of the five 'widespread' species (i.e. occurring at five or more sites) also demonstrates that some species do not appear to be restricted to any one particular surface geology type (Figure 4-59). These particular species either represent highly mobile species that can move through more than one surface geology (Figure 4-59), or they represent species that do not have a specific association with strata and therefore geology plays a less significant role in habitat preference. The distributions of these species also clearly demonstrate that connectivity exists between the alluvial, alluvial-colluvial and hematite-geothite strata.

The higher diversity of troglofauna within the hematite-geothite surface geology suggests that this geology is the primary habitat of the troglofauna at Mulga Downs. Most of the more widespread species occurred within hematite-geothite and alluvial and alluvial-colluvial surface geologies, demonstrating that these particular species are able to move between the geologies. It seems likely that while the hematite-geothite deposits form the primary habitat, the alluvial and alluvial-colluvial deposits represent habitats through which some troglofauna can move and disperse.

Most of the species sampled in this survey were recorded from three or fewer sites. These species appear to be rare and additional data are required for these species in order to model the distributions of these species. These species may have similar widespread distributions to the five more widespread noted above. Alternatively they may have entirely different distribution patterns and may represent much more locally endemic forms. There is insufficient data to demonstrate the close association between different troglofauna species found during this survey; therefore, the use of surrogate species to infer distributions of species sampled in low numbers is not warranted.

Genomic assessments of the recorded troglofauna demonstrated that three (11.1%) of the 27 species sampled represent regionally widespread species: Polyxenidae 'PXD1', Meenoplidae

'widespread' and Meenoplidae 'USF'. The remainder (88.9%) are comprised of species that have not been previously recorded in the Pilbara. This high level of local endemicity indicates that barriers to the dispersal of these species must exist outside of the study area.

The geologies surveyed are all at the footslope of the Chichester range, which is characterised by Marra Mamba iron formations (according to the GSWA surface geology dataset) that also occur within the study area. No bores were surveyed within the Marra Mamba and therefore the fauna associated with this surface geology is not known. The apparent association of troglofauna with hematite-geothite formation suggests that the Marra Mamba iron formations may be just as significant, if not more so, as troglofauna habitat. It is possibly/likely that connectivity exists between these two geologies via the alluvial and alluvial-colluvials, and that there is overlap in fauna assemblages. Surveys are needed within Marra Mamba iron surface geology in order to confirm relationships with its subterranean fauna and that of the surrounding geology.

5.5 IMPACT ASSESSMENT

In assessing development proposals, the EPA's broad objective for subterranean fauna is to ensure there is adequate protection for important habitats for subterranean fauna and that no subterranean fauna species is threatened with extinction. Accordingly, the main aim of this assessment was:

- to determine whether any subterranean fauna species may be restricted solely to the proposed impact areas for the Project and therefore be at risk of extinction from the Project
- determine whether adequate habitat exists outside the proposed impact areas for species recorded within the impact areas.

The proposed impact area for the Project in regard to subterranean fauna has been defined (Figure 1-1). Based on the limited geological and biological data for the study area, the following impacts may affect subterranean fauna:

- Direct loss of troglofauna habitat – excavation of the mine pits will result in direct removal of up to 284 ha of troglofauna habitat which is a primary impact (see section 2.3.4. Most subterranean fauna species were found outside of the area of direct impact, although six troglofauna species were only recorded in the impact area.
- Sediment compaction and/or vibration – there may be some minor vibration and/or compaction impacts on subterranean habitat from the Project (e.g. blasting); however, the actual impact of these effects have not been investigated.
- Nutrient starvation of subterranean habitat – removal of surface vegetation and excavation of the mine pits may lead to a localised reduction in the inflow of nutrients to subterranean habitats underlying the direct impact area, which may lead to reduction in abundance and diversity.
- Contamination – spills (e.g. diesel fuel) may lead to localised contamination of subterranean habitat. As no processing will be undertaken onsite, this potential impact is likely to be minor in scale and restricted to refuelling stations.

Consideration should be given to re-instating nutrient flows where possible, for example establishing vegetation on the proposed waste stock pile. Contamination for spills should be managed as standard operating procedures, for example strategic placement and use of bunds around liquid chemicals. Periodic monitoring of soil and groundwater is recommended to ensure that such contaminants stay below acceptable levels.

As the mine is not proposed to go below the water table, dewatering is not likely to be an issue for subterranean fauna. Specifically, the Project will not result in the direct loss of stygofauna habitat or indirect impacts to troglofauna habitat from altered humidity (see section 2.3.4).

Small-scale groundwater extraction (e.g. for dust suppression during construction) is unlikely to have a significant impact on subterranean fauna.

5.6 RECOMMENDATIONS

5.6.1 Filling data gaps

This survey yielded vastly different results to those previously recorded in the study area, largely attributed to the use of the bore scraping method of sampling which captured a greater number and diversity of subterranean fauna.

The minimum sampling intensity recommended in GS54a was exceeded and the results of the study indicate the presence of a complex troglofauna community; however, insufficient data were obtained from this study to understand how these species relate to each other, or how these species relate to surface geology. The results are complicated by the following:

- a high proportion of single and double records (51.8%)
- a high proportion of new species (88.8%)
- the indication of restricted gene flow, within three species, from troglofauna sampled within the impact and reference areas.

Six potential SRE troglofauna and one potential SRE stygofauna are only known from the proposed impact area. While these species may occur beyond the proposed impact area, broader distributions cannot be confirmed based on current knowledge.

Only one potential SRE stygofauna species was recorded from the proposed impact area. Given the anomalous nature of this species records from a single site, where all other stygofauna were more widely distributed, this species may also represent fauna from a deeper aquifer intersected by this particular bore. The proposed impact area will not extend below the water table, and therefore impacts to stygofauna are likely to be negligible.

Data from additional surveys would improve on the following issues:

- paucity of records (singletons and doubletons)
- understanding of these species and their distribution in relation to surface geology.

Targeted sequencing of the most widespread taxa would also improve knowledge on the extent of the gene flow restrictions occurring at Mulga Downs and its surrounds and therefore define local endemism more clearly.

6 REFERENCES

Barr, T. C. 1968. Cave ecology and the evolution of troglobites. *In:* Dobzhansky, T., Hecht, M. K. & Steere, W. C. (eds) *Evolutionary biology*. North-Holland, Amsterdam, pp. 35–102.

Barranco, P. & Harvey, M. S. 2008. The first indigenous palpigrade from Australia: a new species of *Eukoenenia* (Palpigradi: Eukoeneniidae). *Invertebrate Systematics* **22**: 227–233.

Beesley, P. L., Ross, G. J. B. & Wells, A. 1998. *Mollusca: the southern synthesis*. CSIRO Publishing, Collingwood, Vic.

Bennelongia. 2007. *Stygofauna sampling results for the Devil Creek Development Project, Apache Energy Ltd, at 40 Mile Beach*. Bennelongia Environmental Consultants, Jolimont, WA. Unpublished report prepared for Apache Energy Ltd.

Bennelongia. 2010. *Troglofauna assessment for the Solomon Project: Firetail Deposits*. Bennelongia Environmental Consultants Pty Ltd, Jolimont, WA. Unpublished report prepared for Fortescue Metals Group Ltd.

Biota. 2008. *Marandoo Mine Phase 2 subterranean fauna asessment*. Biota Environmental Sciences Pty Ltd, West Leederville, WA. Unpublished report prepared for Rio Tinto.

BOM. 2012. *Climate statistics for Australian locations*. Commonwealth of Australia, Bureau of Meterology. Available at: http://www.bom.gov.au/climate/data/ (accessed ADD DATE).

Colwell, R. K. & Coddington, J. A. 1994. Estimating terrestrial biodiversity through extrapolation. *Philosophical Transactions of the Royal Society of London B Biological Sciences* **345**: 101–118.

Cracraft, J. 1982. Geographic differentiation, cladistics, and vicariance biogeography: reconstructing the tempo and mode of evolution. *American Zoologist* **22**: 411–424.

Cracraft, J. 1983a. Speciation and its ontology: the empirical consequences of alternative species concepts for understanding patterns and processes of differentiation. *In:* Otte, D. & Endler, J. A. (eds) *Speciation and its consequences*. Sinauer Associates, Sunderland, MA, pp. 28–59.

Cracraft, J. 1983b. Species concepts and speciation analysis. *In:* Johnston, R. F. (ed.) *Current ornithology*. Plennum Press, New York and London, pp. 159–187.

Eberhard, S. M., Halse, S. A. & Humphreys, W. F. 2005. Stygofauna in the Pilbara region, north-west Western Australia: a review. *Journal of the Royal Society of Western Australia* **88**: 167–176.

Eberhard, S. M., Halse, S. A., Williams, M. R., Scanlon, M. D., Cocking, J. & Barron, H. J. 2009. Exploring the relationship between sampling efficiency and short-range endemism for groundwater fauna in the Pilbara region, Western Australia. *Freshwater Biology* **54**: 885–901.

Ecologia. 2011. *Murray Hill Troglofauna Survey*. Ecologia Environment Pty Ltd, West Perth, WA. Unpublished report prepared for Hancock Prospecting.

Edward, K. L. & Harvey, M. S. 2008. Short-range endemism in hypogean environments: the pseudoscorpion genera *Tyrannochthonius* and *Lagynochthonius* (Pseudoscorpiones: Chthoniidae) in the semiarid zone of Western Australia. *Invertebrate Systematics* **22**: 259–293.

EPA. 2003. *Guidance Statement No. 54: Consideration of subterranean fauna in groundwater and caves during environmental impact assessment in Western Australia*. Environmental Protection Authority, Perth, WA.

EPA. 2007. *Guidance Statement Number 54a. Sampling methods and survey considerations for subterranean fauna in Western Australia (Technical appendix to Guidance Statement No. 54)*. Environmental Protection Authority, Perth, WA.

Finston, T. L., Bradbury, J. H., Johnson, M. S. & Knott, B. 2004. When morphology and molecular markers conflict: a case history of subterranean amphipods from the Pilbara, Western Australia. *Animal Biodiversity and Conservation* **27**: 83–94.

Finston, T. L., Francis, C. J. & Johnson, M. S. 2009. Biogeography of the stygobitic isopod *Pygolabis* (Malacostraca: Tainisopidae) in the Pilbara, Western Australia: evidence for multiple colonisations of the groundwater *Molecular Phylogenetics and Evolution* **52**: 448–460.

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

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

Hamilton-Smith, E. & Eberhard, S. M. 2000. Conservation of cave communities in Australia. *In:* Wilkens, H., Culver, D. C. & Humphreys, W. F. (eds) *Ecosystems of the World Vol. 30 - Subterranean ecosystems*. Elsevier, Amsterdam, pp. 647–664.

Harvey, M. S. 1992. The Schizomida (Chelicerata) of Australia. *Invertebrate Taxonomy* **6**: 77–129.

Harvey, M. S. 1993. The systematics of the Hyidae (Pseudoscorpionida: Neobisioidea). *Invertebrate Systematics* **7**: 1–32.

Harvey, M. S. 2001. The Schizomida (Arachnida) of the Seychelle Islands. *Invertebrate Taxonomy* **15**: 681–693.

Harvey, M. S. 2002a. The neglected cousins: what do we know about the smaller arachnid orders? *Journal of Arachnology* **30**: 357–372.

Harvey, M. S. 2002b. Short-range endemism among the Australian fauna: some examples from non-marine environments. *Invertebrate Systematics* **16**: 555–570.

Harvey, M. S. 2011. Two new species of *Synsphyronus* (Pseudoscorpiones: Garypidae) from southern Western Australian granite landforms. *Records of the Western Australian Museum* **26**: 11–22.

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.

Harvey, M. S. & Humphreys, W. F. 1995. Notes on the genus *Draculoides* Harvey (Schizomida: Hubbardiidae), with the description of a new troglobitic species. *Records of the Western Australian Museum, Supplement* **52**: 183–189.

Harvey, M. S. & Leng, M. C. 2008. The first troglobitic pseudoscorpion from the family Olpiidae (Pseudoscorpiones), with remarks on the composition of the family. *Records of the Western Australian Museum* **24**: 387–394.

Harvey, M. S., Rix, M. G., Framenau, V. W., Hamilton, Z. R., Johnson, M. S., Teale, R. J., Humpherys, G. & Humphreys, W. F. 2011. Protecting the innocent: studying short-range endemic taxa enhances conservation outcomes. *Invertebate Sytematics* **25**: 1–10.

Harvey, M. S. & Volschenk, E. S. 2007a. A review of some Australasian Chernetidae: *Sundochernes*, *Troglochernes* and a new genus (Pseudoscorpiones). *Journal of Arachnology* **35**: 238–277.

Harvey, M. S. & Volschenk, E. S. 2007b. Systematics of the Gondwanan pseudoscorpion family Hyidae (Pseudoscorpiones: Neobisioidea); new data and a revised phylogenetic hypothesis. *Invertebrate Systematics* **21**: 365–406.

Harvey, M. S. & Yen, A. L. 1989. *Worms to wasps. An illustrated guide to Australia's terrestrial invertebrates*. Oxford University Press, South Melbourne, Vic.

Hebert, P. D. N., A., C., Ball, S. L. & de Waard, J. R. 2003a. Biological identifications through DNA barcodes. *Proceedings of the Royal Society London B* **270**: 313–321.

Hebert, P. D. N., Ratnasingham, S. & de Waard, J. R. 2003b. Barcoding animal life: Cytochrome c oxidase subunit 1 divergences among closely related species. *Proceedings of the Royal Society London B, Supplement* **270**: 96–99.

Holsinger, J. R. 2000. Ecological derivation, colonization and speciation. *In:* Wilkens, H., Culver, D. C. & Humphreys, W. F. (eds) *Ecosystems of the World Vol. 30 - Subterranean ecosystems*. Elsevier, Amsterdam, pp. 399–415.

Howarth, F. G. 1983. Ecology of cave arthropods. *Annual Review of Entomology* **28**: 365–389.

Howarth, F. G. 1993. High-stress subterranean habitats and evolutionary change in cave-inhabiting arthropods. *American Naturalist, Supplement* **142**: 565–577.

Humphreys, W. F. 1991. Experimental re-establishment of pulse-driven populations in a terrestrial troglobite community. *Journal of Animal Ecology* **60**: 609–623.

Humphreys, W. F. 2000. Background and glossary. *In:* Wilkens, H., Culver, D. C. & Humphreys, W. F. (eds) *Ecosystems of the World Vol. 30 - Subterranean ecosystems*. Elsevier, Amsterdam, pp. 3–14.

Humphreys, W. F. 2008. Rising from Down Under: developments in subterranean biodiversity in Australia from a groundwater fauna perspective. *Invertebrate Systematics* **22**: 85–101.

Karanovic, T. 2006. Subterranean copepods (Crustacea, Copepoda) from the Pilbara Region in Western Australia. *Records of the Western Australian Museum, Supplement* **70**: 239.

Keable, S. J. & Wilson, G. D. F. 2006. New species of *Pygolabis* Wilson, 2003 (Isopoda, Tainisopidae, Crustacea) from Western Australia. *Zootaxa* **1116**: 1–27.

Köhler, F. & Johnson, M. S. 2012. Species limits in molecular phylogenies: a cautionary tale from Australian land snails (Camaenidae: *Amplirhagada* Iredale, 1933). *Zoological Journal of the Linnean Society* **165**: 337–362.

Leighton, K. A. 2004. Climate. *In:* van Vreeswyk, A. M. E., Payne, A. L., Leighton, K. A. & Hennig, P. (eds) *Technical Bulletin 9. An inventory and condition survey of the Pilbara region, Western Australia*. Department of Agriculture, Government of Western Australia, South Perth, WA, pp. 19–38.

Main, B. Y. 1985. Arachnida: Mygalomorphae. *In:* Walton, D. W. (ed.) *Zoological catalogue of Australia Volume 3; Arachnida: Mygalomorphae, Araneomorphar in part, Pseudoscorpionida, Amblypygi and Palpigradi.* Commonwealth of Australia, Canberra, ACT, pp. 1–48.

McKenzie, N. L., van Leeuwen, S. & Pinder, A. M. 2009. Introduction to the Pilbara Biodiversity Survey, 2002–2007. *Records of the Western Australian Museum, Supplement* **78**: 3–89.

Moir, M. L., Brennan, K. E. C. & Harvey, M. S. 2009. Diversity, endemism and species turnover of millipedes within the south-western Australian global biodiversity hotspot. *Journal of Biogeography* **36**: 1958–1971.

Pesce, G. L. & De Laurentiis, P. 1996. Copepods from ground waters of Western Australia. III: *Diacyclops humphreysi* n. sp. and comments on the *Diacyclops crassicaudis*-complex (Crustacea: Copepoda: Cyclopidae). *Crustaceana* **69**: 524–531.

Ponder, W. F. & Colgan, D. J. 2002. What makes a narrow-range taxon? Insights from Australian freshwater snails. *Invertebrate Systematics* **16**: 571–582.

Poulson, T. L. & Lavoie, K. H. 2000. The trophic basis of subsurface ecosystems. *In:* Wilkens, H., Culver, D. C. & Humphreys, W. F. (eds) *Ecosystems of the World Vol. 30 - Subterranean ecosystems*. Elsevier, Amsterdam, pp. 231–250.

Rupert, E. & Barnes, R. D. 1994. *Invertebrate Zoology*. Saunders College Publishing, Philadelphia.

Subterranean Ecology. 2010. *Fortescue Metals Group Solomon Project: Kings Deposits subterranean fauna survey and assessment*. Subterranean Ecology Pty Ltd, Stirling, WA. Unpublished report prepared for Fortescue Metals Group Ltd.

Volschenk, E. S. & Prendini, L. 2008. *Aops oncodactylus*, gen. et sp. nov., the first troglobitic Urodacid (Urodacidae: Scorpiones), with a re-assessment of cavernicolous, troglobitic and troglomorphic scorpions. *Invertebrate Systematics* **22**: 235–257.

Williams, W. D. 1981. *Australian freshwater life. The invertebrates of Australian inland waters. 2nd edition*. The MacMillan Company of Australia Pty Ltd, South Melbourne, Vic.

Wilson, G. D. F. 2003. A new genus of Tainisopidae fam. nov. (Crustacea: Isopoda) from the Pilbara, Western Australia. *Zootaxa* **245**: 1–20.

Appendix 1 Site localities and coordinates (datum, GDA94)

Site code	Latitude (decimal degrees)	Longitude (decimal degrees)	UTM easting	UTM northing	UTM zone
md0247	-22.118322	118.568588	661791	7553242	50K
md0253	-22.123026	118.579277	662888	7552710	50K
md0258	-22.124773	118.592155	664215	7552503	50K
md0259	-22.130163	118.607018	665742	7551890	50K
md0262	-22.13335	118.618851	666959	7551524	50K
md0266	-22.137814	118.63913	669045	7551008	50K
md0268	-22.140776	118.636963	668818	7550682	50K
md0270	-22.14377	118.634781	668589	7550353	50K
md0293	-22.13938	118.614342	666486	7550862	50K
md0295	-22.13599	118.602638	665283	7551250	50K
md0314	-22.138134	118.582176	663170	7551034	50K
md0330	-22.124109	118.56424	661336	7552606	50K
md0371	-22.130049	118.559845	660876	7551953	50K
md0372	-22.133078	118.557487	660629	7551620	50K
md0385	-22.111462	118.531151	657936	7554041	50K
md0386a	-22.157984	118.690254	674294	7548717	50K
md0387	-22.159502	118.689125	674175	7548550	50K
md0393	-22.156727	118.681786	673422	7548865	50K
md0396	-22.161173	118.678467	673074	7548377	50K
md0397	-22.147526	118.674477	672679	7549892	50K
md0398	-22.148979	118.67334	672560	7549733	50K
md0402	-22.154863	118.6689	672095	7549086	50K
md0405	-22.147261	118.6604	671228	7549938	50K
md0408	-22.148682	118.659355	671118	7549782	50K
md0414	-22.162548	118.677277	672950	7548226	50K
md0415	-22.165506	118.675064	672718	7547901	50K
md0420	-22.162304	118.663315	671510	7548269	50K
md0427	-22.1562	118.653778	670534	7548955	50K
md0429	-22.159252	118.651482	670293	7548620	50K
md0430	-22.160656	118.65049	670189	7548466	50K
md0439	-22.154415	118.640854	669203	7549168	50K
md0441	-22.157345	118.638771	668985	7548845	50K
md0462	-22.122181	118.513672	656121	7552873	50K
md0467	-22.117643	118.514809	656244	7553374	50K

Site code	Latitude (decimal degrees)	Longitude (decimal degrees)	UTM easting	UTM northing	UTM zone
md0468	-22.119026	118.513771	656135	7553222	50K
md0470	-22.120459	118.512726	656026	7553064	50K
md0476	-22.123302	118.511734	655920	7552750	50K
md0481	-22.121782	118.510513	655796	7552920	50K
md0482	-22.12221	118.510078	655751	7552873	50K
md0483	-22.12081	118.509911	655735	7553028	50K
md0486	-22.118696	118.509178	655662	7553263	50K
md0487	-22.119913	118.5084	655580	7553129	50K
md0495	-22.116411	118.506348	655372	7553519	50K
md0499	-22.115425	118.504623	655195	7553630	50K
md0509	-22.118998	118.525604	657356	7553213	50K
md0525	-22.114193	118.514961	656263	7553756	50K
md0533	-22.117565	118.526627	657463	7553370	50K
md0552	-22.123091	118.516533	656416	7552769	50K
md0562	-22.125179	118.507912	655524	7552547	50K
md0577	-22.104797	118.507423	655496	7554804	50K
md0578	-22.107954	118.505226	655266	7554456	50K
md0585	-22.107149	118.510956	655858	7554540	50K
md0596	-22.12266	118.513382	656091	7552820	50K
md0599	-22.123266	118.513474	656100	7552753	50K
md0601	-22.12318	118.51413	656168	7552761	50K
md0609	-22.124744	118.525879	657378	7552576	50K
md0612	-22.117664	118.521713	656956	7553364	50K
md0631	-22.107813	118.491325	653832	7554486	50K
md0646	-22.101631	118.481888	652865	7555180	50K
md0671	-22.109659	118.447296	649287	7554326	50K
md0672	-22.112577	118.445053	649053	7554005	50K
md0673	-22.115568	118.442825	648820	7553676	50K
mdh0143	-22.116583	118.508383	655582	7553498	50K
md_kar1	-22.123201	118.783592	683966	7552458	50K
md_kar2	-22.192839	118.752167	680635	7544785	50K
md_kar3	-22.161366	118.723633	677732	7548303	50K
md_kar4	-22.161938	118.711555	676486	7548254	50K
md_kar5	-22.063749	118.519356	656772	7559336	50K
md_kar6	-22.148893	118.65345	670509	7549765	50K

Site code	Latitude (decimal degrees)	Longitude (decimal degrees)	UTM easting	UTM northing	UTM zone
md_kar7	-22.136585	118.635284	668650	7551148	50K
Browns bore	-22.214039	118.519547	656626	7542696	50K
Calamina bore	-22.192766	118.468666	651403	7545103	50K
Ebathacalby bore	-22.248463	118.748825	680219	7538630	50K
Murrays bore	-22.139124	118.520393	656796	7550990	50K
Yampire bore	-22.247131	118.563431	661112	7538986	50K

Appendix 2 Table of sample types relative to field trip and locations

Site code	Visit number	Study area	Bore scrape	Stygofauna haul	Troglobite trap (leaf litter)	Troglobite trap (banana)	Karaman-Chappuis
md0247	T1	reference	X	X			
md0247	T2	reference			X		
md0247	T3	reference	X	X	X		
md0253	T1	reference	X	X			
md0253	T2	reference			X		
md0253	T3	reference	X	X	X		
md0258	T1	reference	X				
md0258	T2	reference			X		
md0258	T3	reference	X		X		
md0259	T1	reference	X	X			
md0259	T2	reference			X		
md0259	T3	reference	X	X	X		
md0262	T1	reference	X	X			
md0262	T2	reference			X		
md0262	T3	reference	X	X	X		
md0266	T1	reference	X	X			
md0266	T2	reference			X		
md0266	T3	reference	X	X	X		
md0268	T1	reference	X				
md0268	T2	reference			X		
md0268	T3	reference	X		X		
md0270	T1	reference	X	X			
md0270	T2	reference			X		
md0270	T3	reference	X	X	X		
md0293	T1	reference	X	X			
md0293	T2	reference			X		
md0293	T3	reference	X	X	X		
md0295	T1	reference	X	X			
md0295	T2	reference			X		
md0295	T3	reference	X	X	X		
md0314	T1	reference	X				
md0314	T2	reference			X		
md0314	T3	reference	X		X		
md0330	T1	reference	X	X			
md0330	T2	reference			X		

Site code	Visit number	Study area	Bore scrape	Stygofauna haul	Troglobite trap (leaf litter)	Troglobite trap (banana)	Karaman-Chappuis
md0330	T3	reference	X	X	X		
md0371	T1	reference	X				
md0371	T2	reference			X		
md0371	T3	reference	X		X		
md0372	T1	reference	X				
md0372	T2	reference			X		
md0372	T3	reference	X		X		
md0385	T1	impact	X	X			
md0385	T2	impact			X		
md0385	T3	impact	X	X	X		
md0386a	T1	reference	X	X			
md0386a	T2	reference			X		
md0386a	T3	reference	X	X	X		
md0387	T1	reference	X	X			
md0387	T2	reference			X		
md0387	T3	reference	X	X	X		
md0393	T1	reference	X	X			
md0393	T2	reference			X		
md0393	T3	reference	X	X	X		
md0396	T1	reference	X	X			
md0396	T2	reference			X		
md0396	T3	reference	X	X	X		
md0397	T1	reference	X	X			
md0397	T2	reference			X		
md0397	T3	reference	X		X		
md0398	T1	reference	X	X			
md0398	T2	reference			X		
md0398	T3	reference	X	X	X		
md0402	T1	reference	X	X			
md0402	T2	reference			X		
md0402	T3	reference	X	X	X		
md0405	T1	reference	X				
md0408	T1	reference	X	X			
md0408	T2	reference			X		
md0408	T3	reference	X	X	X		
md0414	T1	reference	X				

