

Ministers North and Yandicoogina Creek Short-Range Endemic Invertebrate Fauna Survey

Biologic Environmental Survey

Report to BHP Western Australia Iron Ore

April 2021

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EXECUTIVE SUMMARY

BHP Western Australia Iron Ore (BHP WAIO) commissioned Biologic Environmental Survey (Biologic) to undertake a single season targeted short-range endemic (SRE) invertebrate fauna survey covering the Ministers North Miscellaneous Licence area (hereafter referred to as Targeted Survey Area) and a two season Level 2 SRE invertebrate fauna survey within a potential Groundwater Dependent Ecosystem (GDE) in Yandicoogina Creek (hereafter referred to as Level 2 Survey Area). This report presents the combined results of a desktop and field survey assessment of these two survey areas.

The desktop assessment and surveys were carried out in a manner consistent with the Western Australian (WA) Environmental Protection Authority (EPA) and BHP WAIO's requirements for the environmental surveying and reporting of fauna. The desktop assessment yielded 1127 records representing 182 Potential and/or Confirmed SRE invertebrate taxa. Of these, Araneae accounted for the majority of records (77 taxa) with the remaining taxa represented by pseudoscorpions (72 taxa), scorpions (two taxa), millipedes (17 taxa), Isopoda (12 taxa) and snails (two taxa). Fourteen of these taxa are Confirmed SRE species, represented by four spiders and 10 paradoxosomatid millipedes.

During the current surveys, undertaken between the 9th and 13th of September 2019 (dry season) and between the 3rd and 10th of April 2020 (wet season), 70 sites were assessed, of which 32 sites were sampled for SRE invertebrates. The assessments classified the area into six broad habitat categories: Gorge/ Gully, Hillcrest/ Hillslope, Major Drainage Lines, Drainage Area/ Floodplain, Undulating Low Hills, and Sandy/ Stony Plains.

Only one habitat type within the two survey areas is regarded to be of High suitability for SRE fauna, and therefore of high significance: Gorge/ Gully. The habitat type is well distributed within the Level 2 Survey Area representing 20% of the total area surveyed and is associated with the Yandicoogina Creek that occurs well beyond the Level 2 Survey Area boundaries. Gorge/ Gully is less prevalent in the Targeted Survey Area (4%). Both survey areas are dominated by Moderately suitable habitat type Hillcrest/ Hillslope (67% and 64% respectively). This habitat type is found extensively in the immediate areas around the two survey areas. The remaining four habitat types are of Moderate to Low suitability for SRE invertebrate fauna (Major and Minor Drainage Line, Drainage Areas/ Floodplain, Undulating Low Hills) or Low suitability (Sandy/ Stony Plains).

A total of 123 invertebrates were collected from the two survey areas, of which 109 were considered to represent groups known to contain SRE species. These groups were Araneae (one taxon), Pseudoscorpiones (eight taxa), Scorpiones (three taxa), Chilopoda (one taxon), Diplopoda (one taxon), Isopoda (six taxa), and Gastropoda (four taxa).

Specimens of *Karaops* (if all specimens represent the same species) were found in both survey areas. It is likely that the specimens collected in this current survey are one of the four previously collected species in the area. There have been four other species collected within 40 km of the survey areas: *Karaops banyjima, Karaops nyangumarta, Karaops* `ARA001-DNA`, and *Karaops* `ARA002-DNA` (Biologic, 2018; WAM, 2020a).

Olpiid pseudoscorpion specimens collected in the current survey represent five morphospecies, two of which were found in both survey areas. Four morphospecies, *Austrohorus* `sp. PSE121`, *Austrohorus* `sp. PSE121`, *Indolpium* `sp. PSE118`, and *Indolpium* `sp. PSE123` were matched by molecular analysis to specimens previously collected within and nearby the survey areas. One morphospecies, *Xenolpium* `sp. Biologic-PSEU028` was newly collected and could not be matched to any other specimens. *Indolpium* `sp. PSE118` has been collected from sites ~60 km southwest, while the other four morphospecies are only know from the vicinity of the survey areas.

All scorpions encountered in this survey were collected in the Level 2 Survey Area. The *Urodacus* specimen was subadult and could not be identified to species. Five *Lychas* specimens were matched by molecular analysis to others collected ~60 km south-west of the survey areas (*Lychas* `sp. Biologic-SCOR001`), while the other was morphologically identified as part of the well-known species group *Lychas* `multipunctatus complex`.

The spirobolid millipede, *Austrostrophus* `sp. clade A NGW-2020` was found in both two survey areas. Molecular analysis matched these specimens to others collected ~60 km to the south-west.

Buddelundia ‘sp. 49’ was collected in the Targeted Survey Area only in this current survey but has been collected in the Orebody 19-31 area (Biologic, 2014). However, based on communication from Dr Simon Judd, it is possible this species is part of a species complex and may represent two or more taxa. Further specimens would be required to determine the taxonomic status of the species.

The *Bothriembryon* snails were collected in the Level 2 Survey Area only. There is no systematic morphological taxonomy available for *Bothriembryon* in the Pilbara, and while it is currently thought that all Pilbara *Bothriembryon* records constitute the same species (currently referred to as *Bothriembryon* `Pilbara n. sp.`) further molecular and morphological analysis is needed to confirm (C. Whisson, pers. comm., 2020).

1 INTRODUCTION

BHP Western Australia Iron Ore (BHP WAIO) commissioned Biologic Environmental Survey (Biologic) to undertake a single season targeted short-range endemic (SRE) invertebrate fauna survey covering the Ministers North Miscellaneous Licence area (hereafter referred to as Targeted Survey Area) and a two season Level 2 SRE invertebrate fauna survey within a potential Groundwater Dependent Ecosystem (GDE) in Yandicoogina Creek (hereafter referred to as Level 2 Survey Area). The survey areas are located approximately 80 kilometres (km) north-west of Newman Township in the Pilbara region of Western Australia (Figure 1.1) and cover a total area of approximately 92 km^2.

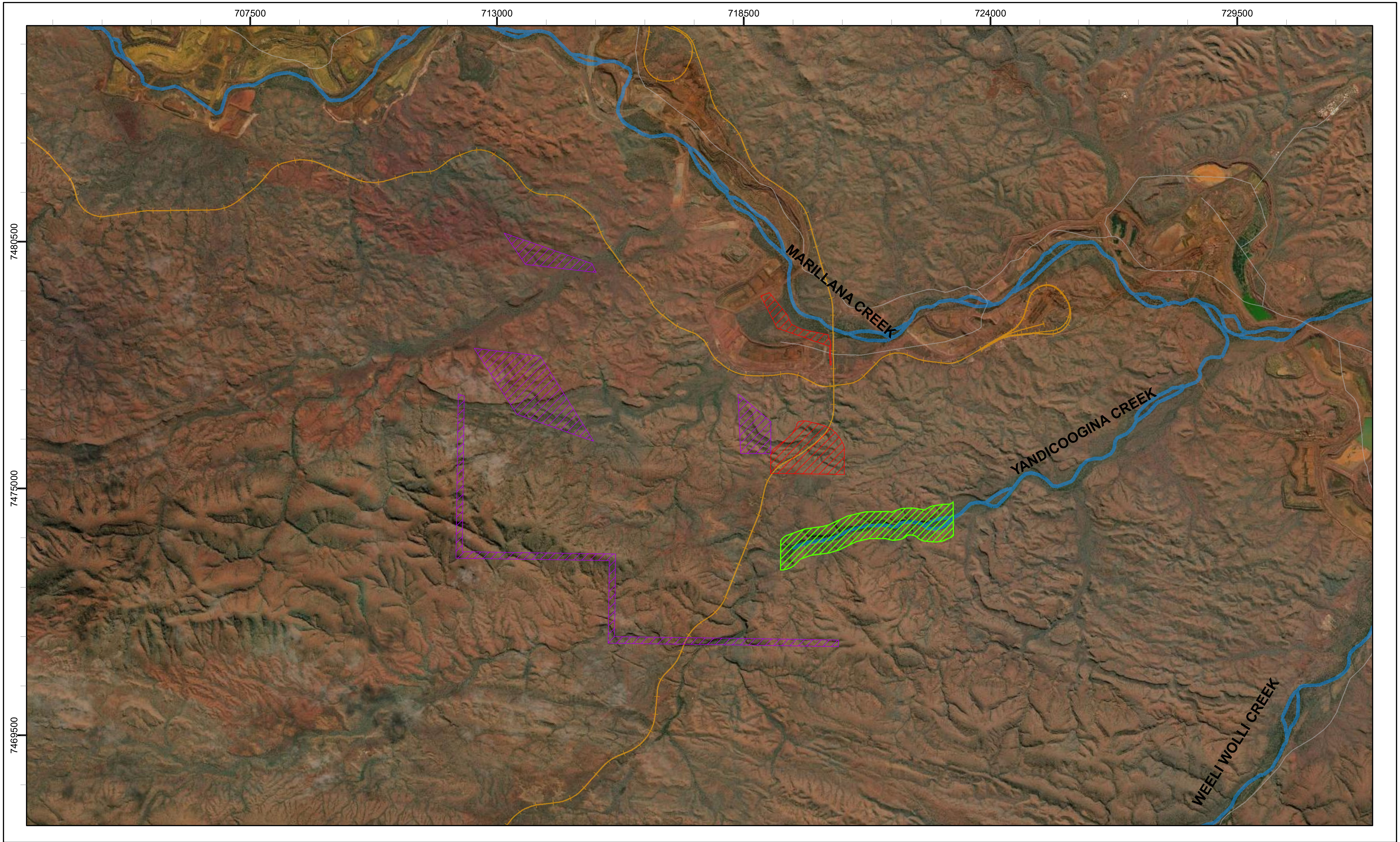
1.1 Short-range endemic fauna

Endemism refers to the restriction of a species to a particular area, whether it is at the continental, national or local scale (Allen, 2010) . Endemism at a local scale is commonly referred to as short-range endemism (Harvey, 2002). Short-range endemism of a species is influenced by several factors including life history, physiology, habitat requirements, dispersal capabilities, biotic and abiotic interactions and historical conditions which not only influence the distribution of a species, but also the tendency for differentiation and speciation (Ponder & Colgan, 2002).

Harvey (2002) proposed a range criterion for terrestrial SRE invertebrate species at less than 10,000 km^2 (or 100 km x 100 km), which has been adopted by regulatory authorities in Western Australia (EPA, 2016b). SRE invertebrate species often share similar biological, behavioural and life history characteristics that influence their restricted distributions and limit their wider dispersal (Harvey, 2002). For example, burrowing taxa such as mygalomorph spiders and *Urodacus* scorpions may only leave their burrows (or a narrow home territory around the burrow) as juveniles dispersing from the maternal burrow, or when males search for a mate. In other cases, SRE taxa are dispersal-limited because of their slow pace of movement and cryptic habitats (such as isopods, millipedes, and snails), while some specialised taxa can be limited by very specific habitat requirements, such as selenopid spiders within fractured rocky outcrops.

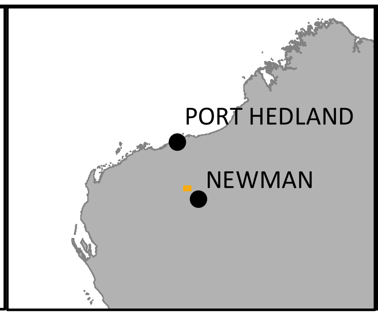
In recent years, a number of taxonomic groups of invertebrates have been highlighted as having a high proportion of species likely to be regarded as SREs (i.e. Harvey, 2002; terrestrial snails, Johnson *et al.*, 2004; freshwater snails, Ponder & Colgan, 2002; Mygalomorph spiders,Rix *et al.*, 2018) . This has led to SRE invertebrate fauna being recognised as comprising a significant biodiversity component of an area and that SRE fauna “may be at a greater risk of changes in conservation status as a result of habitat loss or other threatening processes” (EPA, 2016b).

An increasing number of terrestrial invertebrates appear to exhibit short-range endemism in Western Australia. While protection for listed species (species of conservation significance) and/ or Threatened or Priority Ecological Communities is provided under state and federal legislation, the majority of SRE invertebrate species and communities are not currently listed. This is due largely to incomplete taxonomic or ecological knowledge. As such, the assessment of conservation significance for SRE invertebrates is guided primarily by expert advice provided by the Western Australian Museum (WAM) and other taxonomic experts.



Legend

- Targeted Survey Area
- Level 2 Survey Area
- Targeted Survey Area - Inaccessible
- Rail
- Roads
- Major Creeklines



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BHP Western Australia Iron Ore

Ministers North and Yandicoogina Creek SRE Invertebrate Survey

Figure 1.1: Study Area and Regional Location

Coordinate System: GDA 1994 MGA Zone 50
Projection: Transverse Mercator
Datum: GDA 1994

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2 ENVIRONMENT

2.1 Biogeography

The two survey areas fall within the Pilbara biogeographical region as defined by the Interim Biogeographic Regionalisation of Australia (IBRA) (Thackway & Cresswell, 1995). The Pilbara bioregion is characterised by vast coastal plains and inland mountain ranges with cliffs and deep gorges (Thackway & Cresswell, 1995). Vegetation is predominantly mulga low woodlands or snappy gum over bunch and hummock grasses (Bastin, 2008). Within the Pilbara bioregion there are four subregions: Hamersley, Chichester, Roebourne, and Fortescue Plains.

The two survey areas lie within the Hamersley subregion which contains the southern section of the Pilbara Craton and consists of mountainous areas of Proterozoic sedimentary ranges and plateaux's, dissected by gorges of basalts, shales and dolerite (Kendrick, 2001). The vegetation of the Hamersley subregion is predominantly mulga low woodlands over bunch grass on fine textured soils in valley floors and *Eucalyptus leucophloia* over *Triodia brizoides* (and other *Triodia* spp.) on skeletal soils of the ranges (Kendrick, 2001). The Hamersley subregion drains to either the Fortescue River to the north, the Ashburton River to the south, or the Robe River to the west (Kendrick, 2001).

2.2 Climate

The Pilbara region has a semi-desert to tropical climate with highly variable, mostly summer rainfall (Leighton, 2004; McKenzie *et al.*, 2002). The average annual rainfall over the broader Pilbara area ranges from about 200 – 350 millimetres (mm) (predominantly in January, February and March), although rainfall may vary widely from year to year (van Etten, 2009). The Pilbara climate is heavily influenced by tropical cyclones that develop over the Indian Ocean in the north of Australia (Leighton, 2004). These sometimes cross the northwest coastline, bringing heavy rainfall to inland regions of the Pilbara. Most rainfall generally occurs in the summer wet season from December to June with occasional major rainfall events from tropical cyclones. Temperatures vary significantly throughout the year with average maximum summer temperatures reaching 35°C to 40°C and winter temperatures generally fluctuating between 22°C and 30°C.

Long-term climatic data is not available for Ministers North; however, the Bureau of Meteorology (BoM) weather station at Newman Airport (Station 007176, located 90 km south west of the two survey areas) and Marillana (Station 5009, located 33 km north east of the two survey areas) can be used as reference points for climatic observations in the survey areas.

2.3 Groundwater Dependent Ecosystems

The Level 2 Survey Area is located within a potential Groundwater dependent ecosystem (GDE) in the Yandicoogina Creek system, a major drainage line in the Level 2 Survey Area. GDE's and their associated vegetation are dependent on the presence of groundwater to meet some, or all, of their water requirements, either through surface expression or subsurface presence of groundwater (Hatton & Evans, 1998). GDE classifications are based on unique vegetation communities; and due to the presence of moisture and protective vegetation, these systems may provide significant habitat for SRE invertebrate fauna.

2.4 Desktop Assessment

A desktop assessment was carried out in a manner consistent with the Western Australian (WA) Environmental Protection Authority (EPA) environmental surveying and reporting of fauna, as well as BHP policy and guidance, including the following documents:

- Technical Guidance: Sampling of Short-range Endemic Invertebrate Fauna (EPA, 2016b)
- Technical Guidance: Terrestrial Fauna Surveys (EPA, 2016c)
- Environmental Factor Guideline: Terrestrial Fauna (EPA, 2016a)
- Short-range Endemic Invertebrate Fauna Assessment Methods: Procedure (BHP, 2017)

2.4.1 Review of databases

Five databases were searched for SRE invertebrate fauna records within and surrounding the two survey areas to determine the likely SRE fauna values (Table 2.1).

Table 2.1: Databases searched for the review of previous records

Provider	Database	Reference	Search parameters
DBCA	Threatened and Priority Fauna Database	(DBCA, 2020)	Circle of radius 40 km centred on the coordinates: -22.8158°, 119.1233°
Atlas of Living Australia	Species Occurrence	(ALA, 2020)	Circle of radius 10 km centred on the coordinates: -22.8158°, 119.1233°
Western Australian Museum (WAM)	Arachnids and Myriapods	(WAM, 2020a)	40 x 40 km search area surrounding the survey areas: NW: -22.5337°, 118.8775° SE: -23.1055°, 119.3711°
WAM	Crustaceans	(WAM, 2020b)	40 x 40 km search area surrounding the survey areas: NW: -22.5337°, 118.8775° SE: -23.1055°, 119.3711°
WAM	Molluscs	(WAM, 2020c)	40 x 40 km search area surrounding the survey areas: NW: -22.5337°, 118.8775° SE: -23.1055°, 119.3711°

Within these database searches, records of mygalomorph spiders, selenopid spiders, pseudoscorpions, scorpions, centipedes, millipedes, terrestrial snails, and isopods were targeted. WAM databases were queried within a 1,600 km^2 area surrounding the survey areas. Indeterminate records were excluded, except where generic level characters and distribution information was sufficient to point to a high likelihood that the species could be SRE.

2.4.2 Review of previous studies

Five SRE invertebrate fauna surveys have been conducted in the vicinity of the two survey areas. A summary of the survey effort is shown in Table 2.2. The combination of a high level of habitat assessments conducted in conjunction with fauna sampling across all habitat types present suggests that the region surrounding and including the survey areas have been adequately surveyed for SRE invertebrate fauna.

Table 2.2: Previous reports in the vicinity of the survey areas

Survey Title	Reference	Survey Type	Location	SRE Sampling Sites	Habitat Assessments	Distance from survey area
Ministers North Biological Survey	ecologia (2006)	Biological Survey	Ministers North	23	23	5 km W Level 2 Survey Area
Yandi Mine Short-Range Endemic Invertebrate Survey and Impact Assessment	Biologic (2013)	Two season Level 2	Yandi	34	55	~20 km NW of Level 2 Survey Area
Yandi Tenement Short-Range Endemic Invertebrate Survey	Biologic (2015)	Two season Level 2	Yandi	94	119 (88 wet season & 31 dry season)	15 km NW of Level 2 Survey Area
Ministers North Short-Range Endemic Invertebrate Survey	Biologic (2016)	Two season Level 2	Ministers North	38	91 (40 wet season & 51 dry season)	~5 km W Level 2 Survey Area
Ministers North to Yandi Corridor SRE Invertebrate Fauna Survey	Biologic (2018)	Two season Level 2	Ministers North and Yandi	38	37	~7 km NW of Level 2 Survey Area

3 SURVEY METHODS

3.1 Field survey

3.1.1 Field team and licensing

The SRE fauna sampling for this survey was conducted under a DBCA Regulation 17 "Licence to Take Fauna for Scientific Purposes" (BA27000114) issued to Nihara Gunawardene. The following personnel were involved in the field component of this project:

- Brad Durrant (Principal Zoologist)
- Ryan Ellis (Senior Zoologist)
- Amy Hutchison (Zoologist)
- Emily Eakin-Busher (Graduate Ecologist)

3.1.2 Survey timing and weather

The Targeted and Level 2 SRE invertebrate fauna surveys were undertaken in accordance with relevant EPA guidelines. The first of two sampling trips was conducted during the dry season (September 2019) and the second in the wet season (April 2019). The Level 2 Survey Area was sampled during these two sampling trips. The Targeted Survey Area was sampled in the wet season trip only.

The survey dates were as follows:

- 9^{th} – 13^{th} September 2019 (Trip 1, dry season); and
- 3^{rd} – 10^{th} April 2020 (Trip 2, wet season).

Observed weather conditions prior to and during the surveys are shown in Figure 3.1, alongside long-term climatic data for Newman Airport. The average minimum (13.2 °C) and maximum (32 °C) temperatures during the dry season survey (Trip 1) were slightly higher than the long-term averages for September (12.2 °C and 30.5 °C). No rain was recorded during this survey period and the last recorded rainfall prior to Trip 1 was on August 16^{th}, 2019 (2.4 mm, 4 weeks previously).

The 2019/2020 wet season (November – April) was generally hotter than the long-term average conditions, with mean maximum temperatures ranging from 37.4 °C to 41.5 °C (on average 1.2 °C hotter than the long-term average). Total observed rainfall was significantly higher than average, due to the influence of Tropical Cyclones Blake and Damien, with 198.2 mm falling in January (284% of the long-term average at Newman Airport (BoM, 2020). 17.0 mm of rainfall was recorded on the first day of the wet season survey (Trip 2), though no further rainfall was recorded during the trip (BoM, 2020).

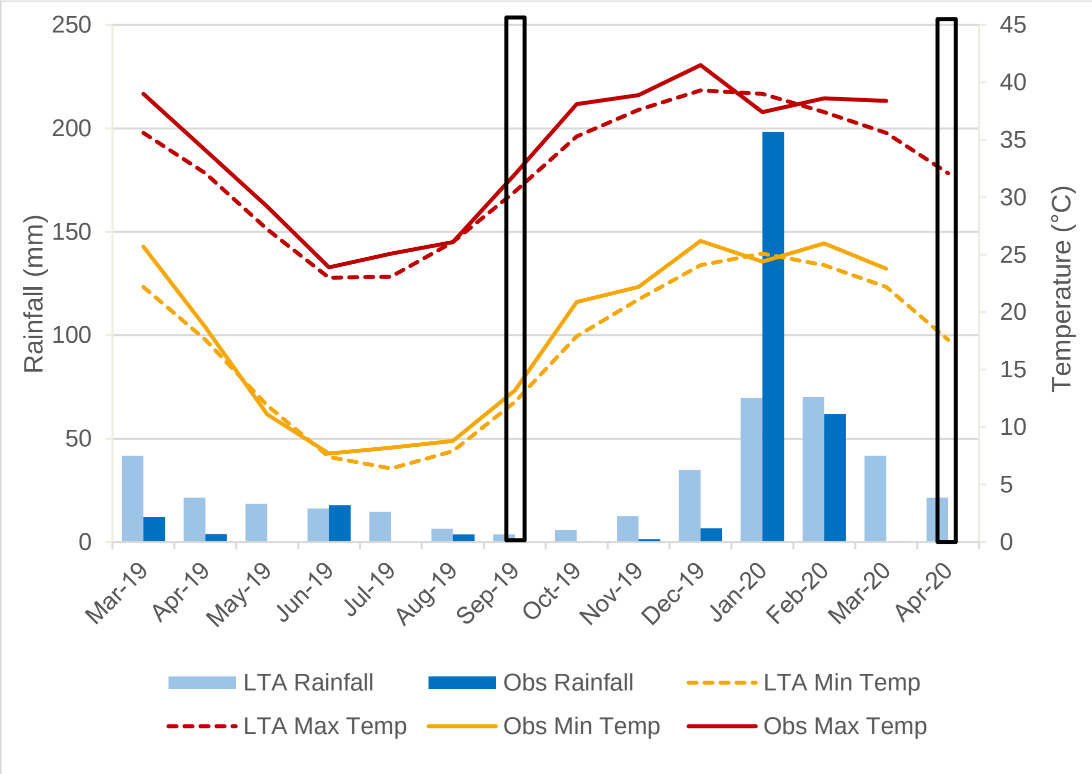


Figure 3.1: Long-term average and current (2019-2020) climatic data for Newman Airport (Station 007176). Approximate survey timing is indicated by the black boxes

3.1.3 Site selection

Habitats considered suitable for SRE terrestrial invertebrates in the Pilbara were targeted for the baseline SRE invertebrate fauna survey, namely gorges/ deep gullies, shallow/ open gullies, ridges/ breakaways, and drainage foci. Sampling was also undertaken in less suitable habitat types, including drainage lines, hillcrests and slopes, and minor rocky outcrops.

3.1.4 Habitat assessment

Habitat assessments were carried out at each site by observation of the physical characteristics of each site. The habitat assessments were aimed at determining the significance of each site as suitable SRE habitat, and hence the likelihood that each site may contain SRE invertebrate fauna (see Appendix A). The broad habitat type in which the site occurred was observed and any site-specific landform characteristics (especially where samples were taken) were also recorded. Further physical characteristics of each site in a 20 x 20 m quadrat were recorded; these were drainage type, aspect, slope, percentage shade, evidence of moisture in soil, soil type and availability, presence of rock outcropping, rock size, percentage litter cover, major vegetation type and evidence of fire and disturbance. The broad habitat type is used for mapping the habitats found in the two survey areas, while the physical characteristics are used to provide an overall picture of the habitat type should an SRE invertebrate be captured in that particular site.

3.1.5 Sampling techniques

The sampling techniques employed for both the Targeted and Level 2 surveys included active foraging, leaf litter sifting, soil sifting and targeted searches for spider and scorpion burrows. The target taxonomic groups were trapdoor spiders (Mygalomorphae), selenopid spiders, scorpions, millipedes, pseudoscorpions, land snails, and isopods.

The sampling methods adopted were carried out in accordance with the following documents:

- Technical Guidance: Sampling of Short-range Endemic Invertebrate Fauna (EPA, 2016b); and
- Short-range Endemic Invertebrate Fauna Assessment Methods: Procedure (BHP, 2017).

Active foraging

Active foraging was undertaken at each sampling site for a minimum of 1.5 person hours and involved various techniques relevant to the following microhabitats:

- Under rocks, within cracks and crevices: suitably sized rocks were overturned, and rocky microhabitats were actively searched for rock dwelling species.
- Woody debris: larger logs and woody debris were investigated and overturned searching for detritivores.
- Vegetation and tree bark: significant vegetation (*e.g.* Mulga, and fig trees) were actively searched, including underneath sheets of bark.
- Burrow searching: active searches were undertaken for mygalomorph spider and scorpion burrows within suitable habitats. Note: searches for burrows are undertaken during foraging time and while walking through the two survey areas, but time taken to excavate burrows is additional to foraging time.

Leaf litter searching

Leaf litter, humus, and soil (to approximately 15 cm below surface where possible) was placed in a sieve at the site and agitated to divide the sample into three grades (>7 mm, >3 mm, >1.4 mm). Each grade was thoroughly searched for target SRE species such as pseudoscorpions, millipedes, snails, and small scorpions. Up to two sifts (~ 1L of material) were conducted at each site, providing enough leaf litter and humus was available.

Specimen preservation and identification

All specimens were euthanised in 100% ethanol to preserve DNA for sequencing. Isopods were transferred to 70% ethanol for storage at the request of Dr Simon Judd.

All isopods were sent directly to Dr Simon Judd for identification and scorpion specimens were identified by Dr Erich Volschenk. All other taxa were identified in-house using available taxonomic keys.

3.1.6 SRE classification

The SRE categories used in this report broadly follow the WAM's revised classification system for SRE invertebrates. This system is based upon the 10,000 km^2 range criterion proposed by Harvey (2002), and uses three broad categories to deal with varying levels of taxonomic certainty that may apply to any given taxon (Table 3.1).

Table 3.1: SRE categorisation used by WAM taxonomists

<table>
<tr><th>Distribution</th><th>Taxonomic Certainty</th><th>Taxonomic Uncertainty</th></tr>
<tr><td>< 10 000 km^2</td><td>Confirmed SRE
• A known distribution of < 10,000 km^2.
• The taxonomy is well known.
• The group is well represented in collections and/ or via comprehensive sampling.</td><td rowspan="2">Potential SRE
• Patchy sampling has resulted in incomplete knowledge of geographic distribution.
• Incomplete taxonomic knowledge.
• The group is not well represented in collections.
• Category applies where there are significant knowledge gaps.

SRE Sub-categories may apply:
A) Data Deficient
B) Habitat Indicators
C) Morphology Indicators
D) Molecular Evidence
E) Research & Expertise</td></tr>
<tr><td>> 10 000 km^2</td><td>Widespread (not an SRE)
• A known distribution of > 10,000 km^2.
• The taxonomy is well known.
• The group is well represented in collections and/ or via comprehensive sampling.</td></tr>
</table>

For taxa which belong to groups which are known to contain SRE species (i.e. mygalomorph spiders, selenopid spiders, scorpions, pseudoscorpions, myriapods, molluscs and crustaceans), the default status is Potential SRE, unless sufficient evidence exists to confirm a Widespread or Confirmed SRE status.

Potential SRE status is sub-categorised by what is currently known about the species in question, i.e., whether there are B) habitat indicators, C) morphology indicators, D) molecular evidence, or E) a weight of general knowledge and experience with the group that suggests a reasonable likelihood that the species could be SRE. In terms of SRE likelihood, the more evidence that exists under sub-categories 'B', 'C', 'D', and 'E', the greater the likelihood that further investigation would confirm that the species is an SRE.

In contrast, when a taxon is considered Potential SRE because of data deficiency (DD) only (sub-category ‘A’), then current information is insufficient to support a reliable assessment of its SRE status; for example, the taxonomy of the genus or family to which the taxon belongs might require significant review before any statement about the likely SRE status can be made or the taxon is not known to include any confirmed SRE species within the region (subject to the extent of prior sampling / taxonomic effort).

Any expert/taxonomist advice about the SRE status of taxa is presented within the broader context of the results from habitat assessment, desktop review, habitat connectivity, and other ecological information collected during the survey. This approach aims to provide a more holistic assessment of SRE likelihood at scales relevant to the project, as well as the standard SRE range criterion of <10,000 km^2 (Harvey, 2002).

3.2 Limitations of the survey

EPA Guidance Statement No. 56 (EPA, 2016c) outlines several potential limitations to fauna surveys, which are presented and discussed in Table 3.2. Other than the unusually dry conditions prior to the wet season survey, it was considered that there were no material limitations to the survey. However, the area is considered to be in BoM Drought Category ‘Serious rainfall deficiency’ (2019 annual rainfall lies below the 10th percentile of all records for the area) (BoM, 2019).

Table 3.2: Survey limitations and constraints

Potential limitation or constraint	Applicability to this survey
Experience of personnel.	No constraint. All senior personnel have more than five years' experience collecting invertebrate fauna specimens.
Proportion of fauna identified.	No constraint. Morphological identifications carried out by established taxonomists Dr Erich Volschenk and Dr Simon Judd. All other identifications carried out in-house using available keys.
Sources of information (recent or historic) and availability of contextual information.	All previous surveys relevant to the planning of the survey were available and consulted.
Proportion of the task achieved.	One two season and one targeted SRE invertebrate fauna survey were completed in each respective survey area.
Disturbances (e.g. fire or flood).	No observation of fire or large-scale flooding was made in the survey areas.
Intensity of survey.	No constraint.
Completeness of survey.	The survey areas, considering current and previous survey effort and habitats covered has been adequately surveyed.
Resources (e.g. degree of expertise available).	All resources required to complete the survey were available.
Remoteness or access issues.	There were access issues with the Targeted Survey Area (Figure 1.1). Tenure access was revoked due to COVID 19 and there were some parts of the Targeted Survey Area that could not be sampled. The majority of the Level 2 Survey Area was accessible. The parts of the survey area that was accessible was entered either by vehicle or on foot.
Scope (what faunal groups were sampled and whether any constraints affect this).	All SRE faunal groups, selenopid spiders, scorpions, pseudoscorpions, myriapods, molluscs and crustaceans were sampled. No constraint.
Timing of survey, weather, seasonality	The conditions prior to and during the wet season survey were considerably hotter and drier than the long-term average conditions. This is likely to have reduced the abundance and activity levels of some invertebrate fauna groups.

4 RESULTS

4.1 Desktop assessment

4.1.1 Database searches

The WAM and NatureMap database searches have provided an up-to-date SRE invertebrate fauna list for the two survey areas and surrounds, containing records from all known previous surveys (with the exception of the most recent Biologic, 2018 survey) within a 40 km radius (congruent with other databases). These searches yielded 1127 records representing 182 Potential and/or Confirmed SRE invertebrate taxa from six higher groups comprising selenopid spiders, mygalomorph spiders, pseudoscorpions, scorpions, millipedes, isopods, and snails (Appendix B).

Of these, Araneae accounted for the majority of records (77 taxa) with remaining taxa being represented by pseudoscorpions (72 taxa), scorpions (2 taxa) and millipedes (17 taxa), Isopoda (12 taxa) and snails (2 taxa). The locations of these records within 40 Km of the two survey areas are shown in Figure 4.1. Fourteen of these taxa are Confirmed SRE species, represented by four spiders and 10 paradoxosomatid millipedes. These are highlighted in red in Figure 4.1. The four spiders are published species whilst only three of the millipedes are formally named. The remaining seven have been given Confirmed status due to the general nature of the *Antichiropus* species in WA being almost always restricted in range. Nineteen taxa are listed in Table 4.1 are Potential SRE recorded within 10 km of the two survey areas. Three of the Potential SRE taxa from were recorded between the current survey area boundaries (Table 4.1).

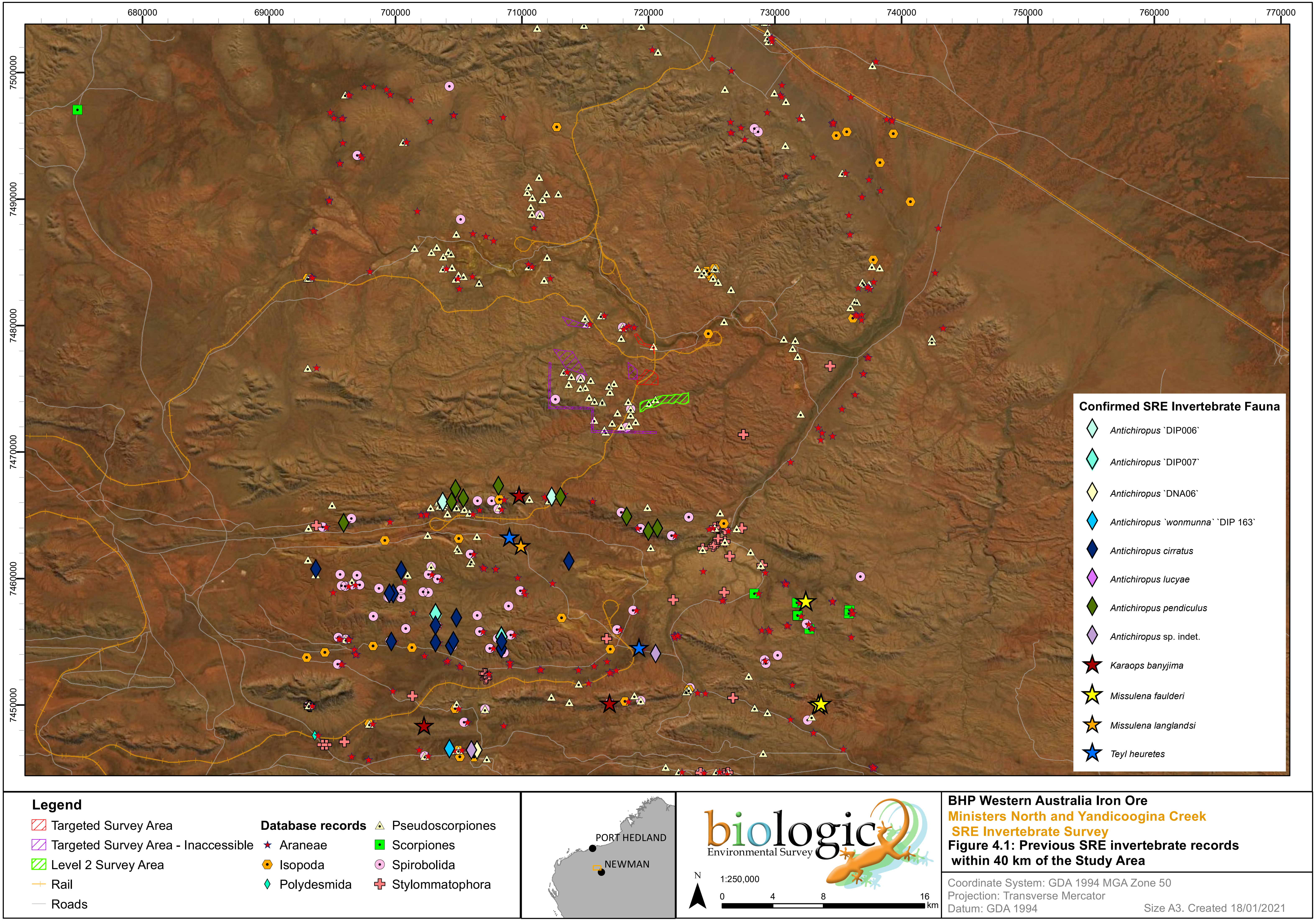
4.1.2 Previous surveys

The Ministers North and Yandicoogina Creek Survey Areas have been well-surveyed for SRE invertebrate fauna in recent years (see Table 2.2). Many of the specimens collected in these surveys are the same as those yielded in the WAM database searches. Most recently, Biologic conducted a survey in the Ministers North to Yandi area in 2018 (Biologic, 2018). The survey recorded five target groups known to contain SREs in seven broad habitat types; these were selenopid spiders, pseudoscorpions, scorpions, millipedes, and isopods. Six of these taxa were regarded as Potential SRE: *Karaops* sp. indet., *Lychas* `*bituberculatus* complex’ *Lychas* `hairy tail complex`, *Buddelundia* sp. `10ma`, *Buddelundia* sp. `49`, and Philosciidae sp. indet.

Table 4.1: Potential SRE invertebrate taxa occurring within 10 km of the Ministers North and Yandicoogina Creek survey areas

NB: Taxa highlighted in green are those found between the two Survey Area boundaries.

Higher Taxa	Family	Genus	Lowest ID	Specimens	Source
Araneae	Barychelidae		Barychelidae sp. indet.	1	WAM DB
	Selenopidae	*Karaops*	*Karaops* `ARA001`	6	WAM DB
	Selenopidae	*Karaops*	*Karaops* sp. indet.	16	Biologic 2018
Pseudoscorpiones	Chthoniidae	*Austrochthonius*	*Austrochthonius* sp. indet.	1	WAM DB
		Lagynochthonius	*Lagynochthonius* sp. S4`	6	WAM DB
			Lagynochthonius `yandi`	1	WAM DB
	Olpiidae	`Genus 7/4`	`Genus 7/4` sp. indet.	4	WAM DB
		Austrohorus	*Austrohorus* `PSE119`	9	WAM DB
			Austrohorus `PSE120`	1	WAM DB
			Austrohorus `PSE121`	1	WAM DB
			Austrohorus `PSE122`	2	WAM DB
			Austrohorus sp. indet.	3	WAM DB
		Beierolpium	*Beierolpium* `PSE126`	1	WAM DB
			Beierolpium sp. indet.	5	WAM DB
		Euryolpium	*Euryolpium* sp. indet.	2	WAM DB
		Indolpium	*Indolpium* `PSE118`	1	WAM DB
			Indolpium `PSE123`	6	WAM DB
			Indolpium sp. indet.	7	WAM DB
			Olpiidae sp. indet.	5	WAM DB
Scorpiones	Buthidae	*Lychas*	*Lychas* ‘hairy tail complex’	3	Biologic 2018
Scorpiones	Buthidae		*Lychas* ‘bituberculatus complex’	2	Biologic 2018
Spirobolida	Trigoniulidae	*Austrostrophus*	*Austrostrophus* stictopygus	4	WAM DB
Isopoda	Armadillidae	*Buddelundia*	*Buddelundia* sp. `10ma`	8	Biologic 2018
			Buddelundia sp. `49`	5	Biologic 2018
	Philosciidae		Philosciidae sp. indet.	10	Biologic 2018



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Ministers North and Yandicoogina Creek SRE Invertebrate Survey
Figure 4.1: Previous SRE invertebrate records within 40 km of the Study Area

Coordinate System: GDA 1994 MGA Zone 50
Projection: Transverse Mercator
Datum: GDA 1994
Size A3. Created 18/01/2021

4.2 Current survey sites

In the dry season survey (Trip 1), habitat assessments were undertaken at 45 sites, with sampling carried out at 23 of these sites. In the wet season survey (Trip 2), 25 new sites were habitat assessed, with sampling carried out at ten of these sites, and 22 of the sites assessed during Trip 1 were re-sampled. Across both trips, habitat assessments were conducted at 70 sites, of which 32 were sampled for invertebrates (Figure 4.2).

4.2.1 Habitat assessment

Habitat assessments were carried out at 70 sites across the two survey areas in two trips (see Appendix C for full details). Forty-five sites were visited in the Level 2 Survey Area and 25 in the Targeted Survey Area. These assessments were used to classify the two survey areas and the intervening area into six broad habitat categories based on the major landform features that primarily determines SRE suitability (Table 4.2). These broad categories, along with aerial photography, were then used to map the extent of these habitat types across the two survey areas (Figure 4.2). A brief description of these broad habitat categories is provided below.

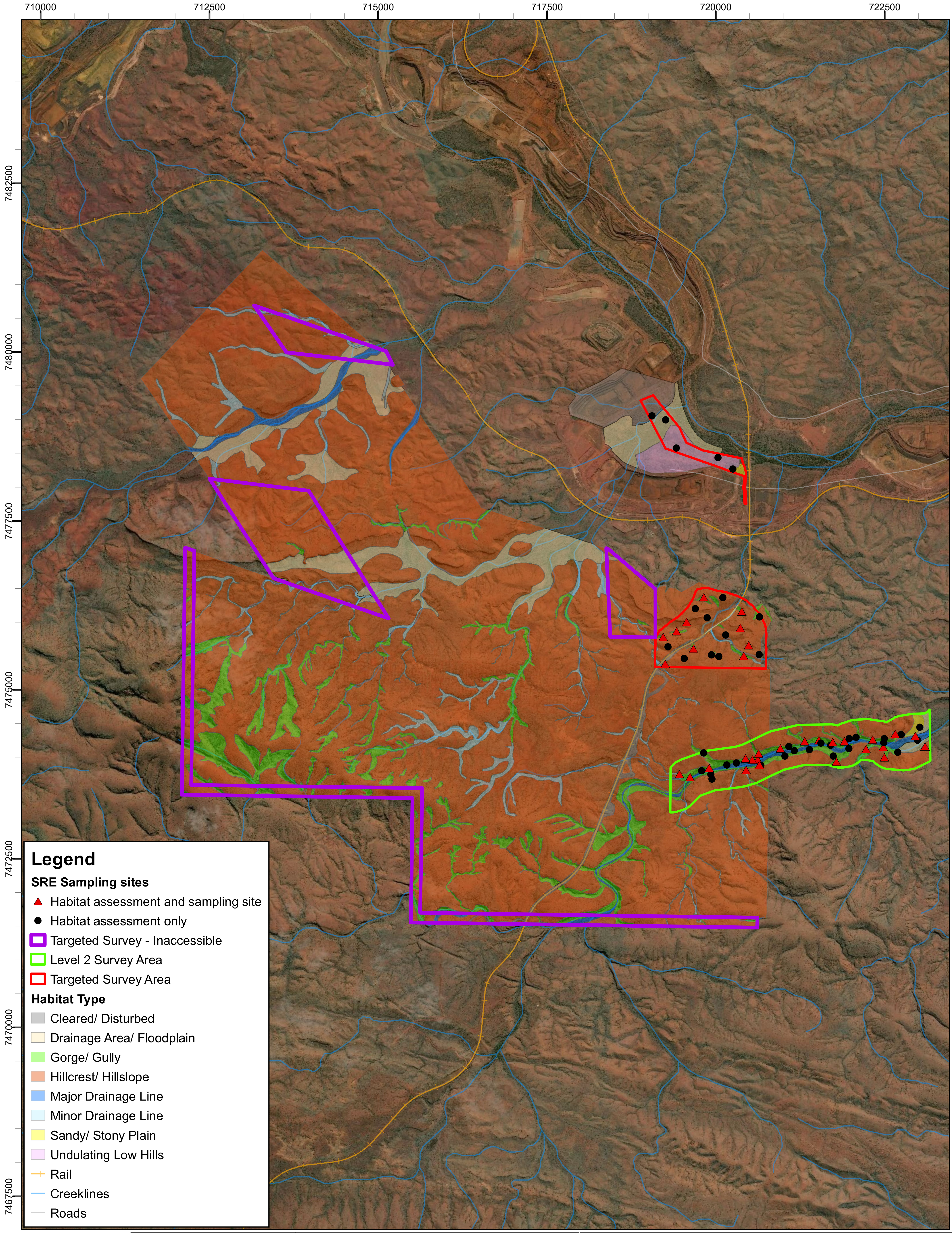
- **Gorge/ Gullies** - This habitat comprises deeply incised rocky landforms with low to moderate gorges carved by moderate or major drainage lines. The base of the gorge is relatively flat and the vertical or near vertical faces offer consistent shade. This habitat zone can form in highly mountainous areas at the base of steep slopes, or in deeply incised rolling hills. The narrower, more meandering courses of river gorges provide plenty of sheltered aspects, complex microhabitats within rocks, dense vegetation, and higher persistence of moisture. This habitat type was the most visited in both the Targeted Survey and the Level 2 Survey (8 and 29 sites respectively in each survey area). The overall SRE suitability of this habitat type is High.
- **Hillcrest/ Hillslope** - This habitat zone comprises the remaining rocky habitats on open (exposed) slopes and hill crests that do not feature major outcrops, ridges, or gullies. Such areas are not highly complex and generally have skeletal soils and sparse open vegetation (often *Triodia* hummock grassland with scattered *Corymbia*/ *Eucalyptus* spp.) that can provide pockets of protection from exposure. Steeper, south-facing hill slopes can also provide some protection. These areas generally have a Moderate- Low suitability for SRE fauna unless there is another landform or vegetation feature providing a more complex microhabitat within this habitat type. While these habitat zones are usually classed Low suitability for SRE fauna, when suitable microhabitats are available as is the case with *Antichiropus*

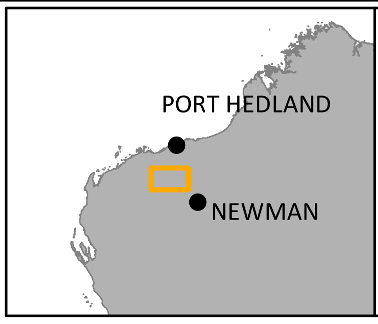
'DIP006' and 'DIP007' (Biologic, 2018), then these habitats can be considered of Moderate suitability. Eleven sites in the Targeted Survey Area and four sites in the Level 2 Survey Area were designated as this habitat type.