Site code	Visit number	Study area	Bore scrape	Stygofauna haul	Troglobite trap (leaf litter)	Troglobite trap (banana)	Karaman-Chappuis
md0414	T2	reference			X		
md0414	T3	reference	X		X		
md0415	T1	reference	X				
md0415	T2	reference			X		
md0415	T3	reference	X		X		
md0420	T1	reference	X	X			
md0420	T2	reference			X		
md0420	T3	reference	X	X	X		
md0427	T1	reference	X	X			
md0427	T2	reference			X		
md0427	T3	reference	X	X	X		
md0429	T1	reference	X				
md0429	T2	reference			X		
md0429	T3	reference	2		X		
md0430	T1	reference	X				
md0430	T2	reference			X		
md0430	T3	reference		X	X		
md0439	T1	reference	X	X			
md0439	T2	reference			X		
md0439	T3	reference	X	X	X		
md0441	T1	reference	X	X			
md0441	T2	reference			X		
md0441	T3	reference	X	X	X		
md0462	T1	impact	X	X			
md0462	T2	impact			X		
md0462	T3	impact	X	X	X		
md0467	T1	impact	X	X			
md0467	T2	impact			X		
md0467	T3	impact	X	X	X		
md0468	T1	impact	X	X			
md0468	T2	impact			X		
md0468	T3	impact	X	X	X		
md0470	T1	impact	X	X			
md0470	T2	impact			X		
md0470	T3	impact	X	X	X		
md0476	T1	impact	X	X		x	

Site code	Visit number	Study area	Bore scrape	Stygofauna haul	Troglobite trap (leaf litter)	Troglobite trap (banana)	Karaman-Chappuis
md0476	T2	impact			X		
md0476	T3	impact	X	X	X		
md0481	T1	impact	X	X			
md0481	T2	impact			X		
md0481	T3	impact	X	X	X		
md0482	T1	impact	X	X		x	
md0482	T2	impact			X		
md0482	T3	impact	X	X	X		
md0483	T1	impact	X	X		x	
md0483	T2	impact			X		
md0483	T3	impact	X	X	X		
md0486	T1	impact	X				
md0487	T1	impact	X	X			
md0487	T2	impact			X		
md0487	T3	impact	X	X	X		
md0495	T1	impact	X	X			
md0495	T2	impact			X		
md0495	T3	impact	X	X	X		
md0499	T1	impact	X	X		x	
md0499	T2	impact			X		
md0499	T3	impact	X	X	X		
md0509	T1	impact	X	X			
md0509	T2	impact			X		
md0509	T3	impact	X	X	X		
md0525	T1	impact	X	X			
md0525	T2	impact			X		
md0525	T3	impact	X	X	X		
md0533	T1	impact	X	X			
md0533	T2	impact			X		
md0533	T3	impact	X	X	X		
md0552	T1	impact	X	X			
md0552	T2	impact			X		
md0552	T3	impact	X	X	X		
md0562	T3	impact	X	X	X		
md0577	T1	impact	X	X			
md0577	T2	impact			X		

Site code	Visit number	Study area	Bore scrape	Stygofauna haul	Troglobite trap (leaf litter)	Troglobite trap (banana)	Karaman-Chappuis
md0577	T3	impact	X	X	X		
md0578	T1	impact	X	X			
md0578	T2	impact			X		
md0578	T3	impact	X	X	X		
md0585	T1	impact	X	X			
md0585	T2	impact			X		
md0585	T3	impact	X	X	X		
md0596	T1	impact	X	X			
md0596	T2	impact			X		
md0596	T3	impact	X	X	X		
md0599	T1	impact	X	X			
md0599	T2	impact			X		
md0599	T3	impact	X	X	X		
md0601	T1	impact	X	X			
md0601	T2	impact			X		
md0601	T3	impact	X	X	X		
md0609	T1	impact	X	X			
md0609	T2	impact			X		
md0609	T3	impact	X	X	X		
md0612	T1	impact	X	X			
md0612	T2	impact			X		
md0631	T1	reference	X	X			
md0631	T2	reference			X		
md0631	T3	reference	X	X	X		
md0646	T1	reference	X	X			
md0646	T2	reference			X		
md0646	T3	reference	X	X	X		
md0671	T1	reference	X				
md0671	T2	reference			X		
md0671	T3	reference	X		X		
md0672	T1	reference	X	X			
md0672	T2	reference			X		
md0672	T3	reference	X	X	X		
md0673	T1	reference	X	X			
md0673	T2	reference			X		
md0673	T3	reference	X	X	X		

Site code	Visit number	Study area	Bore scrape	Stygofauna haul	Troglobite trap (leaf litter)	Troglobite trap (banana)	Karaman-Chappuis
mdh0143	T1	impact	X	X			
mdh0143	T2	impact			X		
mdh0143	T3	impact	X	X	X		
Browns bore	T2	reference		X			
Calamina bore	T2	reference		X			
Ebathacalby bore	T2	reference		X			
Murrays bore	T2	reference		X			
Yampire bore	T2	reference		X			
md_kar1	T3	Reference					X
md_kar2	T3	Reference					X
md_kar3	T3	Reference					X
md_kar4	T3	Reference					X
md_kar5	T3	Reference					X
md_kar6	T3	Reference					X
md_kar7	T3	Reference					X

Appendix 3 Water chemistry readings from stygofauna survey bores

Site code	PH	Temp (°c)	O^2 (ppm)	O^2 (%)	ORP (mv/mm)	TDS (ppm)	Salinity (ppm)	Conductivity (mS)
md0247-T1	6.19	25.7	30.4	2	28	552.5	0.41	942
md0253-T1	6.51	160.9	27.1	1.9	25	357.5	0.26	571
md0259-T1	6.51	132.9	29.8	3.1	43	702	0.53	1165
md0262-T1	6.65	143.4	30.5	2.1	30	565.5	0.42	960
md0266-T1	6.41	137.5	30.7	1.8	26	1118	0.86	1909
md0270-T1	7.27	127	30.8	3.9	55	656.5	0.5	1128
md0293-T1	6.66	52.5	31	4	56	240.5	0.17	413.7
md0295-T1	6.62	88.5	31.2	3.7	53	1371.5	1.07	2369
md0330-T1	5.44	186.9	28.7	1.8	24	611	0.46	1003
md0385-T1	6.38	120.2	30.2	2.8	39	858	0.65	1453
md0386a-T1	6.83	201	25.9	2.1	29	507	0.38	806
md0387-T1	7.62	174.2	29.1	2.1	29	773.5	0.59	1284
md0393-T1	6.94	41.9	28.9	1.6	22	1417	1.11	2344
md0396-T1	6.99	165.6	27.9	2.4	32	1059.5	0.82	1720
md0397-T1	7.8	116.5	30.5	1.6	22	747.5	0.57	1275
md0398-T1	6.58	78.8	29.5	1.5	20	1170	0.9	1956
md0402-T1	7.02	3.3	31.2	1.4	20	676	0.51	1165
md0405-T1	5.84	20.9	31.3	1.1	16	220.35	0.16	379.1
md0408-T1	5.83	69.6	29.6	3	41	448.6	0.33	754
md0420-T1	7.07	147.8	29.3	4.6	64	422.5	0.31	708
md0427-T1	6.61	84.1	29.5	4.6	65	708.5	0.53	1181
md0439-T1	7.08	88.7	30	4.9	70	656.5	0.49	1108
md0441-T1	6.67	82	30.2	3.3	47	500.5	0.37	84
md0462-T1	7.37	116.8	29.6	1.6	22	1053	0.81	1754
md0467-T1	7.13	144.6	29.4	4.2	55	1254.5	0.97	2096
md0468-T1	7.04	153.4	29.7	1.9	27	1144	0.88	1900
md0470-T1	6.83	155.4	30	1.3	18	1137.5	0.88	1911
md0476-T1	7.11	97.4	30.5	0.5	7	1274	0.99	2170
md0481-T1	7.1	76	29.9	2.3	32	1371.5	1.07	2309
md0482-T1	7.1	60.4	29.8	2.8	39	1150.5	0.89	1936
md0483-T1	6.93	90.3	29.8	2.3	33	1248	0.97	2097
md0487-T1	6.67	99.5	31.4	2.4	34	786.5	0.59	1357
md0495-T1	7.07	106	30.9	3.4	49	1423.5	1.11	2434
md0499-T1	6.28	99.4	30.2	1.4	19	221	0.16	376.2
md0509-T1	6.79	96.3	30.2	2.7	38	287.3	0.21	485.7

Site code	PH	Temp (°c)	O^2 (ppm)	O^2 (%)	ORP (mv/mm)	TDS (ppm)	Salinity (ppm)	Conductivity (mS)
md0525-T1	7.07	119.9	28	2.7	37	1189.5	0.92	1941
md0533-T1	6.66	89.5	30.9	2.9	41	461.5	0.34	796
md0552-T1	7.06	29.7	27.9	3.9	53	845	0.64	1372
md0577-T1	6.98	93.8	29.7	1.9	25	929.5	0.71	1555
md0578-T1	7.03	90.2	29.9	3.6	50	806	0.61	1358
md0585-T1	7.11	100	29.2	3.3	45	461.5	0.34	766
md0596-T1	7.29	130.3	29.1	3	41	858	0.65	1426
md0599-T1	7.38	-4.8	27.2	5.1	66	1027	0.8	1658
md0601-T1	7.38	-94	27.5	1.3	17	533	0.4	855
md0609-T1	6.75	72	30.3	2.3	32	409.5	0.3	695
md0612-T1	6.66	120.3	30.4	1.9	26	910	0.7	1549
md0631-T1	7.26	70.9	30.6	3.5	49	955.5	0.73	1630
md0646-T1	7.37	74	30.5	3.1	44	611	0.46	1043
md0672-T1	7.73	81.9	30.1	4.2	59	845	0.64	1440
md0673-T1	7.69	118.4	30.7	3.8	53	1514.5	1.18	2579
mdh0143-T1	6.23	36.1	31	1.9	28	703	0.53	1215
md0247-T3	6.21	16.1	29.7	1.2	16	825.5	0.62	1397
md0253-T3	6.46	135.7	29	2	27	565.5	0.42	935
md0259-T3	6.58	14.3	30.8	2.9	41	669.5	0.5	1144
md0262-T3	6.59	-16.8	32.3	1.3	19	500.5	0.37	878
md0266-T3	6.41	108.1	30.6	2.2	32	1059.5	0.81	1809
md0270-T3	7.05	78.9	29.5	3.4	47	403	0.3	668
md0293-T3	6.5	80.4	32.1	3.9	55	203.45	0.15	355.9
md0295-T3	6.47	6.9	35.1	2.7	42	1404	1.08	2596
md0330-T3	5.55	161.9	30.7	2.1	30	578.5	0.43	991
md0385-T3	6.62	67	32.7	3	44	897	0.68	1589
md0386a-T3	6.88	122	29.4	2.7	38	239.2	0.17	399.1
md0387-T3	7.33	85	28.9	1.2	16	702	0.53	1157
md0393-T3	6.95	-76.7	31.1	1.6	23	1033.5	0.79	1775
md0396-T3	6.9	95.6	30.2	2.1	29	1033.5	0.79	1748
md0398-T3	6.61	-3.9	32.5	1.7	24	1202.5	0.92	2110
md0402-T3	6.98	9.5	32.4	1.1	15	695.5	0.52	1217
md0408-T3	5.53	65.9	32.5	1.7	25	351	0.26	618
md0420-T3	6.88	29.6	31.8	3.6	51	702	0.53	1220
md0427-T3	6.48	42.1	31	3.4	49	370.5	0.27	636
md0429-T3	6.08	80.6	30.4	3.3	46	90.35	0.06	153.2

Site code	PH	Temp (°c)	O^2 (ppm)	O^2 (%)	ORP (mv/mm)	TDS (ppm)	Salinity (ppm)	Conductivity (mS)
md0439-T3	7.09	15.2	28.3	3.6	49	572	0.43	938
md0441-T3	6.6	138.1	28.1	3.8	51	370.5	0.27	602
md0462-T3	7.15	-42.5	32.5	1.1	17	1007.5	0.77	1776
md0467-T3	7.2	29	33.2	1.6	23	891.5	0.75	1752
md0468-T3	6.97	40.6	32	2.5	36	1131	0.87	1970
md0470-T3	6.95	122.8	29.6	2	28	1241.5	0.96	2078
md0476-T3	7.07	25.2	30.8	0.9	13	1241	0.96	2126
md0481-T3	7.12	93.6	30.5	3.3	47	1313	1.02	2226
md0482-T3	7.04	99.5	29.7	3.8	52	1111.5	0.86	1860
md0483-T3	6.86	104.8	29.9	2.6	37	1222	0.95	2058
md0487-T3	6.81	84.6	31	3.2	45	767	0.58	1312
md0495-T3	7.05	99.1	31.6	3.3	48	1404	1.09	2426
md0499-T3	6.16	103.7	30.3	1.3	19	219.7	0.16	371.9
md0509-T3	6.83	86.9	31.4	2.5	35	585	0.43	1006
md0525-T3	6.97	66.3	32	2.5	36	604.5	0.45	1054
md0533-T3	6.71	49.8	32.4	2.8	40	461.5	0.34	812
md0562-T3	6.8	100.2	30	3	42	689	0.52	1163
md0577-T3	6.89	87.1	29.2	2.8	38	258.7	0.19	428.7
md0578-T3	7.11	68	29.1	2	27	277.55	0.2	460.3
md0585-T3	6.39	96.8	30	3	41	422.5	0.31	720
md0596-T3	7.21	-10.6	31.9	2.2	31	1150.5	0.88	2007
md0599-T3	7.35	44.1	31.6	3.3	48	1027	0.78	1775
md0601-T3	7.43	-3.8	31.4	2.6	37	546	0.41	950
md0609-T3	6.69	-31.7	31.6	3.1	45	630.5	0.47	1096
md0631-T3	7.19	7	31.5	4.4	33	942.5	0.72	1630
md0646-T3	7.26	46.7	31	1.6	22	708.5	0.53	1212
md0672-T3	7.44	46.3	33.8	3.8	57	1131	0.87	2038
md0673-T3	7.15	36.5	43	2.6	39	3139.5	2.55	5576
mdh0143-T3	6.48	26.7	31.6	1.5	22	1144	0.88	1991
md_kar1-T3	6.69	91.6	30.6	2.5	36	196.95	0.14	336.2
md_kar2-T3	6.54	77.9	30.1	2	28	75.4	0.05	127.7
md_kar3-T3	6.33	73.2	32.4	2.8	40	66.3	0.05	116
md_kar4-T3	6.2	65.1	31	2.1	30	73.45	0.05	127
md_kar5-T3	6.67	-7.1	30	1.7	23	209.95	0.15	354.2
md_kar6-T3	6.27	47.3	34.8	2	30	100.75	0.07	183.4
md_kar7-T3	6.9	90.7	28.1	1.7	23	54.6	0.04	89.4

Appendix 4 Helix Genomics Report

Helix
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23 May 2012

Erich Volschenk
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Via email

Re. Report on the molecular systematics of Troglofauna and Stygofauna from Murrays Hill

Dear Erich,

Following is a summary of the results of the troglofauna and stygofauna study we have completed. Twenty-nine distinct genetic lineages were detected, which correspond to 29 distinct species. Three species, from the orders Hemiptera and Polyxenida, have been detected previously in the Pilbara and two of those represent species with widespread distributions. The remaining 26 lineages were highly divergent from the specimens available for genetic comparison, suggesting that they have so far not been detected 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 and Dr. Oliver Berry
Helix Molecular Solutions

Background

A broad-scale survey of the sub-surface fauna was initiated as part of the environmental assessment process for the Murrays Hill site in the Pilbara, Western Australia. Fourteen taxonomic groups of subterranean invertebrates were collected. The groups were selected for genetic analysis to establish patterns of biodiversity in the subterranean fauna of the region and compare the results to those obtained during extensive genetic analyses that have been undertaken for the troglobitic fauna elsewhere in the Pilbara.

Objective

Forty-four specimens of troglobitic invertebrates collected at the site, belonging to 14 taxonomic groups (Amphipoda, Araneae, Blattodea, Chilopoda, Coleoptera, Diplopoda, Diplura, Hemiptera, Isopoda, Palpigradi, Pauropoda, Schizomida, Syncarida, Thysanura), were sequenced for variation at the mitochondrial gene cytochrome oxidase subunit I (COXI). In some cases, where amplification of the COXI gene failed, the mitochondrial small ribosomal RNA subunit (12s) was sequenced instead. The specimens were analysed in order to determine the number of species present within each taxonomic group, their relationships to previously detected species in the region, and their distributions in the sampling area.

Executive summary

- Thirteen of the 14 taxonomic orders were sequenced for the mtDNA COXI gene, however the Diplopoda, Isopoda and Thysanura were also sequenced for the 12s gene.
- Phylogenetic analysis and genetic distance measures were employed to estimate the number of species present in each taxonomic group.
- Twenty-nine distinct genetic lineages were detected among the 14 taxonomic orders, which are likely to represent 29 distinct species.
- The majority of species (26) detected in Murrays Hill have so far not been detected in the Pilbara, based on the material available for comparison.
- Three species, from the orders Hemiptera and Polyxenida, have been detected previously in the Pilbara, and two of those appear to belong to widespread species, which have been detected at multiple locations in the Pilbara.

Methods

Forty-four specimens of Troglofauna and Stygofauna collected from the Murrays Hill site (Table 1) were sequenced for variation at the mitochondrial gene cytochrome oxidase subunit I (COXI) using five different primer pairs (LCO1/CI-N-2191, LCO1-long/HCO2-long, LCO1/HCOoutout, LCO1/HCO2, LCO1/CIN2341). All primer combinations failed to amplify DNA for the Thysanura specimens, and because there is a reference data set of 12s sequences from previous Pilbara surveys for that group, the mitochondrial small ribosomal RNA gene (12s) was sequenced for the Thysanura specimens using the primers SR-N-14588 and SR-J-14233 (Simon et al., 1993).

Sequences were edited using SEQUENCHER software (Gene Codes Corporation, Ann Arbor, MI, USA). 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. Bayesian analysis was used to construct the phylogenetic tree, incorporating the model as identified in MODELTEST for each taxonomic group (see Table 2). 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 x 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; see Table 2). Trees produced prior to stationarity were discarded (See Table 2 for model parameters for each taxonomic order).

Amphipoda (Paramelitidae)
Five specimens of Amphipoda were sequenced, assigned on the basis of morphology to two species, Paramelitidae MH1 and Paramelitidae Wittenoom (Table 1). Seventeen specimens representing 16 lineages of Paramelitidae from the Pilbara and Yilgarn regions, which were interpreted to represent 16 distinct species, were included in the phylogenetic analysis as references, nine of which are lodged with the international DNA sequence database Genbank as follows: *Maarrka etheli* (Genbank accession # DQ838031), *Maarrka weeliwollii* (Genbank accession # DQ838032), *Yilgarus* sp. BES9348 (Genbank accession #EF118228), *Kruptus linnaei* (Genbank accession # GU111906), *Molina pleobranchos* (Genbank accession #DQ255962), *Pilbarus millsi* (Genbank accession # DQ490126), *Chydaekata acuminata* (Genbank accession # DQ838024), *Chydaekata* sp. Marillana (Genbank accession # DQ255989) and Paramelitidae sp. T3 (Genbank accession #EF558852). The remaining seven specimens were detected in previous surveys of the Fortescue and DeGrey River basins in the Pilbara (Helix, 2012). Two species of unclassified Bogidiellidae from the Pardoo region were used as outgroups.

Araneae (*Anapistula*)
One specimen of Araneae was sequenced, assigned to the genus *Anapistula* in the family Symphytognathidae, on the basis of morphology (Table 1). No COXI sequences of *Anapistula* are available on Genbank for reference, but for comparison, a sequence of unclassified Symphytognathidae (GenBank accession #GU456913), was included as a reference. Further, a specimen of Araneae from the family Theridiidae, *Robertus neglectus* (GenBank accession # AY231053), was included as the nearest match in Genbank. In addition, seven specimens of Araneae from six locations in the Pilbara from the Upper South Fortescue River basin to Wheelarra Hill east of Newman were included as local references (Helix, 2012). Four of these were assigned to the genus *Anapistula* on the basis of morphology and represented three distinct genetic lineages (Helix, 2012).

Blattodea (*Nocticola*)
Four specimens of Blattodea were sequenced, assigned on the basis of morphology to a single species, *Nocticola* MH1, in the family Nocticolidae (Table 1). There are no COXI sequences of Nocticolidae publically available on the international DNA database GenBank to use as references in the Blattodea phylogeny. However, for reference, 12 specimens of *Nocticola* from eight locations in the Pilbara were included in the analysis (Helix, 2012). One of the specimens represents a widespread species group that has been detected from the Robe River to the Ophthalmia Range. Two sequences of Blattidae *Periplaneta australasiae* (GenBank accession #AM114928) and *Blatta orientalis* (GenBank accession #FJ802746) were used as outgroups.

Chilopoda (Scolopenrdomorpha, *Cryptops*)
Six specimens of Chilopoda (Scolopendromorpha) were sequenced, assigned on the basis of morphology to four species, *Cryptops* Pilbara 1, *Cryptops* Pilbara 2, *Cryptops* MH1 and *Cryptops* MH2 (Table 1). For comparison, a specimen of Cryptopidae, *Scolopocryptops sexspinosus* (Genbank accession #AY288745) was included in the phylogenetic analysis, as were three specimens of Cryptopidae from three locations in the Pilbara, Wonmunna, Munjina and Upper South Fortescue (Helix, 2012). Two specimens of Chilopoda, *Cormocephalus monteithi* from the family Scolopendridae (Genbank accession #HM453309) and *Paralamyctes monteithi* from the family Henicopidae (Genbank accession #AF334321) were used as outgroups.

Coleoptera (Carabidae, *Bembidion*)
Two specimens of Coleoptera were sequenced, assigned on the basis of morphology to a single species, *Bembidion* MH1 (Table 1). For comparison, two specimens of *Bembidion* from Illinois (USA), *B. rapidum* (Genbank accession #DQ059789) and *B. nigripes* (Genbank accession #DQ059789) were included in the phylogenetic analysis as references. In addition, eight specimens of Carabidae from four locations in the Pilbara, ranging from the Upper South Fortescue River to the Turner River, were included as local references (Helix, 2012). Two specimens of Curculionidae, *Lepturinae* sp. (Genbank accession #AB379832) and *Nanostrangalia chujoi* (Genbank accession #FJ559029) were included as outgroups.

Diplopoda (Polyxenidae)
Two specimens of Diplopoda were sequenced, assigned on the basis of morphology to a single species, Polyxenidae MH1 (Table 1). For comparison, twenty-six reference specimens from 12 locations In the Pilbara, from the Robe River to Newman were included in the phylogenetic analysis (Helix,

2012). A specimen of *Polydesmus* sp. (Genbank accession #HQ979247) and a surface specimen of Polydesmida from the Pilbara (Helix, 2012) were used as outgroups.

Diplura (Japygidae, Parajapygidae, Projapygidae)
Six specimens of Diplura were sequenced, assigned on the basis of morphology to three species, in three families, Japygidae MH1, Parajapygidae MH1 and Projapygidae MH1 (Table 1). A specimen of Japygidae from GenBank was included as a reference, *Japyx solifugus* (Genbank accession #AY771989), as well as an unclassified species of Diplura (Genbank accession #HQ943342). For comparison, fourteen specimens of Diplura from the Pilbara, collected from seven locations between Yandeyarra in the Central Pilbara to the Ophthalmia Range near Newman, were included in the phylogenetic analysis as references (Helix, 2012). A specimen of Hemiptera, *Lycorma delicatula*, from the family Fulgoridae (Genbank accession #FJ456942) and a specimen of unclassified Hemiptera (Genbank accession #GU671563) were used as outgroups.

Hemiptera (Meenoplidae)
Two specimens of Hemiptera were sequenced, assigned on the basis of morphology to a single species, Meenoplidae MH1 (Table 1). The family Meenoplidae is well-represented in the Pilbara. For comparison, nine sequences of Meenoplidae from previous surveys in the Pilbara, ranging from the Upper South Fortescue River to Weeli Wolli Creek west of Newman, were included in the analysis (Helix, 2012). One specimen represented a species that is distributed widely in the DeGrey and Fortescue River catchments, whereas the remaining eight were restricted to single locations. In addition, a specimen of unclassified Meenoplidae from the international sequence database Genbank was also included as a reference (Genbank accession #GU671506). Two specimens of Hemiptera, *Lycorma delicatula*, (family Fulgoridae; Genbank accession #FJ456942) and an unclassified specimen (Genbank accession #GU671563) were used as outgroups.

Isopoda (*Troglarmadillo*)
One specimen of Isopoda was sequenced, assigned on the basis of morphology to the species *Troglarmadillo* MH1 (Table 1). For comparison, eight specimens of *Troglarmadillo* from four locations in the Pilbara, from the Turner River in the Central Pilbara to Caramulla Creek east of Newman, were included as references in the phylogenetic analysis (Helix, 2012). Two specimens of the aquatic isopod genus *Haloniscus* were used as outgroups (*Haloniscus* sp. 4; Genbank accession # EU364570, and *Haloniscus longiantennatus*; Genbank accession # EU364578).

Palpigradi
Two specimens of Palpigradi were sequenced, assigned on the basis of morphology to a single species, Palpigradi MH1 (Table 1). A specimen of unclassified Palpigradi, Palpigradi sp. JA-2011 (GenBank accession # JN018169) was included as a reference in the phylogenetic analysis. In addition, seven specimens of Palpigradi from five sites in the Pilbara located between Marillana Creek and Ophthalmia Range were used as local references (Helix, 2012). Sequences of scorpions belonging to genera *Buthus* and *Mesobuthus* were used as outgroups as follows: *Mesobuthus eupeus* (Genbank accession #HM567392), *Buthus atlantis* (Genbank accession #AJ506869).