- **Major Drainage Lines** (including minor drainage)– Major (and minor) Drainage Lines can be densely vegetated, and extensive, but tend to be prone to disturbances from flooding. These areas are dominated by dense shrubland and groves/ thickets of *Acacia* (Mulga and other *Acacia* species) and *Eucalyptus*/ *Corymbia* species; hence, the majority of SRE habitats are based on vegetation and detritus. The density and structure of vegetation influences complexity of detrital microhabitats, and amount of shelter available. Isolation is generally low, as the groves and drainage line habitats form an interconnected network of vegetation-based habitats along the course of the drainage line and flood plains. These types of habitats are generally considered to provide dispersal opportunities for some SRE fauna and hence the suitability of this habitat zone considered Moderate-Low. Eleven sites in the Level 2 Survey Area were classified as this habitat type.
- **Drainage area/ Floodplain** – This habitat zone is characterised by mostly flat, extensive, open areas that may feature pockets of shrubland or open woodland. Similar to drainage lines, slope and aspect are less relevant to SRE suitability but rather the density and structure of vegetation influences complexity of detrital microhabitats, and amount of shelter available. Limited detrital microhabitats can be present though are generally thought unlikely to support SRE species due to high exposure, low complexity, and low isolation (see Appendix A). Only one site in the Targeted Survey Area was designated as this habitat type and is considered of Low SRE suitability.
- **Undulating Low Hills** – Undulating Low Hills are unlikely to support SRE species due to high exposure, low complexity, and low isolation. These low hills can feature some small rockpiles, rock outcrops and breakaways; these isolated features can provide limited shelter for SRE fauna; however, they are unlikely to support the long-term viability of populations. Some Undulating Low Hills can have many of these features whereas others can have very few, hence the habitat type is considered as having varying levels of SRE suitability from Moderate to Low. Three sites in the Targeted Survey Area were classified as this habitat type.
- **Sandy/ Stony Plains** – These areas are mostly flat, extensive, open plains that may feature pockets of shrubland or open woodland and limited detrital microhabitats. They are unlikely to support SRE species due to high exposure, low

complexity, and low isolation. Two sites, one within the Targeted Survey Area and one within the Level 2 Survey Area were sampled within this habitat.

- **Cleared –** Whilst not considered a habitat type, one site was located in a cleared area within the Targeted Survey Area.





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Ministers North and Yandicoogina Creek SRE Invertebrate Survey

Figure 4.2: Survey effort in the Study Area and habitat mapping

Coordinate System: GDA 1994 MGA Zone 50
Projection: Transverse Mercator
Datum: GDA 1994

Size A3. Created 20/07/2020

Table 4.2: Broad Habitat Categories found in the two Survey Areas

Habitat Category	Habitat Suitability	Coverage in the survey areas	Justification	SRE Groups	Representative Site Image
Gorge/ Gully	High	Targeted Survey Area: 4% Level 2 Survey Area: 20%	These habitats are often the most suitable for SRE fauna owing to the high protection from exposure, high complexity and moisture retention, and inherent isolation due to discontinuous landforms. Gorges and south-facing gullies tend to have a higher degree of protection while north-facing gullies tend to be more exposed. The small proportion of the Level 2 Survey Area was considered this habitat type owing to the deep gorge created by Yandicoogina Creek.	Paradoxsomatid millipedes, selenopid spiders, pseudoscorpions and terrestrial isopods.	
Hillcrest/ Hillslope	Moderate/ High	Targeted Survey Area: 69% Level 2 Survey Area: 64%	These habitats contain regular occurrences of rocky habitats, particularly ridges, gullies and outcropping not mapped in the Gorge/Gully habitat that can be important refuges for invertebrate taxa. Likewise, small microhabitats of deeper soils and leaf litter can be important for some species. This habitat type was the most common in both survey areas. Much of it featured low crests and slopes with some higher more complex outcropping in the Level 2 Survey Area.	Paradoxsomatid millipedes, selenopid spiders, pseudoscorpions and terrestrial isopods.	

Habitat Category	Habitat Suitability	Coverage in the survey areas	Justification	SRE Groups	Representative Site Image
Major (and Minor) Drainage Line	Moderate/ Low	Targeted Survey Area: 2% Level 2 Survey Area: 11%	Isolation is generally low as drainage lines and drainage area/ floodplain habitats form an interconnected network of vegetation-based habitats, providing dispersal corridors for some SRE fauna. The Yandicoogina Creek is the main drainage feature in the landscape and for the most part is defined by minor creeklines. However, the Level 2 Survey Area contains a deep gorge through which the creek passes.	Mygalomorph spiders, pseudoscorpions, scorpions, and terrestrial isopods.	
Drainage Area/ Floodplain	Moderate/ Low	Targeted Survey Area: 4% Level 2 Survey Area: 3%	Isolation is generally low as drainage lines and drainage area/ floodplain habitats form an interconnected network of vegetation-based habitats, providing dispersal corridors for some SRE fauna. These kinds of habitats can be important for burrowing species as they often occur on patches of deeper clay-loam soils, and for detritivore species that rely on dense leaf litter; however, they are often widespread and continuous. Both survey areas had very little of this habitat type owing to the generally hilly profile of the entire area.	Mygalomorph spiders, pseudoscorpions, scorpions, and terrestrial isopods.	

Habitat Category	Habitat Suitability	Coverage in the survey areas	Justification	SRE Groups	Representative Site Image
Undulating Low Hills	Moderate/ Low	Targeted Survey Area: 13% Level 2 Survey Area: 0%	These habitats are often comprised of gentle, open hill slopes with shallow gullies and small breakaways. These areas rarely feature dense vegetation and present limited complex sheltered habitats. These habitats often contain small, discontinuous outcrops and boulder piles on plains or open hill slopes. The low levels of habitat complexity, protection and isolation generally make these areas unsuitable for SRE species. The Targeted Survey Area had some low hills in the north, however the Level 2 Survey Area had none of this habitat type.	Mygalomorph spiders, selenopid spiders, pseudoscorpions, scorpions, and terrestrial isopods.	
Sandy/ Stony Plains	Low	Targeted Survey Area: 2% Level 2 Survey Area: 2%	These kinds of habitats can be important for burrowing species as they often occur on patches of deeper clay-loam soils, and for detritivore species that rely on dense leaf litter; however, they are often widespread and continuous. While moderately dense shrubland on the plains can provide patches of detrital microhabitats and deep soils suitable substrate for burrowing taxa, these habitats tend to provide very little protection and are often widespread and continuous. This habitat type was uncommon in both survey areas.	Mygalomorph spiders, pseudoscorpions, scorpions, and terrestrial isopods.	

4.3 Current survey SRE invertebrate fauna results

SRE invertebrate sampling was conducted at 32 of the 70 sites assessed across the two survey trips (Figure 4.3, Appendix C). A total of 123 invertebrates were collected from the two survey areas, of which 109 were considered to represent groups known to contain SRE species. These groups were Araneae (one taxon), Pseudoscorpiones (eight taxa), Scorpiones (three taxa), Chilopoda (one taxon), Diplopoda (one taxon), Isopoda (six taxa), and Gastropoda (four taxa) (Appendix D). Based on further identification and specialist taxonomist information of each group, each taxon was regarded as either Widespread or representing Potential SRE. No Confirmed SRE were collected. Five taxa were considered Widespread and are not discussed further. The remaining 19 Potential SRE taxa are discussed in detail below and are tabulated in Table 4.3.

4.3.1 Araneae

4.3.1.1 Selenopidae

Karaops sp. indet. – Potential SRE

Twenty-nine specimens of *Karaops* were collected from thirteen sites of predominantly Gorge/ Gully habitat during the survey, four of which are located in the Targeted Survey Area (SMNN-88, 98, 99 & 100) and the remaining nine in the Level 2 Survey Area. All specimens were juvenile or female and so could not be identified to species. Many species of *Karaops* are Confirmed SRE; however, due to the lack of identification to species level, these specimens are regarded as Potential SRE (WAM Category ‘A’ Data Deficient, ‘B’ Habitat Indicators and ‘E’ Research and Expertise).

4.3.2 Pseudoscorpiones

4.3.2.1 Garypidae

Synsphyronus \`sp. PSE014 (8/2 long Pilbara)\` – Potential SRE

Five specimens of this garypid pseudoscorpion were collected from rocks at three Targeted Survey Area sites in Hillcrest/ Hillslope and Gorge/ Gully habitat (SMNN-87, 98 & 99) and identified as *Synsphyronus* \`sp. PSE014 (8/2 long Pilbara)\` by Erich Volschenk. There are two records of this morphospecies in the WAM database and these were collected ~13 km SW and ~35 km SSW of the two survey areas. Molecular analysis of three specimens found that they formed a single Operational Taxonomic Unit (OTU) however, this did not match any other known specimens. It should be noted that there are no known sequences for *Synsphyronus* \`sp. PSE014 (8/2 long Pilbara)\` and therefore these may represent the first publicly available sequences. This taxon is regarded as a

Potential SRE (WAM Category ‘A’ Data Deficient, ‘B’ Habitat Indicators and ‘E’ Research and Expertise).

4.3.2.2 Olpiidae

The taxonomy of the Olpiidae is poorly resolved and recent DNA sequencing work indicates there are many more species than previously thought. In addition, there is typically inadequate geographical coverage of specimens to allow for a detailed assessment of SRE status. As a result, all morphospecies of this family are classified as Potential SRE under WAM categories ‘A’ (Data Deficient) and ‘E’ Research and Expertise, until further taxonomic resolution has been developed.

Austrohorus `sp. PSE121` – Potential SRE

Molecular analysis matched six specimens to *Austrohorus* `sp. PSE121`, which was previously recorded from within the Level 2 Survey Area (Biologic, 2016; Wilson *et al.*, 2019). Three specimens were collected in the Targeted Survey Area (SMNN-46, 48 & 80) and three in the Level 2 Survey Area (SMNN-01, 23 & 40), all from Gorge/ Gully habitat.

Austrohorus `sp. PSE122` – Potential SRE

Molecular analysis matched one specimen collected from Gorge/ Gully habitat in the Level 2 Survey Area to *Austrohorus* `sp. PSE122`, which was previously recorded from two sites ~1 km SW of the Level 2 Survey Area (Biologic, 2016; Wilson *et al.*, 2019).

Indolpium `sp. PSE118` – Potential SRE

Molecular analysis matched two specimens collected from Gorge/ Gully habitat in the Level 2 Survey Area (SMNN-40 & 48) to *Indolpium* sp. `PSE118`, which has also been recorded from ~55km SW of the Study Area.

Indolpium `sp. PSE123` – Potential SRE

Molecular analysis matched two specimens from the Targeted Survey Area (SMNN-100; Hillcrest/ Hillslope) and three specimens from the Level 2 Survey Area (SMNN-01, 25 & 33; all Gorge/ Gully) to *Indolpium* `sp. PSE123`. This morphospecies has been previously recorded from the Level 2 Survey Area and from five sites from ~1 km to ~5km west of the Level 2 Survey Area

Xenolpium `sp. Biologic-PSEU028` – Potential SRE

Two specimens from Hillcrest/ Hillslope habitat in the Targeted Survey Area (SMNN-81 & 87) could not be matched with any previous sequences and were subsequently designated as *Xenolpium* `sp. Biologic-PSEU028`.

Olpiidae sp. indet. – Potential SRE

Of the twenty-five olpiid pseudoscorpions collected, 17 were successfully sequenced. The remaining eight could not be identified to genus because of age, condition, or lack of morphological certainty, or failed to sequence when molecular analysis was undertaken.

These eight specimens were recorded from the Targeted Survey Area (SMNN-80) and the Level 2 Survey Area (SMNN-06, 17, 23, 33, 34 & 42), and all from Gorge/ Gully habitat.

4.3.3 Scorpiones

4.3.3.1 Buthidae

Lychas sp. `Biologic-SCOR001` – Potential SRE

Five specimens were collected at four sites, two Level 2 Survey Area sites (SMNY-15 & 17) and two vertebrate fauna survey sites (YAN_1 & YAN_2). The vertebrate fauna sites were part of a vertebrate fauna survey being conducted in the area at the same time as the current survey (GHD, 2020). The Level 2 Survey Area sites were Gorge/ Gully habitat, and the two specimens were collected during leaf sieving and foraging. The three remaining specimens were collected from two GHD sites in vertebrate pitfall traps. YAN_1 was in Hillcrest/Hillslope habitat and YAN_2 was in the Gorge/ Gully area of the Survey Area.

The five specimens were morphologically identified as being part of the *Lychas* `hairy tail complex`, a species group for which growing DNA evidence suggests that it contains many distinct species found throughout the Pilbara, many of which are likely SRE (E. Volschenk, pers. comm., 2020). Four specimens were subject to molecular analysis and were matched to *Lychas* sp. `Biologic-SCOR001`, which has been previously collected from ~60 km SW of the Study Area.

This taxon is regarded as a Potential SRE (WAM Category 'A' Data Deficient and 'E' Research and Expertise).

Lychas `multipunctatus complex` – Potential SRE

One specimen of this species was collected in a vertebrate pitfall trap by the concurrent vertebrate fauna survey (GHD, 2020). The specimen was collected in the Level 2 Survey Area (YAN_2) in what appears to be Gorge/ Gully habitat.

As with *Lychas* 'hairy tail complex,' the taxonomy of this group is poorly developed and hence the species complex is likely to contain SRE species (E. Volschenk, pers. comm., 2020). This taxon is therefore regarded as a Potential SRE (WAM Category 'A' Data Deficient and 'E' Research and Expertise).

4.3.3.2 Urodacidae

Urodacus sp. indet. – Potential SRE

One *Urodacus* juvenile specimen, possibly belonging to the *Urodacus butleri* or *Urodacus* 'hammersley black group', was collected while foraging at a Level 2 Survey Area Gorge/ Gully site, SMNN-11. There are no database records for these species in the immediate area and so the specimen may represent a new species.

This taxon most likely belongs to one of five *Urodacus* species complexes and is regarded as a Potential SRE (WAM Category 'A' Data Deficient and 'E' Research and Expertise).

4.3.4 Diplopoda

4.3.4.1 Trigoniulidae

Austrostrophus `sp. clade A NGW-2020` – Potential SRE

Three specimens of *Austrostrophus* were collected from three sites, one in Hillcrest/ Hillslope habitat in the Targeted Survey Area (SMNN-100) and two in Gorge/ Gully habitat in the Level 2 Survey Area (SMNN-11 & 34). Species in this genus are known to occupy rocky habitats such as gorges, gullies, and ridges throughout the Pilbara.

Molecular analysis matched the three specimens to *Austrostrophus* `sp. clade A NGW-2020` which has been recorded from ~60km SW of the Study Area. *Austrostrophus* `sp. clade A NGW-2020` is genetically distinct from the one formally named species of *Austrostrophus*, *A. stictopygus*, and it is now thought that *A. stictopygus* represents a species complex (M. Harvey, pers. comm., 2020)

This morphospecies is designated as Potential SRE (WAM Category 'A' Data Deficient and 'E' Research and Expertise).

4.3.5 Isopoda

4.3.5.1 Armadillidae

Four isopod morphospecies were identified from the material collected from the survey area, all belonging to the Buddelundiinae subfamily. Two have been collected previously from the Ministers North area and a third collected within 100 km of the survey areas (S. Judd pers. comm.). A fourth morphospecies likely belongs to a species complex and requires further taxonomic work. All are considered Potential SRE. Two additional juvenile specimens could not be identified further due to their condition and are designated as indeterminate.

Buddelundia `sp. 10ma` - Potential SRE

Only one specimen was collected from a vertebrate fauna pitfall trap (GHD, 2020). The specimen was collected in YAN_2, a Gorge/ Gully site in the Level 2 Survey Area. This morphospecies has been collected previously from the Ministers North area (Biologic, 2018) in Breakaway/ Cliff and Gorge/ Gully habitats. Based on taxonomist assessment, the distribution of this species is limited (< 60 km linear distribution, S. Judd, pers. comm) and it is considered to be a Potential SRE (WAM Category ‘A’ Data Deficient and ‘E’ Research and Expertise).

Buddelundia `sp. 48` - Potential SRE

This morphospecies was collected from five sites within Gorge/ Gully habitat, one in the Target Survey Area (SMNN-86), and four in the Level 2 Survey Area (SMNN-02, 11, 21, & 25). It has not been collected previously from this area (S. Judd, pers. comm.). The reference specimen for this morphospecies was collected in the Angelo River area (60 km SW of the two survey areas), with another specimen collected from the Turee Syncline (65 km SW of the two survey areas). Due to the low number of collections and the short distance to the localities of the other specimens, this morphospecies is considered to be Potential SRE (WAM Category ‘A’ Data Deficient and ‘E’ Research and Expertise).

Buddelundia `sp. 49` - Potential SRE

One female of this morphospecies was collected from a Hillcrest/ Hillslope habitat in the Targeted Survey Area (SMNN-100). This morphospecies was previously collected in the Biologic 2018 survey at Hillcrest/ Hillslope and Minor Drainage habitat. It has also been collected at Orebody 19 and Wheelarra North (100 km SE of the two survey areas); however, Dr Simon Judd notes that this morphospecies is most likely a species complex with limited distribution. The disjunct distribution of population suggests that there may be two or more taxa represented by the morphospecies. As a result of the limited distribution, this morphospecies is considered to be a Potential SRE (WAM Category ‘A’ Data Deficient and ‘E’ Research and Expertise).

Buddelundiinae sp. indet. – Potential SRE

A single female specimen in poor condition was collected at Site SMNN-98, in a Gorge/ Gully habitat in the Targeted Survey Area. It belongs to an undescribed genus closely related to *Buddelundia*. This undescribed genus is mostly found in the Pilbara region and is far less frequently encountered than *Buddelundia*, as such, it represents a Potential SRE species (WAM Category ‘A’ Data Deficient and ‘E’ Research and Expertise).

Buddelundia sp. indet. - Potential SRE

Two juvenile *Buddelundia* specimens in poor condition were collected from two sites (Level 2 Survey Area site SMNN-40 and Targeted Survey Area site SMNN-99) both within Gorge/ Gully habitat type. Due to their immaturity and condition they could not be placed into any of the morphospecies listed above. They may represent one or more of these morphospecies or they may represent a separate species altogether. As such, they are identified here as Potential SRE species (WAM Category 'A' Data Deficient).

4.3.6 Gastropoda

4.3.6.1 Bothriembryontidae

Bothriembryon sp. indet. – Potential SRE

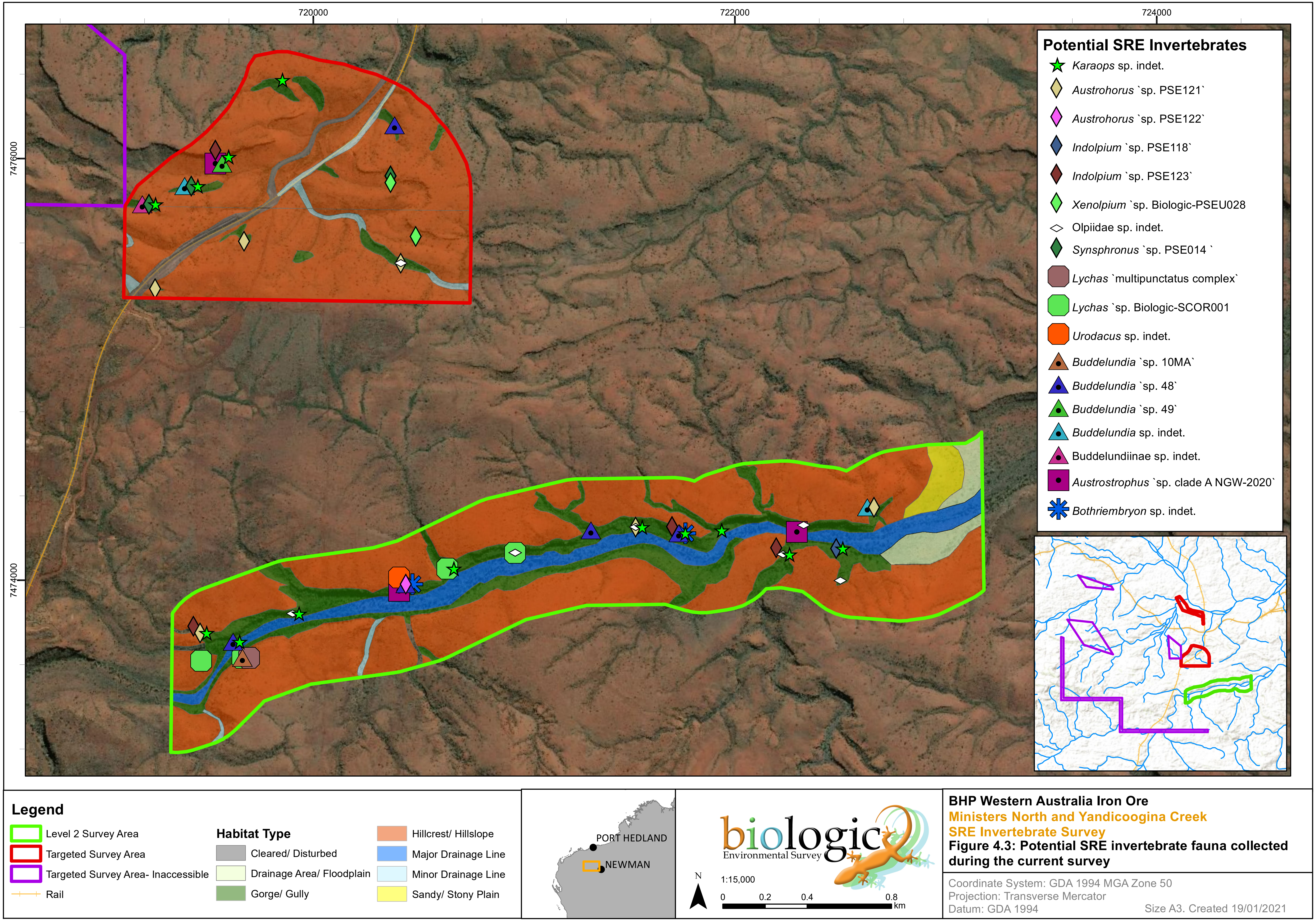
This endemic land snail genus has a Gondwanan distribution in Australia, however, relictual species do occur in the drier areas of Australia. In the Pilbara region, molecular data has shown there may be many SRE species within the genus (Whisson & Kirkendale, 2014). Three live snails and three shells were collected from two Gorge/ Gully sites in the Level 2 Survey Area (SMNN11 and 25). Currently, only one morphospecies is listed in the WAMDB for Mollusca, this is *Bothriembryontidae* `Pilbara' n. sp (WAM, 2020b). Further taxonomic and molecular work is required in this genus to ascertain species boundaries (C. Whisson, pers. comm., 2020). The specimens from this survey are designated as Potential SRE (WAM Category 'A' Data Deficient and 'E' Research and Expertise).

Table 4.3: Potential SRE invertebrate recorded during the current survey

Taxon	Locality	Site	SRE Habitat	SRE Status	No.
ARACHNIDA					
Araneae					
Selenopidae					
***Karaops* sp. indet.**	Targeted Survey Area - Ministers North	SMNN-100	Hillcrest/ Hillslope	Potential SRE	1
	Targeted Survey Area - Ministers North	SMNN-88	Gorge/ Gully	Potential SRE	1
	Targeted Survey Area - Ministers North	SMNN-98	Gorge/ Gully	Potential SRE	1
	Targeted Survey Area - Ministers North	SMNN-99	Gorge/ Gully	Potential SRE	1
	Level 2 Survey Area - Yandicoogina Creek	SMNN-01	Gorge/ Gully	Potential SRE	1
	Level 2 Survey Area - Yandicoogina Creek	SMNN-02	Gorge/ Gully	Potential SRE	1
	Level 2 Survey Area - Yandicoogina Creek	SMNN-06	Gorge/ Gully	Potential SRE	1
	Level 2 Survey Area - Yandicoogina Creek	SMNN-15	Gorge/ Gully	Potential SRE	1
	Level 2 Survey Area - Yandicoogina Creek	SMNN-23	Gorge/ Gully	Potential SRE	1
	Level 2 Survey Area - Yandicoogina Creek	SMNN-25	Gorge/ Gully	Potential SRE	1
	Level 2 Survey Area - Yandicoogina Creek	SMNN-30	Gorge/ Gully	Potential SRE	1
	Level 2 Survey Area - Yandicoogina Creek	SMNN-33	Gorge/ Gully	Potential SRE	1
	Level 2 Survey Area - Yandicoogina Creek	SMNN-43	Gorge/ Gully	Potential SRE	1
Pseudoscorpiones					
Garypidae					
***Synsphyronus* `sp. PSE014 `**	Targeted Survey Area - Ministers North	SMNN-87	Hillcrest/ Hillslope	Potential SRE	2
	Targeted Survey Area - Ministers North	SMNN-98	Gorge/ Gully	Potential SRE	2
	Targeted Survey Area - Ministers North	SMNN-99	Gorge/ Gully	Potential SRE	1
Olpiidae					
***Austrohorus* `sp. PSE121`**	Targeted Survey Area - Ministers North	SMNN-46	Gorge/ Gully	Potential SRE	1
	Targeted Survey Area - Ministers North	SMNN-48	Gorge/ Gully	Potential SRE	1
	Targeted Survey Area - Ministers North	SMNN-80	Gorge/ Gully	Potential SRE	1
	Level 2 Survey Area - Yandicoogina Creek	SMNN-01	Gorge/ Gully	Potential SRE	1
	Level 2 Survey Area - Yandicoogina Creek	SMNN-23	Gorge/ Gully	Potential SRE	1
	Level 2 Survey Area - Yandicoogina Creek	SMNN-40	Gorge/ Gully	Potential SRE	1

Taxon	Locality	Site	SRE Habitat	SRE Status	No.
***Austrohorus* `sp. PSE122`**	Level 2 Survey Area - Yandicoogina Creek	SMNN-11	Gorge/ Gully	Potential SRE	1
***Indolpium* `sp. PSE118`**	Level 2 Survey Area - Yandicoogina Creek	SMNN-40	Gorge/ Gully	Potential SRE	1
	Level 2 Survey Area - Yandicoogina Creek	SMNN-43	Gorge/ Gully	Potential SRE	1
***Indolpium* `sp. PSE123`**	Targeted Survey Area - Ministers North	SMNN-100	Hillcrest/ Hillslope	Potential SRE	2
	Level 2 Survey Area - Yandicoogina Creek	SMNN-01	Gorge/ Gully	Potential SRE	1
	Level 2 Survey Area - Yandicoogina Creek	SMNN-25	Gorge/ Gully	Potential SRE	1
	Level 2 Survey Area - Yandicoogina Creek	SMNN-33	Gorge/ Gully	Potential SRE	1
Olpiidae sp. indet.	Targeted Survey Area - Ministers North	SMNN-80	Gorge/ Gully	Potential SRE	1
	Level 2 Survey Area - Yandicoogina Creek	SMNN-06	Gorge/ Gully	Potential SRE	1
	Level 2 Survey Area - Yandicoogina Creek	SMNN-17	Gorge/ Gully	Potential SRE	2
	Level 2 Survey Area - Yandicoogina Creek	SMNN-23	Gorge/ Gully	Potential SRE	1
	Level 2 Survey Area - Yandicoogina Creek	SMNN-33	Gorge/ Gully	Potential SRE	2
	Level 2 Survey Area - Yandicoogina Creek	SMNN-34	Gorge/ Gully	Potential SRE	1
	Level 2 Survey Area - Yandicoogina Creek	SMNN-42	Gorge/ Gully	Potential SRE	1
***Xenolpium* `sp. Biologic-PSEU028`**	Targeted Survey Area - Ministers North	SMNN-81	Hillcrest/ Hillslope	Potential SRE	1
	Targeted Survey Area - Ministers North	SMNN-87	Hillcrest/ Hillslope	Potential SRE	1
Scorpiones					
Buthidae					
***Lychas* `*multipunctatus* complex`**	Level 2 Survey Area - Yandicoogina Creek	YAN_2	Gorge/ Gully	Potential SRE	1
***Lychas* `sp. Biologic-SCOR001`**	Level 2 Survey Area - Yandicoogina Creek	SMNN-15	Gorge/ Gully	Potential SRE	1
	Level 2 Survey Area - Yandicoogina Creek	SMNN-17	Gorge/ Gully	Potential SRE	1
	Level 2 Survey Area - Yandicoogina Creek	YAN_2	Gorge/ Gully	Potential SRE	1
	Level 2 Survey Area - Yandicoogina Creek	YAN_1	Hillcrest/ Hillslope	Potential SRE	1
Urodacidae					
***Urodacus* sp. indet.**	Level 2 Survey Area - Yandicoogina Creek	SMNN-11	Gorge/ Gully	Potential SRE	1
DIPLOPODA					
Spirobolida					
Trigoniulidae					
***Austrostrophus* `sp. clade A NGW-2020`**	Targeted Survey Area - Ministers North	SMNN-100	Hillcrest/ Hillslope	Potential SRE	1
	Level 2 Survey Area - Yandicoogina Creek	SMNN-11	Gorge/ Gully	Potential SRE	1

Taxon	Locality	Site	SRE Habitat	SRE Status	No.
	Level 2 Survey Area - Yandicoogina Creek	SMNN-34	Gorge/ Gully	Potential SRE	1
GASTROPODA					
Bothriembryontidae					
Bothriembryon sp. indet.	Level 2 Survey Area - Yandicoogina Creek	SMNN-11	Gorge/ Gully	Potential SRE	1
	Level 2 Survey Area - Yandicoogina Creek	SMNN-25	Gorge/ Gully	Potential SRE	1
MALACOSTRACA					
Isopoda					
Armadillidae					
***Buddelundia* `sp. 10MA`**	Level 2 Survey Area - Yandicoogina Creek	YAN_2	Gorge/ Gully	Potential SRE	1
***Buddelundia* `sp. 48`**	Targeted Survey Area - Ministers North	SMNN-86	Gorge/ Gully	Potential SRE	1
	Level 2 Survey Area - Yandicoogina Creek	SMNN-02	Gorge/ Gully	Potential SRE	1
	Level 2 Survey Area - Yandicoogina Creek	SMNN-11	Gorge/ Gully	Potential SRE	1
	Level 2 Survey Area - Yandicoogina Creek	SMNN-21	Gorge/ Gully	Potential SRE	1
	Level 2 Survey Area - Yandicoogina Creek	SMNN-25	Gorge/ Gully	Potential SRE	1
***Buddelundia* `sp. 49`**	Targeted Survey Area - Ministers North	SMNN-100	Hillcrest/ Hillslope	Potential SRE	1
***Buddelundia* sp. indet.**	Targeted Survey Area - Ministers North	SMNN-99	Gorge/ Gully	Potential SRE	1
	Level 2 Survey Area - Yandicoogina Creek	SMNN-40	Gorge/ Gully	Potential SRE	1
Buddelundiinae sp. indet.	Targeted Survey Area - Ministers North	SMNN-98	Gorge/ Gully	Potential SRE	1
Grand Total					**79**



BHP Western Australia Iron Ore

Ministers North and Yandicoogina Creek

SRE Invertebrate Survey

Figure 4.3: Potential SRE invertebrate fauna collected during the current survey

Coordinate System: GDA 1994 MGA Zone 50
Projection: Transverse Mercator
Datum: GDA 1994

Size A3. Created 19/01/2021

5 DISCUSSION

5.1 SRE habitat

Gorge/ Gully habitat comprises rugged, sometimes steep-sided rocky valleys incised into the surrounding landscape. Vegetation within this habitat is variable depending on position in landscape and can be dense and complex in areas of soil deposition or sparse and simple where erosion has occurred. The vertical or near vertical faces offer consistent shade, plenty of sheltered aspects, complex microhabitats, and higher persistence of moisture. These habitats are often highly suitable for SRE fauna owing to the high protection from exposure, high complexity and moisture retention, and inherent isolation due to discontinuous landforms. Although Gorge/ Gully habitat comprises 24% of available habitat in the two survey areas (4% of Targeted Survey Area and 20% of Level 2 Survey Area), just over half of the survey effort (37 of 70 sites) was spent within it due to its suitability for SRE species. Hence, most of the invertebrate specimens collected in this survey were from this habitat type.

The Yandicoogina Creek gorge of the Level 2 Survey Area was deep and well protected from the elements, however the high energy system of a riverine gorge would also mean that the isolation would be reduced due to flooding events. The presence of a number of Potential SRE species at multiple sites within the Level 2 Survey Area would point to a relatively high degree of connectivity throughout the gorge system and beyond the Survey Area.

The Gorge/ Gully sites of the Targeted Survey Area were not associated with the Major Drainage of the Yandicoogina Creek and represent shallower gullies found within the more widespread Hillcrest/ Hillslope habitat. The Gorge/Gully habitat of the Targeted Survey Area were less deeply incised than those found in the Level 2 Survey Area and hence would afford less protection and isolation from the elements. However, the likelihood that Potential SRE species from this habitat type in the Targeted Survey Area being restricted to the Survey Area would be low due to their regular occurrence throughout the Hillcrest/ Hillslope habitat.

Hillcrest/ Hillslope was the most common habitat type in both survey areas comprising 69% (Targeted) and 64% (Level 2). This habitat type is ranked as High to Moderate suitability for SREs. This habitat type is spread throughout the immediate area between the inaccessible sections of the Targeted Survey Area (Figure 4.2) as well as around the Level 2 Survey Area. It would be reasonable to assume that the Potential SRE species occurring in this habitat type within the Targeted Survey Area and the Level 2 Survey Area would also be likely to occur in the Hillcrests and Hillslopes of the intervening areas. The remaining habitat types in the two survey areas were classed as Moderate to Low suitability for SRE invertebrate fauna and occur well beyond both survey area boundaries as well.

5.2 SRE invertebrate fauna

Of the nineteen Potential SRE species, six were found in both survey areas. Specimens of *Karaops* (for which it is reasonable to assume all belong to a single species) were found well distributed, primarily in Gorge/ Gully and Hillcrest/ Hillslope habitat in both survey areas. There have been four other species collected within 40 km of the survey areas: *Karaops banyjima, Karaops nyangumarta, Karaops* `ARA001-DNA`, and *Karaops* `ARA002-DNA` (Biologic, 2018; WAM, 2020a), and it is highly likely that the selenopids collected in this current survey would align with one of these species.

Olpiid pseudoscorpion specimens collected in the current survey represent five morphospecies, two of which were found in both survey areas. Four morphospecies, *Austrohorus* `sp. PSE121`, *Austrohorus* `sp. PSE121`, *Indolpium* `sp. PSE118`, and *Indolpium* `sp. PSE123` were matched by molecular analysis to specimens previously collected within and nearby the survey areas. One morphospecies, *Xenolpium* `sp. Biologic-PSEU028` was newly collected and could not be matched to any other specimens. *Indolpium* `sp. PSE118` has been collected from sites ~60 km southwest, while the other four morphospecies are only know from the vicinity of the survey areas. *Synsphyronus* `sp. PSE014` was only collected in the Targeted Survey Area, however, it has been collected previously from Mining Area C (Biota, 2011).

All scorpions encountered in this survey were collected in the Level 2 Survey Area. The *Urodacus* specimen was subadult and could not be identified to species and therefore it is not possible to say what level of distribution this species would have through the survey area. Five *Lychas* specimens were matched by molecular analysis to others collected ~60 km south-west of the survey areas (*Lychas* `sp. Biologic-SCOR001`), while the other was morphologically identified as part of the well-known species group *Lychas* `multipunctatus complex`.

The spirobolid millipede, *Austrostrophus* `sp. clade A NGW-2020` was found in both survey areas. Molecular analysis matched these specimens to others collected ~60 km to the south-west.

Buddelundia 'sp. 49' was collected in the Targeted Survey Area only but is also known from Orebody 19 - 31 (Biologic, 2014). However, based on communication from Dr Simon Judd, it is possible this species is part of a species complex and may represent two or more taxa and further specimens would be required to determine the taxonomic status of the species. Buddelundiinae sp. indet. was collected in the Targeted Survey Area; however, the taxonomic status of the specimen is too uncertain to determine the likely regional distribution of this potentially new genus (S. Judd, pers. comm., 2020).

The *Bothriembryon* snails were collected in the Level 2 Survey Area only. There is no systematic morphological taxonomy available for *Bothriembryon* in the Pilbara, and while it is currently thought that all Pilbara *Bothriembryon* records constitute the same species (currently referred to as *Bothriembryon* \`Pilbara n. sp.\`) further molecular and morphological analysis is needed to confirm (C. Whisson, pers. comm., 2020).

6 CONCLUSION

The desktop study identified that both survey areas are likely to contain highly prospective habitat for SREs, with 168 SRE invertebrate taxa recorded in the search area. The current field survey recorded six habitat types, of which two were ranked as High and Moderate to High (Gorge/ Gully and Hillcrest/ Hillslope), and nineteen Potential SRE taxa. None of the Potential SRE taxa appear likely to be restricted to either the Targeted Survey Area or the Level 2 Survey Area.

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Appendix A: Factors affecting the suitability of habitat for Short Range Endemic Invertebrate Fauna.

Habitat assessments at each site were aimed at determining the significance of features and landforms that may constitute suitable SRE habitat, and hence the likelihood that the site may support SRE invertebrate fauna. Each habitat type or broad habitat unit was ranked based on three major factors that can influence the persistence of SRE species in an environment; these are degree of isolation, protection and habitat complexity. These factors are briefly outlined below and illustrated in Figure 1.

Isolation: This factor is based on the level of connectivity between sites which share similar habitat characteristics. Degree of isolation is the most important factor when it comes to the level of risk, as any fauna with limited dispersal characteristics, regardless of the habitat preference, will likely be an isolated population. Examples include ranges and high ridges in the Pilbara, peaks like Mt Meharry have been shown to harbour significant SRE species (Durrant, 2011).

Protection: This factor primarily covers protection from exposure to the elements. With respect to the Pilbara region however, protection from disturbance is also very important for the long-term viability of SRE habitats and communities, *i.e.* protection from fire, flood and invasive species.

Protection is provided at two levels; the site level where the structural composition of the site (aspect, slope *etc.*) can provide protection from exposure and disturbance by providing physical barriers (*e.g.* gorges and gullies); and the habitat level where certain microhabitat characteristics, associated with habitat complexity, provide more direct protection, particularly from exposure (*i.e.* leaf litter, rocky substrates, canopy cover and soil depth).

Habitat complexity: This factor drives species richness and often abundance at a site, *i.e.* the more complex a site is, the more species and individuals it is likely to support. This is particularly important as a number of SRE groups are predators; the richness and abundance of prey species are critical to their survival.

Complexity, with respect to SREs, is based around a number of microhabitat types:

- Leaf litter: both depth and structural variation;
- Rocky substrates: loose rocks and crevices;
- Vegetation variation: flora richness and structural variation; and
- Soil: depth and structural variation.

Similarly, the complexity of the habitat is important to detritivore SRE taxa (isopods, millipedes and some snails), which rely upon decaying leaf litter, woody debris and organic matter for survival. Examples in the Pilbara include deep gullies and gorges, where many of these areas contain most of the above microhabitat types and therefore tend to be the richest areas.

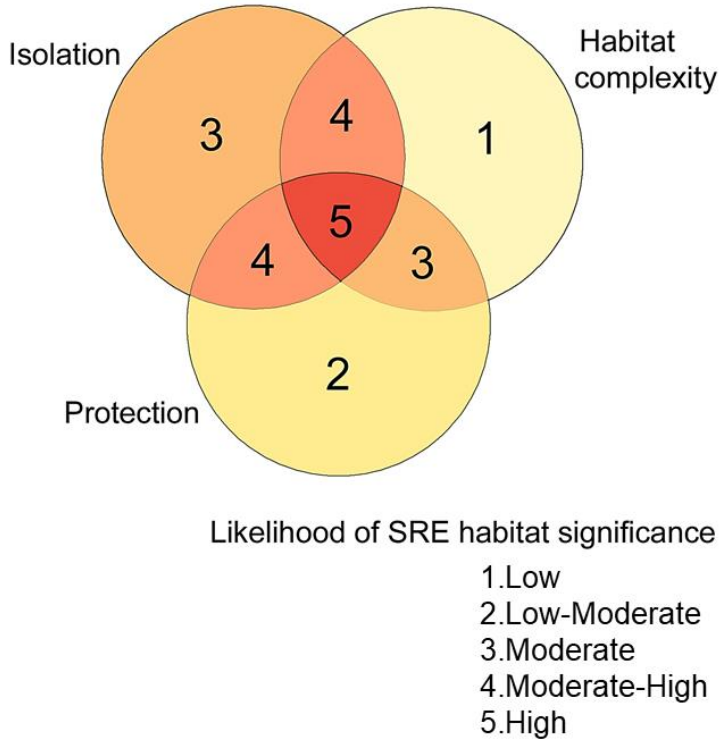

Figure 1. Habitat assessment diagram.

Appendix B: WAM Database SRE Invertebrate Fauna Records

Higher Taxon	Family	Lowest Taxonomic ID	Status	Count
Arachnida				
Araneae	**Actinopodidae**	*Missulena* `*marillana*`	**Potential SRE**	**3**
		Missulena faulderi	**Confirmed SRE**	**3**
		Missulena langlandsi	**Confirmed SRE**	**4**
		Missulena rutraspina	**Widespread**	**2**
		Missulena sp. indet.	**Potential SRE**	**5**
	Barychelidae	*Aurecocrypta* `HD1`	**Potential SRE**	**1**
		Aurecocrypta `MYG057`	**Potential SRE**	**1**
		Aurecocrypta `MYG246`	**Potential SRE**	**2**
		Aurecocrypta `MYG315`	**Potential SRE**	**2**
		Aurecocrypta `MYG316`	**Potential SRE**	**2**
		Aurecocrypta `MYG317`	**Potential SRE**	**1**
		Aurecocrypta sp. indet.	**Potential SRE**	**3**
		Barychelidae sp. indet.	**Potential SRE**	**5**
		Idiommata `MYG111`	**Potential SRE**	**2**
		Idiommata sp. indet.	**Potential SRE**	**1**
		Synothele `MYG055`	**Potential SRE**	**2**
		Synothele `MYG309`	**Potential SRE**	**5**
		Synothele `MYG311`	**Potential SRE**	**3**
		Synothele `*xkarara*`	**Potential SRE**	**4**
		Synothele sp. indet.	**Potential SRE**	**8**
	Halonoproctidae	*Conothele* `MYG002`	**Potential SRE**	**12**
		Conothele `MYG279`	**Potential SRE**	**2**
		Conothele `MYG281`	**Potential SRE**	**3**
		Conothele `MYG282`	**Potential SRE**	**18**
		Conothele `MYG333`	**Potential SRE**	**2**
		Conothele `MYG525`	**Potential SRE**	**1**
		Conothele `MYG527`	**Potential SRE**	**7**
		Conothele `MYG533`	**Potential SRE**	**1**
		Conothele `MYG534`	**Potential SRE**	**1**
		Conothele `MYG539`	**Potential SRE**	**2**
		Conothele `MYG608`	**Potential SRE**	**1**
		Conothele sp. indet.	**Potential SRE**	**4**
	Idiopidae	Eucyrtops sp. indet.	**Potential SRE**	**3**
		Gaius sp. indet.	**Potential SRE**	**1**
		Gaius tealei	**Widespread**	**20**
		Idiopidae sp. indet.	**Potential SRE**	**12**
		Idiosoma `MYG083`	**Potential SRE**	**3**
		Idiosoma `MYG085`	**Potential SRE**	**3**
		Idiosoma `MYG233`	**Potential SRE**	**1**
		Idiosoma `MYG305`	**Potential SRE**	**2**
		Idiosoma `MYG384`	**Potential SRE**	**7**
		Idiosoma sp. indet.	**Potential SRE**	**34**
	Nemesiidae	*Aname* `*marillana* group`	**Potential SRE**	**5**
		Aname `MYG104`	**Potential SRE**	**1**
		Aname `MYG331`	**Potential SRE**	**1**
		Aname `MYG341`	**Potential SRE**	**1**
		Aname `MYG370`	**Potential SRE**	**1**
		Aname `MYG377`	**Potential SRE**	**1**
		Aname sp. indet.	**Potential SRE**	**63**
		Kwonkan `MYG006`	**Potential SRE**	**22**
		Kwonkan `MYG033`	**Potential SRE**	**7**
		Kwonkan `MYG088`	**Potential SRE**	**3**
		Kwonkan `MYG098`	**Potential SRE**	**1**
		Kwonkan `MYG195`	**Potential SRE**	**40**
		Kwonkan `MYG197`	**Potential SRE**	**3**

Higher Taxon	Family	Lowest Taxonomic ID	Status	Count
		Kwonkan `MYG321`	Potential SRE	1
		Kwonkan `MYG323`	Potential SRE	10
		Kwonkan `MYG324`	Potential SRE	1
		Kwonkan `MYG325`	Potential SRE	6
		Kwonkan `MYG336`	Potential SRE	3
		Kwonkan `MYG337`	Potential SRE	7
		Kwonkan `MYG338`	Potential SRE	4
		Kwonkan `MYG339`	Potential SRE	14
		Kwonkan `MYG340`	Potential SRE	2
		Kwonkan `MYG341`	Potential SRE	1
		Kwonkan `MYG378`	Potential SRE	1
		Kwonkan `MYG379`	Potential SRE	7
		Kwonkan `MYG484`	Potential SRE	7
		Kwonkan `MYG524`	Potential SRE	1
		Kwonkan `MYG648`	Potential SRE	2
		Kwonkan `MYG653`	Potential SRE	1
		Kwonkan sp. indet.	Potential SRE	23
		Nemesiidae sp. indet.	Potential SRE	11
		Swolnpes `MYG234`	Potential SRE	1
		Teyl heuretes	Confirmed SRE	2
	Selenopidae	*Karaops* `ARA001`	Potential SRE	16
		Karaops `ARA002`	Potential SRE	1
		Karaops banyjima	Confirmed SRE	6
		Karaops sp. indet.	Potential SRE	7
Pseudoscorpiones	Atemnidae	*Anatemnus* sp. indet.	Potential SRE	1
		Oratemnus sp. indet.	Widespread	17
	Chernetidae	*Haplochernes* sp. indet.	Widespread	3
		Nesidiochernes sp. indet.	Potential SRE	1
		Sundochernes `PSE090`	Potential SRE	1
		Sundochernes sp. indet.	Potential SRE	1
		Troglochernes `PSE072`	Potential SRE	5
		Troglochernes sp. indet.	Potential SRE	1
	Chthoniidae	*Austrochthonius* `pilbara`	Widespread	11
		Austrochthonius sp. indet.	Widespread	2
		Chthoniidae `sp. HLX PC056`	Potential SRE	1
		Chthoniidae `sp. HLX PC057`	Potential SRE	1
		Lagynochthonius `PSE039`	Potential SRE	3
		Lagynochthonius `PSE043`	Potential SRE	1
		Lagynochthonius `PSE045`	Potential SRE	2
		Lagynochthonius `PSE096`	Potential SRE	1
		Lagynochthonius `PSE097`	Potential SRE	1
		Lagynochthonius `sp. 2`	Potential SRE	2
		Lagynochthonius `sp. Packsaddle`	Potential SRE	2
		Lagynochthonius `sp. S4`	Potential SRE	6
		Lagynochthonius `yandi`	Potential SRE	1
		Lagynochthonius sp. indet.	Potential SRE	1
		Tyrannochthonius `HD1`	Potential SRE	1
		Tyrannochthonius `PSE046`	Potential SRE	3
		Tyrannochthonius `PSE050`	Potential SRE	3
		Tyrannochthonius `PSE055`	Potential SRE	1
		Tyrannochthonius `sp. B37`	Potential SRE	1
		Tyrannochthonius `sp. indet.`	Potential SRE	1
		Tyrannochthonius `sp. MA`	Potential SRE	1
		Tyrannochthonius `sp. S4`	Potential SRE	5
		Tyrannochthonius `sp. S5`	Potential SRE	1
	Garypidae	*Synsphyronus* `PSE014 long hand 2`	Potential SRE	1
		Synsphyronus gracilis	Widespread	5
		Synsphyronus heptatrichus	Widespread	10