Pauropoda
Two specimens of Pauropoda were sequenced, assigned to a single species, Pauropoda MH1, on the basis of morphology (Table 1). No COXI sequences of Pauropoda are available on GenBank, however, for comparison, four specimens of Pauropoda from four sites in the Pilbara were included in the phylogenetic analysis as references. Two specimens of Scolopendridae (Chilopoda) were used as outgroups: *Cormocephalus monteithi* (Genbank accession #HM453309) and *Ethmostigmus rubripes* (GenBank accession # AF370836).

Schizomida (*Draculoides*)
Two specimens of Schizomida were sequenced, assigned to a single species, *Draculoides* MH1, on the basis of morphology (Table 1). For comparison, four voucher specimens of *Draculoides* and five voucher specimens of *Paradraculoides* from the family Hubbardiidae were included in the phylogenetic analysis as follows: *Draculoides vinei* (Genbank accession # EU272694), *Draculoides julianneae* (Genbank accession # EU272686), *Draculoides bramstokeri* (Genbank accession # EU272683), *Draculoides mesozeirus* (Genbank accession # EU272730), *Paradraculoides anachoretus* (Genbank accession # EU272709) , *Paradraculoides bythius* (Genbank accession # EU272715), *Paradraculoides gnophicola* (Genbank accession # EU272722.1), *Paradracuoides kryptus* (Genbank

accession # EU272724), *Paradraculoides* sp. (Genbank accession # EU272697). Two additional genera from the family Hubardiidae were also included, *Bamazomus* sp. (Genbank accession # EU272676) and *Brignolozomus woodwardi* (Genbank accession # EU272675) from Queensland. Ten specimens from four locations in the Pilbara, ranging from the Upper South Fortescue River to the Hancock Range, were included as local references (Helix, 2012). The specimens were assigned to the genus *Draculoides* based on morphology. Two specimens of Palpigradi were used as outgroups, Palpigradi sp. JA-2011 (GenBank accession #JN018169) and Palpigradi sp. 2 JA-2011 (GenBank accession #JN018214).

Syncarida (Bathynellidae and Parabathynellidae)
Five specimens of Syncarida were sequenced, assigned to two species, Bathynellidae MH1 and Parabathynellidae MH1 (Table 1). For comparison, five sequences of Parabathynellidae from the Yilgarn were included as references, *Billibathynella* sp. 2 (GenBank accession #EU350247), Parabathynellidae gen A sp. 4 (GenBank accession #EU350221), *Atopobathynella glenayleensis* (Genbank accession #EU350256), *Atopobathynella* sp. 1 (GenBank accession # EU350252) and *A. hinzeae* (Genbank accession #EU350245). In addition, ten specimens of Bathynellidae and 14 specimens of Parabathynellidae from the Pilbara were included as local references (Helix, 2012). Two specimens of Amphipoda, *Chydaekata acuminata* (Genbank accession #DQ838024) and *Maarrka etheli* (Genbank accession #DQ838031) were included as outgroups.

Thysanura (Atelurinae and Nicoletiidae)
Four Thysanura, assigned on the basis of morphology to two species, Atelurinae MH1 and *Trinemura* MH1 in the family Nicoletiidae, were sequenced (Table 1). No sequences of Nicoletiidae are lodged with Genbank, however, for comparison, a specimen of Atelurinae was included as a reference, *Atelura formicaria* (GenBank accession #EU084035). Further, six specimens of Atelurinae from six locations in the Pilbara, and seven specimens of Nicoletiidae from six locations in the Pilbara ranging from Barrow Island to the Ophthalmia Range near Newman, were included as local references (Helix, 2012). Two specimens of Thysanura from the family Lepismatidae were used as outgroups, *Thermobia* sp. (Genbank accession #AF252405) and *Ctenolepisma* sp. (Genbank accession #AF252404).

Results
Amphipoda (Paramelitidae)
A 594 – 686 bp fragment of the COXI gene was obtained from three of the specimens (Appendix 1). Specimens PES5797 and PES5605 failed to yield a DNA sequence.

Phylogenetic analysis
The phylogenetic analysis, which contained the three new specimens from Murrays Hill in addition to the 17 reference specimens, revealed the presence of 17 lineages (AA – AQ; Figure 1). The specimens from Murrays Hill were placed in a single lineage, AQ (Figure 1). No reference specimens were placed in lineage AQ, however it formed a moderately well-supported clade with lineage AC, which contained two specimens from the Upper South Fortescue River (Figure 1).

Differentiation within and between lineages
The 17 lineages differed from one another by between 5.1 and 25.0% sequence divergence (Table 3). Lineage AQ from Murrays Hill differed from the reference lineages by between 19.4 and 23.4% sequence divergence (Table x). The three individuals with lineage AQ differed on average by 1.6% (Table 4).

Araneae (*Anapistula*)
A 686 bp fragment of COXI was obtained from the *Anapistula* specimen (Appendix 1).

Phylogenetic analysis
The phylogenetic analysis, which included the one new specimen analysed here from Murrays Hill, in addition to the nine reference specimens, revealed the presence of eight lineages (ArA – ArH; Figure 2). The new specimen from Murrays Hill was placed in lineage ArC (Figure 2). No reference specimens were placed in lineage ArC, but the lineage was placed in a well-supported clade that contained three reference lineages of *Anapistula* from the Upper South Fortescue River basin, the Central Pilbara and Mindy-Coondiner (Figure 2).

Differentiation within and between lineages

The eight lineages differed from one another by between 12.4 and 25.5% sequence divergence (Table 5a). Lineage ArC, containing the new specimen from Murrays Hill, differed from the reference specimens by between 12.4 and 25.5% sequence divergence (Table 5a). In particular, lineage ArC differed from the three lineages of *Anapistula* by between 12.4 and 13.4% sequence divergence (Table 5a). Differentiation between individuals within lineages ranged from 0.8 – 2.5% sequence divergence (Table 5b).

Blattodea (*Nocticola*)

The four specimens yielded a 616 base-pair (bp) fragment of COXI (Appendix 1).

Phylogenetic analysis

The phylogenetic analysis, which contained the four new specimens from Murrays Hill analysed here, as well as 12 reference specimens of *Nocticola*, revealed the presence of eleven lineages (haplotypes or clusters of highly similar haplotypes (genetic distances ≤ 3%) separated from other such clusters by long branch lengths; BA - BK; Figure 3). The four specimens from Murrays Hill were placed in two genetic lineages, BJ and BK (Figure 3). No reference specimens were contained in lineages BJ or BK, however, the two lineages formed a well-supported clade with lineage BF, which contained a specimen from Christmas Creek (Figure 3).

Differentiation within and between lineages

The 11 lineages of Blattodea differed from one another by between 4.6 and 26.6% sequence divergence (Table 6). Lineage BJ and BK, which contained the specimens from Murrays Hill, differed from one another by 4.6% sequence divergence and from the reference lineages by between 9.1 and 26.3% sequence divergence (Table 6). The three individuals from Murrays Hill within lineage BJ differed from one another on average by 2.8% (Table 7).

Chilopoda (Scolopendromorpha, *Cryptops*)

A DNA sequence ranging from 625 – 686 bp was obtained from five of the six specimens (Appendix 1). One specimen, PES6069, failed to yield a DNA sequence.

Phylogenetic analysis

The phylogenetic analysis, which included the five specimens analysed here, in addition to four reference specimens, revealed the presence of eight distinct genetic lineages (ScA - ScH; Figure 4).The five specimens from Murrays Hill were placed in four distinct genetic lineages (ScE, ScF, ScG and ScH; Figure 4). One lineage, ScE, contained two specimens (991-5262 and PES5889); the remaining three lineages each contained a single specimen (Figure 4). No reference specimens were placed in lineages ScE - ScH from Murrays Hill (Figure 4). Lineages ScE - ScH formed a well-supported clade (Figure 4).

Differentiation within and between lineages

The eight lineages of Chilopoda differed from one another by between 15.8 and 24.1% sequence divergence (Table 8). The four lineages detected in Murrays Hill differed from the reference lineages by between 21.3 and 23.9% sequence divergence (Table 8). The two specimens within lineage ScE differed by 0.6% sequence divergence.

Coleoptera (Carabidae, *Bembidion*)

A 456 bp fragment of COXI was obtained from the two specimens (Appendix 1).

Phylogenetic analysis

The phylogenetic analysis, which included the two specimens of *Bembidion* analysed here, in addition to ten reference specimens, revealed the presence of 11 distinct genetic lineages (CaA – CaK; Figure 5). The two specimens from Murrays Hill were placed in lineage CaK (Figure 5). The specimens of *Bembidion* from Murrays Hill did not show close affinities to the voucher specimens of *Bembidion* (Figure 5). Instead the specimens were placed in a moderately well-supported clade containing specimens assigned to the tribe Anillini on the basis of morphology, from the Upper South Fortescue River (Figure 5).

Differentiation within and between lineages

The 11 lineages differed from one another by between 3.6 and 20.8% sequence divergence (Table 9). The lineage detected in Murrays Hill, CaK, differed from the reference lineages by between 12.7 and

18.5% sequence divergence (Table 9). The two specimens within lineage CaK differed from one another by 3.1% sequence divergence (Table x).

Diplopoda (Polyxenidae)
One specimen yielded a 547 bp fragment of COXI (Appendix 1) and both specimens yielded a 422 bp fragment of the 12s gene (Appendix 2).

Phylogenetic analysis
The COXI phylogenetic analysis, which contained the one new specimen from Murrays Hill analysed here, as well as 26 reference specimens of Polyxenida from locations in the Pilbara from the Robe River to Newman, revealed the presence of 13 genetic lineages (Figure 6). The new specimen from Murrays Hill was placed in genetic lineage PN (Figure 6). Lineage PN contained seven reference specimens from seven locations, Beasley River, Hamersley Range, Marillana Creek, Robe Headwaters, Turee Syncline, Upper South Fortescue River and Wonmunna (Figure 6). Lineage PN formed a relatively well-supported clade with lineages PK-PL-PM, PO and PP from West Turner, the Robe River and Hamersley Range (Figure 6).

Differentiation between within and between lineages
The 13 lineages differed from one another by between 0.2 and 18.8% sequence divergence at COXI (Table 10). Lineage PN differed from the remaining lineages by between 3.1 and 17.1% sequence divergence (Table 10). Differentiation between individuals within lineage PN averaged 0.7% sequence divergence (Table 11). The two specimens from Murrays Hill differed from one another by 0.5% sequence divergence at the 12s gene.

Diplura (Japygidae, Parajapygidae, Projapygidae)
Five specimens yielded a 686 – 820 bp fragment of COXI (Appendix 1). A single specimen of Projapygidae, PES5937, failed to yield a DNA sequence.

Phylogenetic analysis
The phylogenetic analysis, which contained the five new specimens analysed here in addition to the 16 reference and GenBank specimens, revealed the presence of 20 distinct genetic lineages (Figure 7). There was a single lineage of Anajapygidae (DB), eight lineages of Japygidae (DC – DH, DQ and DR), three lineages of Parajapygidae (DI, DJ and DS) and seven lineages of Projapygidae DK – DP and DT; Figure 7). Three of the four family clades were well-supported; the clade containing the Japygidae was moderately well-supported (posterior probability= 0.92; Figure 7).

The two new specimens of Japygidae were placed in two of the lineages (DQ and DR; Figure 7). The two new specimens of Parajapygidae were placed in a single lineage, DS, and the specimen of Projapygidae was placed in lineage DT (Figure 7). None of the four lineages containing the new specimens contained reference specimens. Japygidae lineages DQ and DR from Murrays Hill formed a well-supported clade with lineage DH from the Central Pilbara (Figure 7). Parajapygidae lineage DS from Murrays Hill formed a well-supported clade with lineages DI and DJ from Munjina (Figure 7).

Differentiation within and between lineages
The eight lineages of Japygidae differed from one another by between 11.0 and 20.2% sequence divergence (Table 12a). The two lineages from Murrays Hill, DQ and DR, differed from one another by 13.0% sequence divergence and from the reference lineages of Japygidae by between 12.8 and 20.0% sequence divergence (Table 12a). The three lineages of Parajapygidae differed from one another by between 3.0 and 16.9% sequence divergence (Table 12b). The lineage from Murrays Hill, DS, differed from the reference lineages of Parajapygidae by between 15.2 and 16.9% sequence divergence (Table 12b). The two individuals from Murrays Hill in lineage DS differed from one another by 3.0% sequence divergence. The seven lineages of Projapygidae differed from one another by between 11.3 and 18.7% sequence divergence (Table 12c). The lineage from Murrays Hill, DT, differed from the reference lineages of Projapygidae by between 14.3 and 18.7% sequence divergence (Table 12c).

Hemiptera (Meenoplidae)
The two specimens yielded a 686 bp fragment of COXI (Appendix 1).

Phylogenetic analysis

The phylogenetic analysis, which contained the two new specimens analysed here, in addition to the ten reference specimens, revealed the presence of ten distinct genetic lineages (MA-MJ; Figure 8). The two new specimens from Murrays Hill were placed in two distinct lineages (MB, MG; Figure 8). Both specimens were placed in lineages containing reference specimens. Lineage MB contained the reference specimen representing the widespread species, and lineage MG contained the reference specimen from the Upper South Fortescue River catchment (Figure 3).

Differentiation between within and between lineages
The ten lineages of Meenoplidae differed from one another by between 4.5 and 25.0% sequence divergence (Table 13). The two lineages detected in Murrays Hill (MB, MG) differed from one another by 15.1% sequence divergence and from the remaining lineages by between 10.2 and 22.9% sequence divergence (Table 13). The two specimens within lineage MB differed from one another by 0.9% sequence divergence and the two specimens within lineage MG differed from one another by 0.3% sequence divergence (Table 14).

Isopoda (*Troglarmadillo*)
The specimen (PES5180) failed to yield a DNA sequence for COXI or 12s (Table 1).

Palpigradi
The two specimens yielded a 701-706 bp fragment of COXI (Appendix 1).

Phylogenetic analysis
The phylogenetic analysis, which contained the two new specimens from Murrays Hill analysed here, in addition to the eight reference specimens, revealed the presence of ten distinct genetic lineages (PaA - PaJ; Figure 10). The two new specimens were placed in two distinct lineages (PaI and PaJ; Figure 10). No reference specimens were placed in the lineages containing the new specimens (Figure 10).

Genetic differentiation between lineages
The ten lineages differed from one another by between 19.1 and 36.5% sequence divergence (Table 15). The two new specimens from Murrays Hill differed from one another by 33.4% sequence divergence and from the remaining lineages by between 23.6 and 36.5% sequence divergence (Table 15).

Pauropoda
A 642 to 686 bp fragment of COXI was obtained from the two specimens (Appendix 1).

Phylogenetic analysis
The phylogenetic analysis, which included the two new specimens from Murrays Hill analysed here, in addition to the four reference specimens, revealed the presence of six distinct genetic lineages (PrA – PrF; Figure 11). The two new specimens were placed in two distinct genetic lineages (PrE and PrF; Figure 11). No reference specimens were placed in the lineages containing the new specimens, however, specimen PES5884 formed a well-supported clade with an unclassified specimen of Pauropoda from Marillana Creek (Figure 11).

Differentiation within and between lineages
The six lineages of Pauropoda differed from one another by between 19.5 and 34.7% sequence divergence (Table 16). The two specimens from Murrays Hill differed from one another by 30.3% sequence divergence, and from the reference specimens by between 19.5 and 34.7% sequence divergence (Table 16).

Schizomida (*Draculoides*)
A 712-845 bp fragment of COXI was obtained from the two specimens (Appendix 1).

Phylogenetic analysis
The phylogenetic analysis, which included the two new specimens from Murrays Hill analysed here, in addition to 23 reference specimens of Hubbardiidae, revealed the presence of 25 distinct genetic lineages (SzA - SzY; Figure 12). The two specimens from Murrays Hill were placed in two distinct lineages, SzL and ScM (Figure 12). No reference lineages were placed in either lineage SzL or ScM

(Figure 2). The two lineages formed a clade that was distinct from the remainder of the reference specimens, but it was not well-supported (Figure 12).

Genetic differentiation between lineages
The 25 lineages of Schizomida differed from one another by between 5.2 and 19.3% sequence divergence (Table 17). The two lineages from Murrays Hill, SzL and SzM, differed from one another by 13.3% sequence divergence, and from the reference lineages by between 11.8 and 19.2% sequence divergence (Table 17).

Syncarida (Bathynellidae and Parabathynellidae)
Four of the Syncarida yielded a 686 – 704 bp fragment of the COXI gene. One specimen, PES5968 failed to yield a DNA sequence.

Phylogenetic analysis
The phylogenetic analysis, which included the four specimens from Murrays Hill, in addition to the 29 reference specimens, revealed the presence of 21 lineages of Parabathynellidae and 12 lineages of Bathynellidae (Figure 13). The four specimens from Murrays Hill were each placed in a separate genetic lineage (Bathynellidae SBA and SBB, and Parabathynellidae SPT and SPU; Figure 13). No reference specimens were placed in the lineages containing the Murrays Hill specimens (Figure 13). Parabathynellidae lineage SPT from Murrays Hill formed a well-supported clade with the lineage of *Atopobathynella* sp. 1 from the Yilgarn (Figure 13). Bathynellidae lineages SBA and SBB from Murrays Hill formed a well-supported clade with two lineages from Ophthalmia in the Fortescue River basin and two lineages from the DeGrey River basin, Eel Creek and Yarrie Station (Figure 13).

Genetic differentiation between lineages
The two Bathynellidae lineages from Murrays Hill differed from one another by 18.0% sequence divergence, and from the reference specimens of Bathynellidae by between 16.4 and 25.3% sequence divergence (Table 18). The two Parabathynellidae specimens from Murrays Hill differed from one another by 21.6% sequence divergence, and from the reference specimens of Parabathynellidae by between 14.8 and 24.0% sequence divergence (Table 19).

Thysanura (Ateluriinae and Nicoletiidae)
All four specimens failed to yield a DNA sequence for COXI. Because we have a substantial data set of reference sequences for 12s, the four specimens were sequenced for 12s and three of them (PES5124, PES5266 and PES5964) yielded a 392 - 431 bp fragment of that gene (Appendix 2).

Phylogenetic analysis
The phylogenetic analysis revealed the presence of eight distinct genetic lineages of Ateluriinae (TAA, TAD, TAE, TAH, TAI, TAK, TAM, TAN; Figure 14). The specimen of Ateluriinae from Murrays Hill was placed in lineage TAN (Figure 14). No reference specimens were placed in lineage TAN, and it showed no close genetic relationships with reference specimens, being placed outside of the clade containing the reference specimens (Figure 14). The phylogenetic analysis also revealed the presence of nine distinct genetic lineages of Nicoletiidae (TNA – TNI; Figure 14). The specimens of *Trinemura* (Nicoletiidae) from Murrays Hill were placed in lineages TNH and TNI (Figure 14). No reference specimens were placed in lineages TNH or TNI, however lineages TNH and TNI formed a well-supported clade with lineages TNB, TNE and TNF from Phil's Creek and the Upper South Fortescue River basin (Figure 14). In particular, lineage TNH formed a well-supported clade with lineage TNB, which contained a specimen from Phil's Creek assigned to the genus *Trinemura*, on the basis of morphology (Figure 14).

Differentiation between lineages
The eight Ateluriinae lineages differed from one another by between 4.1 and 27.3% sequence divergence (Table 20a). Lineage TAN differed from the reference lineages by between 15.8 and 26.1% sequence divergence (Table 20a). The nine Nicoletiidae lineages differed from one another by between 6.2 and 21.5% sequence divergence (Table 20b). Lineage TNH differed from the reference lineages by between 12.0 and 18.4% sequence divergence and lineage TNI differed from the reference lineages by between 12.0 and 20.9% sequence divergence (Table 20b). Lineages TNH and TNI differed from one another by 12.6% sequence divergence (Table 20b).

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. However, the authours also stated that individuals of the same species rarely differ by >2% sequence divergence (Hebert et al., 2003a). Thus, there is a "grey" area between 2 and 8%, where the level of sequence variation requires further consideration.

The mitochondrial gene 12s is widely used in insect systematics (Simon et al., 1996; Caterino et al., 2000), although in contrast to the mitochondrial gene COXI, fewer broadscale comparative studies are available to provide a basis for species discrimination. Nonetheless, 12s has proven useful for establishing phylogenetic relationships in many insect groups (Caterino et al., 2000). The 12s gene evolves approximately 1.5 times (Mueller, 2006) to three times (Hebert, 2003a) more slowly than COXI. Hence we would expect that the threshold for species discrimination using 12s would be, by inference, lower than COXI. If we take 8% as the threshold for species delineation using COXI, a reasonable threshold for defining species using 12s might then be expected to range from 2.6 – 5.3% sequence divergence, and by the same logic, individuals of the same species might expect to differ by no more than 0.7 to 1.3% sequence divergence.

Using these guidelines, we can draw some conclusions about the level of biodiversity in each of the 14 taxonomic orders assessed in Murrays Hill.

Amphipoda (Paramelitidae)

The low level of sequence divergence between the three specimens from Murrays Hill indicates that they belong to a single species. This supports their morphological assignment to the single species Paramelitidae MH1. While showing a genetic relationship to a lineage of Paramelitidae from the Upper South Fortescue River, the two lineages are genetically differentiated and represent two distinct species. Based on the material available for genetic comparison, lineage AQ from Murrays Hill has not been detected previously in the Pilbara. No DNA sequence was obtained for the specimen assigned to the species Paramelitidae Wittenoom.

Araneae (*Anapistula*)

The high level of sequence divergence between the new specimen analysed here and the reference specimens indicates that it is likely to belong to a distinct species, which has so far not been detected in the Pilbara, based on the material available for genetic comparison. The specimen was placed in a well-supported clade containing reference specimens of *Anapistula*, supporting its morphological placement in that genus, however it is likely to represent a new species owing to the high level of sequence divergence between it and the reference lineages of *Anapistula*.

Blattodea (*Nocticola*)

The low level of sequence divergence among the three individuals of *Nocticola* from Murrays Hill within lineage BJ indicates that they are likely to belong to a single species. Further, the relatively low level of sequence divergence between lineages BJ and BK from Murrays Hill also suggests that they belong to a single species. This supports their morphological assignment to the single species *Nocticola* MH1. However, the level of sequence divergence observed between the two lineages, while relatively low, is greater than that generally observed between individuals of the same species, and suggests that gene flow is limited to small spatial scales, causing isolated populations to become genetically differentiated. Thus the populations may have conservation significance, as they may reflect incipient species. The species *Nocticola* MH1 does not appear to have been detected previously in the Pilbara, based on the material available for genetic comparison, however, species *Nocticola* MH1 may share a relatively recent common ancestor with a population of *Nocticola* from Christmas Creek.

Chilopoda (Scolopendromorpha, *Cryptops*)

The high level of sequence divergence between the four lineages detected in Murrays Hill, ScE, ScF, ScG and ScH, indicates that they belong to four distinct species. The low level of sequence divergence between the two individuals in lineage ScE indicates that they belong to the same species. There was relatively poor correspondence between morphological and genetic assignments. The two specimens in lineage ScE were assigned to two distinct species based on morphology, MH1

and MH2. The two specimens assigned to species MH2 on the basis of morphology, were placed in two distinct lineages, ScE and ScH. However, the two specimens that were assigned to species Pilbara 1 and Pilbara 2 were indeed placed in two distinct genetic lineages, supporting their assignment to two distinct species based on morphology.

Coleoptera (Carabidae, *Bembidion*)
The moderately low level of sequence divergence between the two specimens in the lineage detected in present study, CaK, suggests that they are likely to belong to the same species. However, the two specimens showed a greater level of genetic differentiation than is usually observed between individuals of the same species, but less variation than is usually observed between distinct species. In the absence of morphological or ecological differences, we would likely consider the differentiation to be intra-specific, however, gene flow in this group appears to be restricted on short spatial scales between the two sites in the sampling area. Such isolation can be the precursor to allopatric speciation. In contrast, the high level of sequence divergence between lineage CaK and the reference lineages indicates that it is likely to be a distinct species, that has not so far been detected in the Pilbara, based on the material available for genetic comparison.

Diplopoda (Polyxenida)
The low level of sequence divergence between the two specimens at the 12s gene (0.5%) indicates that they belong to the same species. This level of sequence divergence would roughly correspond to 0.75% to 1.5% sequence divergence at COXI, using the conversion factors of a 1.5× to 3× faster rate of evolution for COXI. This supports the morphological assignment of both specimens to the single species Polyxenidae MH1. The low level of sequence divergence between specimens within lineage PN at COXI indicates that they belong to a single species. Thus lineage PN represents a species that was detected at multiple sites from the Robe River to Wonmunna, approximately 70 km west of Newman. Further, the lineage shows a close genetic affinity and relatively low levels of sequence divergence (<4%) to additional lineages from West Turner, Robe River and Hamersley Range. The group may represent a widespread species that shows genetic variation associated with geography, or the variation may represent incipient speciation, arising from limited gene flow among geographically differentiated populations.

Diplura (Japygidae, Parajapygidae, Projapygidae)
The taxonomic assignments of the five specimens to three families are supported by the molecular data.

The high level of sequence divergence between Japygidae lineages DQ and DR from Murrays Hill indicates that they represent two distinct species, in contrast to their assignment to a single species, Japygidae MH1, on the basis of morphology. Further, the high level of sequence divergence between lineages DQ and DR and the reference lineages indicates that the species have not so far been detected in the Pilbara, based on the material available for genetic comparison, although lineage DR may share a relatively recent common ancestor with a species of Japygidae from the central Pilbara.

The low level of sequence divergence between the two specimens of Parajapygidae from Murrays Hill in lineage DS (3.0%) indicates that they belong to the same species. This is supported by their assignment to the single species MH1 on the basis of morphology. However, the two specimens show greater sequence divergence than is typically observed between individuals of the same species, although substantially less than is generally observed between distinct species. This suggests that gene flow may be impeded over small spatial scales. The high level of sequence divergence between lineage DS and the reference lineages indicates that the species has not so far been detected in the Pilbara, based on the material available for genetic comparison, although it may share a relatively recent common ancestor with a species of Parajapygidae from Munjina.

The high level of sequence divergence between Projapygidae lineage DT from Murrays Hill and the reference lineages indicates that the species has not so far been detected in the Pilbara, based on the material available for genetic comparison.