Higher Taxon	Family	Lowest Taxonomic ID	Status	Count
		Synsphyronus sp. indet.	**Potential SRE**	**3**
	Garypinidae	*Solinus* `sp. nov.`	**Potential SRE**	**1**
		Solinus sp. indet.	**Potential SRE**	**3**
	Hyidae	*Indohya* `PSE005`	**Potential SRE**	**8**
		Indohya `PSE150`	**Potential SRE**	**1**
	Olpiidae	`Genus 7/4` `PSE118`	**Potential SRE**	**1**
		`Genus 7/4` sp. indet.	**Potential SRE**	**5**
		`PSEAAA` `HD4`	**Potential SRE**	**1**
		Austrohorus `M1`	**Potential SRE**	**1**
		Austrohorus `M2`	**Potential SRE**	**1**
		Austrohorus `PSE119`	**Potential SRE**	**9**
		Austrohorus `PSE120`	**Potential SRE**	**1**
		Austrohorus `PSE121`	**Potential SRE**	**1**
		Austrohorus `PSE122`	**Potential SRE**	**2**
		Austrohorus sp. indet.	**Potential SRE**	**5**
		Beierolpium `8/2`	**Potential SRE**	**2**
		Beierolpium `8/4`	**Potential SRE**	**2**
		Beierolpium `HD1`	**Potential SRE**	**1**
		Beierolpium `HD2`	**Potential SRE**	**1**
		Beierolpium `M1`	**Potential SRE**	**1**
		Beierolpium `PSE126`	**Potential SRE**	**1**
		Beierolpium `sp. 1`	**Potential SRE**	**2**
		Beierolpium `sp. 8/2`	**Potential SRE**	**5**
		Beierolpium `sp. 8/3`	**Potential SRE**	**25**
		Beierolpium `sp. 8/4 (small)`	**Potential SRE**	**11**
		Beierolpium `sp. 8/4 lge`	**Potential SRE**	**3**
		Beierolpium `sp. 8/4 small`	**Potential SRE**	**1**
		Beierolpium `sp. 8/4`	**Potential SRE**	**31**
		Beierolpium sp. indet.	**Potential SRE**	**10**
		Euryolpium sp. indet.	**Potential SRE**	**10**
		Indolpium `PSE118`	**Potential SRE**	**1**
		Indolpium `PSE123`	**Potential SRE**	**6**
		Indolpium `PSE124`	**Potential SRE**	**1**
		Indolpium `PSE125`	**Potential SRE**	**1**
		Indolpium sp. indet.	**Potential SRE**	**22**
		Olpiidae `Helix sp. H-PO016`	**Potential SRE**	**1**
		Olpiidae `sp. MA`	**Potential SRE**	**1**
		Olpiidae sp. indet.	**Potential SRE**	**34**
		Xenolpium `PSE033`	**Potential SRE**	**1**
		Xenolpium `PSE120`	**Potential SRE**	**2**
		Xenolpium `sp. 1`	**Potential SRE**	**4**
		Xenolpium `sp. 2`	**Potential SRE**	**1**
		Xenolpium sp. indet.	**Potential SRE**	**24**
Scorpiones	**Buthidae**	*Lychas* sp. indet.	**Potential SRE**	**1**
	Urodacidae	*Urodacus* sp. indet.	**Potential SRE**	**7**
Crustacea				
Isopoda	**Armadillidae**	Armadillidae sp. indet.	**Potential SRE**	**7**
		Buddelundia `10ma`	**Potential SRE**	**6**
		Buddelundia `14cr`	**Potential SRE**	**1**
		Buddelundia `sp. 77`	**Potential SRE**	**6**
		Buddelundia sp. indet.	**Potential SRE**	**11**
	Philosciidae	?*Andricophiloscia* sp. indet.	**Potential SRE**	**1**
		Laevophiloscia sp. indet.	**Potential SRE**	**1**
		Philosciidae `sp. B03`	**Potential SRE**	**2**
		Philosciidae `sp. B04`	**Potential SRE**	**1**
		Philosciidae `sp. B10`	**Potential SRE**	**1**
		Philosciidae `sp. B16`	**Potential SRE**	**1**
		Philosciidae sp. indet.	**Potential SRE**	**2**

Higher Taxon	Family	Lowest Taxonomic ID	Status	Count
Diplopoda				
Polydesmida	**Paradoxosomatidae**	*Antichiropus* `DIP006`	**Confirmed SRE**	**2**
		Antichiropus `DIP007`	**Confirmed SRE**	**2**
		Antichiropus `DNA06`	**Confirmed SRE**	**1**
		Antichiropus `wonmunna` `DIP 163`	**Confirmed SRE**	**4**
		Antichiropus cirratus	**Confirmed SRE**	**22**
		Antichiropus lucyae	**Confirmed SRE**	**3**
		Antichiropus pendiculus	**Confirmed SRE**	**11**
		Antichiropus sp. indet.	**Confirmed SRE**	**3**
		Paradoxosomatidae sp. indet.	**Confirmed SRE**	**1**
Spirobolida	**Trigoniulidae**	*Austrostrophus* `clade A`	**Potential SRE**	**1**
		Austrostrophus `clade E`	**Potential SRE**	**4**
		Austrostrophus `DIP018`	**Potential SRE**	**4**
		Austrostrophus sp. indet.	**Potential SRE**	**79**
		Austrostrophus stictopygus	**Potential SRE**	**66**
		Trigoniulidae sp. indet.	**Potential SRE**	**6**
	(blank)	Spirobolida sp. indet.	**Potential SRE**	**1**
Gastropoda				
Stylommatophora	**Bothriembryontidae**	*Bothriembryon* `Pilbara` n.sp.	**Potential SRE**	**107**
	Camaenidae	Gen. nov. `Mount Robinson` n.sp.	**Potential SRE**	**7**

Appendix C: Site Data

Site	Survey Area	Latitude	Longitude	Date	Habitat Type	Landform	SRE Suitability	Slope	Aspect	Outcropping	Leaf Litter Availability	Soil Type	Drainage	Shade Availability
SMNN-01	Level 2	-22.8296	119.1385	10/09/2019	Gorge/Gully	Cliff	Moderate / High	Steep	South/ West	Major Outcropping	Few Small Patches	Loamy Sand	Gully	High 80-100%
SMNN-02	Level 2	-22.8300	119.1400	10/09/2019	Gorge/Gully	Cliff	Moderate	Low	South	Moderate Outcropping	Few Large Patches	Loamy Sand	Creek	High 80-100%
SMNN-03	Level 2	-22.8291	119.1417	10/09/2019	Major Drainage Line	Major Drainage Line	Moderate / Low	Flat	Flat	Negligible	Many Small Patches	Clay Loam	Creek	Medium 40-60%
SMNN-04	Level 2	-22.8296	119.1430	10/09/2019	Hillcrest/ Upper Hillslope	Breakaway	Moderate / Low	Steep	North	Major Outcropping	Few Small Patches	Loamy Sand	Negligible	Negligible <5%
SMNN-05	Level 2	-22.8302	119.1432	10/09/2019	Hillcrest/ Upper Hillslope	Other	Low	Flat	Flat	Limited Outcropping	None Discernible	Loamy Sand	Negligible	Negligible <5%
SMNN-06	Level 2	-22.8287	119.1427	10/09/2019	Gorge/Gully	Cliff	Moderate / High	Steep	South	Extensive Outcropping	Many Small Patches	Loamy Sand	Negligible	High 80-100%
SMNN-07	Level 2	-22.8275	119.1497	10/09/2019	Major Drainage Line	Major Drainage Line	Moderate / Low	Flat	Flat	Limited Outcropping	Evenly Spread	Loamy Sand	River	Medium 40-60%
SMNN-08	Level 2	-22.8283	119.1502	10/09/2019	Gorge/Gully	Cliff	Moderate / Low	Steep	North	Major Outcropping	Few Small Patches	Loamy Sand	Negligible	Negligible <5%
SMNN-09	Level 2	-22.8282	119.1500	10/09/2019	Major Drainage Line	Boulders/ Rockpiles	Moderate / High	Flat	Flat	Major Outcropping	Few Large Patches	Loamy Sand	Wetland	Med to High 60-80%
SMNN-10	Level 2	-22.8275	119.1489	10/09/2019	Gorge/Gully	Cliff	Moderate / High	Flat	South	Limited Outcropping	Many Small Patches	Loamy Sand	Creek	High 80-100%
SMNN-11	Level 2	-22.8274	119.1479	10/09/2019	Gorge/Gully	Cliff	Moderate / High	Low	South	Moderate Outcropping	Few Large Patches	Loamy Sand	Negligible	High 80-100%
SMNN-12	Level 2	-22.8280	119.1466	10/09/2019	Major Drainage Line	Major Drainage Line	Moderate / Low	Flat	Flat	Limited Outcropping	Evenly Spread	Loamy Sand	Creek	Low to Med 20-40%
SMNN-13	Level 2	-22.8283	119.1453	10/09/2019	Major Drainage Line	Major Drainage Line	Moderate / Low	Flat	Flat	Limited Outcropping	Many Large Patches	Loamy Sand	Creek	Med to High 60-80%
SMNN-14	Level 2	-22.8268	119.1419	10/09/2019	Gorge/Gully	Breakaway	Moderate / Low	Steep	West	Major Outcropping	Few Small Patches	Loamy Sand	Negligible	Low to Med 20-40%
SMNN-15	Level 2	-22.8267	119.1498	11/09/2019	Gorge/Gully	Cliff	Moderate	Steep	West	Moderate Outcropping	None Discernible	Loamy Sand	Negligible	High 80-100%
SMNN-16	Level 2	-22.8289	119.1480	11/09/2019	Gorge/Gully	Gully	Moderate / High	Flat	North/ West	Major Outcropping	Few Large Patches	Loamy Sand	Gully	High 80-100%
SMNN-17	Level 2	-22.8260	119.1530	11/09/2019	Gorge/Gully	Outcropping at end of ridge line	Moderate	Moderate	South	Major Outcropping	Few Small Patches	Loamy Sand	Negligible	Medium 40-60%

Site	Survey Area	Latitude	Longitude	Date	Habitat Type	Landform	SRE Suitability	Slope	Aspect	Outcropping	Leaf Litter Availability	Soil Type	Drainage	Shade Availability
SMNN-18	Level 2	-22.8270	119.1537	11/09/2019	Gorge/Gully	Hillslope	Moderate / Low	Steep	North	Major Outcropping	None Discernible	Loamy Sand	Negligible	Low 5-20%
SMNN-19	Level 2	-22.8258	119.1542	11/09/2019	Gorge/Gully	Cliff	Moderate	Low	South	Negligible	None Discernible	Loamy Sand	Negligible	High 80-100%
SMNN-20	Level 2	-22.8263	119.1550	11/09/2019	Major Drainage Line	Major Drainage Line	Moderate / Low	Flat	Flat	Negligible	Few Large Patches	Loamy Sand	Creek	Low to Med 20-40%
SMNN-21	Level 2	-22.8250	119.1564	11/09/2019	Gorge/Gully	Gully	Moderate / High	Steep	South/ West	Major Outcropping	Few Small Patches	Loamy Sand	Negligible	High 80-100%
SMNN-22	Level 2	-22.8261	119.1572	11/09/2019	Gorge/Gully	Hillslope	Moderate / Low	Moderate	North	Major Outcropping	None Discernible	Loamy Sand	Negligible	Low to Med 20-40%
SMNN-23	Level 2	-22.8248	119.1585	11/09/2019	Gorge/Gully	Boulders/ Rockpiles	Moderate	Steep	South	Major Outcropping	Few Small Patches	Loamy Sand	Negligible	Medium 40-60%
SMNN-24	Level 2	-22.8255	119.1602	11/09/2019	Major Drainage Line	Major Drainage Line	Moderate / Low	Flat	Flat	Negligible	Few Large Patches	Loamy Sand	Creek	Low to Med 20-40%
SMNN-25	Level 2	-22.8251	119.1605	11/09/2019	Gorge/Gully	Cliff	Moderate	Steep	South	Major Outcropping	Few Small Patches	Loamy Sand	Negligible	Low to Med 20-40%
SMNN-26	Level 2	-22.8269	119.1606	11/09/2019	Gorge/Gully	Boulders/ Rockpiles	Moderate / Low	Moderate	North/ East	Moderate Outcropping	Scarce	Loamy Sand	Negligible	Low 5-20%
SMNN-27	Level 2	-22.8277	119.1611	11/09/2019	Gorge/Gully	Gully	Moderate	Flat	North	Major Outcropping	Many Small Patches	Loamy Sand	Gully	High 80-100%
SMNN-28	Level 2	-22.8252	119.1588	11/09/2019	Major Drainage Line	Major Drainage Line	Moderate / Low	Flat	Flat	Negligible	Evenly Spread	Loamy Sand	Creek	Negligible <5%
SMNN-29	Level 2	-22.8246	119.1629	11/09/2019	Gorge/Gully	Cliff	Moderate	Moderate	South	Limited Outcropping	Few Small Patches	Loamy Sand	Negligible	High 80-100%
SMNN-30	Level 2	-22.8249	119.1622	11/09/2019	Gorge/Gully	Gully	Moderate / High	Low	South/ East	Moderate Outcropping	Few Small Patches	Loamy Sand	Negligible	High 80-100%
SMNN-31	Level 2	-22.8259	119.1629	11/09/2019	Gorge/Gully	Wetland	Moderate / High	Flat	Flat	Limited Outcropping	Many Large Patches	Clay Loam	Wetland	Med to High 60-80%
SMNN-32	Level 2	-22.8244	119.1639	12/09/2019	Gorge/Gully	Cliff	Moderate	Flat	South	Moderate Outcropping	Few Small Patches	Loamy Sand	Negligible	High 80-100%
SMNN-33	Level 2	-22.8259	119.1653	12/09/2019	Gorge/Gully	Gully	Moderate / High	Moderate	West	Minor Outcropping	Evenly Spread	Loamy Sand	Creek	High 80-100%
SMNN-34	Level 2	-22.8246	119.1663	12/09/2019	Gorge/Gully	Cliff	Moderate	Low	South	Limited Outcropping	Few Small Patches	Loamy Sand	Negligible	High 80-100%
SMNN-35	Level 2	-22.8254	119.1738	12/09/2019	Hillcrest/ Upper Hillslope	Ridge line	Moderate / Low	Very Steep	North	Major Outcropping	Few Small Patches	Loamy Sand	Negligible	Low to Med 20-40%
SMNN-36	Level 2	-22.8246	119.1727	12/09/2019	Major Drainage Line	Sand Plain	Moderate / Low	Flat	Flat	Negligible	Scarce	Sand	Negligible	Negligible <5%
SMNN-37	Level 2	-22.8241	119.1724	12/09/2019	Major Drainage Line	Major Drainage Line	Moderate / Low	Flat	Flat	Negligible	Many Small Patches	Loamy Sand	Creek	Low to Med 20-40%

Site	Survey Area	Latitude	Longitude	Date	Habitat Type	Landform	SRE Suitability	Slope	Aspect	Outcropping	Leaf Litter Availability	Soil Type	Drainage	Shade Availability
SMNN-38	Level 2	-22.8229	119.1730	12/09/2019	Sandy/ Stony Plain	Stony Plain	Low	Flat	Flat	Negligible	Few Small Patches	Clayey Sand	Negligible	Low 5-20%
SMNN-39	Level 2	-22.8239	119.1704	12/09/2019	Hillcrest/ Upper Hillslope	Boulders/ Rockpiles	Moderate	Steep	South	Major Outcropping	Scarce	Loamy Sand	Negligible	Medium 40-60%
SMNN-40	Level 2	-22.8238	119.1695	12/09/2019	Gorge/Gully	Cliff	Moderate / High	Steep	South/ West	Major Outcropping	Scarce	Loamy Sand	Negligible	High 80-100%
SMNN-41	Level 2	-22.8262	119.1699	12/09/2019	Gorge/Gully	Ironstone Outcrops	Moderate / Low	Low	North	Major Outcropping	Scarce	Loamy Sand	Negligible	Low 5-20%
SMNN-42	Level 2	-22.8270	119.1680	12/09/2019	Gorge/Gully	Gully	Moderate	Moderate	North	Major Outcropping	Many Small Patches	Loamy Sand	Gully	High 80-100%
SMNN-43	Level 2	-22.8256	119.1678	12/09/2019	Gorge/Gully	Cliff	Moderate / Low	Cliff	North	Negligible	Many Small Patches	Loamy Sand	Gully	High 80-100%
SMNN-44	Level 2	-22.8250	119.1679	12/09/2019	Major Drainage Line	Major Drainage Line	Moderate / Low	Flat	Flat	Negligible	Few Small Patches	Clayey Sand	Creek	Medium 40-60%
SMNN-45	Level 2	-22.8245	119.1680	12/09/2019	Gorge/Gully	Breakaway	Moderate / High	Steep	South	Major Outcropping	Many Small Patches	Loamy Sand	Negligible	High 80-100%
SMNN-46	Targeted	-22.8149	119.1362	6/04/2020	Gorge/Gully	Gully	Moderate / High	Moderate	North/ West	Extensive Outcropping	Few Large Patches	Clay Loam	Gully	Low to Med 20-40%
SMNN-47	Targeted	-22.8142	119.1389	6/04/2020	Undulating Low Hills	Stony Plain	Low	Low	Flat	Negligible	None Discernible	Clay Loam	Sheet Flow	Negligible <5%
SMNN-48	Targeted	-22.8128	119.1402	6/04/2020	Gorge/Gully	Gully	Moderate / High	Steep	South/ West	Extensive Outcropping	Few Large Patches	Clay Loam	Gully	Med to High 60-80%
SMNN-79	Targeted	-22.8138	119.1439	6/04/2020	Hillcrest/ Upper Hillslope	Hillslope	Low	Low	North	Negligible	Scarce	Clay Loam	Negligible	Negligible <5%
SMNN-80	Targeted	-22.8137	119.1475	6/04/2020	Gorge/Gully	Gully	Moderate	Steep	South	Extensive Outcropping	Few Small Patches	Clay Loam	Gully	Low 5-20%
SMNN-81	Targeted	-22.8122	119.1481	6/04/2020	Hillcrest/ Hillslope	Breakaway	Moderate	Steep	South	Extensive Outcropping	Few Small Patches	Clay Loam	Negligible	Low 5-20%
SMNN-82	Targeted	-22.8109	119.1448	6/04/2020	Hillcrest/ Upper Hillslope	Hillslope	Low	Moderate	South	Limited Outcropping	None Discernible	Clay Loam	Negligible	Negligible <5%
SMNN-83	Targeted	-22.8136	119.1428	6/04/2020	Gorge/Gully	Gully	Moderate	Steep	North	Extensive Outcropping	Few Small Patches	Clay Loam	Gully	Low to Med 20-40%
SMNN-84	Targeted	-22.8135	119.1497	7/04/2020	Hillcrest/ Upper Hillslope	Hillslope	Low	Moderate	South/ East	Limited Outcropping	None Discernible	Clay Loam	Negligible	Low 5-20%
SMNN-85	Targeted	-22.8085	119.1497	7/04/2020	Hillcrest/ Upper Hillslope	Hillslope	Low	Moderate	North	Limited Outcropping	None Discernible	Clay Loam	Negligible	Negligible <5%
SMNN-86	Targeted	-22.8078	119.1471	7/04/2020	Gorge/Gully	Gully	Moderate	Moderate	West	Extensive Outcropping	Few Small Patches	Clay Loam	Gully	Low to Med 20-40%
SMNN-87	Targeted	-22.8099	119.1469	7/04/2020	Hillcrest/ Hillslope	Breakaway	Moderate / High	Very Steep	South	Extensive Outcropping	Scarce	Clay Loam	Negligible	Medium 40-60%
SMNN-88	Targeted	-22.8059	119.1416	7/04/2020	Gorge/Gully	Gully	Moderate / High	Steep	South	Major Outcropping	Few Large Patches	Clay Loam	Gully	Low 5-20%

Site	Survey Area	Latitude	Longitude	Date	Habitat Type	Landform	SRE Suitability	Slope	Aspect	Outcropping	Leaf Litter Availability	Soil Type	Drainage	Shade Availability
SMNN-89	Targeted	-22.8075	119.1404	7/04/2020	Hillcrest/ Upper Hillslope	Hillslope	Low	Low	North/ East	Negligible	None Discernible	Clay Loam	Negligible	Negligible <5%
SMNN-90	Targeted	-22.8060	119.1444	7/04/2020	Hillcrest/ Upper Hillslope	Hillslope	Low	Low	South/ East	Limited Outcropping	None Discernible	Clay Loam	Negligible	Negligible <5%
SMNN-91	Targeted	-22.8087	119.1421	7/04/2020	Hillcrest/ Upper Hillslope	Footslope	Low	Steep	East	Negligible	None Discernible	Clay Loam	Negligible	Negligible <5%
SMNN-92	Targeted	-22.7887	119.1455	7/04/2020	Sandy/ Stony Plain	Stony Plain	Low	Flat	Flat	Negligible	Scarce	Clay Loam	Creek	Low 5-20%
SMNN-93	Targeted	-22.7872	119.1434	7/04/2020	Undulating Low Hills	Hillslope	Low	Low	South/ East	Limited Outcropping	Few Small Patches	Clay Loam	Negligible	Negligible <5%
SMNN-94	Targeted	-22.7860	119.1373	7/04/2020	Undulating Low Hills	Hillslope	Low	Low	North	Negligible	None Discernible	Clay Loam	Negligible	Negligible <5%
SMNN-95	Targeted	-22.7818	119.1338	7/04/2020	Cleared	Cleared	N/A	Flat	Flat	Negligible	None Discernible	Clay Loam	Negligible	Negligible <5%
SMNN-96	Targeted	-22.7823	119.1357	7/04/2020	Drainage Area/ Floodplain	Drainage Area/ Floodplain	Low	Flat	Flat	Negligible	Scarce	Clay Loam	Sheet Flow	Negligible <5%
SMNN-97	Targeted	-22.8126	119.1365	8/04/2020	Hillcrest/ Upper Hillslope	Hillslope	Low	Moderate	South	Negligible	None Discernible	Clay Loam	Negligible	Negligible <5%
SMNN-98	Targeted	-22.8113	119.1358	8/04/2020	Gorge/Gully	Gully	Moderate / Low	Steep	South	Major Outcropping	None Discernible	Clay Loam	Gully	Negligible <5%
SMNN-99	Targeted	-22.8105	119.1378	8/04/2020	Gorge/Gully	Gully	Moderate / High	Moderate	South	Major Outcropping	Few Small Patches	Clay Loam	Gully	Low to Med 20-40%
SMNN-100	Targeted	-22.8092	119.1392	8/04/2020	Hillcrest/ Hillslope	Cliff	Moderate / High	Cliff	South	Major Outcropping	Scarce	Clay Loam	Negligible	Medium 40-60%

Appendix D: Fauna Data

Taxon	Locality	Site	SRE Habitat	SRE Status	No.
ARACHNIDA					
Araneae					
Selenopidae					
***Karaops* sp. indet.**	Targeted Survey Area - Ministers North	SMNN-100	Hillcrest/ Hillslope	Potential SRE	1
	Targeted Survey Area - Ministers North	SMNN-88	Gorge/ Gully	Potential SRE	1
	Targeted Survey Area - Ministers North	SMNN-98	Gorge/ Gully	Potential SRE	1
	Targeted Survey Area - Ministers North	SMNN-99	Gorge/ Gully	Potential SRE	1
	Level 2 Survey Area - Yandicoogina Creek	SMNN-01	Gorge/ Gully	Potential SRE	1
	Level 2 Survey Area - Yandicoogina Creek	SMNN-02	Gorge/ Gully	Potential SRE	1
	Level 2 Survey Area - Yandicoogina Creek	SMNN-06	Gorge/ Gully	Potential SRE	1
	Level 2 Survey Area - Yandicoogina Creek	SMNN-15	Gorge/ Gully	Potential SRE	1
	Level 2 Survey Area - Yandicoogina Creek	SMNN-23	Gorge/ Gully	Potential SRE	1
	Level 2 Survey Area - Yandicoogina Creek	SMNN-25	Gorge/ Gully	Potential SRE	1
	Level 2 Survey Area - Yandicoogina Creek	SMNN-30	Gorge/ Gully	Potential SRE	1
	Level 2 Survey Area - Yandicoogina Creek	SMNN-33	Gorge/ Gully	Potential SRE	1
	Level 2 Survey Area - Yandicoogina Creek	SMNN-43	Gorge/ Gully	Potential SRE	1
Pseudoscorpiones					
Garypidae					
***Synsphyronus* `sp. PSE014 `**	Targeted Survey Area - Ministers North	SMNN-87	Hillcrest/ Hillslope	Potential SRE	2
	Targeted Survey Area - Ministers North	SMNN-98	Gorge/ Gully	Potential SRE	2
	Targeted Survey Area - Ministers North	SMNN-99	Gorge/ Gully	Potential SRE	1
Olpiidae					
***Austrohorus* `sp. PSE121`**	Targeted Survey Area - Ministers North	SMNN-46	Gorge/ Gully	Potential SRE	1
	Targeted Survey Area - Ministers North	SMNN-48	Gorge/ Gully	Potential SRE	1
	Targeted Survey Area - Ministers North	SMNN-80	Gorge/ Gully	Potential SRE	1
	Level 2 Survey Area - Yandicoogina Creek	SMNN-01	Gorge/ Gully	Potential SRE	1

Taxon	Locality	Site	SRE Habitat	SRE Status	No.
	Level 2 Survey Area - Yandicoogina Creek	SMNN-23	Gorge/ Gully	Potential SRE	1
	Level 2 Survey Area - Yandicoogina Creek	SMNN-40	Gorge/ Gully	Potential SRE	1
***Austrohorus* `sp. PSE122`**	Level 2 Survey Area - Yandicoogina Creek	SMNN-11	Gorge/ Gully	Potential SRE	1
***Indolpium* `sp. PSE118`**	Level 2 Survey Area - Yandicoogina Creek	SMNN-40	Gorge/ Gully	Potential SRE	1
	Level 2 Survey Area - Yandicoogina Creek	SMNN-43	Gorge/ Gully	Potential SRE	1
***Indolpium* `sp. PSE123`**	Targeted Survey Area - Ministers North	SMNN-100	Hillcrest/ Hillslope	Potential SRE	2
	Level 2 Survey Area - Yandicoogina Creek	SMNN-01	Gorge/ Gully	Potential SRE	1
	Level 2 Survey Area - Yandicoogina Creek	SMNN-25	Gorge/ Gully	Potential SRE	1
	Level 2 Survey Area - Yandicoogina Creek	SMNN-33	Gorge/ Gully	Potential SRE	1
Olpiidae sp. indet.	Targeted Survey Area - Ministers North	SMNN-80	Gorge/ Gully	Potential SRE	1
	Level 2 Survey Area - Yandicoogina Creek	SMNN-06	Gorge/ Gully	Potential SRE	1
	Level 2 Survey Area - Yandicoogina Creek	SMNN-17	Gorge/ Gully	Potential SRE	2
	Level 2 Survey Area - Yandicoogina Creek	SMNN-23	Gorge/ Gully	Potential SRE	1
	Level 2 Survey Area - Yandicoogina Creek	SMNN-33	Gorge/ Gully	Potential SRE	2
	Level 2 Survey Area - Yandicoogina Creek	SMNN-34	Gorge/ Gully	Potential SRE	1
	Level 2 Survey Area - Yandicoogina Creek	SMNN-42	Gorge/ Gully	Potential SRE	1
***Xenolpium* `sp. Biologic-PSEU028`**	Targeted Survey Area - Ministers North	SMNN-81	Hillcrest/ Hillslope	Potential SRE	1
	Targeted Survey Area - Ministers North	SMNN-87	Hillcrest/ Hillslope	Potential SRE	1
Scorpiones					
Buthidae					
***Lychas* `*multipunctatus* complex`**	Level 2 Survey Area - Yandicoogina Creek	YAN_2	Gorge/ Gully	Potential SRE	1
***Lychas* `sp. Biologic-SCOR001`**	Level 2 Survey Area - Yandicoogina Creek	SMNN-15	Gorge/ Gully	Potential SRE	1
	Level 2 Survey Area - Yandicoogina Creek	SMNN-17	Gorge/ Gully	Potential SRE	1
	Level 2 Survey Area - Yandicoogina Creek	YAN_2	Gorge/ Gully	Potential SRE	1
	Level 2 Survey Area - Yandicoogina Creek	YAN_1	Hillcrest/ Hillslope	Potential SRE	1
Urodacidae					
***Urodacus* sp. indet.**	Level 2 Survey Area - Yandicoogina Creek	SMNN-11	Gorge/ Gully	Potential SRE	1

Taxon	Locality	Site	SRE Habitat	SRE Status	No.
CHILOPODA					
Geophilomorpha					
Geophilomorpha sp. indet.	Targeted Survey Area - Ministers North	SMNN-88	Gorge/ Gully	Widespread	1
	Level 2 Survey Area - Yandicoogina Creek	SMNN-11	Gorge/ Gully	Widespread	1
	Level 2 Survey Area - Yandicoogina Creek	SMNN-34	Gorge/ Gully	Widespread	1
Scolopendromorpha					
Scolopendridae					
***Cormocephalus* sp. indet.**	Targeted Survey Area - Ministers North	SMNN-100	Hillcrest/ Hillslope	Widespread	1
DIPLOPODA					
Spirobolida					
Trigoniulidae					
***Austrostrophus* `sp. clade A NGW-2020`**	Targeted Survey Area - Ministers North	SMNN-100	Hillcrest/ Hillslope	Potential SRE	1
	Level 2 Survey Area - Yandicoogina Creek	SMNN-11	Gorge/ Gully	Potential SRE	1
	Level 2 Survey Area - Yandicoogina Creek	SMNN-34	Gorge/ Gully	Potential SRE	1
GASTROPODA					
Achatinidae					
Eremopeas interioris	Level 2 Survey Area - Yandicoogina Creek	SMNN-09	Major Drainage Line	Widespread	1
	Level 2 Survey Area - Yandicoogina Creek	SMNN-43	Gorge/ Gully	Widespread	1
Bothriembryontidae					
Bothriembryon sp. indet.	Level 2 Survey Area - Yandicoogina Creek	SMNN-11	Gorge/ Gully	Potential SRE	1
	Level 2 Survey Area - Yandicoogina Creek	SMNN-25	Gorge/ Gully	Potential SRE	1
Pupillidae					
***Gastrocopta* sp. indet.**	Level 2 Survey Area - Yandicoogina Creek	SMNN-09	Major Drainage Line	Widespread	1
	Level 2 Survey Area - Yandicoogina Creek	SMNN-34	Gorge/ Gully	Widespread	1
***Pupoides* sp. indet.**	Level 2 Survey Area - Yandicoogina Creek	SMNN-09	Major Drainage Line	Widespread	1
MALACOSTRACA					
Isopoda					

Taxon	Locality	Site	SRE Habitat	SRE Status	No.
Armadillidae					
***Buddelundia* `sp. 10MA`**	Level 2 Survey Area - Yandicoogina Creek	YAN_2	Gorge/ Gully	Potential SRE	1
***Buddelundia* `sp. 16`**	Targeted Survey Area - Ministers North	SMNN-100	Hillcrest/ Hillslope	Widespread	1
	Targeted Survey Area - Ministers North	SMNN-88	Gorge/ Gully	Widespread	1
	Level 2 Survey Area - Yandicoogina Creek	SMNN-02	Gorge/ Gully	Widespread	1
	Level 2 Survey Area - Yandicoogina Creek	SMNN-10	Gorge/ Gully	Widespread	1
	Level 2 Survey Area - Yandicoogina Creek	SMNN-25	Gorge/ Gully	Widespread	1
	Level 2 Survey Area - Yandicoogina Creek	SMNN-34	Gorge/ Gully	Widespread	1
***Buddelundia* `sp. 48`**	Targeted Survey Area - Ministers North	SMNN-86	Gorge/ Gully	Potential SRE	1
	Level 2 Survey Area - Yandicoogina Creek	SMNN-02	Gorge/ Gully	Potential SRE	1
	Level 2 Survey Area - Yandicoogina Creek	SMNN-11	Gorge/ Gully	Potential SRE	1
	Level 2 Survey Area - Yandicoogina Creek	SMNN-21	Gorge/ Gully	Potential SRE	1
	Level 2 Survey Area - Yandicoogina Creek	SMNN-25	Gorge/ Gully	Potential SRE	1
***Buddelundia* `sp. 49`**	Targeted Survey Area - Ministers North	SMNN-100	Hillcrest/ Hillslope	Potential SRE	1
***Buddelundia* sp. indet.**	Targeted Survey Area - Ministers North	SMNN-99	Gorge/ Gully	Potential SRE	1
	Level 2 Survey Area - Yandicoogina Creek	SMNN-40	Gorge/ Gully	Potential SRE	1
Buddelundiinae sp. indet.	Targeted Survey Area - Ministers North	SMNN-98	Gorge/ Gully	Potential SRE	1
Grand Total					**79**

Appendix E: Molecular Report



Ministers North and Yandicoogina Creek Short-range Endemic Invertebrate Fauna

Molecular Systematics Analysis

Biologic Environmental Survey

Report to BHP Billiton Iron Ore Pty Ltd

July 2020

DOCUMENT STATUS				
Version No.	Authors	Review / Approved for Issue	Approved for Issue to	
			Name	Date
1	J. Huey, S. Floeckner	Nihara Gunawardene	Suzi Wild	23/07/2020

GLOSSARY

COI	Cytochrome Oxidase subunit 1, a mitochondrial gene commonly used in phylogenetic studies and used as a DNA barcode to identify species
GenBank	Annotated open access sequence database of all publicly available nucleotide sequences and their protein translations
OTU	Operational taxonomic unit – species-equivalent taxonomic unit based on COI or 12S cluster similarity

1 INTRODUCTION

BHP Billiton Iron Ore Pty Ltd commissioned Biologic Environmental Survey (Biologic) to undertake a molecular systematics analysis (DNA barcoding) of 29 short-range endemic (SRE) invertebrate fauna specimens collected from Ministers North and Yandicoogina Creek Survey Areas (hereafter referred to as the Study Area).

1.1 Aims and objectives

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

- Undertake DNA sequencing of 29 subterranean fauna specimens to obtain barcoding sequences of the mitochondrial gene Cytochrome Oxidase I (COI; Hebert *et al.*, 2003b);
- Investigate the interspecific and intraspecific relationships between sequences of each higher taxonomic group (*i.e.* use the results of the DNA analysis to indicate how many different species/ OTUs are likely to occur within each genus or relevant higher taxon, based on published species-thresholds); and
- Investigate the relationships between sequences from the Study Area and relevant previous sequences from the wider Pilbara region, using available DNA databases (*i.e.* compare the results of the current analysis with accessible DNA databases to assess whether any of the species/ OTUs from the Study Area have been collected previously or more widely beyond the Study Area).

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

2 METHODS

2.1 Sub-sample preparation

Biologic undertook a targeted SRE invertebrate fauna survey covering the Ministers North Misc. License (Targeted Survey Area) and a Level 2 SRE invertebrate fauna survey covering a portion of Yandicoogina Creek (Level 2 Survey Area) (Biologic, 2020). From this work, eight potential SRE morphospecies required further clarification of species identifications and regional distributions.

- *Lychas* sp.'hairy tail'
- *Synsyphronus* sp. indet.
- *Indolpium* sp. MNY01
- *Indolpium* sp. MNY02
- *Xenolpium* sp. MNY01
- *Xenolpium* sp. MNY02
- Olpiidae sp. indet.

- *Austrostrophus* sp. indet.

A total of 29 specimens collected from the Study Area by Biologic were selected for molecular systematics analysis (Table 2.1). The specimens were chosen based on their geographic spread across the Study Area to assist with understanding species distributions. Adequate redundancy in specimen selection was incorporated to account for any potential sequence generation failure. Specimens in good condition were chosen to increase their DNA extraction potential.

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

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

Class/Subclass	Order	Number of samples	PCR success	Sequence success	% sequence success
Arachnida	Scorpiones	4	4	4	100.00%
Arachnida	Pseudoscorpiones	22	21	20	90.09%
Diplopoda	Spirobolida	3	3	3	100.00%
TOTAL		**29**	**28**	**27**	**93.10%**

2.2 DNA extraction, amplification and sequencing

DNA extraction and sequencing methods followed Cullen and Harvey (2017, 2018), as follows:

Subsampled tissue/specimen was placed directly into ATL buffer for extraction using the *QIAGEN DN-easy* Blood and Tissue extraction kit, and DNA extraction followed the manufacturer's protocols. DNA extractions were amplified by Polymerase Chain Reaction (PCR) using Folmer PCR primers (LCO1490, HCO2198; Folmer *et al.*, 1994) to assess the variability of COI.

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

2.3 Specimen selection for comparative analysis

DNA comparisons were typically conducted at the order level (Table 2.1). However, in cases where there was an abundance of sequences, secondary comparisons were also undertaken at the family level. For groups where taxonomic clarification at the order level was not possible due to low numbers of specimens, comparisons between sequences remained at the class level. See the relevant section of the Results and Discussion for clarification of the taxonomic resolution for each analysis.

Comparative sequences were from different sources, using two separate methods.

Sources

- Biologic Sequence Library: sequences produced from previous jobs undertaken by Biologic, which is comprised of 3,076 quality assured DNA sequences.
- GenBank: Annotated open access sequence database of all publicly available nucleotide sequences and their protein translations.
- Previous molecular data from the study area, available in Wilson *et al.* (2019).

Methods

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

The final datasets for each taxonomic group were supplemented with an appropriate outgroup sequence to root the final phylogeny, and any duplicate sequences (identical sequences from the same specimen found in multiple databases) were removed.

2.4 Analysis and interpretation of sequence alignments/divergence

For each taxonomic group, the selected sequences were aligned using the MAFFT (Multiple Alignment using Fast Fourier Transform) algorithm (Katoh *et al.*, 2002). Trees were constructed on resulting alignments using the RaxML (Stamatakis, 2014) plugin in GENEIOUS Prime, using 1,000 bootstrap replicates and the GTR+G substitution model.

To delimit taxonomic units using molecular data, we applied a genetic distance based threshold method, combined with our morphological identifications. Fauna-specific genetic distance thresholds for delimiting species and OTUs were used wherever possible, based on published literature and available previous reports. Where these thresholds were not available, the assessment used average divergence thresholds for related groups or higher taxa developed by broad-level studies (*e.g.* Hebert *et al.*, 2003a).

In general, ≤8% COI divergence is seen as appropriate to determine OTUs (Hebert et al., 2003a), however, higher or lower divergences are sometimes justified depending on the organism studied. Unless otherwise stated, we considered sequences that exhibited COI divergences ≤8% to belong to the same OTU.

2.5 Constraints and Limitations

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

The databases used for regional comparisons were limited to GenBank and Biologic's Sequence Library. While these sequence databases, in combination, comprise a large portion of the subterranean fauna genetic work undertaken for Rio Tinto in the Pilbara region, it is acknowledged that there may be many other relevant sequences from third party project areas nearby or elsewhere in the region that were not available for comparison at the time of the study. GenBank is dynamic database, and the addition of new sequences and altered taxonomic classifications could not be included into this report if they occurred after 14th of July 2020.

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

3 RESULTS AND DISCUSSION

A total of 29 specimens were processed for sequencing by Biologic. Sequences were successfully derived for 28 of these specimens (96.55% of specimens), with one failing to produce a PCR product. Of these 28 sequences, one did not produce a high-quality sequence. This left 27 high quality sequences for analysis (93.1% of sequences). The orders of the sequences are tabulated in Table 2.1.

In total, eight OTUs have been designated to specimens from the Study Area, five of these have so far been collected within 40 km of the Study Area (Table 3.1). The results of each taxonomic group's analysis are described in the subsequent sections.

Table 3.1: Summary of species and OTUs recovered from 27 samples successfully sequenced in this study, organised by taxon.

Species/OTU	Number of specimens from Study	Unique to Study Area?	Linear Distance
Spirobolida	**3**		
Austrostrophus `sp. clade A NGW-2020`	3	No	64.62km
Pseudoscorpiones	**20**		

Species/OTU	Number of specimens from Study	Unique to Study Area?	Linear Distance
Synsphyronus `sp. PSE014`	3	Yes	1.15km
Indolpium `sp. PSE123`	6	Yes	7.31km
Xenolpium `sp. Biologic-PSEU028`	2	Yes	0.28km
Austrohorus `sp. PSE121`	6	Yes	3.56km
Austrohorus `sp. PSE122`	1	Yes	4.02km
Indolpium `sp. PSE118`	2	No	56.9km
Scorpiones	**4**		
Lychas `sp. Biologic-SCOR001`	4	No	63.06km

3.1 Spirobolida

The three specimens sequenced from the study area fell into a single OTU, with 9 other specimens (Fig 3.1.1). *Austrostrophus* `sp. clade A NGW-2020` had intraspecific genetic divergences less than 5.05%, and was greater than 7.45% divergent from the next closest OTU (Table 3.1.1). *Austrostrophus* `sp. clade A NGW-2020` was not restricted to the study area, and had a linear distribution of over 64km (Table 3.1).

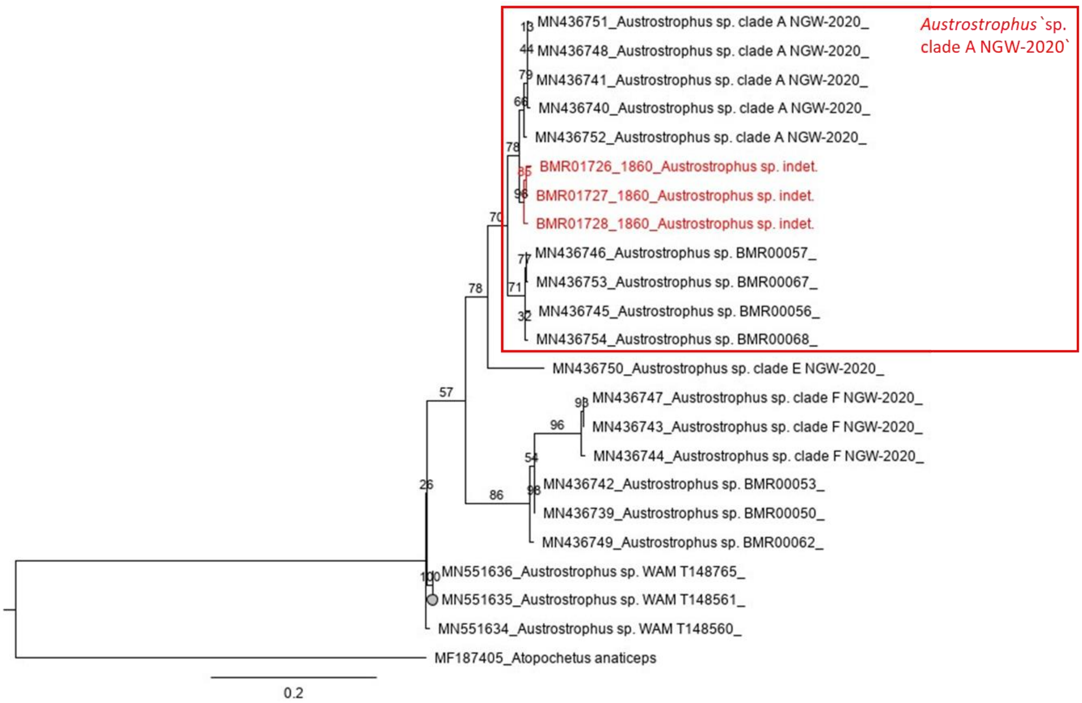

Figure 3.1.1: Maximum Likelihood phylogeny showing relationships among specimens. Numbers are bootstrap values.

Table 3.1.1: Genetic distances among specimens. Colours correspond to OTUs in Fig 3.1.1, and grey boxes indicate intraspecific genetic distances.

COI pairwise distances (%)	BMR01726	BMR01727	BMR01728	MN436740	MN436741	MN436748	MN436751	MN436752	MN436745	MN436746	MN436753	MN436754	MN436750	MN551634	MN551635	MN551636	MN436739	MN436742	MN436749	MN436743	MN436747	MN436744	MF187405
BMR01726_1860_Austrostrophus sp. indet.		0.91	1.22	2.83	2.43	2.58	2.58	2.28	5.02	4.56	4.71	4.71	7.75	8.36	8.21	8.21	9.84	9.73	9.73	10.03	9.92	10.39	18.87
BMR01727_1860_Austrostrophus sp. indet.	0.91		0.91	2.52	2.13	2.28	2.28	1.98	4.71	4.26	4.41	4.41	7.60	8.36	8.21	8.21	9.53	9.42	9.42	10.03	9.92	10.39	18.72
BMR01728_1860_Austrostrophus sp. indet.	1.22	0.91		2.52	2.13	2.28	2.28	1.98	4.71	4.26	4.41	4.41	7.45	8.36	8.21	8.21	9.53	9.42	9.42	10.03	9.92	10.39	18.57
MN436740_Austrostrophus sp. clade A NGW-2020_	2.83	2.52	2.52		0.31	0.47	0.47	1.10	4.72	4.25	4.40	4.40	7.86	7.70	7.55	7.55	9.12	9.12	8.96	9.75	9.43	9.90	19.06
MN436741_Austrostrophus sp. clade A NGW-2020_	2.43	2.13	2.13	0.31		0.15	0.15	0.76	4.41	3.95	4.10	4.10	7.75	7.60	7.45	7.45	9.06	8.97	8.97	9.57	9.43	9.90	18.11
MN436748_Austrostrophus sp. clade A NGW-2020_	2.58	2.28	2.28	0.47	0.15		0.30	0.91	4.56	4.10	4.26	4.26	7.90	7.75	7.60	7.60	9.22	9.12	9.12	9.73	9.59	10.07	18.27
MN436751_Austrostrophus sp. clade A NGW-2020_	2.58	2.28	2.28	0.47	0.15	0.30		0.91	4.26	4.10	4.26	4.26	7.60	7.45	7.30	7.30	8.91	8.82	8.82	9.42	9.27	9.74	17.96
MN436752_Austrostrophus sp. clade A NGW-2020_	2.28	1.98	1.98	1.10	0.76	0.91	0.91		4.56	4.10	4.26	4.26	7.90	7.90	7.75	7.75	9.22	9.12	9.12	9.73	9.59	10.07	18.42
MN436745_Austrostrophus sp. BMR00056_	5.02	4.71	4.71	4.72	4.41	4.56	4.26	4.56		0.76	0.91	0.91	7.60	7.60	7.75	7.75	8.91	8.82	8.51	10.49	10.57	10.71	17.96
MN436746_Austrostrophus sp. BMR00057_	4.56	4.26	4.26	4.25	3.95	4.10	4.10	4.10	0.76		0.15	0.46	7.75	7.14	7.30	7.30	8.75	8.66	8.36	10.03	10.08	10.39	18.42
MN436753_Austrostrophus sp. BMR00067_	4.71	4.41	4.41	4.40	4.10	4.26	4.26	4.26	0.91	0.15		0.61	7.90	7.30	7.45	7.45	8.91	8.82	8.51	10.18	10.24	10.55	18.57
MN436754_Austrostrophus sp. BMR00068_	4.71	4.41	4.41	4.40	4.10	4.26	4.26	4.26	0.91	0.46	0.61		7.90	6.99	7.14	7.14	8.59	8.51	8.21	9.88	9.92	10.07	18.42
MN436750_Austrostrophus sp. clade E NGW-2020_	7.75	7.60	7.45	7.86	7.75	7.90	7.60	7.90	7.60	7.75	7.90	7.90		8.36	8.51	8.51	9.38	9.42	9.73	11.09	11.06	11.04	20.24
MN551634_Austrostrophus sp. WAM T148560_	8.36	8.36	8.36	7.70	7.60	7.75	7.45	7.90	7.60	7.14	7.30	6.99	8.36		1.22	1.22	7.97	7.90	7.90	8.82	8.94	9.42	18.72
MN551635_Austrostrophus sp. WAM T148561_	8.21	8.21	8.21	7.55	7.45	7.60	7.30	7.75	7.75	7.30	7.45	7.14	8.51	1.22		0.00	8.13	8.06	8.06	9.57	9.76	10.23	18.42
MN551636_Austrostrophus sp. WAM T148765_	8.21	8.21	8.21	7.55	7.45	7.60	7.30	7.75	7.75	7.30	7.45	7.14	8.51	1.22	0.00		8.13	8.06	8.06	9.57	9.76	10.23	18.42
MN436739_Austrostrophus sp. BMR00050_	9.84	9.53	9.53	9.12	9.06	9.22	8.91	9.22	8.91	8.75	8.91	8.59	9.38	7.97	8.13	8.13		0.00	1.09	5.16	5.20	5.36	19.88
MN436742_Austrostrophus sp. BMR00053_	9.73	9.42	9.42	9.12	8.97	9.12	8.82	9.12	8.82	8.66	8.82	8.51	9.42	7.90	8.06	8.06	0.00		1.22	5.02	5.20	5.36	19.48
MN436749_Austrostrophus sp. BMR00062_	9.73	9.42	9.42	8.96	8.97	9.12	8.82	9.12	8.51	8.36	8.51	8.21	9.73	7.90	8.06	8.06	1.09	1.22		5.32	5.37	5.52	19.18
MN436743_Austrostrophus sp. clade F NGW-2020_	10.03	10.03	10.03	9.75	9.57	9.73	9.42	9.73	10.49	10.03	10.18	9.88	11.09	8.82	9.57	9.57	5.16	5.02	5.32		0.00	0.81	19.48
MN436747_Austrostrophus sp. clade F NGW-2020_	9.92	9.92	9.92	9.43	9.43	9.59	9.27	9.59	10.57	10.08	10.24	9.92	11.06	8.94	9.76	9.76	5.20	5.20	5.37	0.00		0.65	19.54
MN436744_Austrostrophus sp. clade F NGW-2020_	10.39	10.39	10.39	9.90	9.90	10.07	9.74	10.07	10.71	10.39	10.55	10.07	11.04	9.42	10.23	10.23	5.36	5.36	5.52	0.81	0.65		19.68
MF187405_Atopochetus anaticeps	18.87	18.72	18.57	19.06	18.11	18.27	17.96	18.42	17.96	18.42	18.57	18.42	20.24	18.72	18.42	18.42	19.88	19.48	19.18	19.48	19.54	19.68	

3.2 Pseudoscorpiones

The 20 successfully sequenced pseudoscorpion specimens belonged to two families; these were Garypidae and Olpiidae, which are addressed separately below.