Hemiptera (Meenoplidae)
The high level of sequence divergence between the two lineages detected in Murrays Hill, MB and MG, indicates that they represent two distinct species, in contrast to their morphological assignments to the same species. The low level of sequence divergence between the two specimens within

lineage MB indicates that they belong to a single species, which is widespread throughout the Pilbara. The reference specimen representing this lineage was collected from the upper South Fortescue River basin. Similarly, the low level of sequence divergence between the two specimens within lineage MG indicates that they belong to a single species. The reference specimen representing this lineage was also collected from the upper South Fortescue River basin.

Palpigradi

The high level of sequence divergence between the two lineages detected in Murrays Hill, PaI and PaJ, indicates that they belong to two distinct species, in contrast to their morphological assignment to the same species. Further, the two species are highly genetically distinct from the reference specimens, indicating that they are likely to belong to two new species that have so far not been detected in the Pilbara, based on the material available for genetic comparison.

Pauropoda

The high level of sequence divergence between the two lineages of Pauropoda detected in Murrays Hill, PrE and PrF, indicates that they belong to two distinct species, in contrast to their assignment to the same species based on morphology. Further, the two species are highly genetically distinct from the reference specimens, are likely to represent species that have so far not been detected in the Pilbara, based on the material available for genetic comparison.

Schizomida (*Draculoides*)

The high level of sequence divergence between the two lineages detected in Murrays Hill, SzL and SzM, indicates that they belong to two distinct species, in contrast to their assignment to a single species on the basis of morphology. Further, the high level of sequence divergence between them and the reference specimens indicates that they have not so far been detected in the Pilbara, based on the material available for genetic comparison. Because the genus *Draculoides* was polyphyletic in the present analysis (the composite lineages did not arise from a single common ancestor), we cannot unequivocally place the new specimens in that genus using the present data set.

Syncarida (Bathynellidae and Parabathynellidae)

The high level of sequence divergence between the two lineages of Bathynellidae from Murrays Hill indicates that they belong to two distinct species, in contrast to their assignment to a single species on the basis of morphology. Similarly, the high level of sequence divergence between the two lineages of Parabathynellidae from Murrays Hill indicates that they belong to two distinct species, in contrast to their assignment to a single species on the basis of morphology. Further, the high level of sequence divergence between the four species from Murrays Hill from the reference specimens indicates that they have not so far been detected in the Pilbara or Yilgarn, based on the material available for genetic comparison. Parabathynellidae lineage SPT from Murrays Hill was placed in a clade containing the reference specimens of Atopobathynellidae. While the clade was not well-supported, this finding may provide a basis for examining its relationship to that genus.

Thysanura (Atelurinae and Nicoletiidae)

The high level of sequence divergence between the Atelurinae lineage TAN from Murrays Hill and the reference specimens indicates that it represents a distinct species that has so far not been detected in the Pilbara, based on the material available for genetic comparison. The high level of sequence divergence between the two Nicoletiidae lineages TNH and TNI from Murrays Hill indicates that they belong to two distinct species. This contrasts with their assignment to the single species *Trinemura* MH1 on the basis of morphology. Further, the high level of sequence divergence between the two Nicoletiidae lineages TNH and TNI from Murrays Hill and the reference specimens indicates that they represents two distinct species that have so far not been detected in the Pilbara, based on the material available for genetic comparison. Atelurinae lineage TAN shows no close genetic affinities to reference specimens, however, lineages TNH and TNI show close genetic affinities with lineages TNB, TNE and TNF from Phil's Creek and the Upper South Fortescue River basin. In particular, lineage TNH shows genetic affinities to lineage TNB, which contains a specimen assigned to the genus *Trinemura* from Phil's Creek, supporting its placement in that genus. However, the Murrays Hill lineages differ from the reference lineages by ≥12% sequence divergence, and because 12s evolves 1.5 to 3 times more slowly than COXI (Hebert et al, 2003a; Mueller, 2006), this corresponds to >18% sequence divergence at COXI. Hence the two lineages of Nicoletiidae from Murrays Hill are likely to represent new species.

In summary, 29 distinct genetic lineages were detected among the 37 specimens for which DNA sequences were obtained. The majority of the lineages were not detected at other sites in the Pilbara, based on the material available for comparison. Three species, two from the order Hemiptera and one from the order Polyxenida appeared to belong to species that have been detected previously and two, one Hemiptera and one Polyxenida, have widespread distributions in the Pilbara.

References

Caterino MS, Cho S, Sperling FAH (2000). The current state of insect molecular systematics: A thriving Tower of Babel. Annual Review of Entomology 45: 1-54.

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 (2012). Unpublished data as per data sharing agreement.

Mueller RL (2006). Evolutionary rates, divergence dates and the performance of mitochondrial genes in Bayesian Phylogenetic analysis. Systematic Biology 55: 289-300.

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

Simon, C., Fratl, F, Beckenbach, A., Crespi, B., Liu, H., Flook, P. (1996) Evolution, weighting, and phylogenetic utility of mitochondrial gene sequences and a compilation of conserved polymerase chain reaction primers. Annals of the Entomological Society 87: 651-701.

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 used in the present study and the genetic lineage to which they were assigned based on variation at the COIX and 12s genes. *= not previously detected in the Pilbara.

Lab No.	Order	Species	Helix ID	Genetic lineage
PES-5797	Amphipoda	Paramelitidae 'MH1'	BX31	No data
PES-5173	Amphipoda	Paramelitidae 'MH1'	BX32	AQ*
PES-5924	Amphipoda	Paramelitidae 'MH1'	BX33	AQ*
PES-5941	Amphipoda	Paramelitidae 'MH1'	BX34	AQ*
PES-5605	Amphipoda	Paramelitidae 'Wittenoom'	BX35	No data
PES-5149	Araneae	Anapistula 'MH1'	BX1	ArC*
PES-5125	Blattodea	Nocticola 'MH1'	BX20	BJ*
PES-5215	Blattodea	Nocticola 'MH1'	BX21	BK*
PES-5436	Blattodea	Nocticola 'MH1'	BX22	BJ*
PES-5781	Blattodea	Nocticola 'MH1'	BX23	BJ*
PES-0968	Chilopoda	Cryptops 'pilbara1'	BX11	ScF*
PES-3783	Chilopoda	Cryptops 'pilbara2'	BX12	ScG*
991-5262	Chilopoda	Cryptops 'MH1'	BX13	ScE*
PES-5889	Chilopoda	Cryptops 'MH2'	BX8	ScE*
PES-5272	Chilopoda	Cryptops 'MH2'	BX9	ScH*
PES-6069	Chilopoda	Cryptops 'MH2'	BX10	No data
PES-5290	Coleoptera	Bembidion 'MH1'	BX6	CaK*
PES-5285	Coleoptera	Bembidion 'MH1'	BX7	CaK*
PES-6026	Diplopoda	Polyxenidae 'MH1'	BX38	PN
PES-5132	Diplopoda	Polyxenidae 'MH1'	BX39	PN
PES-5195	Diplura	Japygidae 'MH1'	BX16	DQ*
PES-5952	Diplura	Japygidae 'MH1'	BX17	DR*
PES-5141	Diplura	Parajapygidae 'MH1'	BX29	DS*
PES-5190	Diplura	Parajapygidae 'MH1'	BX30	DS*
PES-5878	Diplura	Projapygidae 'MH1'	BX40	DT*
PES-5937	Diplura	Projapygidae 'MH1'	BX41	No data
PES-5862	Hemiptera	Meenoplidae 'MH1'	BX18	MG
PES-5869	Hemiptera	Meenoplidae 'MH1'	BX19	MB
PES-5180	Isopoda	Troglarmadillo 'MH1'	BX44	No data
PES-5788	Palpigradi (whip scorpion)	Palpigradi 'MH1'	BX24	PaI*
PES-5871	Palpigradi (whip scorpion)	Palpigradi 'MH1'	BX25	PaJ*
PES-5884	Pauropoda	Pauropoda 'MH1'	BX36	PrE*
PES-6086	Pauropoda	Pauropoda 'MH1'	BX37	PrF*
PES-5578	Schizomida	Draculoides 'MH1'	BX14	SzL*
PES-5735	Schizomida	Draculoides 'MH1'	BX15	SzM*
PES-5293	Syncarida	Bathynellidae 'MH1'	BX4	SBA*
PES-5816	Syncarida	Bathynellidae 'MH1'	BX5	SBB*
PES-5958	Syncarida	Parabathynellidae 'MH1'	BX26	SPT*
PES-5968	Syncarida	Parabathynellidae 'MH1'	BX27	No data
PES-5981	Syncarida	Parabathynellidae 'MH1'	BX28	SPU*
PES-5253	Zygentoma (Thysanura)	Atelurinae 'MH1'	BX2	No data
PES-5124	Zygentoma (Thysanura)	Atelurinae 'MH1'	BX3	TAN*
PES-5266	Zygentoma (Thysanura)	Trinemura 'MH1'	BX42	TNI*
PES-5964	Zygentoma (Thysanura)	Trinemura 'MH1'	BX43	TNH*

Table 2. Model parameters used in the construction of phylogenies using Bayesian analysis for each of the 14 taxonomic orders included in Murrays Hill.

Taxonomic group	Model	No. generations	Split frequency	No. burn-in trees
Amphipoda	GTR+I+G	1 x 10^6	0.0117	5000
Araneae	GTR+I+G	1 x 10^6	0.0028	3000
Blattodea	GTR+G	1 x 10^6	0.0123	4000
Chilopoda	GTR+I+G	1 x 10^6	0.0087	3000
Coleoptera	GTR+I+G	1 x 10^6	0.0040	3000
Diplopoda	GTR+I+G	1 x 10^6	0.0107	3000
Diplura	TIM3+G	1 x 10^6	0.0018	3000
Hemiptera	GTR+I	1 x 10^6	0.0005	2000
Isopoda				
Palpigradi	GTR+G	1 x 10^6	0.0010	2500
Pauropoda	GTR+I+G	1 x 10^6	0.0015	3000
Schizomida	GTR+I+G	2 x 10^6	0.0142	5000
Syncarida	GTR+I+G	1 x 10^6	0.0092	3000
Thysanura	TIM3+G	1 x 10^6	0.0016	3000

Table 3. Mean COXI distances (below diagonal) between lineages of Amphipoda. Distances between lineages from Murrays Hill and the reference lineages are highlighted in yellow. Above diagonal= standard error.

Lineage	AA	AB	AC	AD	AE	AF	AG	AH	AI	AJ	AK	AL	AM	AN	AO	AP	AQ
AA		0.010	0.014	0.016	0.016	0.015	0.015	0.018	0.018	0.017	0.016	0.015	0.015	0.016	0.018	0.015	0.015
AB	0.076		0.016	0.016	0.018	0.018	0.018	0.017	0.018	0.017	0.017	0.017	0.017	0.016	0.018	0.017	0.017
AC	0.203	0.224		0.017	0.016	0.016	0.016	0.018	0.018	0.016	0.017	0.016	0.016	0.015	0.018	0.016	0.015
AD	0.221	0.224	0.218		0.017	0.018	0.017	0.018	0.019	0.019	0.017	0.017	0.016	0.017	0.018	0.017	0.016
AE	0.232	0.233	0.224	0.226		0.010	0.015	0.016	0.009	0.015	0.015	0.017	0.016	0.015	0.017	0.017	0.016
AF	0.249	0.252	0.239	0.234	0.089		0.014	0.016	0.012	0.014	0.015	0.016	0.016	0.015	0.018	0.016	0.015
AG	0.236	0.250	0.239	0.219	0.198	0.192		0.016	0.017	0.015	0.016	0.017	0.015	0.016	0.018	0.016	0.016
AH	0.247	0.232	0.249	0.234	0.205	0.200	0.199		0.016	0.016	0.016	0.018	0.017	0.017	0.018	0.018	0.018
AI	0.256	0.249	0.244	0.241	0.051	0.085	0.213	0.210		0.015	0.016	0.018	0.018	0.017	0.018	0.018	0.017
AJ	0.233	0.223	0.243	0.249	0.177	0.181	0.195	0.215	0.161		0.015	0.016	0.015	0.016	0.019	0.017	0.016
AK	0.242	0.223	0.250	0.215	0.173	0.184	0.201	0.193	0.174	0.164		0.016	0.016	0.015	0.017	0.016	0.016
AL	0.226	0.228	0.241	0.213	0.229	0.219	0.247	0.230	0.236	0.228	0.240		0.015	0.015	0.019	0.016	0.017
AM	0.228	0.217	0.226	0.195	0.232	0.222	0.225	0.237	0.232	0.193	0.229	0.202		0.015	0.019	0.015	0.016
AN	0.211	0.200	0.212	0.208	0.203	0.213	0.233	0.224	0.215	0.210	0.216	0.202	0.204		0.018	0.015	0.016
AO	0.226	0.239	0.250	0.243	0.228	0.246	0.248	0.243	0.249	0.246	0.215	0.250	0.240	0.226		0.019	0.018
AP	0.219	0.221	0.211	0.215	0.221	0.243	0.218	0.234	0.224	0.222	0.216	0.236	0.210	0.211	0.244		0.016
AQ	0.208	0.219	0.205	0.194	0.219	0.224	0.233	0.225	0.234	0.228	0.216	0.233	0.222	0.216	0.232	0.207	

Table 4. Mean COXI distances (D) within lineages of Amphipoda. s.e.= standard error.

Lineage	D	s.e.
AC	0.027	0.006
AQ	0.016	0.004

Table 5a. Mean COXI distances (below diagonal) between lineages of Araneae. Distances between lineages from Murrays Hill and the remaining lineages are highlighted in yellow. Above diagonal= standard error.

Lineage	ArA	ArB	ArC	ArD	ArE	ArF	ArG	ArH
ArA		0.014	0.018	0.018	0.017	0.019	0.019	0.018
ArB	0.124		0.018	0.018	0.016	0.018	0.019	0.019
ArC	0.230	0.224		0.019	0.017	0.015	0.014	0.016
ArD	0.221	0.221	0.255		0.015	0.020	0.019	0.019
ArE	0.175	0.152	0.190	0.143		0.019	0.019	0.018
ArF	0.217	0.233	0.134	0.242	0.228		0.015	0.016
ArG	0.226	0.237	0.128	0.252	0.215	0.140		0.015
ArH	0.214	0.223	0.124	0.242	0.196	0.133	0.135	

Table 5b. Mean COXI distances (D) within lineages of Araneae. s.e.= standard error.

Lineage	D	s.e.
ArA	0.008	0.004
ArG	0.025	0.007

Table 6. Mean COXI distances (below diagonal) between lineages of Blattodea. Distances between lineages from Murrays Hill and the remaining lineages are highlighted in yellow. Lineages are grouped into major clades BA and BB. Above diagonal= standard error.

Lineage	BA	BB	BC	BD	BE	BF	BG	BH	BI	BJ	BK
BA		0.015	0.016	0.015	0.016	0.016	0.015	0.016	0.016	0.016	0.016
BB	0.155		0.018	0.018	0.018	0.018	0.018	0.018	0.018	0.018	0.018
BC	0.244	0.262		0.012	0.012	0.012	0.012	0.012	0.012	0.012	0.013
BD	0.227	0.254	0.111		0.012	0.013	0.012	0.014	0.013	0.013	0.013
BE	0.232	0.243	0.114	0.101		0.014	0.012	0.014	0.013	0.013	0.013
BF	0.240	0.266	0.123	0.127	0.136		0.011	0.013	0.012	0.011	0.011
BG	0.235	0.247	0.115	0.115	0.112	0.104		0.013	0.011	0.012	0.012
BH	0.235	0.243	0.127	0.141	0.141	0.112	0.112		0.012	0.013	0.013
BI	0.241	0.250	0.121	0.140	0.126	0.122	0.099	0.113		0.011	0.012
BJ	0.242	0.263	0.121	0.133	0.133	0.091	0.123	0.122	0.116		0.007
BK	0.237	0.245	0.122	0.131	0.127	0.097	0.110	0.113	0.110	0.046	

Table 7. Mean COXI distances (D) within lineages of Blattodea. s.e.= standard error.

Lineage	D	s.e.
BC	0.024	0.005
BI	0.032	0.007
BJ	0.028	0.005

Table 8. Mean COXI distances (below diagonal) between lineages of Chilopoda (Scolopendromorpha). Above diagonal= standard error.

Lineage	ScA	ScB	ScC	ScD	ScE	ScF	ScG	ScH
ScA		0.014	0.014	0.016	0.017	0.015	0.016	0.016
ScB	0.158		0.014	0.016	0.015	0.016	0.016	0.017
ScC	0.170	0.166		0.016	0.015	0.016	0.015	0.016
ScD	0.190	0.211	0.216		0.017	0.016	0.017	0.017
ScE	0.234	0.229	0.230	0.241		0.015	0.015	0.014
ScF	0.213	0.220	0.227	0.214	0.201		0.015	0.016
ScG	0.233	0.239	0.236	0.240	0.182	0.169		0.015
ScH	0.218	0.223	0.225	0.213	0.174	0.173	0.186	

Table 9. Mean COXI distances (below diagonal) between lineages of Carabidae. Distances between lineages detected in Murrays Hill and the remaining lineages are highlighted in yellow. Above diagonal= standard error.

Lineage	CaA	CaB	CaC	CaD	CaE	CaF	CaG	CaH	CaI	CaJ	CaK
CaA		0.009	0.011	0.009	0.016	0.015	0.017	0.018	0.017	0.017	0.015
CaB	0.036		0.011	0.010	0.018	0.017	0.018	0.019	0.018	0.018	0.016
CaC	0.062	0.058		0.010	0.018	0.017	0.017	0.019	0.018	0.018	0.016
CaD	0.043	0.048	0.048		0.016	0.016	0.016	0.018	0.017	0.017	0.014
CaE	0.163	0.169	0.173	0.152		0.016	0.017	0.018	0.016	0.016	0.016
CaF	0.145	0.162	0.168	0.144	0.151		0.015	0.018	0.017	0.017	0.016
CaG	0.173	0.177	0.178	0.163	0.161	0.133		0.019	0.017	0.018	0.017
CaH	0.192	0.196	0.189	0.176	0.171	0.180	0.194		0.019	0.017	0.016
CaI	0.185	0.199	0.192	0.169	0.174	0.176	0.179	0.208		0.016	0.016
CaJ	0.166	0.177	0.185	0.156	0.170	0.163	0.179	0.164	0.154		0.017
CaK	0.144	0.159	0.164	0.127	0.164	0.151	0.178	0.182	0.185	0.172	

Table 10. Mean COXI distances (below diagonal) between lineages of Diplopoda. Distances between lineages detected in Murrays Hill and the remaining lineages are highlighted in yellow. Above diagonal= standard error.

Lineage	PA-PB	PC	PD	PE-PF	PG-PH-PI	PJ	PK-PL-PM	PN	PO	PP	PQ	PR	PS
PA-PB		0.012	0.013	0.012	0.012	0.013	0.013	0.013	0.014	0.012	0.016	0.016	0.014
PC	0.092		0.009	0.010	0.010	0.012	0.012	0.012	0.013	0.010	0.015	0.015	0.015
PD	0.112	0.052		0.011	0.011	0.012	0.012	0.012	0.013	0.010	0.015	0.015	0.015
PE-PF	0.089	0.079	0.089		0.007	0.009	0.012	0.012	0.012	0.008	0.015	0.014	0.014
PG-PH-PI	0.092	0.084	0.097	0.048		0.008	0.011	0.012	0.012	0.008	0.014	0.014	0.014
PJ	0.097	0.085	0.097	0.051	0.045		0.009	0.010	0.009	0.005	0.014	0.014	0.015
PK-PL-PM	0.119	0.107	0.110	0.110	0.105	0.053		0.007	0.005	0.004	0.014	0.014	0.014
PN	0.111	0.106	0.105	0.106	0.107	0.059	0.038		0.007	0.005	0.014	0.014	0.014
PO	0.117	0.112	0.113	0.105	0.107	0.049	0.024	0.031		0.002	0.015	0.015	0.014
PP	0.066	0.051	0.055	0.039	0.038	0.011	0.013	0.015	0.002		0.014	0.014	0.014
PQ	0.175	0.162	0.165	0.168	0.160	0.144	0.159	0.158	0.150	0.108		0.015	0.016
PR	0.177	0.192	0.189	0.174	0.169	0.167	0.171	0.171	0.168	0.125	0.183		0.015
PS	0.145	0.170	0.171	0.147	0.149	0.148	0.155	0.150	0.149	0.112	0.188	0.168	

Table 11. Mean COXI distances (D) within lineages of Diplopoda. s.e.= standard error.

Lineage	D	s.e.
PA-PB	0.024	0.007
PE-PF	0.023	0.006
PG-PH-PI	0.028	0.006
PK-PL-PM	0.023	0.004
PN	0.007	0.002

Table 12. Mean COXI distances (below diagonal) between lineages of Diplura. Above diagonal= standard error. Lineages are grouped by family clades; Jap= Japygidae, Para= Parajapygidae, Pro= Projapygidae, Ana=Anajapygidae.

a. Japygidae

Lineage	DC	DD	DE	DF	DG	DH	DQ	DR
DC		0.015	0.014	0.014	0.014	0.014	0.013	0.014
DD	0.168		0.014	0.013	0.014	0.014	0.014	0.016
DE	0.185	0.181		0.011	0.013	0.014	0.012	0.013
DF	0.186	0.161	0.112		0.013	0.014	0.012	0.013
DG	0.190	0.163	0.142	0.158		0.014	0.013	0.014
DH	0.202	0.182	0.172	0.183	0.169		0.013	0.013
DQ	0.179	0.171	0.138	0.137	0.128	0.157		0.012
DR	0.200	0.185	0.147	0.163	0.153	0.149	0.130	

b. Parajapygidae

Lineage	DI	DJ	DS
DI		0.013	0.013
DJ	0.152		0.014
DS	0.152	0.169	

c. Projapygidae

Lineage	DK	DL	DM	DN	DO	DP	DT
DK		0.011	0.013	0.015	0.014	0.014	0.013
DL	0.113		0.012	0.014	0.014	0.013	0.013
DM	0.143	0.134		0.013	0.013	0.013	0.013
DN	0.170	0.187	0.160		0.013	0.014	0.014
DO	0.183	0.181	0.145	0.141		0.014	0.014
DP	0.156	0.162	0.146	0.156	0.152		0.013
DT	0.168	0.168	0.168	0.187	0.168	0.143	

Table 13. Mean COXI distances (below diagonal) between lineages of Hemiptera (Meenoplidae). Above diagonal= standard error. Distances between lineages detected in Murrays Hill and the remaining lineages are highlighted in yellow.

Lineage	MA	MB	MC	MD	ME	MF	MG	MH	MI	MJ
MA		0.014	0.013	0.014	0.014	0.015	0.015	0.017	0.018	0.018
MB	0.167		0.010	0.012	0.012	0.013	0.013	0.015	0.015	0.015
MC	0.163	0.102		0.011	0.012	0.012	0.013	0.017	0.015	0.016
MD	0.157	0.121	0.107		0.012	0.012	0.014	0.016	0.016	0.015
ME	0.163	0.136	0.128	0.111		0.013	0.014	0.015	0.015	0.015
MF	0.178	0.157	0.138	0.142	0.158		0.014	0.016	0.015	0.015
MG	0.192	0.151	0.131	0.164	0.168	0.141		0.016	0.016	0.016
MH	0.250	0.229	0.221	0.227	0.223	0.210	0.217		0.012	0.013
MI	0.234	0.224	0.203	0.212	0.189	0.207	0.205	0.127		0.008
MJ	0.236	0.215	0.203	0.191	0.187	0.208	0.205	0.137	0.045	

Table 14. Mean COXI distances (D) within lineages of Hemiptera. s.e.= standard error.

Lineage	D	s.e.
MB	0.009	0.003
MG	0.003	0.002

Table 15. Mean COXI distances (below diagonal) between lineages of Palpigradi. Distances between lineages detected in Murrays Hill and the remaining lineages are highlighted in yellow. Above diagonal= standard error.

Lineage	PaA	PaB	PaC	PaD	PaE	PaF	PaG	PaH	PaI	PaJ
PaA		0.015	0.016	0.015	0.016	0.016	0.017	0.017	0.015	0.018
PaB	0.217		0.016	0.016	0.016	0.018	0.017	0.018	0.016	0.018
PaC	0.255	0.264		0.014	0.015	0.019	0.016	0.016	0.016	0.018
PaD	0.250	0.261	0.191		0.016	0.017	0.017	0.016	0.015	0.018
PaE	0.240	0.250	0.243	0.274		0.017	0.016	0.016	0.015	0.018
PaF	0.231	0.254	0.244	0.234	0.224		0.018	0.017	0.017	0.019
PaG	0.291	0.304	0.279	0.314	0.276	0.255		0.017	0.017	0.017
PaH	0.272	0.306	0.256	0.277	0.276	0.231	0.274		0.016	0.017
PaI	0.269	0.261	0.263	0.260	0.266	0.236	0.295	0.279		0.017
PaJ	0.345	0.362	0.330	0.341	0.365	0.323	0.285	0.306	0.334	

Table 16. Mean COXI distances (below diagonal) between lineages of Pauropoda. Distances between lineages detected in Murrays Hill and the remaining lineages are highlighted in yellow. Above diagonal= standard error.

Lineage	PrA	PrB	PrC	PrD	PrE	PrF
PrA		0.017	0.017	0.017	0.017	0.017
PrB	0.331		0.016	0.016	0.018	0.018
PrC	0.330	0.246		0.015	0.018	0.018
PrD	0.321	0.251	0.213		0.018	0.019
PrE	0.195	0.313	0.330	0.318		0.019
PrF	0.292	0.337	0.315	0.347	0.303	

Table 17. Mean COXI distances (below diagonal) between lineages of Schizomida. Distances between lineages from Murrays Hill and the reference lineages are highlighted in yellow. Above diagonal= standard error.

Lineage	SzA	SzB	SzC	SzD	SzE	SzF	SzG	SzH	SzI	SzJ	SzK	SzL	SzM	SzN	SzO	SzP	SzQ	SzR	SzS	SzT	SzU	SzV	SzW
SzA		0.014	0.016	0.016	0.016	0.015	0.014	0.015	0.015	0.015	0.016	0.016	0.013	0.015	0.014	0.015	0.015	0.015	0.016	0.016	0.015	0.015	0.015
SzB	0.177		0.014	0.014	0.013	0.014	0.014	0.014	0.013	0.014	0.013	0.015	0.014	0.013	0.012	0.015	0.013	0.014	0.014	0.015	0.014	0.014	0.013
SzC	0.167	0.139		0.011	0.011	0.011	0.011	0.013	0.013	0.013	0.012	0.014	0.013	0.013	0.012	0.014	0.014	0.014	0.014	0.015	0.014	0.014	0.014
SzD	0.177	0.169	0.094		0.012	0.013	0.012	0.014	0.012	0.013	0.012	0.014	0.014	0.013	0.013	0.014	0.014	0.014	0.013	0.014	0.014	0.014	0.014
SzE	0.190	0.141	0.091	0.112		0.011	0.012	0.014	0.013	0.013	0.012	0.015	0.014	0.013	0.013	0.014	0.014	0.014	0.014	0.015	0.014	0.014	0.013
SzF	0.185	0.138	0.084	0.122	0.102		0.011	0.014	0.012	0.013	0.012	0.014	0.014	0.013	0.012	0.014	0.013	0.014	0.013	0.015	0.014	0.013	0.013
SzG	0.162	0.151	0.099	0.118	0.109	0.092		0.014	0.014	0.013	0.013	0.015	0.014	0.014	0.013	0.015	0.014	0.014	0.014	0.015	0.014	0.014	0.014
SzH	0.180	0.157	0.138	0.147	0.157	0.138	0.141		0.013	0.013	0.013	0.015	0.014	0.013	0.012	0.014	0.014	0.014	0.015	0.014	0.014	0.014	0.014
SzI	0.180	0.120	0.131	0.139	0.147	0.131	0.147	0.125		0.013	0.008	0.015	0.014	0.013	0.013	0.014	0.013	0.013	0.013	0.014	0.013	0.014	0.013
SzJ	0.178	0.139	0.156	0.151	0.164	0.144	0.152	0.141	0.115		0.013	0.016	0.014	0.014	0.013	0.014	0.015	0.014	0.015	0.015	0.014	0.013	0.014
SzK	0.164	0.131	0.120	0.120	0.144	0.126	0.135	0.125	0.052	0.138		0.014	0.014	0.013	0.013	0.014	0.013	0.013	0.013	0.014	0.013	0.013	0.013
SzL	0.181	0.162	0.156	0.158	0.165	0.158	0.158	0.154	0.148	0.165	0.139		0.015	0.015	0.014	0.016	0.015	0.016	0.015	0.016	0.016	0.016	0.014
SzM	0.149	0.151	0.143	0.157	0.162	0.149	0.135	0.147	0.151	0.147	0.139	0.133		0.013	0.013	0.013	0.012	0.013	0.014	0.015	0.013	0.014	0.013
SzN	0.170	0.149	0.128	0.146	0.144	0.139	0.144	0.138	0.130	0.143	0.126	0.158	0.141		0.014	0.014	0.014	0.014	0.013	0.014	0.014	0.013	0.013
SzO	0.177	0.125	0.128	0.146	0.154	0.138	0.130	0.133	0.119	0.138	0.117	0.160	0.145	0.141		0.013	0.013	0.013	0.015	0.015	0.013	0.013	0.014
SzP	0.180	0.182	0.164	0.160	0.170	0.164	0.162	0.154	0.154	0.147	0.146	0.192	0.147	0.151	0.141		0.015	0.015	0.014	0.015	0.012	0.011	0.015
SzQ	0.169	0.146	0.149	0.151	0.172	0.149	0.157	0.143	0.139	0.162	0.126	0.160	0.118	0.139	0.138	0.162		0.009	0.013	0.015	0.014	0.013	0.010
SzR	0.178	0.147	0.144	0.146	0.165	0.151	0.160	0.139	0.130	0.157	0.120	0.165	0.125	0.141	0.135	0.172	0.055		0.014	0.016	0.014	0.014	0.010
SzS	0.193	0.177	0.164	0.149	0.175	0.157	0.157	0.172	0.138	0.164	0.126	0.162	0.160	0.154	0.158	0.162	0.157	0.157		0.014	0.014	0.015	0.013
SzT	0.190	0.171	0.174	0.183	0.188	0.172	0.172	0.167	0.146	0.153	0.155	0.188	0.171	0.153	0.164	0.174	0.172	0.187	0.147		0.014	0.014	0.015
SzU	0.173	0.166	0.155	0.156	0.158	0.155	0.158	0.155	0.142	0.147	0.127	0.180	0.137	0.153	0.136	0.091	0.145	0.143	0.150	0.154		0.009	0.014
SzV	0.180	0.167	0.160	0.165	0.169	0.152	0.156	0.159	0.143	0.152	0.135	0.167	0.141	0.154	0.143	0.089	0.160	0.162	0.159	0.156	0.062		0.013
SzW	0.172	0.135	0.146	0.156	0.160	0.151	0.149	0.144	0.131	0.154	0.123	0.148	0.115	0.133	0.148	0.164	0.063	0.060	0.157	0.187	0.143	0.152	

Table 18. Mean COXI distances (below diagonal) between lineages of Syncarida –Bathynellidae. Distances between lineages from Murrays Hill and the remaining lineages are highlighted in yellow. Above diagonal= standard error.

Lineage	SBA	SBB	SBC	SBD	SBE	SBF	SBG	SBH	SBI	SBJ	SBK	SBL
SBA		0.015	0.015	0.019	0.015	0.015	0.016	0.016	0.015	0.017	0.015	0.015
SBB	0.180		0.015	0.020	0.014	0.014	0.015	0.016	0.014	0.016	0.015	0.014
SBC	0.203	0.195		0.020	0.015	0.015	0.017	0.017	0.017	0.016	0.018	0.017
SBD	0.210	0.219	0.207		0.019	0.020	0.021	0.019	0.020	0.021	0.018	0.019
SBE	0.191	0.166	0.176	0.200		0.013	0.016	0.016	0.015	0.016	0.015	0.015
SBF	0.200	0.164	0.188	0.198	0.147		0.015	0.017	0.016	0.016	0.016	0.016
SBG	0.253	0.241	0.285	0.269	0.238	0.255		0.015	0.015	0.018	0.015	0.015
SBH	0.216	0.209	0.256	0.214	0.228	0.238	0.224		0.010	0.017	0.013	0.013
SBI	0.216	0.199	0.240	0.221	0.216	0.238	0.217	0.082		0.017	0.013	0.013
SBJ	0.245	0.246	0.248	0.269	0.256	0.264	0.271	0.235	0.230		0.016	0.016
SBK	0.210	0.190	0.254	0.221	0.226	0.232	0.224	0.135	0.136	0.237		0.011
SBL	0.215	0.199	0.251	0.214	0.226	0.226	0.214	0.132	0.137	0.243	0.098	

Table 19. Mean COXI distances (below diagonal) between lineages of Syncarida –Parabathynellidae. Distances between lineages from Murrays Hill and the reference lineages are highlighted in yellow. Above diagonal= standard error.

Lineage	SPA	SPB	SPC	SPD	SPE	SPF	SPG	SPH	SPI	SPJ	SPK	SPL	SPM	SPN	SPO	SPP	SPQ	SPR	SPS	SPT	SPU
SPA		0.017	0.015	0.015	0.015	0.015	0.016	0.016	0.016	0.016	0.016	0.016	0.018	0.019	0.019	0.019	0.018	0.017	0.016	0.016	0.016
SPB	0.156		0.016	0.016	0.015	0.017	0.018	0.019	0.017	0.018	0.018	0.018	0.016	0.019	0.019	0.019	0.018	0.021	0.019	0.018	0.019
SPC	0.201	0.143		0.011	0.011	0.015	0.015	0.016	0.014	0.015	0.016	0.015	0.017	0.019	0.018	0.019	0.018	0.016	0.017	0.016	0.016
SPD	0.200	0.150	0.089		0.008	0.014	0.015	0.015	0.014	0.015	0.016	0.015	0.018	0.019	0.019	0.018	0.018	0.016	0.017	0.016	0.015
SPE	0.182	0.140	0.085	0.048		0.015	0.014	0.014	0.014	0.014	0.016	0.015	0.016	0.018	0.017	0.018	0.017	0.015	0.016	0.015	0.015
SPF	0.204	0.192	0.194	0.188	0.173		0.015	0.015	0.014	0.015	0.016	0.016	0.017	0.019	0.019	0.019	0.017	0.016	0.016	0.015	0.016
SPG	0.205	0.190	0.182	0.180	0.164	0.182		0.014	0.014	0.015	0.015	0.015	0.017	0.018	0.018	0.018	0.018	0.016	0.015	0.015	0.015
SPH	0.211	0.210	0.223	0.211	0.186	0.216	0.179		0.014	0.015	0.013	0.014	0.018	0.019	0.018	0.019	0.018	0.016	0.015	0.015	0.015
SPI	0.199	0.170	0.163	0.166	0.145	0.192	0.144	0.192		0.008	0.015	0.015	0.016	0.017	0.018	0.019	0.016	0.016	0.015	0.014	0.014
SPJ	0.198	0.172	0.179	0.163	0.152	0.204	0.144	0.182	0.066		0.015	0.015	0.015	0.018	0.018	0.019	0.017	0.016	0.015	0.014	0.014
SPK	0.222	0.212	0.222	0.210	0.200	0.210	0.195	0.155	0.198	0.191		0.015	0.018	0.019	0.019	0.019	0.018	0.017	0.017	0.015	0.015
SPL	0.235	0.201	0.209	0.209	0.189	0.230	0.202	0.164	0.216	0.221	0.179		0.018	0.020	0.019	0.019	0.018	0.017	0.016	0.016	0.016
SPM	0.209	0.170	0.184	0.177	0.162	0.209	0.167	0.200	0.167	0.154	0.221	0.205		0.016	0.015	0.017	0.017	0.016	0.018	0.017	0.019
SPN	0.242	0.221	0.219	0.215	0.206	0.240	0.203	0.223	0.205	0.194	0.242	0.255	0.171		0.015	0.014	0.016	0.018	0.017	0.016	0.018
SPO	0.221	0.205	0.207	0.211	0.187	0.228	0.190	0.211	0.196	0.188	0.217	0.211	0.138	0.159		0.016	0.016	0.017	0.018	0.017	0.017
SPP	0.255	0.214	0.248	0.238	0.223	0.248	0.213	0.225	0.215	0.205	0.251	0.244	0.188	0.144	0.188		0.016	0.017	0.017	0.015	0.019
SPQ	0.236	0.225	0.213	0.209	0.198	0.230	0.211	0.236	0.196	0.203	0.255	0.246	0.175	0.159	0.186	0.159		0.017	0.016	0.017	0.018
SPR	0.238	0.225	0.219	0.206	0.203	0.216	0.200	0.214	0.208	0.203	0.218	0.226	0.157	0.171	0.152	0.150	0.174		0.014	0.015	0.016
SPS	0.219	0.220	0.237	0.216	0.206	0.235	0.200	0.211	0.195	0.184	0.227	0.232	0.171	0.160	0.190	0.150	0.152	0.140		0.014	0.015
SPT	0.235	0.234	0.237	0.227	0.215	0.213	0.200	0.231	0.195	0.186	0.218	0.240	0.197	0.178	0.174	0.153	0.180	0.152	0.148		0.015
SPU	0.231	0.214	0.226	0.201	0.191	0.228	0.216	0.211	0.194	0.183	0.212	0.235	0.190	0.207	0.188	0.198	0.219	0.219	0.222	0.216	

Table 20. Mean COXI distances (below diagonal) between lineages of Thysanura. Distances between lineages from Murrays Hill and the remaining lineages are highlighted in yellow. Above diagonal= standard error.

a. Atelurinae

Lineage	TAA	TAD	TAE	TAH	TAK	TAI	TAM	TAN
TAA		0.011	0.013	0.014	0.013	0.015	0.021	0.018
TAD	0.041		0.012	0.012	0.014	0.015	0.023	0.020
TAE	0.078	0.058		0.013	0.013	0.015	0.023	0.019
TAH	0.078	0.061	0.067		0.015	0.014	0.022	0.019
TAK	0.084	0.079	0.074	0.087		0.014	0.023	0.019
TAI	0.096	0.094	0.099	0.090	0.070		0.023	0.020
TAM	0.259	0.247	0.273	0.225	0.264	0.257		0.022
TAN	0.164	0.181	0.177	0.171	0.158	0.180	0.261	

b. Nicoletiidae

Lineage	TNA	TNB	TNC	TND	TNE	TNF	TNG	TNH	TNI
TNA		0.020	0.019	0.019	0.021	0.021	0.018	0.020	0.020
TNB	0.181		0.021	0.021	0.019	0.020	0.024	0.017	0.019
TNC	0.166	0.204		0.013	0.021	0.021	0.022	0.020	0.020
TND	0.168	0.197	0.062		0.021	0.020	0.022	0.020	0.019
TNE	0.202	0.162	0.215	0.206		0.015	0.024	0.016	0.016
TNF	0.192	0.161	0.199	0.190	0.113		0.024	0.015	0.017
TNG	0.115	0.202	0.180	0.187	0.216	0.214		0.023	0.024
TNH	0.162	0.125	0.175	0.169	0.128	0.120	0.184		0.015
TNI	0.184	0.159	0.177	0.165	0.154	0.153	0.209	0.126	

Figure 1. Bayesian analysis of COXI haplotypes of Amphipoda. Numbers on major nodes correspond to posterior probabilities; values <50% are not shown. Specimens from Murrays Hill are highlighted in yellow; Genbank reference specimens are highlighted in turquoise. Scale bar= number of substitutions per site.

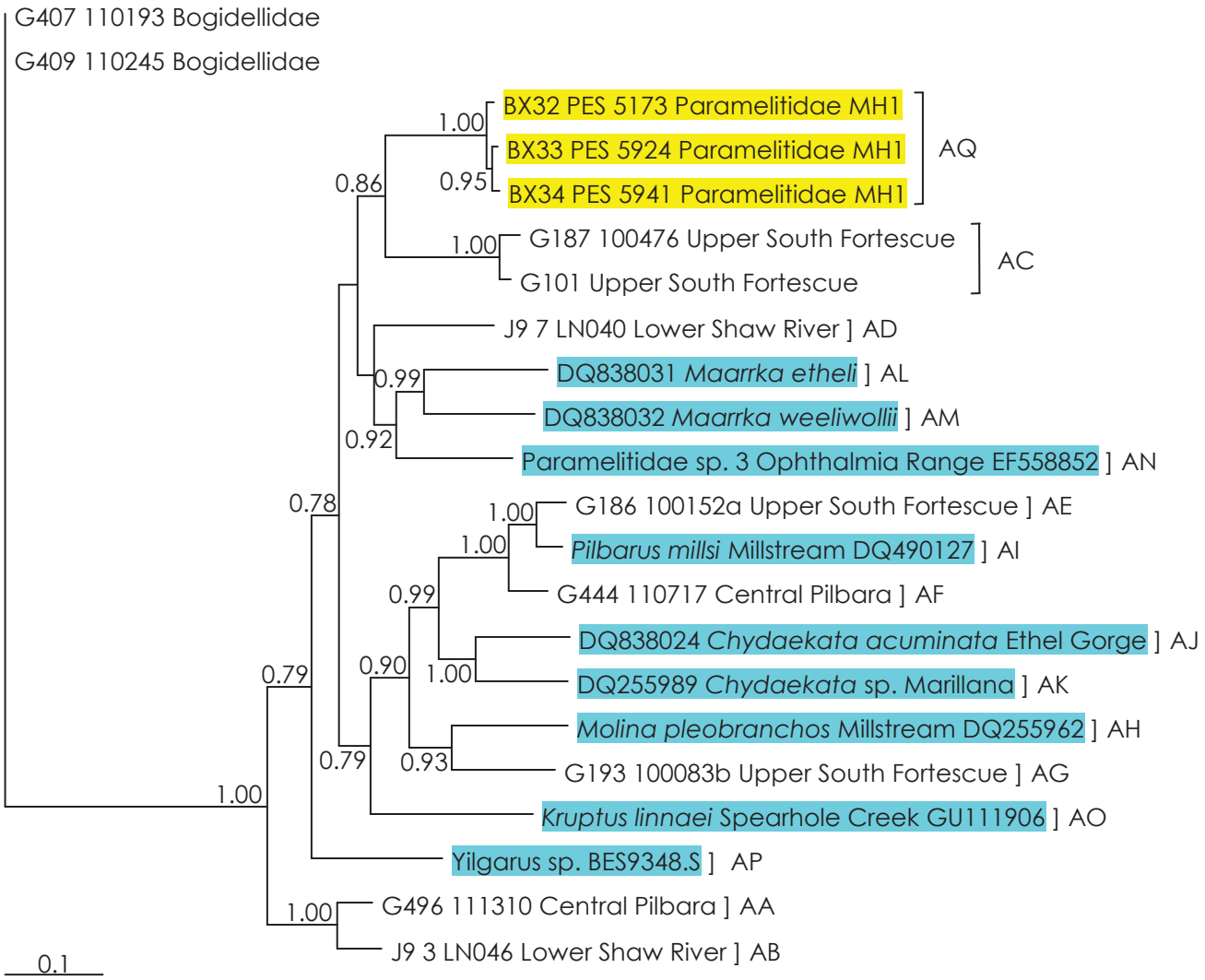


Figure 2. Bayesian analysis of COXI haplotypes of Araneae. Numbers on major nodes correspond to posterior probabilities; values <50% are not shown. Specimens from Murrays Hill are highlighted in yellow; Genbank reference specimens are highlighted in turquoise. Scale bar= number of substitutions per site.

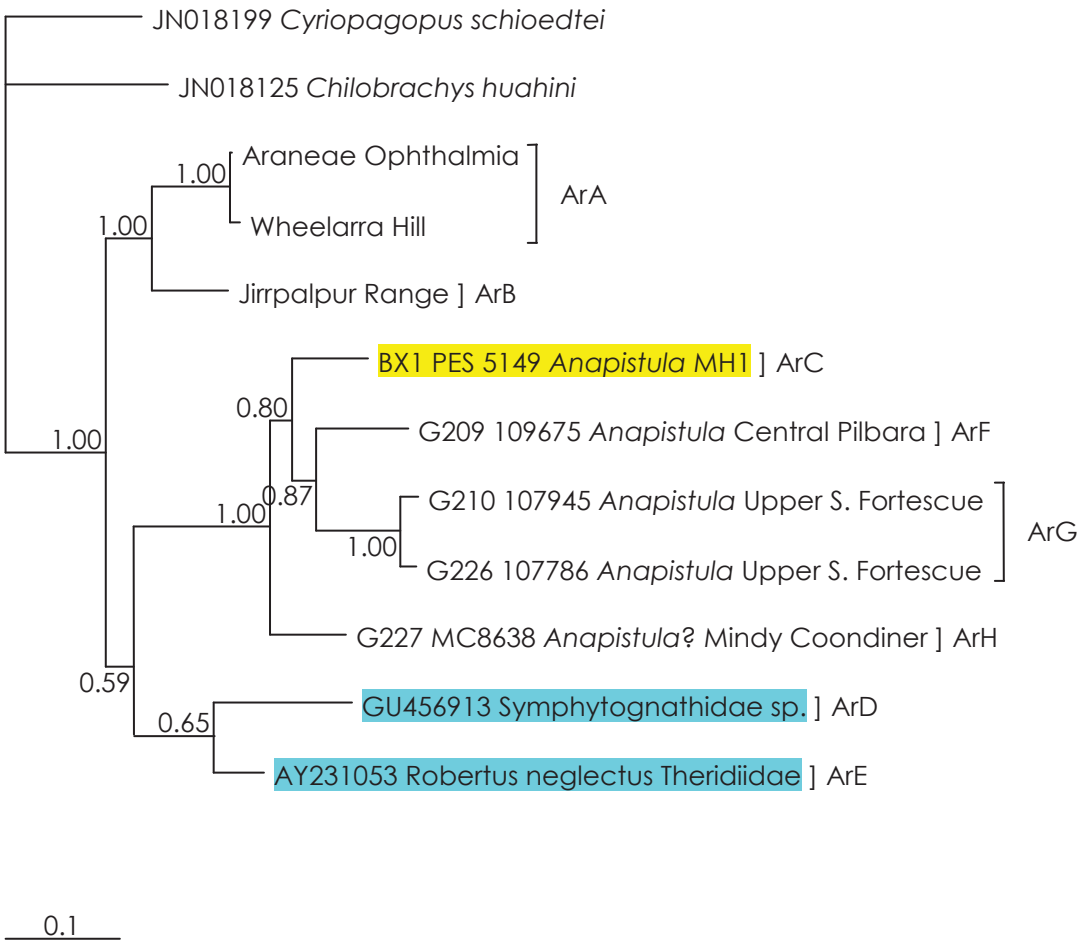


Figure 3. Bayesian analysis of COXI haplotypes of Blattodea. Numbers on major nodes correspond to posterior probabilities; values <50% are not shown. Specimens from Murrays Hill are highlighted in yellow. Scale bar= number of substitutions per site.

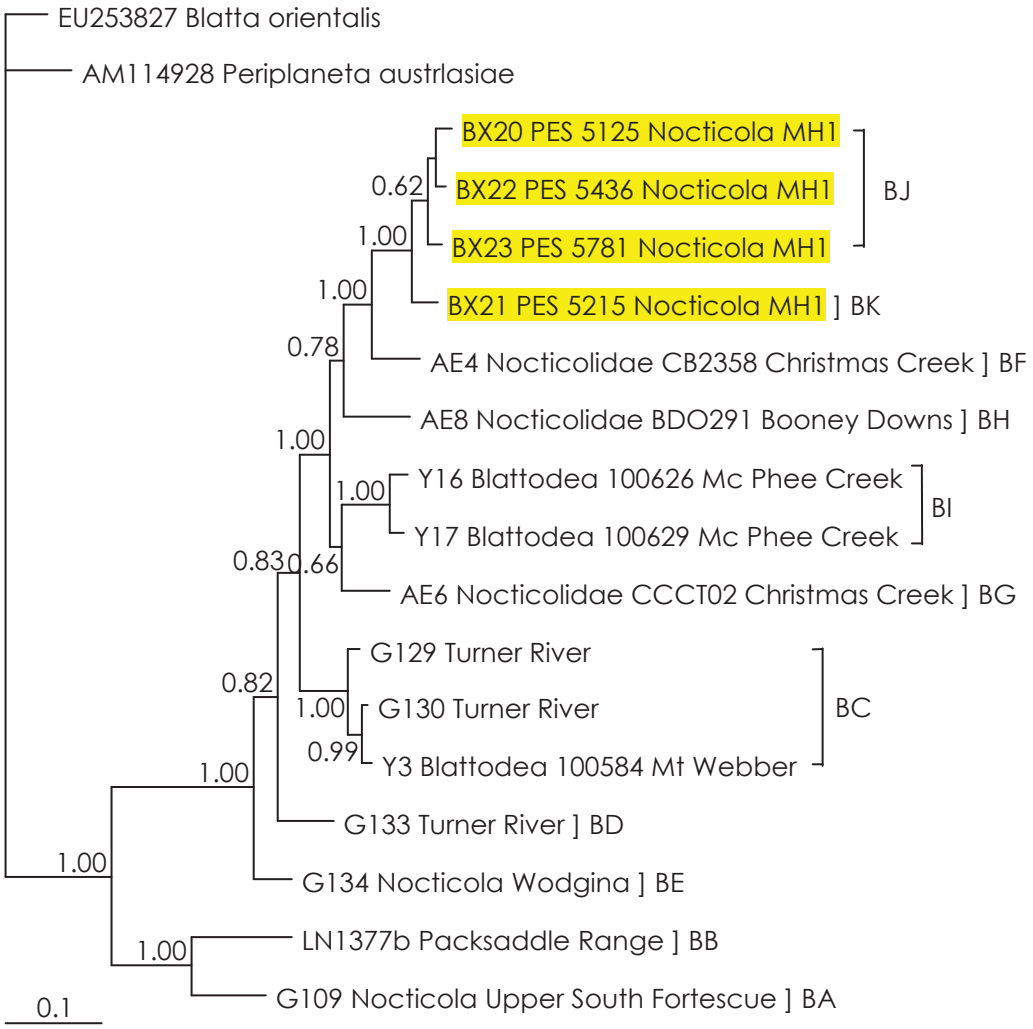


Figure 4. Bayesian analysis of COXI haplotypes of Chilopoda. Numbers on major nodes correspond to posterior probabilities; values <50% are not shown. Specimens from Murrays Hill are highlighted in yellow; Genbank reference specimens are highlighted in turquoise. Scale bar= number of substitutions per site.