3.2.1 Garypidae

The three samples that were successfully sequenced formed a single OTU, that did not match any other sequences in the analysis (Fig. 3.2.1.1). This OTU, *Synsphyronus* `sp. PSE014`, had low intraspecific genetic distances (<1.38%), and was over 17% divergent from the next closest related OTU (Table 3.2.1.1). *Synsphyronus* `sp. PSE014` was restricted to the Study Area (Targeted Survey Area only) and had a linear geographic distance 1.15km (Table 3.1).

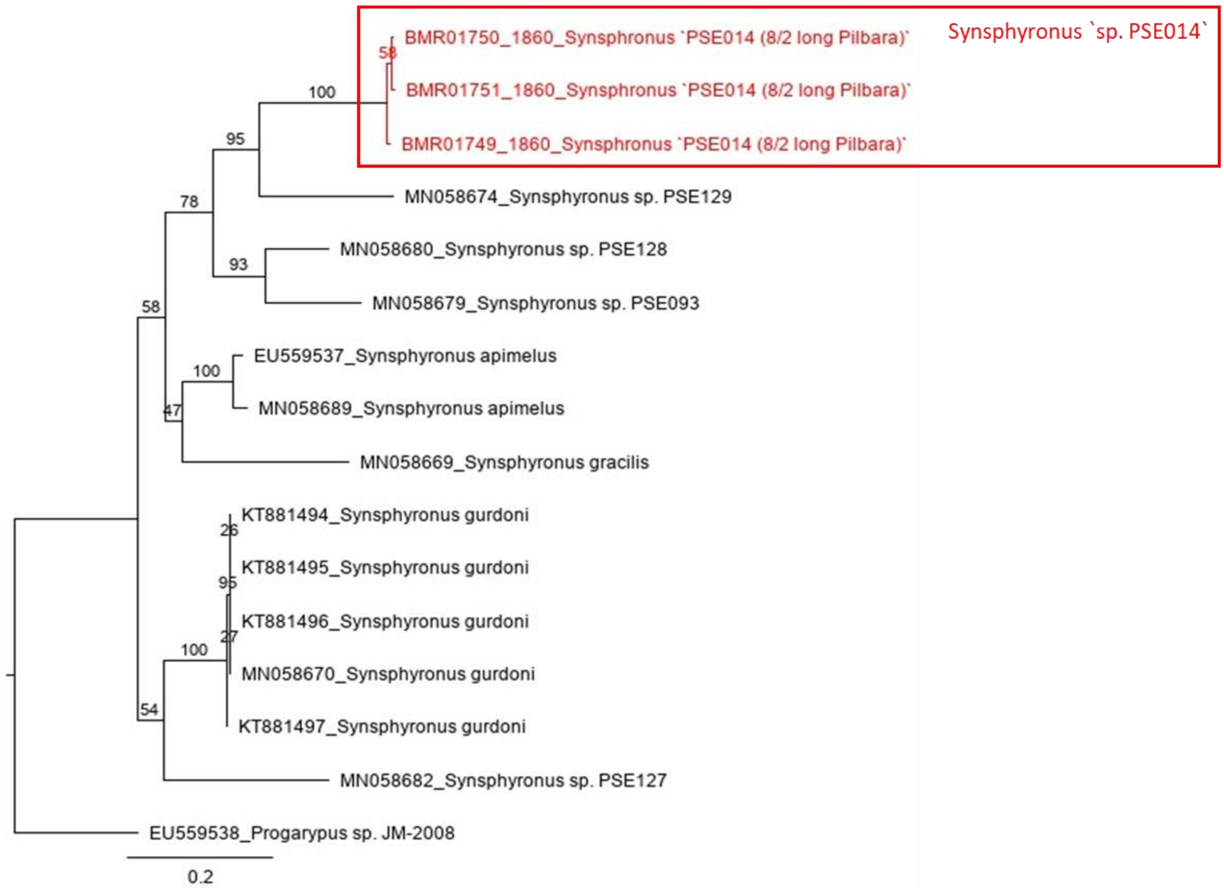

Figure 3.2.1.1: Maximum Likelihood phylogeny showing relationships among specimens. Numbers are bootstrap values.

Table 3.2.1.1: Genetic distances among specimens. Colours correspond to OTUs in Fig 3.2.1.1, and grey boxes indicate intraspecific genetic distances.

COI pairwise distances (%)	BMR01749	BMR01750	BMR01751	MN058674	EU559537	MN058689	KT881494	KT881495	KT881496	MN058670	KT881497	MN058669	MN058682	MN058679	MN058680	EU559538
BMR01749_1860_Synsphronus `PSE014 (8/2 long Pilbara)`		1.07	1.38	17.43	17.89	18.27	18.81	18.81	18.81	18.81	18.50	20.80	20.49	18.35	16.67	22.02
BMR01750_1860_Synsphronus `PSE014 (8/2 long Pilbara)`	1.07		0.61	17.25	18.02	18.40	18.93	18.93	18.93	18.93	18.63	20.61	20.15	18.47	16.79	21.99
BMR01751_1860_Synsphronus `PSE014 (8/2 long Pilbara)`	1.38	0.61		17.10	18.02	18.40	18.63	18.63	18.63	18.63	18.32	20.76	20.31	18.47	16.95	21.99
MN058674_Synsphyronus sp. PSE129	17.43	17.25	17.10		18.78	18.71	19.24	19.24	19.24	19.24	18.93	20.46	21.07	18.32	17.10	20.61
EU559537_Synsphyronus apimelus	17.89	18.02	18.02	18.78		2.99	13.74	13.74	13.74	13.74	13.28	16.49	16.49	15.57	16.03	17.56
MN058689_Synsphyronus apimelus	18.27	18.40	18.40	18.71	2.99		14.31	14.31	14.31	14.31	13.84	16.98	17.14	15.72	15.88	18.87
KT881494_Synsphyronus gurdoni	18.81	18.93	18.63	19.24	13.74	14.31		0.00	0.00	0.00	0.46	16.95	16.18	18.32	17.71	16.95
KT881495_Synsphyronus gurdoni	18.81	18.93	18.63	19.24	13.74	14.31	0.00		0.00	0.00	0.46	16.95	16.18	18.32	17.71	16.95
KT881496_Synsphyronus gurdoni	18.81	18.93	18.63	19.24	13.74	14.31	0.00	0.00		0.00	0.46	16.95	16.18	18.32	17.71	16.95
MN058670_Synsphyronus gurdoni	18.81	18.93	18.63	19.24	13.74	14.31	0.00	0.00	0.00		0.46	16.95	16.18	18.32	17.71	16.95
KT881497_Synsphyronus gurdoni	18.50	18.63	18.32	18.93	13.28	13.84	0.46	0.46	0.46	0.46		16.79	15.73	17.86	17.25	16.64
MN058669_Synsphyronus gracilis	20.80	20.61	20.76	20.46	16.49	16.98	16.95	16.95	16.95	16.95	16.79		20.46	17.56	18.02	23.21
MN058682_Synsphyronus sp. PSE127	20.49	20.15	20.31	21.07	16.49	17.14	16.18	16.18	16.18	16.18	15.73	20.46		19.85	19.08	19.24
MN058679_Synsphyronus sp. PSE093	18.35	18.47	18.47	18.32	15.57	15.72	18.32	18.32	18.32	18.32	17.86	17.56	19.85		12.37	20.31
MN058680_Synsphyronus sp. PSE128	16.67	16.79	16.95	17.10	16.03	15.88	17.71	17.71	17.71	17.71	17.25	18.02	19.08	12.37		19.85
EU559538_Progarypus sp. JM-2008	22.02	21.99	21.99	20.61	17.56	18.87	16.95	16.95	16.95	16.95	16.64	23.21	19.24	20.31	19.85	

3.2.2 Olpiidae

The 17 olpiid specimens that were successfully sequenced formed five distinct OTUs (Fig. 3.2.2.1). Four OTUs *Austrohorus* `sp. PSE121`, *Austrohorus* `sp. PSE122`, *Indolpium* `sp. PSE118` and *Indolpium* `sp. PSE123` matched sequences from a previous molecular analysis of specimens from the Study Area (Biologic, 2016; Wilson *et al.*, 2019). *Indolpium* `sp. PSE118` also matching specimens from GenBank (Fig 3.2.2.1). One of these OTUs, *Xenolpium* `sp. Biologic-PSE028` did not match any other specimens in the analysis, and was found at two sites, 0.28km apart (Table 3.1).

Austrohorus `sp. PSE121` and *Indolpium* `sp. PSE123` were found in both the Targeted and Level 2 Survey Areas as well as in 40 km area around the Study Area. *Austrohorus* `sp. PSE122` was a singleton only found in the Level 2 Survey Area but matched previously collected specimens from within 40 km around the Study Area. ***Xenolpium* `sp. Biologic-PSE028`** was collected in the Targeted Survey Area only; no other matching specimens from previous work could be found. Based on current collections, these four were restricted to the Study Area and so revealed small linear distances (Table 3.1). Only *Indolpium* `sp. PSE118` matched specimens from a much larger area, revealing a linear distance over 56km.

It must be noted that *Austrohorus* `sp. PSE122`, *Indolpium* `sp. PSE118`, and *Indolpium* `sp. PSE123`, all had high genetic divergences within species (Table 3.2.2.1). For example, *Indolpium* `sp. PSE118` had genetic distances as high as 10.61%, and if a smaller intraspecific genetic threshold was applied (e.g., 8%), the OTU could be split into four. However, if a 9% threshold is applied, consistent with Wilson *et al.* (2019), the specimens collapse into a single OTU, with a maximum genetic distance of 10.61%. In addition, *Indolpium* `sp. PSE123` had intraspecific genetic divergences as high as 9.03%, which was consistent with previous work (Wilson *et al.*, 2019). In both instances, detailed morphological and molecular research may be required to resolve the true species boundaries, and until that time, we are conservatively pooling specimens into these OTUs. The phylogenetic analysis also revealed considerable instability in the generic identifications. This is consistent with olpiid taxonomy, and considerable work is required to stabilise the generic concepts.

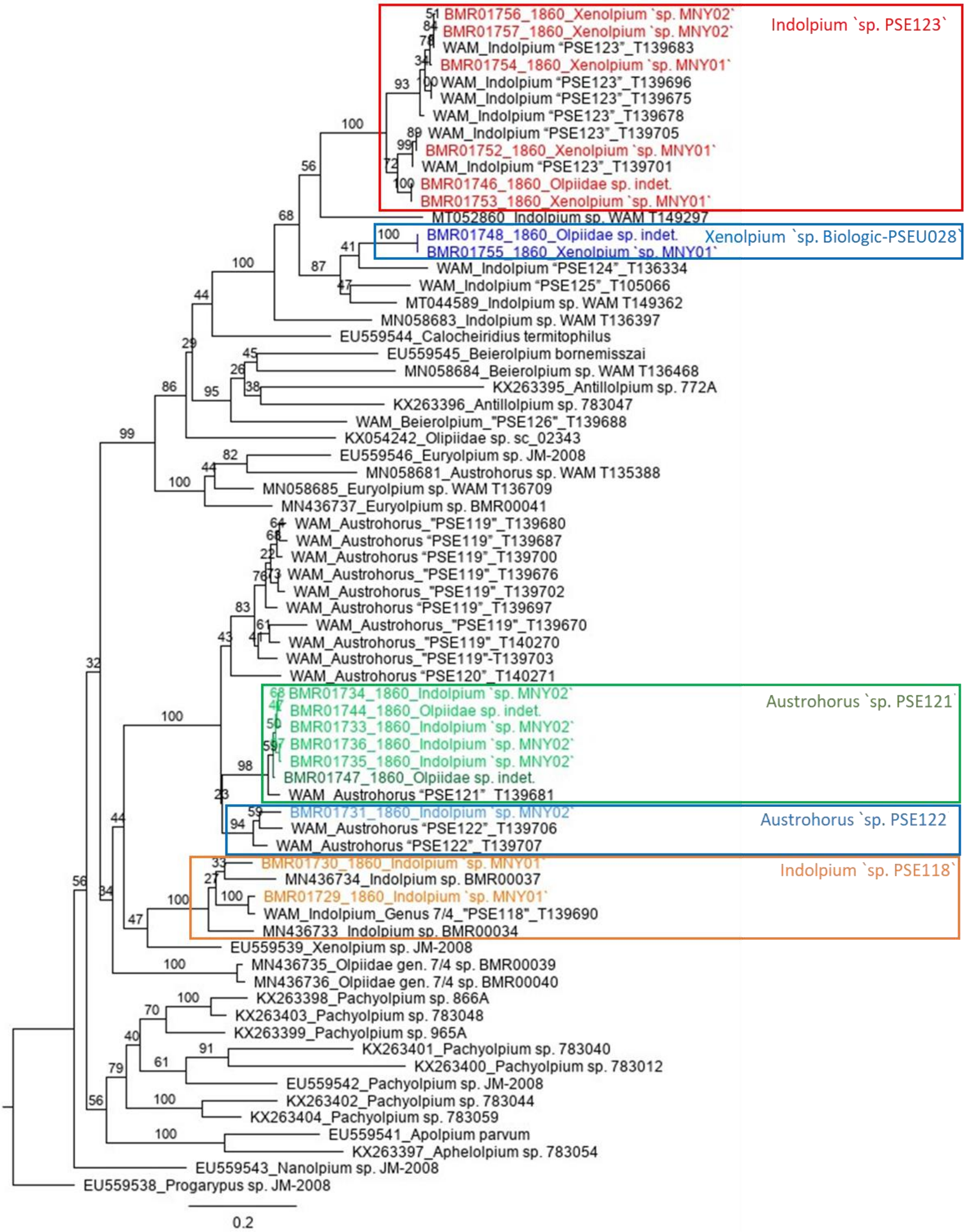

Figure 3.2.2.1: Maximum Likelihood phylogeny showing relationships among specimens. Numbers are bootstrap values.

Table 3.2.2.1: Genetic distances among specimens. Colours correspond to OTUs in Fig 3.2.2.1, and grey boxes indicate intraspecific genetic distances.