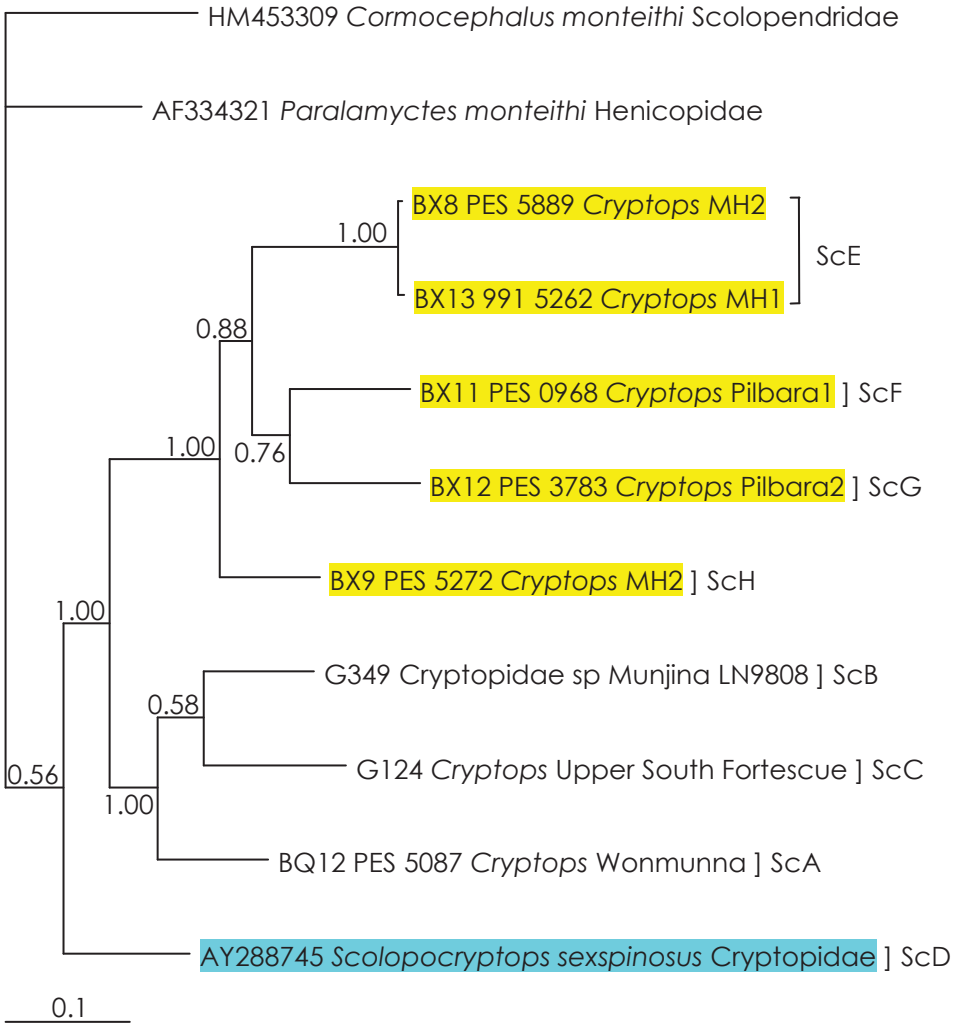


Figure 5. Bayesian analysis of COXI haplotypes of Coleoptera. Numbers on major nodes correspond to posterior probabilities; values <50% are not shown. Specimens from Murrays Hill are highlighted in yellow; Genbank reference specimens are highlighted in turquoise. Scale bar= number of substitutions per site.

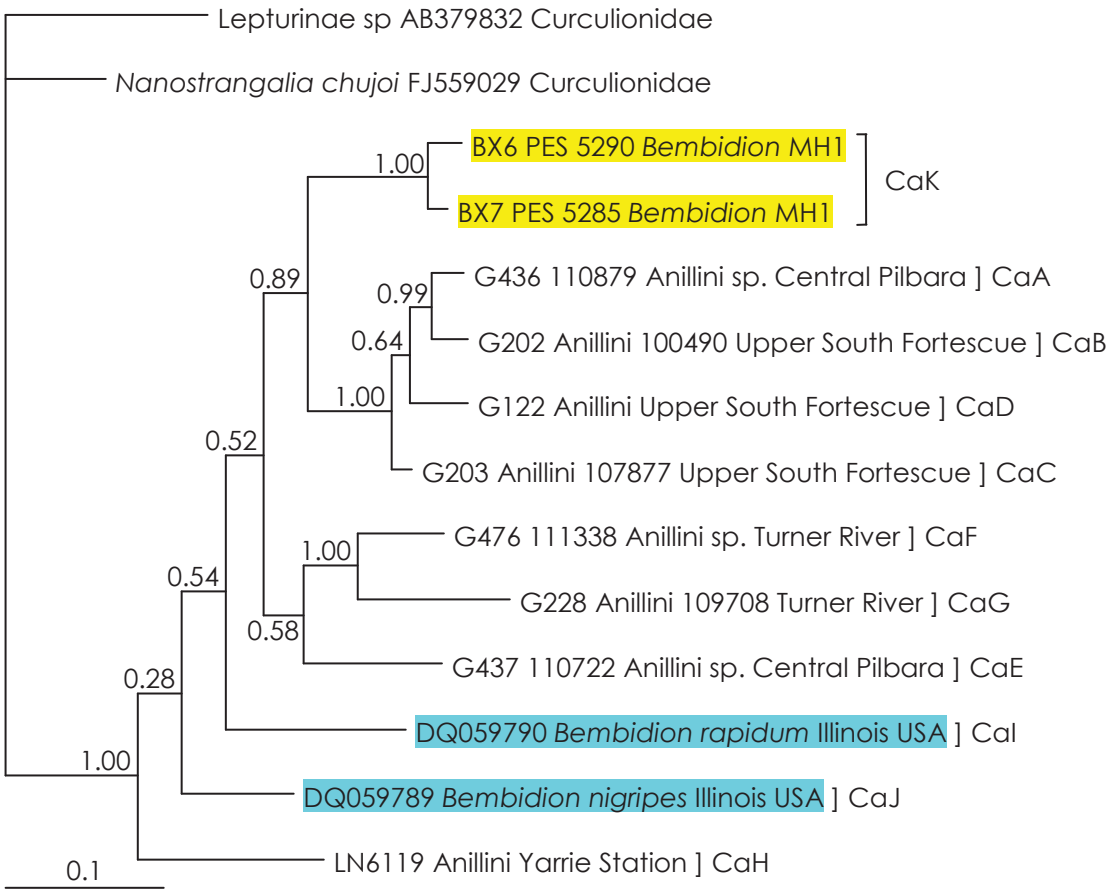


Figure 6. Bayesian analysis of COXI haplotypes of Diplopoda. Numbers on major nodes correspond to posterior probabilities; values <50% are not shown. Specimens from Murrays Hill are highlighted in yellow; Genbank reference specimens are highlighted in turquoise. Scale bar= number of substitutions per site.

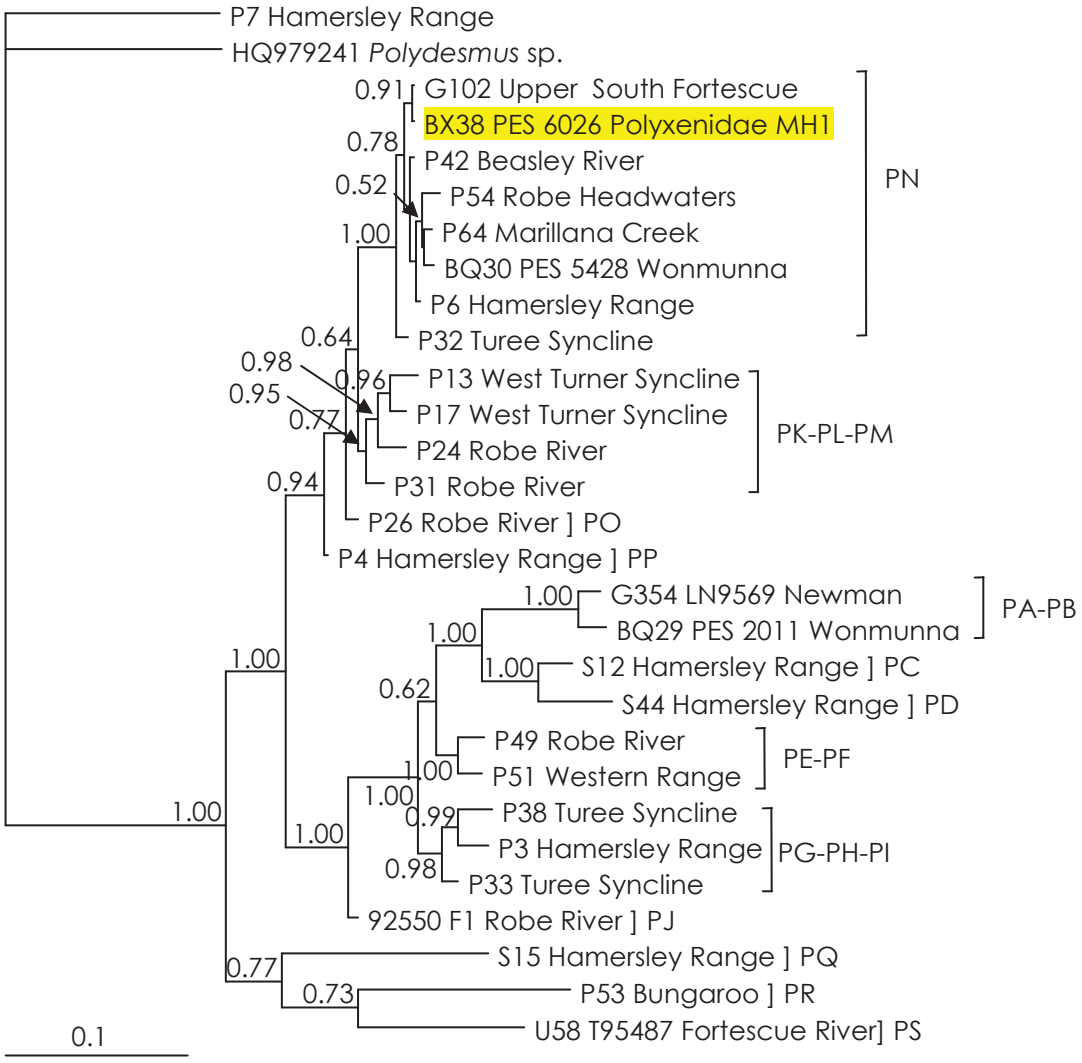


Figure 7. Bayesian analysis of COXI haplotypes of Diplura. Numbers on major nodes correspond to posterior probabilities; values <50% are not shown. Specimens from Murrays Hill are highlighted in yellow; Genbank reference specimens are highlighted in turquoise. Scale bar= number of substitutions per site.

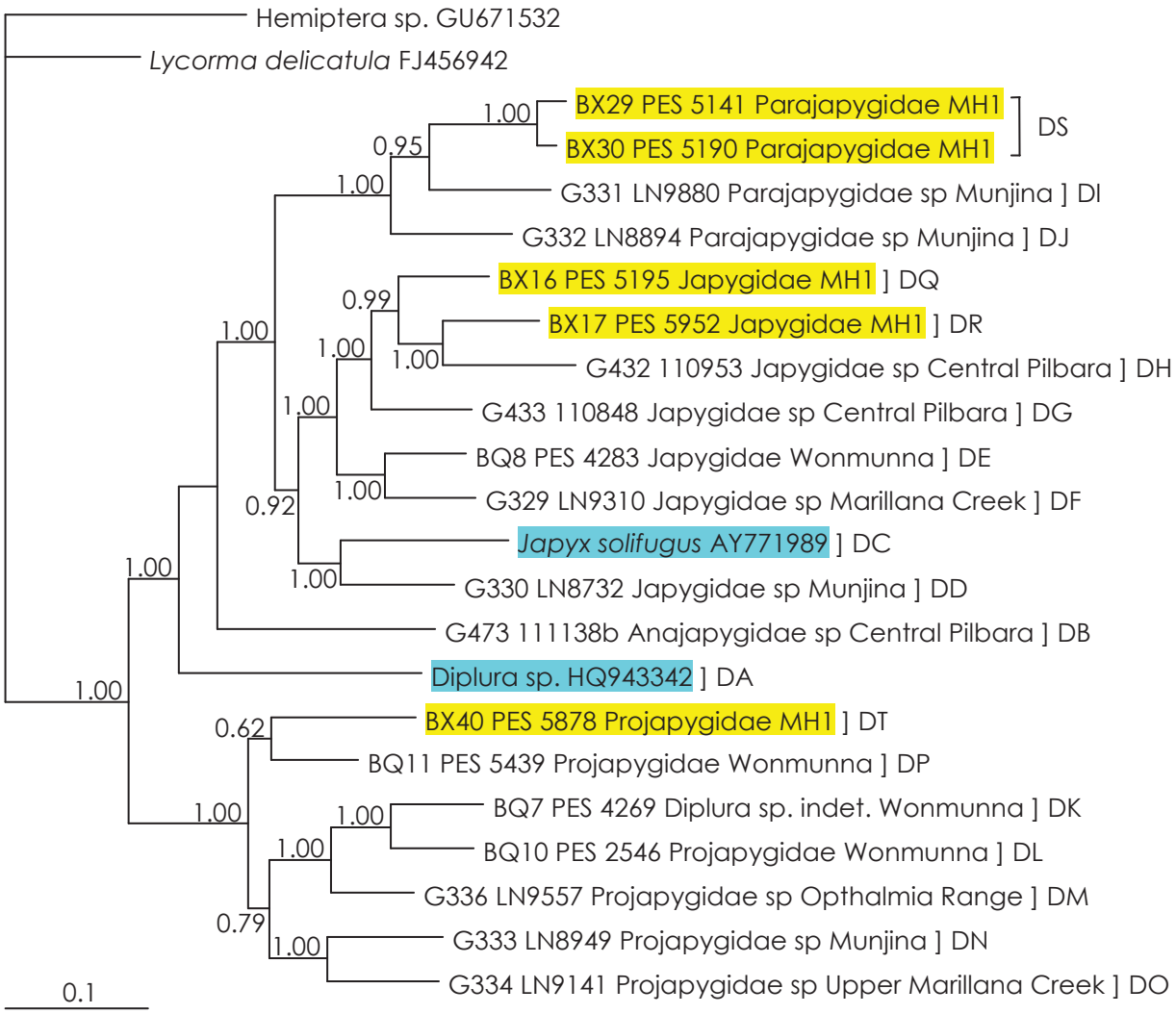


Figure 8. Bayesian analysis of COXI haplotypes of Hemiptera (Meenoplidae). Numbers on major nodes correspond to posterior probabilities; values <50% are not shown. Specimens from Murrays Hill are highlighted in yellow; Genbank reference specimens are highlighted in turquoise. Scale bar= number of substitutions per site.

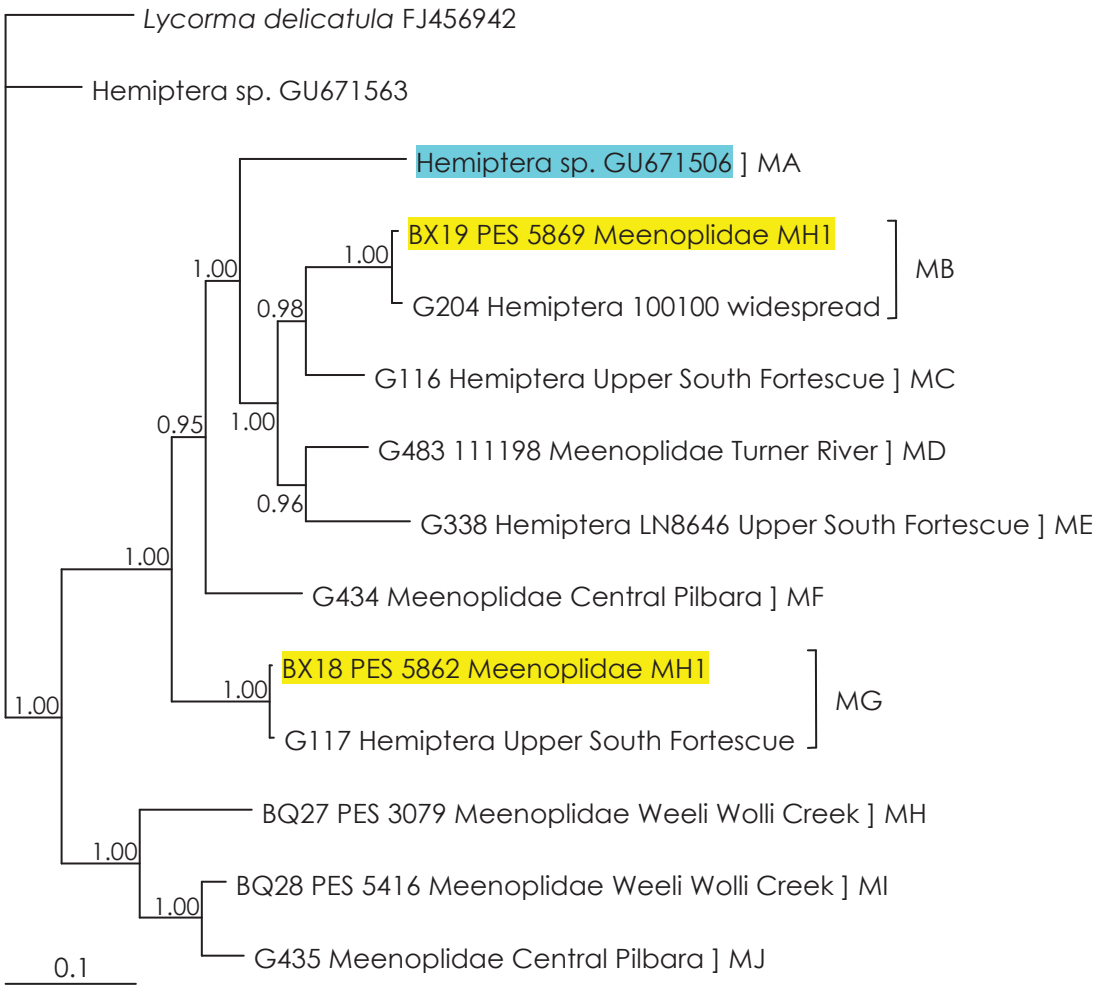


Figure 10. Bayesian analysis of COXI haplotypes of Palpigradi from Murrays Hill. Numbers on major nodes correspond to posterior probabilities; values <50% are not shown. Specimens from Murrays Hill are highlighted in yellow; Genbank reference specimens are highlighted in turquoise. Scale bar= number of substitutions per site.

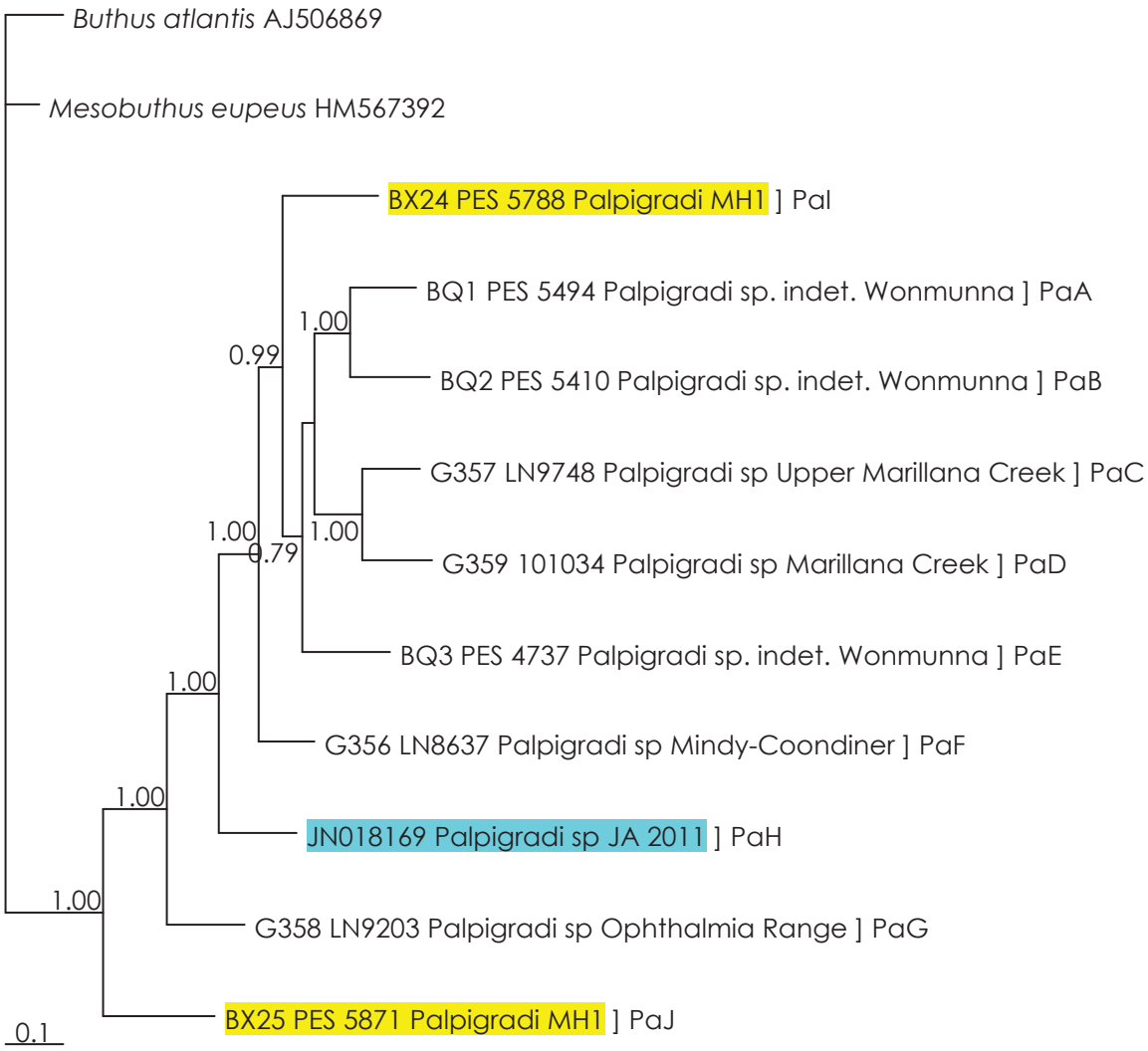


Figure 11. Bayesian analysis of COXI haplotypes of Pauropoda from Murrays Hill. Numbers on major nodes correspond to posterior probabilities; values <50% are not shown. Specimens from Murrays Hill are highlighted in yellow. Scale bar= number of substitutions per site.

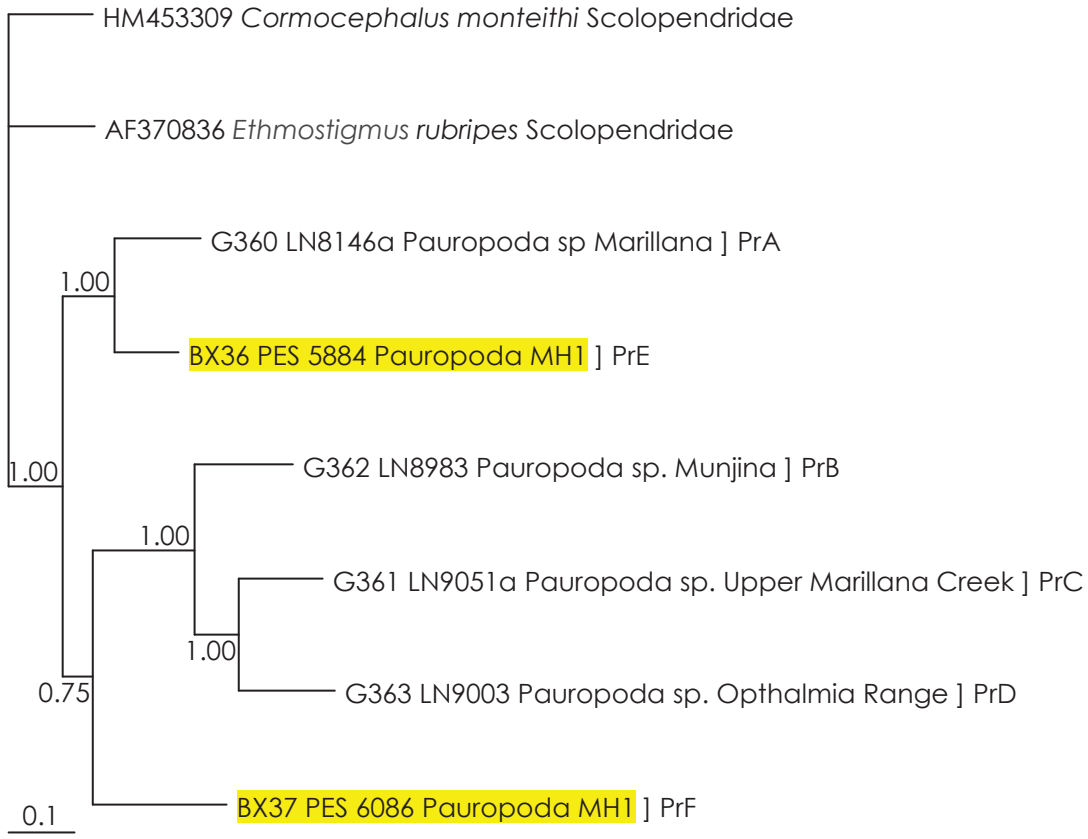


Figure 12. Bayesian analysis of COXI haplotypes of Schizomida from Murrays Hill. Numbers on major nodes correspond to posterior probabilities; values <50% are not shown. Specimens from Murrays Hill are highlighted in yellow; Genbank references sequences are highlighted in turquoise. Scale bar= number of substitutions per site.

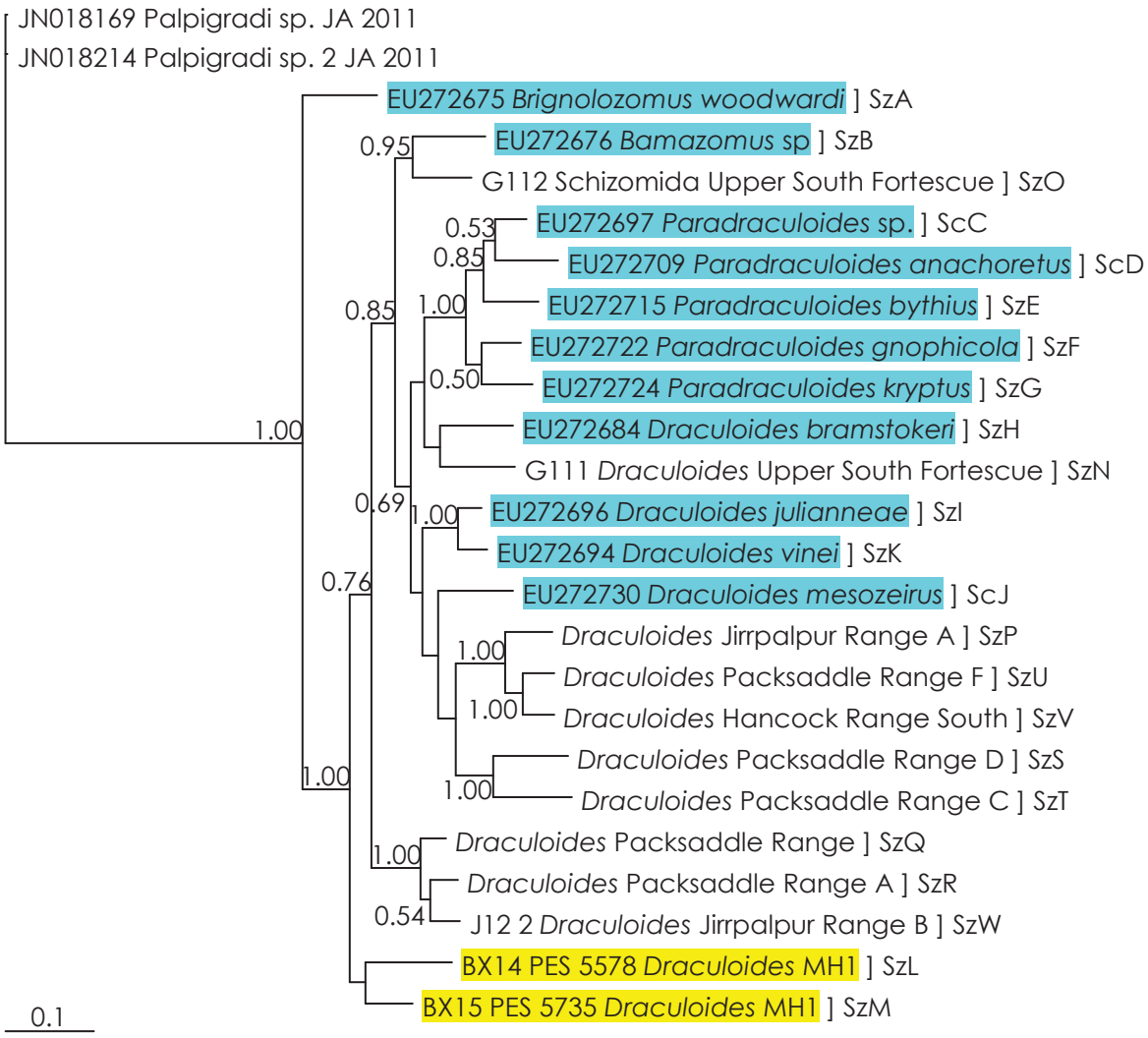


Figure 13. Bayesian analysis of COXI haplotypes of Syncarida from Murrays Hill. Numbers on major nodes correspond to posterior probabilities; values <50% are not shown. Specimens from Murrays Hill are highlighted in yellow; the Genbank reference sequence is highlighted in turquoise. Scale bar= number of substitutions per site. Lineages are prefaced by SB (Syncarida, Bathynellidae) or SP (Syncarida, Parabathynellidae).

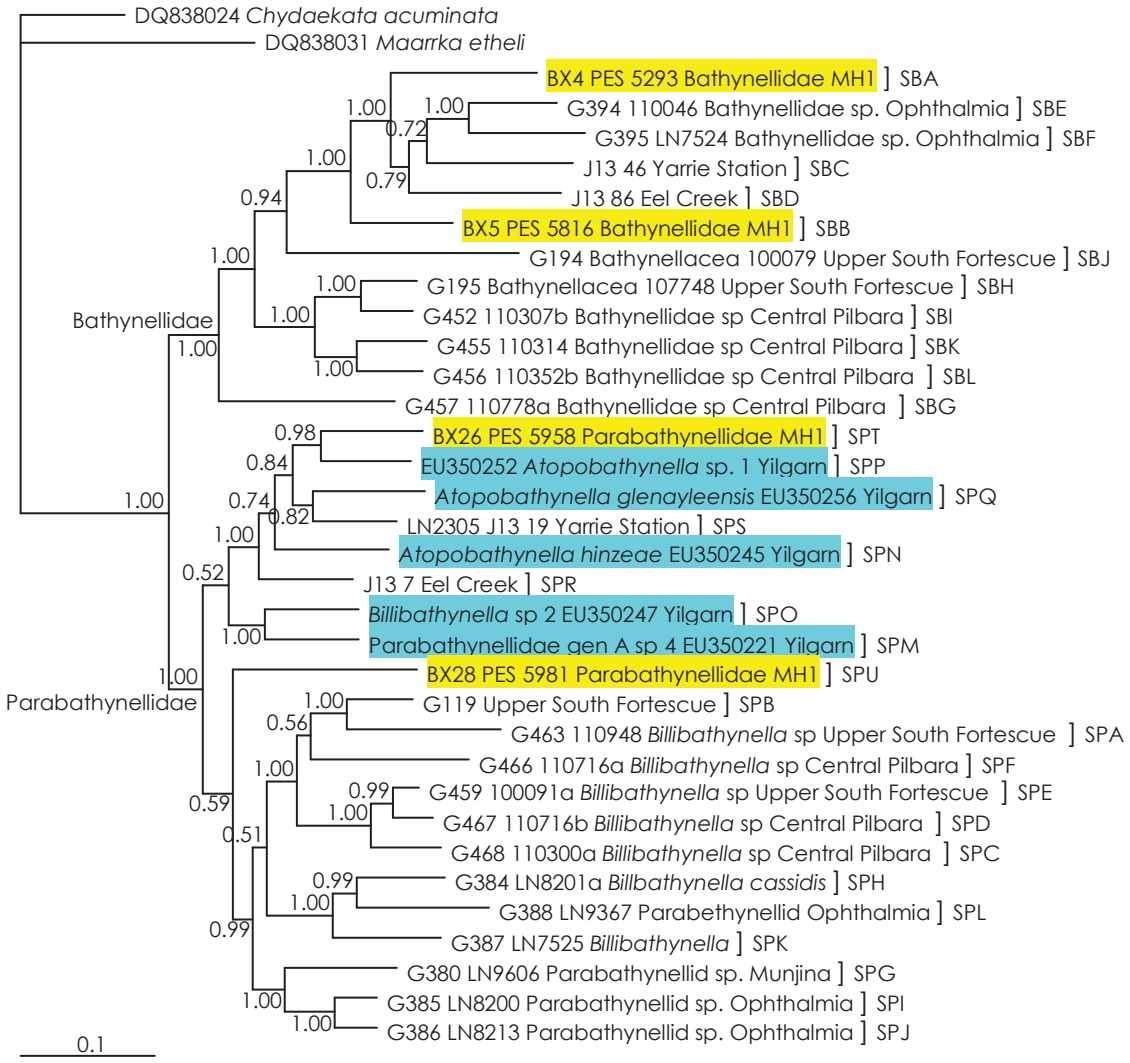
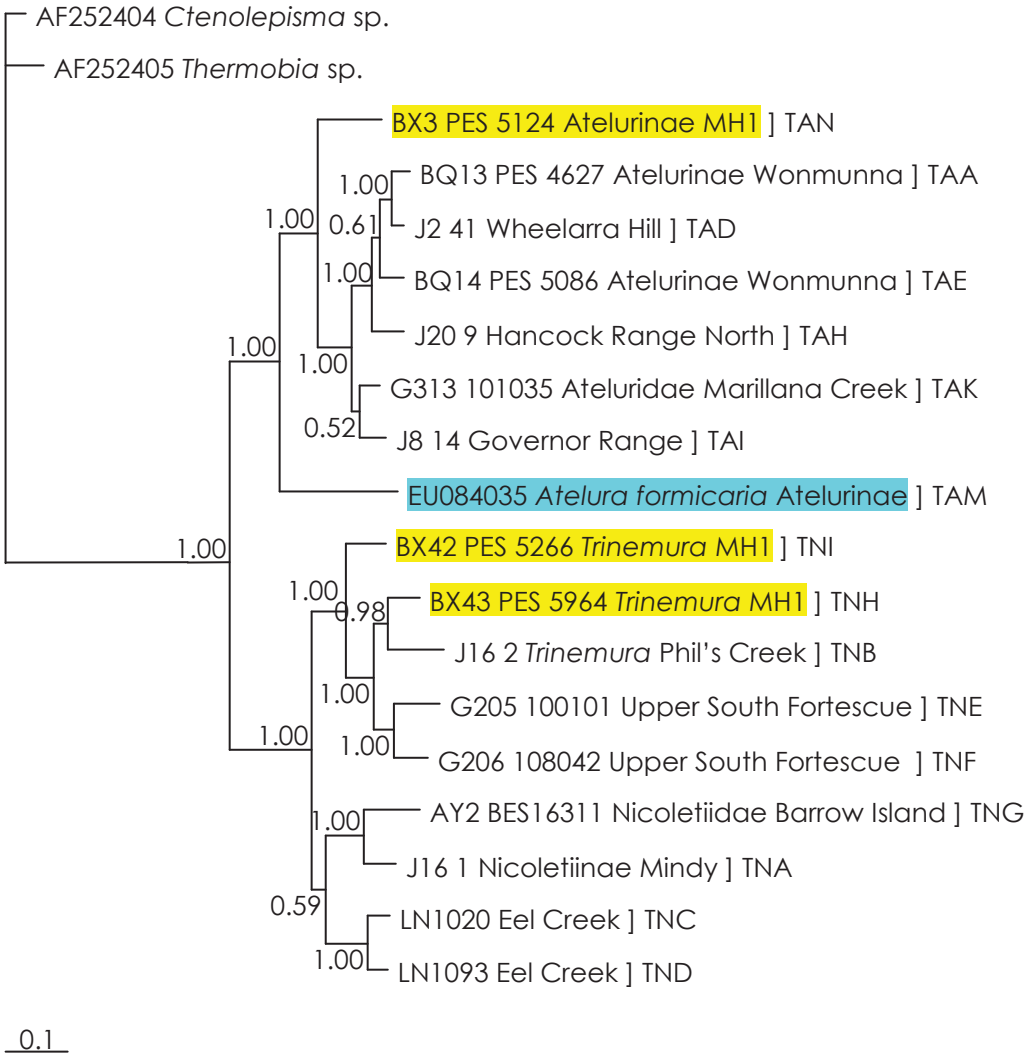


Figure 14. Bayesian analysis of 12s haplotypes of Thysanura (Atelurinae and Nicoletiidae) from Murrays Hill. Numbers on major nodes correspond to posterior probabilities; values <50% are not shown. Specimens from Murrays Hill are highlighted in yellow; Genbank reference specimens are highlighted in turquoise. Scale bar= number of substitutions per site. Lineages are prefaced by TA (Thysanura, Atelurinae) or TN (Thysanura, Nicoletiidae).



Appendix 1. COXI sequences of Troglofauna from Murrays Hill used in the present study.

#BX32_PES-5173_Paramelitidae_MH1
----------ATCCCCAAGAAGTCTAATTGAAAATGAC
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TAATTACTTCTTCTTTAGTTGACATAGGCTCCGGAACTGGATGAACAATCTATCCCCCTC
TTGCATCATCCTTATCTCATAATGGTCCTTCCATAGATTTTACAATTTTCTCCCTTCATA
TAGCAGGAGCATCCTCTATTCTTGGGGCCATCAACTTTATCACAACCATTCTTAATATAC
GATCTATTACTATAACAATAGACCGAACCCCTATATTTGTTTGATCAGTATTTATTACTG
CTATTCTATTACTATTATCACTTCCAGTACTAGCTGGAGCAATTACAATACTTTTAACAG
ACCGTAACTTTAATACTTCATTTTTTGATCCTAGAGGGGGAGGGGACCCAATTCTATTCC
AACACCTGTTTTGATTTTTTGGTCACCCTGAAGTTTAGTCATAGC

#BX37_PES-6086_Pauropoda_MH1_PrF
ATAAAGATATTGGAACACTTTACTTTATCTTAGGATTATGAGCCTCCATACTTGGAGCTT
CCCTAAGCCTAATCATCCGTATAGAACTAAGAAAACCAGGAAGATTTCTAAGAAATGACC
ACATCTATAACGTAGTAGTTACAGCACACGCCTTTGTAATAATCTTCTTTGTAGTAATAC
CTTTAATAATAGGAGCATTTGGTAACTGACTCACCCCAATAATGCTAAATACGCCTGATA
TGGCCTTCCCCCGAATAAACAACCTAAGCTTCTGATTTCTCCCCCCCTCCCTTCTTCTAT
TAACATTATCCTCACTAGTTAGATCAGGTGTAGGAACTGGATGAACAGTCTATCCTCCAC
TAGCCGGACAAATAGCTCACGAAGGACTATCAGTAGACCTAGCCATTTTCTCCCTTCACA
TTGCGGGAGCCTCCTCCATTCTAGGAGCAATTAACTTCATAACCACAATTATCAACATAA
AACCAACAAACATAAAAATAGAATCAACTCCCTTGTTCATTTGAGCTGTATTTTTAACAG
CAGTATTACTGCTAATATCTCTCCCAGTTCTCGCTGGAGCAATCACTATACTACTAACAG
ATCGTAATTTTAATACTTCATTTTTCGACCCTAACGGAGGAGGAGACCCTATCTTGTTCC
AACATTTATTTTGATTTTTTGGTCAC------------------

#BX38_PES-6026_Polyxenidae_MH1
----------------CAATTAAAATTACGATCACATAACAACATAGTAATAGCCCCAGC
TAATACTGGTAAAGACAAAAGCAGCAGCACAGCAGTAATACCCACCGACCAAACAAACAA
```

AGGAATCTTTTCAAAGGACATACCAACTGTACGCATGTTAATAATAGTCGTAATAAAATT
AATAGCTCCTAAAATAGATGAAACACCAGCCAAATGCAAAGAAAAAATCGCCAAATCAAC
AGAACCCCCCCCCATGAGCAATTACTCCCGCTAACGGAGGATAAACAGTCCATCCAGTACC
AACCCCCTGACCAACCATAGAAGAAGACAATAATAAAATAAATGAAGGTGGCAGCAACCA
AAAACTCATATTATTCATCCGAGGAAAGGCCATATCAGGAGCACCTAATATAAGAGGCAC
CAACCAATTTCCAAATCCACCAATCATAATAGGTATGACCATAAAAAAAAATCATAACAAA
AGCATGAGCAGTGACAATAGTATTATAAATCTGATCATCTCCAATCAATCTTCCAACACT
CCCTAACTCAATACGAATTAATA

#BX14_PES-5578_Draculoides_MH1
----------GCTGGCATTTTAGGAAGAG
CACTTAGTATTATAATTCGAATTGAACTAGGAACACCCAGAAGATTTTTAGGAAATGACC
ATCTTTATAATGTCATTGTAACAGCCCATGCATTTGTTATAATCTTTTTTATAGTCATAC
CAGTAATAATCGGAGGATTTGGAAATTGATTAATTCCATTAATAATTGGGGCACCAGATA
TAGCATTTCCACGAATAAATAACCTTTCATTTTGACTTCTCATCCCATCTTTACTTTTCC
TGCTATTTTCCTCAATAATTTCAATAGGAGTAGGAACCGGATGAACTGTCTATCCACCTC
TTTCTAGAATTAACTTTCATAGAGGAGCCGCAGTTGACTTTACAATCTTTTCTTTACACA
TCGCGGGAATTTCTTCAATTTTAGGTGCTATTAACTTCATTACTACTATTAGAAATATAC
GAACACCAGGAATAACACTAGAACGAATCCCTCTATTCATTTGATCAGTATTACTAACAG
CCATTCTTCTTCTCCTCTCACTACCAGTACTAGCAGGCGCCATTACAATACTTCTCCTAG
ACCGAAACTTTAATACATCATTCTTTGATCCAATAGGAGGAGGAGATCCAATTTTATATC
AACATTTATTCTGATTCTTTGGACACCCAGAAGTCTACATCTTAATTTTACCAGGTTTTG
GAATTATCTCACATATTATTAGACACTATACAGG----------

#BX15_PES-5735_Draculoides_MH1
ATAAAGATATTGGAACTTTATACTTAATTTTTGGAATATGAGCAGGAATTTTAGGAAGAG
CTCTAAGCATTATAATTCGAATTGAACTAGGCACACCAAGAAGATTTTTAGGAAATGATC
ACCTTTATAATGTCATCGTTACAGCCCATGCATTTGTAATAATTTTCTTTATAGTTATAC
CAGTAATAATTGGTGGATTTGGAAACTGATTAATTCCTCTGATAATTGGAGCACCAGATA
TAGCATTTCCACGAATAAACAACCTATCATTTTGATTACTTATTCCATCCCTATTATTTT
TATTATTTTCATCAATAATTTCAATAGGAGTTGGAACAGGGTGAACTGTTTATCCCCCTC
TATCAAGAATTAATTTTCACAGGGGAGCTGCAGTTGACTTTACAATTTTTTCTCTTCACA
TTGCAGGAATTTCTTCAATTTTAGGAGCTATTAACTTTATTACCACTATTAGAAATATAC
GAACCCCAGGAATATCTCCAGAACGAGTACCTTTATTTATTTGATCAGTTCTATTAACAG
CAATTTTACTTCTTCTTTCTCTACCTGTACTTGCTGGAGCAATTACAATACTTCTTCTAG
ATCGAAACTTTAATACATCATTCTTTGATCCAATAGGAGGAGGAGACCCAATCTTATACC
AACATTTATTTTGATTCTTTGGTCACCCAGAAGTTTACATCTTAATTCTACCAGGATTTG
GAATTATTTCTCATATTATTAGACATTATACAGGAAAAAAAGAACCTTTTGGTACACTTG
GAATAATTTATGCAATAATAGCAATTGGCCTCCTAGGTTTTATTGTATGAGC-ACACCAT
ATATTTAC----------

#BX4_PES-5293_Bathynellidae_MH1
GTGACCAAAAAATCAAAATAGATGCTGGTATAAAATTGGGTCTCCCCCGCCTGCAGGGTC
AAAGAAAGAAGTATTGATATTTCGATCTGTTAAAAGTATAGTGATCCCCCCTGCTAATAC
CGGAAGAGCAAGAAGTAAAAGAAGGGCAGTGATAAATACAGACCAAGCAAATAATGGAAG
TAATTCTATTATTAATCCCATAGCACGTATATTTCATACTGTCCTAAGGAAGTTTACAGC
CCCTAGAATAGAAGAAGCTCCAGCTAAATGTAAAGAGAAAATAGCAAGATCGACAGAGAC
TCCCCTGTGAGAGATATTTCTAGCAAGAGGGGGATAAACAGTTCAGCCTGTTCCTACCCC
TCTTTCTACTACTCTCCTTCTAACTAAGAGGATTAGAGAAGGAATGAGAAGTCAAAATCT
TAAATTATTCAAGCGGGGAAATGCTATATCGGGGGCTCTAATTATTATAGGAACTAATCA
ATTACCAAACCCTCCTATTATTAAAGGCATAACTATAAAGAAAATTATAACAAAAGCATG
AGCAGTGACGATAGTATTATAAATTTGGTCGTCACCAATTAAAGTTCCTGGCTGTCCTAG
TTCTATTCGAATAATCACACTTATTCCTGTTCCTACTATTCCAGCTCAAGCACCCAGAAT
TAGATATAAAGTACCAATATCTTTAT

#BX5_PES-5816_Bathynellidae_MH1
GTGACCAAAAAATCAAAATAAATGTTGATATAAAATAGGGTCTCCCCCTCCAGCAGGATC

AAAAAAAGAAGTATTAATATTACGATCTGTAAGAAGTATAGTAATTCCTCCTGCTAAAAC
TGGTAAAGATAAAAGTAACAGGACTGCAGTAATTAGAACAGACCACGCGAATAGTGGTAA
AAGCTCTATTATTAGGCCTATTGCTCGTATATTTCATAGAGTTCTTAAAAAATTAATAGC
TCCTAAAATAGAGGAAGCACCTGCTAAGTGGAGAGAAAAAATTGCAAGATCCACTGATAC
TCCTCTATGAGAAATATTTCTAGCTAGAGGTGGATATACAGTTCATCCGGTTCCTACCCC
CCTTTCAACTACTCTTCTTCTTACAAGTAGAAAGAGGGAAGGGACTAAAAGTCAAAATCT
TAAATTATTTATTCGAGGGAAGGCTATATCAGGAGCTCTGATTATTATAGGAACTAATCA
ATTTCCAAACCCCCCTATCATTAAAGGCATAACTATAAAGAAAATTATAATAAAAGCATG
AGCTGTTACAATTGTATTATAAATTTGATCATCTCCAATTAAGCTTCCTGGCTGTCCAAG
TTCCATTCGAATAATAACTCTTATTCCGGTTCCTACTATTCCAGCCCAGGCTCCTAAAAT
TAAATATAAGGTTCCAATATCTTTAT

#BX26_PES-5958_Parabathynellidae_MH1
ATAAAGATATTGGAACAATATATTTATTATTTGGAGCATGAGCAGGAATATTAGGAACAG
GATTAAGTATAATTATTCGTCTAGAACTAGGACAATCCGGACCATTAATAGGAAATGACC
AAATATATAATGTTATTGTTACTGCTCATGCTTTTGTAATAATTTTTTTTATAGTTATAC
CTATTATAATTGGAGGATTTGGAAATTGATTAATTCCTTTAATAGTAAATTGTCCTGATA
TAGCATTTCCACGTATAAATAATATAAGGTTCTGATTATTACCTCCATCTTTATTACTTC
TATTAAGAAGAAGGATAATTGAAAGTGGTGTTGGTACTGGATGAACAGTGTACCCTCCTT
TAGCATTAAATATTTTTCATAGAGGACCTTCTGTTGATTTAGCTATTTTTTCTTTACATA
TTGCAGGTGCTTCATCTATTTTAGGAGCCATYAACTTTATTACTACTATTATTAATATAC
GTTCTCCAGGATTAGTCATAGATCGTTTACCGTTATTTTGTTGAGCTGTATTTATTACGG
CTATTTTATTATTACTTTCTTTACCTGTATTAGCCGGAGGAATTACAATACTTTTAACTG
ATCGTAATTTAAACACTTCATTTTTTGACCCAGCTGGAGGAGGAGACCCAATTTTATACC
AGCATTTATTTTGATTTTTTGGACATCCAGAAGTTTATATTTTA--

#BX28_PES-5981_Parabathynellidae_MH1
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GTTTAAGTATGCTTATTCGTATTGAATTAGGTCAACCTAGAGCTTTTTTGGGTAACGAGC
AGATTTTTAACGTAATTGTTACTGCACATGCATTTGTCATAATTTTTTTTATAGTCATAC
CGATTATAATTGGGGGATTCGGTAATTGAATAATTCCATTAATATTAAATTCACCGGATA
TAGCTTTTCCACGTATAAATAACATAAGATTCTGATTGTTACCACCTTCCTTAACTTTAC
TGTTATCAAGAAGAATCATTGAAAGAGGTGTTGGAACTGGATGAACTGTTTACCCACCTC
TTGCCTCTTCTTTATTTCATAGCGGCCCATCTGTTGATTTAGCCATTTTTTCTCTACATA
TTGCAGGAGCCTCGTCTATTTTAGGAGCTATTAATTTTATTTCAACTGTGATTAACATAC
GAATAATTCAAATATCACTAGACCGAATTCCACTATTTGTGTGAGCTGTATTTATTACAG
CTATTCTGTTATTATTATCTTTGCCAGTTTTAGCAGGAGGTATTACTATATTATTAACCG
ACCGTAACTTAAACACCTCATTTTTTGATCCAGCAGGAGGAGGTGATCCAATTCTTTATC
AACATCTTTTCTGATTTTTTGGTCACCCTGAAGTTTA-

Appendix 2. 12s sequences of specimens from Murrays Hill used in the present study.

#BX3_PES-5124_Atelurinae_MH1
TAAACTAGGATTAGATACCCTATTATTCTTAATGTAAATGTTG------TATGGGTAGTA
TCAGTTGTGATCTAAAAACTCAAAGGATTTGGCGGTACTTTAATCCCTTCAGAGGAGCCT
GTCCTGTAATTGATGGTCCACGTTATTG-GTTACTTCTTTTGGTAAAA------CAGTTT
GTATATCGCCGTCGTTCAGGAAATATTTTTAAGGTAGATAATTTTCTATAATTCTTATTG
GAATTTAAGGCAGGTCAAGGTGCAGTTTATGGAGAGGGAAGAGATGGGCTACAATATATT
TTATATAAAACGGATTATTTGGTTAAACATGAA---TAAGAAGGAGGATTTGAATATAAT
TTTT---A-TGGATAAGGGTGAATTGGGCTCTAAGGTATGCACACATCG----------

#BX42_PES-5266_Trinemura_MH1
NAAACTAGGATTAGATACCCTATTATTAGTGATGTAAATGAGTAAG---CTTAGGTATTA
GTTG--GTGTTCATGAAACCTAGAGAATTTGGCGGTATTTTAGTCTTTTTAGAGGAATCT
GTCCTATAATCGATAATCCGCGTTGTT--ATTACCTGTTTTGATTGAG-------AGTTT
GTATATCGCCGTCA-GAAGGGAATTTTTAGAGGATTTGTAATTCTTGGAAGTTTGTATGG
GGAAGGATGACAGGTCAAGGTGCAGCTAATGAATAGGGAGGAGATGGATTACAATATGTG
TTATATANAACGGATTCTTGAGNTAGGTTGGGATNN---GAAGGTGGATTTAAAAGTAAT
TTTT---ATAATATAGGGATGAAGGTGGCTCTAAAGTGTGCACACATCGCCCGTCACTCT
CATTAATTGTGAGATAAGTCGTAACATA

#BX43_PES-5964_Trinemura_MH1
TAAACTAGGATTAGATACCCTATTATTAGCAGCATAAAAAAGTAGG---CTTAGGTATTA
ATTG--ATGTTCATGAAACCTAGAGAATTTGGCGGTATTTTAGTCTTTTTAGAGGAACCT
GTCCTATAATCGATAATCCACGTTGTT--ATTACCTGTTTTGATTTAT-------AGTTT
GTATATCGCCGTCATAAGGGAATTTTTT--GAGAATGTTTAATTTCTAAAAGGTTGAGAG
AGAGG-ATGACAGGTCAAGGTGCAGCTTATGAATAGGGAGGTGATGGGTTACAATATAAG
GAATGTATGACGAATTTTCAGGATGGGGTTGTT---TAAGAAGGTGGATTTAAAAGTAAT
TTGT---AGAATATACTGGTGAAGGTGGCTCTAAAATGTGCACACATCGCCCG-TCACTC
TCATTAATTGTGAGATAAGTCGTAACATA

#BX38_PES-6026_Polyxenidae_MH1
TAAACTAGGATTAGATACCCTATTATGAAGTTAATTTTGATTGCCATGGTAGTAGATAAT
TGAAACCTAAAGATTTTGGCGGTAATTTAAGCTCATTAGAGGAATTTGTTATGTAAATGA
TGATCCCCGTGGGGTGTACTTTATTAATTGTTTGTATACCGCCGTTGATTTGATAATTTT
TAGAAGATAATGGAATTTTTGTTAGTAGAGATTGTCTTTTAAATCAGGTCGAGGTGCAGC
TTTATTAAAGGTTTAAATGAATTACAATTTTTGTTTGAATACGGATTAATTATTTGAATT
ATTTATGAAGGAGGATTTAAAAGTAAAATTTTAATGGAATGAAAATTTGATTGTGGCTCT
AAATTATGTACATATCGCCCGTCACTCTCGTTAAAATATGAGATAAGTCGTAACATAGTA
AA

#BX39_PES-5132_Polyxenidae_MH1
TAAACTAGGATTAGATACCCTATTATGAAGTTAATTTTGATTGCCATGGTAGTAGATAAT
TGAAACCTAAAGATTTTGGCGGTAATTTAAGCTCATTAGAGGAATTTGTTATGTAAATGA
TGATCCCCGTGGGGTGTACTTTATTAATTGTTTGTATACCGCCGTTGATTTGATAATTTT
TAGAGGATAATGAAATTTTTGTTAGTAGAGATTGTCTTTTAAATCAGGTCGAGGTGCAGC
TTTATTAAAGGTTTAAATGAATTACAATTTTTGTTTGAATACGGATTAATTATTTGAATT
ATTTATGAAGGAGGATTTAAAAGTAAAATTTTAATGGAATGAAAATTTGATTGTGGCTCT
AAATTATGTACATATCGCCCGTCACTCTCGTTAAAATATGAGATAAGTCGTAACATAGTA
AA

Appendix 5 Drill Log Data for <25m.

BoreID	Depth range (m)	Code
MD0386A	0-2	NAM
MD0386A	2-4	NAM
MD0386A	4-6	NAM
MD0386A	6-8	NAM
MD0386A	8-10	NAM
MD0386A	10-12	NAM
MD0386A	12-14	NAM
MD0386A	14-16	NAM
MD0386A	16-18	NAM
MD0386A	18-20	NAM
MD0386A	20-22	NAM
MD0386A	22-24	NAM
MD0387	0-2	NAM
MD0387	2-4	NAM
MD0387	4-6	NAM
MD0387	6-8	NAM
MD0387	8-10	NAM
MD0387	10-12	NAM
MD0387	12-14	NAM
MD0387	14-16	NAM
MD0387	16-18	NAM
MD0387	18-20	NAM
MD0387	20-22	NAM
MD0387	22-24	NAM
MD0398	0-2	NAM
MD0398	2-4	NAM
MD0398	4-6	NAM
MD0398	6-8	NAM
MD0398	8-10	NAM
MD0398	10-12	NAM
MD0398	12-14	NAM
MD0398	14-16	NAM
MD0398	16-18	NAM
MD0398	18-20	NAM
MD0398	20-22	NAM
MD0398	22-24	NAM
MD0397	0-2	NAM

BoreID	Depth range (m)	Code
MD0397	2-4	NAM
MD0397	4-6	NAM
MD0397	6-8	NAM
MD0397	8-10	NAM
MD0397	10-12	NAM
MD0397	12-14	NAM
MD0397	14-16	NAM
MD0397	16-18	NAM
MD0397	18-20	NAM
MD0397	20-22	NAM
MD0397	22-24	NAM
MD0420	0-2	ALU
MD0420	2-4	ALU
MD0420	4-6	ALU
MD0420	6-8	ALU
MD0420	8-10	ALU
MD0420	10-12	ALU
MD0420	12-14	GZ
MD0420	14-16	GZ
MD0420	16-18	GZ
MD0420	18-20	GZ
MD0420	20-22	NAM
MD0420	22-24	NAM
MD0430	0-2	ALU
MD0430	2-4	ALU
MD0430	4-6	ALU
MD0430	6-8	ALU
MD0430	8-10	ALU
MD0430	10-12	ALU
MD0430	12-14	ALU
MD0430	14-16	ALU
MD0430	16-18	ALU
MD0430	18-20	ALU
MD0430	20-22	ALU
MD0430	22-24	ALU
MD0429	0-2	ALU
MD0429	2-4	ALU

BoreID	Depth range (m)	Code
MD0429	4-6	ALU
MD0429	6-8	ALU
MD0429	8-10	ALU
MD0429	10-12	ALU
MD0429	12-14	ALU
MD0429	14-16	ALU
MD0429	16-18	ALU
MD0429	18-20	ALU
MD0429	20-22	ALU
MD0429	22-24	ALU
MD0262	0-2	NAM
MD0262	2-4	NAM
MD0262	4-6	NAM
MD0262	6-8	NAM
MD0262	8-10	NAM
MD0262	10-12	NAM
MD0262	12-14	NAM
MD0262	14-16	NAM
MD0262	16-18	NAM
MD0262	18-20	NAM
MD0262	20-22	NAM
MD0262	22-24	NAM
MD0314	0-2	ALU
MD0314	2-4	ALU
MD0314	4-6	ALU
MD0314	6-8	ALU
MD0314	8-10	CC
MD0314	10-12	CC
MD0314	12-14	CC
MD0314	14-16	NAM
MD0314	16-18	NAM
MD0314	18-20	NAM
MD0314	20-22	NAM
MD0314	22-24	NAM
MD0253	0-2	NAM
MD0253	2-4	NAM
MD0253	4-6	NAM
MD0253	6-8	NAM
MD0253	8-10	NAM

BoreID	Depth range (m)	Code
MD0253	10-12	NAM
MD0253	12-14	NAM
MD0253	14-16	NAM
MD0253	16-18	NAM
MD0253	18-20	NAM
MD0253	20-22	NAM
MD0253	22-24	NAM
MD0372	0-2	ALU
MD0372	2-4	ALU
MD0372	4-6	ALU
MD0372	6-8	ALU
MD0372	8-10	ALU
MD0372	10-12	ALU
MD0372	12-14	ALU
MD0372	14-16	ALU
MD0372	16-18	ALU
MD0372	18-20	ALU
MD0372	20-22	ALU
MD0372	22-24	ALU
MD0371	0-2	ALU
MD0371	2-4	ALU
MD0371	4-6	ALU
MD0371	6-8	ALU
MD0371	8-10	ALU
MD0371	10-12	ALU
MD0371	12-14	ALU
MD0371	14-16	ALU
MD0371	16-18	ALU
MD0371	18-20	ALU
MD0371	20-22	ALU
MD0371	22-24	NAM
MD0330	0-2	ALU
MD0330	2-4	ALU
MD0330	4-6	ALU
MD0330	6-8	ALU
MD0330	8-10	ALU
MD0330	10-12	ALU
MD0330	12-14	GZ
MD0330	14-16	NAM

BoreID	Depth range (m)	Code
MD0330	16-18	NAM
MD0330	18-20	NAM
MD0330	20-22	NAM
MD0330	22-24	NAM
MD0247	0-2	NAM
MD0247	2-4	NAM
MD0247	4-6	NAM
MD0247	6-8	NAM
MD0247	8-10	NAM
MD0247	10-12	NAM
MD0247	12-14	NAM
MD0247	14-16	NAM
MD0247	16-18	NAM
MD0247	18-20	NAM
MD0247	20-22	NAM
MD0247	22-24	NAM
MD0259	0-2	ALU
MD0259	2-4	ALU
MD0259	4-6	NAM
MD0259	6-8	NAM
MD0259	8-10	NAM
MD0259	10-12	NAM
MD0259	12-14	NAM
MD0259	14-16	NAM
MD0259	16-18	NAM
MD0259	18-20	NAM
MD0259	20-22	NAM
MD0259	22-24	NAM
MD0270	4-6	ALU
MD0270	6-8	ALU
MD0270	8-10	ALU
MD0270	10-12	ALU
MD0270	12-14	ALU
MD0270	14-16	GZ
MD0270	16-18	NAM
MD0270	18-20	NAM
MD0270	20-22	NAM
MD0270	22-24	NAM
MD0270	0-2	ALU

BoreID	Depth range (m)	Code
MD0270	2-4	ALU
MD0268	0-2	GZ
MD0268	2-4	GZ
MD0268	4-6	GZ
MD0268	6-8	GZ
MD0268	8-10	GZ
MD0268	10-12	GZ
MD0268	12-14	NAM
MD0268	14-16	NAM
MD0268	16-18	NAM
MD0268	18-20	NAM
MD0268	20-22	NAM
MD0268	22-24	NAM
MD0601	0-2	GZ
MD0601	2-4	GZ
MD0601	4-6	GZ
MD0601	6-8	NAM
MD0601	8-10	NAM
MD0601	10-12	NAM
MD0601	12-14	NAM
MD0601	14-16	NAM
MD0601	16-18	NAM
MD0601	18-20	NAM
MD0601	20-22	NAM
MD0601	22-24	NAM
MD0599	0-2	GZ
MD0599	2-4	GZ
MD0599	4-6	NAM
MD0599	6-8	NAM
MD0599	8-10	NAM
MD0599	10-12	NAM
MD0599	12-14	NAM
MD0599	14-16	NAM
MD0599	16-18	NAM
MD0599	18-20	NAM
MD0599	20-22	NAM
MD0599	22-24	NAM
MD0552	0-2	GZ
MD0552	2-4	GZ

BoreID	Depth range (m)	Code
MD0552	4-6	GZ
MD0552	6-8	GZ
MD0552	8-10	GZ
MD0552	10-12	GZ
MD0552	12-14	GZ
MD0552	14-16	GZ
MD0552	16-18	GZ
MD0552	18-20	GZ
MD0552	20-22	GZ
MD0552	22-24	NAM
MD0482	0-2	GZ
MD0482	2-4	GZ
MD0482	4-6	GZ
MD0482	6-8	GZ
MD0482	8-10	GZ
MD0482	10-12	GZ
MD0482	12-14	NAM
MD0482	14-16	NAM
MD0482	16-18	NAM
MD0482	18-20	NAM
MD0482	20-22	NAM
MD0482	22-24	NAM
MD0481	0-2	GZ
MD0481	2-4	GZ
MD0481	4-6	GZ
MD0481	6-8	GZ
MD0481	8-10	GZ
MD0481	10-12	GZ
MD0481	12-14	GZ
MD0481	14-16	GZ
MD0481	16-18	GZ
MD0481	18-20	GZ
MD0481	20-22	GZ
MD0481	22-24	GZ
MD0483	0-2	GZ
MD0483	2-4	GZ
MD0483	4-6	GZ
MD0483	6-8	NAM
MD0483	8-10	JER
MD0483	10-12	JER
MD0483	12-14	JER
MD0483	14-16	JER
MD0483	16-18	JER
MD0483	18-20	JER
MD0483	20-22	JER
MD0483	22-24	JER
MD0486	0-2	JER
MD0486	2-4	JER
MD0486	4-6	JER
MD0486	6-8	JER
MD0486	8-10	JER
MD0486	10-12	JER
MD0486	12-14	JER
MD0486	14-16	JER
MD0486	16-18	JER
MD0486	18-20	JER
MD0486	20-22	JER
MD0486	22-24	JER
MD0487	0-2	GZ
MD0487	2-4	GZ
MD0487	4-6	GZ
MD0487	6-8	NAM
MD0487	8-10	NAM
MD0487	10-12	NAM
MD0487	12-14	NAM
MD0487	14-16	NAM
MD0487	16-18	NAM
MD0487	18-20	NAM
MD0487	20-22	JER
MD0487	22-24	JER
MD0578	0-2	ALU
MD0578	2-4	ALU
MD0578	4-6	ALU
MD0578	6-8	ALU
MD0578	8-10	ALU
MD0578	10-12	GZ
MD0578	12-14	GZ
MD0578	14-16	GZ

BoreID	Depth range (m)	Code
MD0578	16-18	GZ
MD0578	18-20	GZ
MD0578	20-22	GZ
MD0578	22-24	GZ
MD0577	0-2	ALU
MD0577	2-4	ALU
MD0577	4-6	ALU
MD0577	6-8	ALU
MD0577	8-10	ALU
MD0577	10-12	ALU
MD0577	12-14	NAM
MD0577	14-16	NAM
MD0577	16-18	NAM
MD0577	18-20	NAM
MD0577	20-22	NAM
MD0577	22-24	NAM
MD0427	0-2	ALU
MD0427	2-4	ALU
MD0427	4-6	ALU
MD0427	6-8	ALU
MD0427	8-10	ALU
MD0427	10-12	ALU
MD0427	12-14	ALU
MD0427	14-16	ALU
MD0427	16-18	ALU
MD0427	18-20	ALU
MD0427	20-22	ALU
MD0427	22-24	ALU
MD0499	0-2	GZ
MD0499	2-4	GZ
MD0499	4-6	GZ
MD0499	6-8	GZ
MD0499	8-10	GZ
MD0499	10-12	GZ
MD0499	12-14	NAM
MD0499	14-16	NAM
MD0499	16-18	NAM
MD0499	18-20	NAM
MD0499	20-22	NAM

BoreID	Depth range (m)	Code
MD0499	22-24	JER
MD0495	0-2	GZ
MD0495	2-4	GZ
MD0495	4-6	NAM
MD0495	6-8	NAM
MD0495	8-10	NAM
MD0495	10-12	NAM
MD0495	12-14	NAM
MD0495	14-16	NAM
MD0495	16-18	NAM
MD0495	18-20	NAM
MD0495	20-22	NAM
MD0495	22-24	NAM
MDh0143	0-2	GZ
MDh0143	2-4	GZ
MDh0143	4-6	GZ
MDh0143	6-8	GZ
MDh0143	8-10	NAM
MDh0143	10-12	NAM
MDh0143	12-14	JER
MDh0143	14-16	JER
MDh0143	16-18	JER
MDh0143	18-20	JER
MDh0143	20-22	JER
MDh0143	22-24	JER
MD0467	0-2	GZ
MD0467	2-4	GZ
MD0467	4-6	GZ
MD0467	6-8	GZ
MD0467	8-10	GZ
MD0467	10-12	GZ
MD0467	12-14	GZ
MD0467	14-16	GZ
MD0467	16-18	GZ
MD0467	18-20	GZ
MD0467	20-22	GZ
MD0467	22-24	GZ
MD0468	0-2	GZ
MD0468	2-4	GZ

BoreID	Depth range (m)	Code
MD0468	4-6	GZ
MD0468	6-8	GZ
MD0468	8-10	GZ
MD0468	10-12	GZ
MD0468	12-14	GZ
MD0468	14-16	GZ
MD0468	16-18	GZ
MD0468	18-20	GZ
MD0468	20-22	NAM
MD0468	22-24	NAM
MD0470	0-2	GZ
MD0470	2-4	GZ
MD0470	4-6	GZ
MD0470	6-8	GZ
MD0470	8-10	GZ
MD0470	10-12	GZ
MD0470	12-14	GZ
MD0470	14-16	GZ
MD0470	16-18	GZ
MD0470	18-20	NAM
MD0470	20-22	NAM
MD0470	22-24	JER
MD0596	0-2	GZ
MD0596	2-4	GZ
MD0596	4-6	GZ
MD0596	6-8	NAM
MD0596	8-10	NAM
MD0596	10-12	NAM
MD0596	12-14	NAM
MD0596	14-16	NAM
MD0596	16-18	NAM
MD0596	18-20	NAM
MD0596	20-22	NAM
MD0596	22-24	NAM
MD0462	0-2	GZ
MD0462	2-4	GZ
MD0462	4-6	NAM
MD0462	6-8	NAM
MD0462	8-10	NAM

BoreID	Depth range (m)	Code
MD0462	10-12	NAM
MD0462	12-14	NAM
MD0462	14-16	NAM
MD0462	16-18	NAM
MD0462	18-20	NAM
MD0462	20-22	NAM
MD0462	22-24	NAM
MD0612	0-2	GZ
MD0612	2-4	GZ
MD0612	4-6	GZ
MD0612	6-8	GZ
MD0612	8-10	NAM
MD0612	10-12	NAM
MD0612	12-14	NAM
MD0612	14-16	NAM
MD0612	16-18	NAM
MD0612	18-20	NAM
MD0612	20-22	NAM
MD0612	22-24	NAM
MD0385	0-2	GZ
MD0385	2-4	GZ
MD0385	4-6	GZ
MD0385	6-8	GZ
MD0385	8-10	NAM
MD0385	10-12	NAM
MD0385	12-14	NAM
MD0385	14-16	NAM
MD0385	16-18	NAM
MD0385	18-20	NAM
MD0385	20-22	NAM
MD0385	22-24	NAM
MD0533	0-2	GZ
MD0533	2-4	NAM
MD0533	4-6	NAM
MD0533	6-8	NAM
MD0533	8-10	NAM
MD0533	10-12	NAM
MD0533	12-14	NAM
MD0533	14-16	NAM

BoreID	Depth range (m)	Code
MD0533	16-18	NAM
MD0533	18-20	NAM
MD0533	20-22	NAM
MD0533	22-24	NAM
MD0509	0-2	NAM
MD0509	2-4	NAM
MD0509	4-6	NAM
MD0509	6-8	NAM
MD0509	8-10	NAM
MD0509	10-12	NAM
MD0509	12-14	NAM
MD0509	14-16	NAM
MD0509	16-18	NAM
MD0509	18-20	NAM
MD0509	20-22	NAM
MD0509	22-24	NAM
MD0609	0-2	ALU
MD0609	2-4	ALU
MD0609	4-6	ALU
MD0609	6-8	GZ
MD0609	8-10	GZ
MD0609	10-12	GZ
MD0609	12-14	GZ
MD0609	14-16	GZ
MD0609	16-18	GZ
MD0609	18-20	NAM
MD0609	20-22	NAM
MD0609	22-24	NAM
MD0525	0-2	GZ
MD0525	2-4	GZ
MD0525	4-6	GZ
MD0525	6-8	GZ
MD0525	8-10	GZ
MD0525	10-12	GZ
MD0525	12-14	GZ
MD0525	14-16	GZ
MD0525	16-18	NAM
MD0525	18-20	NAM
MD0525	20-22	NAM

BoreID	Depth range (m)	Code
MD0525	22-24	NAM
MD0585	0-2	ALU
MD0585	2-4	ALU
MD0585	4-6	GZ
MD0585	6-8	GZ
MD0585	8-10	NAM
MD0585	10-12	NAM
MD0585	12-14	NAM
MD0585	14-16	NAM
MD0585	16-18	NAM
MD0585	18-20	NAM
MD0585	20-22	NAM
MD0585	22-24	NAM
MD0671	0-2	ALU
MD0671	2-4	ALU
MD0671	4-6	ALU
MD0671	6-8	ALU
MD0671	8-10	ALU
MD0671	10-12	ALU
MD0671	12-14	ALU
MD0671	14-16	ALU
MD0671	16-18	ALU
MD0671	18-20	GZ
MD0671	20-22	GZ
MD0671	22-24	GZ
MD0672	0-2	ALU
MD0672	2-4	ALU
MD0672	4-6	ALU
MD0672	6-8	ALU
MD0672	8-10	ALU
MD0672	10-12	ALU
MD0672	12-14	ALU
MD0672	14-16	ALU
MD0672	16-18	ALU
MD0672	18-20	ALU
MD0672	20-22	ALU
MD0672	22-24	ALU
MD0673	0-2	ALU
MD0673	2-4	ALU

BoreID	Depth range (m)	Code
MD0673	4-6	ALU
MD0673	6-8	ALU
MD0673	8-10	ALU
MD0673	10-12	ALU
MD0673	12-14	ALU
MD0673	14-16	ALU
MD0673	16-18	ALU
MD0673	18-20	ALU
MD0673	20-22	ALU
MD0673	22-24	ALU
MD0646	0-2	ALU
MD0646	2-4	ALU
MD0646	4-6	ALU
MD0646	6-8	ALU
MD0646	8-10	ALU
MD0646	10-12	ALU
MD0646	12-14	ALU
MD0646	14-16	ALU
MD0646	16-18	ALU
MD0646	18-20	ALU
MD0646	20-22	ALU
MD0646	22-24	NAM
MD0631	0-2	ALU
MD0631	2-4	ALU
MD0631	4-6	ALU
MD0631	6-8	ALU
MD0631	8-10	ALU
MD0631	10-12	ALU
MD0631	12-14	ALU
MD0631	14-16	ALU
MD0631	16-18	ALU
MD0631	18-20	GZ
MD0631	20-22	GZ
MD0631	22-24	GZ
MD0476	0-2	GZ
MD0476	2-4	GZ
MD0476	4-6	GZ
MD0476	6-8	GZ
MD0476	8-10	GZ

BoreID	Depth range (m)	Code
MD0476	10-12	GZ
MD0476	12-14	GZ
MD0476	14-16	GZ
MD0476	16-18	GZ
MD0476	18-20	GZ
MD0476	20-22	GZ
MD0476	22-24	GZ
MD0396	0-2	ALU
MD0396	2-4	ALU
MD0396	4-6	ALU
MD0396	6-8	ALU
MD0396	8-10	NAM
MD0396	10-12	NAM
MD0396	12-14	NAM
MD0396	14-16	NAM
MD0396	16-18	NAM
MD0396	18-20	NAM
MD0396	20-22	NAM
MD0396	22-24	NAM
MD0393	0-2	ALU
MD0393	2-4	ALU
MD0393	4-6	ALU
MD0393	6-8	ALU
MD0393	8-10	NAM
MD0393	10-12	NAM
MD0393	12-14	NAM
MD0393	14-16	NAM
MD0393	16-18	NAM
MD0393	18-20	NAM
MD0393	20-22	NAM
MD0393	22-24	NAM
MD0415	0-2	ALU
MD0415	2-4	ALU
MD0415	4-6	ALU
MD0415	6-8	ALU
MD0415	8-10	ALU
MD0415	10-12	GZ
MD0415	12-14	GZ
MD0415	14-16	GZ

BoreID	Depth range (m)	Code
MD0415	16-18	NAM
MD0415	18-20	NAM
MD0415	20-22	NAM
MD0415	22-24	NAM
MD0414	0-2	ALU
MD0414	2-4	ALU
MD0414	4-6	ALU
MD0414	6-8	GZ
MD0414	8-10	GZ
MD0414	10-12	GZ
MD0414	12-14	NAM
MD0414	14-16	NAM
MD0414	16-18	NAM
MD0414	18-20	NAM
MD0414	20-22	NAM
MD0414	22-24	NAM
MD0402	0-2	GZ
MD0402	2-4	GZ
MD0402	4-6	GZ
MD0402	6-8	NAM
MD0402	8-10	NAM
MD0402	10-12	NAM
MD0402	12-14	NAM
MD0402	14-16	NAM
MD0402	16-18	NAM
MD0402	18-20	NAM
MD0402	20-22	NAM
MD0402	22-24	NAM
MD0408	0-2	ALU
MD0408	2-4	ALU
MD0408	4-6	GZ
MD0408	6-8	GZ
MD0408	8-10	GZ
MD0408	10-12	GZ
MD0408	12-14	NAM
MD0408	14-16	NAM
MD0408	16-18	NAM
MD0408	18-20	NAM
MD0408	20-22	NAM

BoreID	Depth range (m)	Code
MD0408	22-24	NAM
MD0441	0-2	ALU
MD0441	2-4	ALU
MD0441	4-6	ALU
MD0441	6-8	ALU
MD0441	8-10	ALU
MD0441	10-12	ALU
MD0441	12-14	ALU
MD0441	14-16	ALU
MD0441	16-18	ALU
MD0441	18-20	ALU
MD0441	20-22	ALU
MD0441	22-24	ALU
MD0439	0-2	ALU
MD0439	2-4	ALU
MD0439	4-6	ALU
MD0439	6-8	ALU
MD0439	8-10	ALU
MD0439	10-12	ALU
MD0439	12-14	ALU
MD0439	14-16	ALU
MD0439	16-18	ALU
MD0439	18-20	ALU
MD0439	20-22	ALU
MD0439	22-24	ALU
MD0293	0-2	ALU
MD0293	2-4	ALU
MD0293	4-6	ALU
MD0293	6-8	ALU
MD0293	8-10	ALU
MD0293	10-12	ALU
MD0293	12-14	GZ
MD0293	14-16	GZ
MD0293	16-18	GZ
MD0293	18-20	NAM
MD0293	20-22	NAM
MD0293	22-24	NAM
MD0295	0-2	GZ
MD0295	2-4	NAM

BoreID	Depth range (m)	Code
MD0295	4-6	NAM
MD0295	6-8	NAM
MD0295	8-10	NAM
MD0295	10-12	NAM
MD0295	12-14	NAM
MD0295	14-16	NAM
MD0295	16-18	NAM
MD0295	18-20	NAM
MD0295	20-22	NAM
MD0295	22-24	NAM
MD0266	0-2	ALU
MD0266	2-4	JER
MD0266	4-6	JER
MD0266	6-8	JER
MD0266	8-10	JER
MD0266	10-12	JER
MD0266	12-14	JER
MD0266	14-16	JER
MD0266	16-18	JER
MD0266	18-20	JER
MD0266	20-22	JER
MD0266	22-24	JER
MD0562	0-2	CC
MD0562	2-4	CC
MD0562	4-6	CC
MD0562	6-8	CC
MD0562	8-10	CC
MD0562	10-12	GZ
MD0562	12-14	GZ
MD0562	14-16	GZ
MD0562	16-18	GZ
MD0562	18-20	GZ
MD0562	20-22	GZ
MD0562	22-24	GZ

Geological Codes: NAM, nammuldi; ALU, Tertiary alluvial; JER, Jerrinah; CC, Calcrete.