COI Genetic Distances (%)	BMR01729	T139690	BMR01730	MN436734	MN436733	EU559539	BMR01731	T139706	T139707	T139670	T139676	T139702	T139680	T139687	T139700	T139697	T139703	T140270	BMR01733	BMR01734	BMR01744	BMR01735	BMR01736	BMR01747	T139681	T140271	MN436735	MN436736	EU559538	EU559542	EU559543	KX263398	KX263403	KX263399	KX263402	KX263404	KX263401	KX263400	EU559541	KX263397	BMR01746	BMR01753	BMR01752	T139701	T139705	BMR01754	BMR01756	BMR01757	T139683	T139675	T139696	T139678	BMR01748	BMR01755	MT044589	T105066	T136334	MN058683	MT052860	EU559544	T139688	EU559545	MN058684	KX263396	EU559546	MN058685	MN436737	MN058681	KX054242	KX263395
BMR01729_1860_Indolpium `sp. MNY01`		1.76	8.24	10.61	9.47	16.49	21.37	22.91	22.69	24.01	22.91	22.91	23.79	23.57	23.79	22.47	22.69	23.57	20.31	20.31	20.46	20.76	20.61	20.92	23.57	23.35	17.56	18.02	19.24	22.44	21.37	20.00	19.08	20.31	22.29	20.15	21.26	24.89	23.51	22.42	22.60	22.60	23.97	25.99	26.43	23.36	23.66	23.51	24.45	25.11	25.11	24.45	23.21	23.21	24.58	24.45	26.43	21.53	21.53	21.03	25.11	22.14	25.04	24.77	23.82	20.46	22.03	23.51	24.58	26.49
WAM_Indolpium_Genus 7/4_"PSE118"_T139690	1.76		8.37	9.91	10.57	17.62	23.79	23.35	22.25	23.79	23.13	22.69	23.57	23.35	23.57	22.69	23.13	23.79	23.57	23.57	23.57	24.01	23.79	24.01	23.57	23.57	18.50	18.50	21.37	23.35	24.23	21.37	20.71	21.81	23.57	21.15	23.00	25.11	25.55	23.79	24.01	24.01	25.55	25.55	25.99	23.35	23.79	23.57	23.57	24.23	24.23	23.57	24.67	24.67	25.33	24.45	25.99	22.03	22.47	22.85	25.11	23.35	25.55	26.76	24.67	21.37	22.17	24.89	25.55	27.48
BMR01730_1860_Indolpium `sp. MNY01`	8.24	8.37		8.78	9.31	14.50	20.46	22.47	20.93	20.49	21.81	20.71	20.71	21.37	22.03	20.49	20.93	20.93	18.17	18.17	18.47	18.63	18.47	18.78	20.71	20.71	17.25	16.95	19.54	22.44	18.78	18.78	17.25	17.71	21.07	19.54	24.11	25.34	23.21	20.62	22.75	22.75	23.51	24.67	25.11	21.99	22.29	22.14	22.69	23.79	23.79	23.35	23.97	23.97	25.04	25.11	25.77	22.60	20.61	21.18	24.01	21.22	23.36	24.77	21.37	18.93	21.67	21.07	23.21	26.03
MN436734_Indolpium sp. BMR00037	10.61	9.91	8.78		10.31	15.95	19.77	22.47	20.49	20.93	20.04	19.60	20.04	20.93	20.71	20.26	19.16	19.82	19.47	19.62	19.77	20.08	19.92	19.92	20.71	21.37	17.79	17.48	18.24	20.69	19.31	19.16	18.24	19.92	20.53	19.47	23.63	24.50	24.20	22.42	22.37	22.37	23.28	24.67	24.89	22.21	22.52	22.37	22.69	23.35	23.35	22.69	23.59	23.59	23.59	23.57	24.45	23.44	20.99	20.95	23.13	22.67	24.66	23.92	21.76	19.47	21.23	22.21	23.59	26.72
MN436733_Indolpium sp. BMR00034	9.47	10.57	9.31	10.31		16.03	20.15	20.71	20.04	22.25	22.03	21.37	21.59	22.91	22.47	21.81	20.93	21.59	18.32	18.17	18.32	18.63	18.47	18.47	21.37	21.59	16.34	16.49	20.92	22.44	19.54	19.54	19.24	18.93	20.31	19.70	23.16	24.89	22.75	20.95	22.29	22.29	23.51	25.55	25.77	22.75	23.05	22.90	24.01	24.45	24.45	24.23	23.66	23.66	24.89	25.55	26.21	23.05	21.22	18.28	22.91	21.68	25.04	23.22	22.75	20.61	20.07	22.14	22.14	25.27
EU559539_Xenolpium sp. JM-2008	16.49	17.62	14.50	15.95	16.03		16.95	18.94	18.06	19.82	18.06	17.62	18.72	18.72	18.72	17.62	18.50	18.06	16.64	16.79	16.95	17.25	17.25	16.49	16.96	19.16	17.41	17.25	18.63	19.54	18.32	18.47	17.71	18.78	19.54	18.78	22.68	24.43	21.07	20.13	23.66	23.66	24.12	24.01	24.23	22.44	22.29	22.14	21.37	22.91	22.91	22.91	21.99	21.99	22.90	21.15	23.35	21.37	21.22	20.57	22.47	20.92	23.66	22.60	21.68	20.31	20.25	21.07	21.83	25.88
BMR01731_1860_Indolpium `sp. MNY02`	21.37	23.79	20.46	19.77	20.15	16.95		5.95	5.73	12.12	10.79	10.79	11.45	12.34	11.89	11.23	10.57	10.35	11.60	11.60	11.91	11.60	11.60	11.76	12.12	13.00	21.07	20.76	17.86	21.37	20.31	20.15	19.85	19.85	20.31	20.46	22.45	25.34	22.90	24.71	25.04	25.04	25.95	25.99	26.21	26.41	26.41	26.41	25.77	25.99	25.99	26.65	26.11	26.11	25.65	24.45	27.31	25.65	26.41	24.85	26.43	24.28	25.65	24.30	22.75	23.66	21.85	24.43	25.65	28.63
WAM_Austrohorus PSE122_T139706	22.91	23.35	22.47	22.47	20.71	18.94	5.95		6.39	10.79	10.79	10.35	11.45	11.45	12.34	11.89	11.89	10.35	11.67	11.45	11.67	11.45	11.45	12.12	11.89	12.78	22.91	22.91	20.26	21.15	23.13	20.26	20.93	20.49	19.16	20.71	22.85	25.77	22.91	24.89	25.33	25.33	25.55	25.55	25.33	27.09	26.87	26.87	26.87	26.21	26.21	26.87	26.21	26.21	25.55	24.67	26.87	27.31	26.87	25.50	25.11	25.33	25.11	25.44	23.79	25.55	23.20	27.09	26.65	29.02
WAM_Austrohorus PSE122?T139707	22.69	22.25	20.93	20.49	20.04	18.06	5.73	6.39		11.45	9.69	9.03	9.69	10.79	10.79	9.91	8.59	9.03	11.23	11.01	11.23	11.01	11.01	11.67	11.89	12.34	20.93	19.82	19.60	20.93	20.49	19.38	18.72	20.49	19.82	20.26	25.37	25.55	24.45	25.77	24.67	24.67	25.99	25.99	26.21	26.21	25.99	25.99	25.99	26.21	26.21	26.65	27.97	27.97	26.65	24.67	26.87	26.87	25.99	24.17	24.45	23.79	25.11	23.90	24.23	24.45	21.39	24.67	24.45	28.80
WAM_Austrohorus_"PSE119"_T139670	24.01	23.79	20.49	20.93	22.25	19.82	12.12	10.79	11.45		8.37	7.71	7.93	9.25	8.81	9.25	8.81	6.61	14.76	14.10	14.32	14.10	14.10	14.10	14.32	11.67	22.91	22.25	20.26	23.79	23.35	22.03	21.15	21.59	21.37	21.15	27.75	26.21	23.79	26.21	27.97	27.97	27.31	27.31	27.09	26.21	25.99	25.99	25.99	26.65	26.65	27.31	27.97	27.97	25.77	27.09	27.75	27.09	28.19	26.16	27.09	26.65	26.21	26.10	22.69	26.43	25.00	25.55	26.65	28.14
WAM_Austrohorus_"PSE119"_T139676	22.91	23.13	21.81	20.04	22.03	18.06	10.79	10.79	9.69	8.37		1.10	3.30	3.74	2.86	3.52	5.07	5.95	12.56	11.89	12.12	11.45	11.89	11.45	11.23	11.45	21.15	21.15	18.50	22.47	22.03	20.93	20.26	22.03	20.26	20.93	24.48	24.89	23.13	25.55	25.99	25.99	26.65	26.65	26.43	24.89	24.67	24.67	24.67	25.33	25.33	25.99	27.75	27.75	26.21	24.67	26.87	26.43	26.21	25.50	25.33	25.77	24.67	24.34	21.37	24.01	22.42	25.33	25.99	27.48
WAM_Austrohorus_"PSE119"_T139702	22.91	22.69	20.71	19.60	21.37	17.62	10.79	10.35	9.03	7.71	1.10		3.08	4.85	3.97	4.63	5.73	6.17	12.78	12.12	12.34	11.67	12.12	11.67	11.45	11.67	21.59	20.93	18.94	21.81	22.03	20.26	20.26	21.81	20.71	20.71	24.48	24.23	23.13	24.89	25.77	25.77	26.43	26.43	26.21	24.67	24.45	24.45	24.45	25.11	25.11	25.77	27.31	27.31	25.77	24.23	26.43	26.21	25.33	25.50	25.11	25.55	24.23	24.34	22.25	23.79	22.42	25.11	24.89	27.04
WAM_Austrohorus_"PSE119"_T139680	23.79	23.57	20.71	20.04	21.59	18.72	11.45	11.45	9.69	7.93	3.30	3.08		2.20	2.20	4.63	6.17	6.83	13.88	13.22	13.44	12.78	13.22	12.78	13.00	12.12	22.03	21.37	20.26	23.35	22.47	21.37	20.71	21.81	22.25	20.93	26.26	25.77	24.45	26.65	25.99	25.99	27.09	27.09	26.87	24.45	24.23	24.23	24.23	24.67	24.67	25.55	29.30	29.30	27.53	26.65	27.09	27.31	25.55	26.38	25.77	26.87	25.77	25.44	22.47	25.11	23.97	25.77	26.43	27.70
WAM_Austrohorus PSE119_T139687	23.57	23.35	21.37	20.93	22.91	18.72	12.34	11.45	10.79	9.25	3.74	4.85	2.20		2.20	4.63	6.61	6.83	13.00	12.78	13.00	12.34	12.78	12.34	12.12	11.01	22.03	22.03	19.60	24.23	22.47	21.59	20.49	21.81	22.25	20.71	25.96	26.43	24.23	26.87	25.99	25.99	26.65	26.65	26.43	24.45	24.23	24.23	24.23	24.67	24.67	25.55	28.19	28.19	27.09	25.77	26.87	27.31	25.55	26.16	25.55	26.65	25.55	25.88	21.59	25.33	23.71	25.55	26.87	27.26
WAM_Austrohorus PSE119_T139700	23.79	23.57	22.03	20.71	22.47	18.72	11.89	12.34	10.79	8.81	2.86	3.97	2.20	2.20		4.19	5.73	5.95	13.22	12.56	12.78	12.56	13.00	12.12	12.78	12.78	21.81	21.81	19.82	24.23	22.91	21.81	20.49	22.91	22.47	21.37	25.52	26.43	24.67	26.87	26.87	26.87	27.97	27.97	27.75	25.77	25.55	25.55	25.55	25.99	25.99	26.87	28.86	28.86	27.75	26.43	27.75	27.97	26.43	26.38	25.77	26.87	25.55	25.66	21.81	25.33	23.71	26.21	27.31	27.48
WAM_Austrohorus PSE119_T139697	22.47	22.69	20.49	20.26	21.81	17.62	11.23	11.89	9.91	9.25	3.52	4.63	4.63	4.63	4.19		5.95	5.95	11.89	11.67	11.89	11.23	11.67	11.45	11.89	11.45	21.37	20.93	19.82	23.13	22.03	20.04	19.82	22.47	21.81	21.59	25.07	25.77	23.13	26.43	26.21	26.21	27.31	27.31	27.53	25.33	25.55	25.55	25.55	26.65	26.65	26.43	27.97	27.97	26.65	25.33	27.53	27.31	25.99	25.50	25.55	25.55	25.99	24.78	22.69	24.01	22.94	25.33	25.55	26.82
WAM_Austrohorus_"PSE119"-T139703	22.69	23.13	20.93	19.16	20.93	18.50	10.57	11.89	8.59	8.81	5.07	5.73	6.17	6.61	5.73	5.95		5.29	11.67	11.45	11.67	11.45	11.45	11.01	11.23	11.89	21.15	20.93	20.49	22.91	22.47	21.15	20.26	22.91	21.59	21.59	26.86	26.43	24.01	26.65	25.33	25.33	26.21	26.21	26.43	25.11	24.89	24.89	24.89	25.99	25.99	25.55	29.08	29.08	27.09	25.99	27.75	25.99	26.43	25.06	24.89	25.11	25.33	24.56	22.69	25.33	22.68	25.33	25.33	28.36
WAM_Austrohorus_"PSE119"_T140270	23.57	23.79	20.93	19.82	21.59	18.06	10.35	10.35	9.03	6.61	5.95	6.17	6.83	6.83	5.95	5.95	5.29		11.89	12.12	12.34	12.12	12.12	11.67	11.89	11.45	21.59	21.15	19.60	22.47	21.81	20.49	19.60	20.71	18.94	21.15	26.11	26.43	23.57	25.77	26.65	26.65	26.43	26.43	26.65	25.55	25.33	25.33	25.33	26.43	26.43	26.65	28.41	28.41	25.99	25.33	26.87	25.55	25.33	25.50	25.55	25.33	25.11	25.22	22.03	24.67	21.91	24.67	25.99	27.92
BMR01733_1860_Indolpium `sp. MNY02`	20.31	23.57	18.17	19.47	18.32	16.64	11.60	11.67	11.23	14.76	12.56	12.78	13.88	13.00	13.22	11.89	11.67	11.89		0.92	1.22	1.37	1.37	1.53	3.30	11.89	20.76	20.61	18.63	21.22	19.39	20.46	19.08	20.00	20.76	21.07	24.47	25.34	21.68	22.91	25.65	25.65	26.41	28.41	28.63	25.80	25.80	25.80	25.99	27.09	27.09	27.53	25.95	25.95	26.11	26.21	28.63	25.65	24.28	23.63	24.67	25.34	25.80	23.84	22.75	22.29	22.03	23.51	25.19	26.49
BMR01734_1860_Indolpium `sp. MNY02`	20.31	23.57	18.17	19.62	18.17	16.79	11.60	11.45	11.01	14.10	11.89	12.12	13.22	12.78	12.56	11.67	11.45	12.12	0.92		0.61	1.07	1.07	1.22	3.30	11.89	20.15	20.00	18.63	21.37	19.54	20.76	19.24	20.31	20.92	21.22	23.99	25.50	21.68	23.24	25.95	25.95	26.72	28.86	29.08	26.11	26.11	26.11	26.43	27.53	27.53	27.97	26.26	26.26	26.57	26.43	28.86	25.95	24.73	24.08	24.89	25.19	25.80	23.99	22.44	22.60	22.38	23.51	25.34	26.49
BMR01744_1860_Olpiidae sp. indet.	20.46	23.57	18.47	19.77	18.32	16.95	11.91	11.67	11.23	14.32	12.12	12.34	13.44	13.00	12.78	11.89	11.67	12.34	1.22	0.61		1.37	1.37	1.53	3.52	12.12	20.46	20.31	18.78	21.83	19.70	20.92	19.24	20.31	21.07	21.37	24.23	25.95	21.53	23.24	26.11	26.11	26.87	28.86	29.08	26.26	26.26	26.26	26.43	27.53	27.53	27.97	26.26	26.26	26.41	26.43	28.86	25.80	24.73	24.54	25.11	25.50	26.11	23.84	22.14	22.75	22.38	23.36	25.50	26.64
BMR01735_1860_Indolpium `sp. MNY02`	20.76	24.01	18.63	20.08	18.63	17.25	11.60	11.45	11.01	14.10	11.45	11.67	12.78	12.34	12.56	11.23	11.45	12.12	1.37	1.07	1.37		0.31	1.37	3.52	12.12	20.46	20.31	18.78	21.53	19.24	20.92	19.54	20.31	20.76	21.83	24.23	25.50	22.14	23.24	25.95	25.95	26.72	28.63	28.86	26.11	26.11	26.11	26.21	27.31	27.31	27.75	26.41	26.41	26.57	26.65	29.08	26.26	24.58	24.24	25.11	25.34	25.80	23.99	22.75	22.90	23.09	23.36	25.19	26.64
BMR01736_1860_Indolpium `sp. MNY02`	20.61	23.79	18.47	19.92	18.47	17.25	11.60	11.45	11.01	14.10	11.89	12.12	13.22	12.78	13.00	11.67	11.45	12.12	1.37	1.07	1.37	0.31		1.37	3.52	12.12	20.46	20.31	18.47	21.37	19.08	20.61	19.54	20.31	20.61	21.83	24.47	25.34	21.99	23.08	25.80	25.80	26.57	28.41	28.63	25.95	25.95	25.95	25.99	27.09	27.09	27.53	26.26	26.26	26.41	26.43	28.86	26.11	24.43	24.24	25.11	25.19	25.80	23.68	22.75	22.90	22.91	23.05	25.19	26.64
BMR01747_1860_Olpiidae sp. indet.	20.92	24.01	18.78	19.92	18.47	16.49	11.76	12.12	11.67	14.10	11.45	11.67	12.78	12.34	12.12	11.45	11.01	11.67	1.53	1.22	1.53	1.37	1.37		2.86	11.89	20.15	20.00	17.86	21.53	19.08	20.46	19.39	19.70	20.92	21.22	24.23	25.34	21.68	22.59	25.65	25.65	26.41	28.19	28.41	25.80	25.80	25.80	25.77	26.87	26.87	27.31	26.11	26.11	25.95	26.21	29.52	25.80	24.58	23.93	24.67	25.34	25.50	23.84	22.60	22.14	22.03	23.21	24.73	26.34
WAM_Austrohorus PSE121_T139681	23.57	23.57	20.71	20.71	21.37	16.96	12.12	11.89	11.89	14.32	11.23	11.45	13.00	12.12	12.78	11.89	11.23	11.89	3.30	3.30	3.52	3.52	3.52	2.86		11.67	21.15	21.37	20.71	22.25	20.93	20.49	20.49	21.37	20.49	21.15	24.93	26.21	23.35	24.67	25.77	25.77	26.87	26.87	27.09	25.11	24.89	24.89	24.89	25.99	25.99	26.43	27.97	27.97	26.43	24.67	28.86	26.65	24.45	24.17	22.91	24.89	25.99	25.00	22.25	23.13	21.13	25.33	25.11	28.58
WAM_Austrohorus PSE120?T140271	23.35	23.57	20.71	21.37	21.59	19.16	13.00	12.78	12.34	11.67	11.45	11.67	12.12	11.01	12.78	11.45	11.89	11.45	11.89	11.89	12.12	12.12	12.12	11.89	11.67		22.91	22.91	21.15	22.47	22.69	23.13	22.25	21.37	22.25	20.49	28.78	26.65	24.23	26.87	27.53	27.53	26.65	26.65	26.87	26.65	26.43	26.43	26.43	27.97	27.97	27.31	29.08	29.08	26.21	26.21	27.75	29.52	25.55	24.84	25.99	27.09	28.41	26.54	23.57	26.21	23.71	24.67	26.21	30.12
MN436735_Olpiidae gen. 7/4 sp. BMR00039	17.56	18.50	17.25	17.79	16.34	17.41	21.07	22.91	20.93	22.91	21.15	21.59	22.03	22.03	21.81	21.37	21.15	21.59	20.76	20.15	20.46	20.46	20.46	20.15	21.15	22.91		1.83	20.76	20.61	19.39	20.00	18.47	19.24	20.92	20.76	23.87	24.28	21.07	19.97	24.43	24.43	24.89	24.45	24.67	23.97	23.82	23.82	23.35	23.79	23.79	24.45	23.05	23.05	25.04	24.23	27.09	23.82	24.12	19.96	22.91	23.21	23.66	22.91	22.29	19.85	22.38	21.53	23.66	26.34
MN436736_Olpiidae gen. 7/4 sp. BMR00040	18.02	18.50	16.95	17.48	16.49	17.25	20.76	22.91	19.82	22.25	21.15	20.93	21.37	22.03	21.81	20.93	20.93	21.15	20.61	20.00	20.31	20.31	20.31	20.00	21.37	22.91	1.83		21.22	20.15	19.54	20.15	18.02	19.39	21.07	21.22	24.23	24.12	21.07	19.97	25.04	25.04	25.50	25.33	25.55	24.43	24.28	24.28	24.01	24.89	24.89	25.11	23.82	23.82	25.95	24.45	26.65	24.28	24.58	20.57	23.35	23.66	24.12	23.07	22.75	20.46	22.20	21.37	23.05	26.49
EU559538_Progarypus sp. JM-2008	19.24	21.37	19.54	18.24	20.92	18.63	17.86	20.26	19.60	20.26	18.50	18.94	20.26	19.60	19.82	19.82	20.49	19.60	18.63	18.63	18.78	18.78	18.47	17.86	20.71	21.15	20.76	21.22		20.61	17.86	18.17	17.25	18.32	20.76	19.08	23.40	23.21	22.14	21.44	25.34	25.34	25.34	26.65	26.87	25.19	25.19	25.04	25.33	26.21	26.21	26.43	23.36	23.36	23.51	22.91	26.65	25.04	23.21	22.71	24.67	24.28	25.50	24.61	22.60	20.76	22.56	22.90	24.43	28.17
EU559542_Pachyolpium sp. JM-2008	22.44	23.35	22.44	20.69	22.44	19.54	21.37	21.15	20.93	23.79	22.47	21.81	23.35	24.23	24.23	23.13	22.91	22.47	21.22	21.37	21.83	21.53	21.37	21.53	22.25	22.47	20.61	20.15	20.61		19.85	17.25	18.02	17.10	18.02	16.79	20.67	20.15	21.37	22.59	23.05	23.05	23.36	23.13	22.91	25.04	24.89	24.89	23.57	24.01	24.01	23.57	22.29	22.29	22.90	21.37	23.57	23.51	23.66	21.18	22.25	22.75	25.04	25.23	23.36	22.14	22.56	23.82	21.99	27.56
EU559543_Nanolpium sp. JM-2008	21.37	24.23	18.78	19.31	19.54	18.32	20.31	23.13	20.49	23.35	22.03	22.03	22.47	22.47	22.91	22.03	22.47	21.81	19.39	19.54	19.70	19.24	19.08	19.08	20.93	22.69	19.39	19.54	17.86	19.85		18.32	17.71	16.79	20.61	19.70	25.06	23.51	22.44	22.75	22.90	22.90	24.89	25.77	26.21	23.82	23.66	23.66	23.57	24.23	24.23	24.45	23.97	23.97	23.05	24.23	24.67	22.90	22.14	21.03	23.13	23.51	24.89	23.38	21.22	20.15	21.14	23.05	21.99	26.79
KX263398_Pachyolpium sp. 866A	20.00	21.37	18.78	19.16	19.54	18.47	20.15	20.26	19.38	22.03	20.93	20.26	21.37	21.59	21.81	20.04	21.15	20.49	20.46	20.76	20.92	20.92	20.61	20.46	20.49	23.13	20.00	20.15	18.17	17.25	18.32		6.41	12.98	18.32	16.79	22.09	21.68	21.83	21.77	22.14	22.14	23.36	23.13	23.57	22.75	22.90	22.75	21.81	22.47	22.47	22.47	22.29	22.29	23.21	22.69	23.79	22.90	22.14	20.88	22.03	23.66	24.58	24.61	23.21	21.37	21.67	22.75	21.83	27.71
KX263403_Pachyolpium sp. 783048	19.08	20.71	17.25	18.24	19.24	17.71	19.85	20.93	18.72	21.15	20.26	20.26	20.71	20.49	20.49	19.82	20.26	19.60	19.08	19.24	19.24	19.54	19.54	19.39	20.49	22.25	18.47	18.02	17.25	18.02	17.71	6.41		11.45	17.86	16.64	20.19	20.92	21.83	21.44	23.36	23.36	24.58	25.33	25.33	23.51	23.66	23.51	22.91	23.57	23.57	23.79	22.90	22.90	24.12	22.47	25.77	23.51	21.68	20.88	21.37	23.36	24.58	24.77	22.90	21.07	22.56	23.05	22.44	27.56
KX263399_Pachyolpium sp. 965A	20.31	21.81	17.71	19.92	18.93	18.78	19.85	20.49	20.49	21.59	22.03	21.81	21.81	21.81	22.91	22.47	22.91	20.71	20.00	20.31	20.31	20.31	20.31	19.70	21.37	21.37	19.24	19.39	18.32	17.10	16.79	12.98	11.45		17.10	15.88	20.55	20.46	20.76	20.30	22.44	22.44	22.90	23.79	23.79	22.44	22.29	22.14	22.03	22.91	22.91	23.13	23.66	23.66	22.14	23.79	25.33	22.44	23.36	22.10	23.57	23.05	23.97	24.61	21.07	20.76	21.49	22.44	22.29	27.25
KX263402_Pachyolpium sp. 783044	22.29	23.57	21.07	20.53	20.31	19.54	20.31	19.16	19.82	21.37	20.26	20.71	22.25	22.25	22.47	21.81	21.59	18.94	20.76	20.92	21.07	20.76	20.61	20.92	20.49	22.25	20.92	21.07	20.76	18.02	20.61	18.32	17.86	17.10		11.91	22.21	22.75	20.61	21.60	21.83	21.83	22.29	22.69	22.69	21.68	21.83	21.68	22.25	23.13	23.13	23.13	22.44	22.44	22.29	23.13	26.43	23.21	22.14	22.41	25.11	23.51	24.73	23.99	21.37	21.37	21.31	23.21	22.75	26.79
KX263404_Pachyolpium sp. 783059	20.15	21.15	19.54	19.47	19.70	18.78	20.46	20.71	20.26	21.15	20.93	20.71	20.93	20.71	21.37	21.59	21.59	21.15	21.07	21.22	21.37	21.83	21.83	21.22	21.15	20.49	20.76	21.22	19.08	16.79	19.70	16.79	16.64	15.88	11.91		22.33	21.99	19.85	21.77	22.44	22.44	22.60	24.23	23.79	22.75	22.90	22.75	23.35	24.01	24.01	23.79	22.90	22.90	22.60	24.01	26.87	22.90	21.68	21.49	23.35	22.75	23.66	25.54	22.14	21.07	21.67	22.29	20.76	25.73
KX263401_Pachyolpium sp. 783040	21.26	23.00	24.11	23.63	23.16	22.68	22.45	22.85	25.37	27.75	24.48	24.48	26.26	25.96	25.52	25.07	26.86	26.11	24.47	23.99	24.23	24.23	24.47	24.23	24.93	28.78	23.87	24.23	23.40	20.67	25.06	22.09	20.19	20.55	22.21	22.33		22.33	24.58	26.01	26.49	26.49	28.62	30.12	30.12	29.34	29.57	29.34	30.12	30.42	30.42	28.93	26.37	26.37	28.74	28.78	30.86	26.72	29.69	24.23	31.45	25.53	27.08	27.20	26.37	24.47	25.30	28.62	28.03	31.53
KX263400_Pachyolpium sp. 783012	24.89	25.11	25.34	24.50	24.89	24.43	25.34	25.77	25.55	26.21	24.89	24.23	25.77	26.43	26.43	25.77	26.43	26.43	25.34	25.50	25.95	25.50	25.34	25.34	26.21	26.65	24.28	24.12	23.21	20.15	23.51	21.68	20.92	20.46	22.75	21.99	22.33		25.19	23.90	26.87	26.87	26.57	27.31	27.09	27.48	27.33	27.18	27.31	27.97	27.97	27.53	25.95	25.95	26.41	27.53	29.08	26.41	27.63	25.76	26.43	26.41	27.48	28.33	25.19	23.21	28.06	26.41	26.41	30.46
EU559541_Apolpium parvum	23.51	25.55	23.21	24.20	22.75	21.07	22.90	22.91	24.45	23.79	23.13	23.13	24.45	24.23	24.67	23.13	24.01	23.57	21.68	21.68	21.53	22.14	21.99	21.68	23.35	24.23	21.07	21.07	22.14	21.37	22.44	21.83	21.83	20.76	20.61	19.85	24.58	25.19		17.35	24.43	24.43	24.73	26.65	26.65	25.65	25.95	25.80	26.87	26.87	26.87	27.31	24.43	24.43	25.04	26.21	29.52	24.12	25.65	23.02	27.75	26.41	27.63	26.47	24.28	23.51	23.80	23.66	23.51	29.39
KX263397_Aphelolpium sp. 783054	22.42	23.79	20.62	22.42	20.95	20.13	24.71	24.89	25.77	26.21	25.55	24.89	26.65	26.87	26.87	26.43	26.65	25.77	22.91	23.24	23.24	23.24	23.08	22.59	24.67	26.87	19.97	19.97	21.44	22.59	22.75	21.77	21.44	20.30	21.60	21.77	26.01	23.90	17.35		23.57	23.57	23.73	25.77	25.99	23.08	22.91	22.91	24.67	25.77	25.77	25.77	22.91	22.91	23.24	22.47	27.53	23.57	23.73	22.71	26.65	23.57	24.06	25.13	24.71	20.30	24.28	24.55	24.88	28.07
BMR01746_1860_Olpiidae sp. indet.	22.60	24.01	22.75	22.37	22.29	23.66	25.04	25.33	24.67	27.97	25.99	25.77	25.99	25.99	26.87	26.21	25.33	26.65	25.65	25.95	26.11	25.95	25.80	25.65	25.77	27.53	24.43	25.04	25.34	23.05	22.90	22.14	23.36	22.44	21.83	22.44	26.49	26.87	24.43	23.57		0.00	4.58	3.97	4.85	8.09	8.24	8.24	8.37	8.15	8.15	7.93	14.81	14.81	15.57	17.84	18.50	15.27	15.57	19.66	25.33	21.53	23.66	23.99	24.28	22.29	22.74	24.73	20.46	24.96
BMR01753_1860_Xenolpium `sp. MNY01`	22.60	24.01	22.75	22.37	22.29	23.66	25.04	25.33	24.67	27.97	25.99	25.77	25.99	25.99	26.87	26.21	25.33	26.65	25.65	25.95	26.11	25.95	25.80	25.65	25.77	27.53	24.43	25.04	25.34	23.05	22.90	22.14	23.36	22.44	21.83	22.44	26.49	26.87	24.43	23.57	0.00		4.58	3.97	4.85	8.09	8.24	8.24	8.37	8.15	8.15	7.93	14.81	14.81	15.57	17.84	18.50	15.27	15.57	19.66	25.33	21.53	23.66	23.99	24.28	22.29	22.74	24.73	20.46	24.96
BMR01752_1860_Xenolpium `sp. MNY01`	23.97	25.55	23.51	23.28	23.51	24.12	25.95	25.55	25.99	27.31	26.65	26.43	27.09	26.65	27.97	27.31	26.21	26.43	26.41	26.72	26.87	26.72	26.57	26.41	26.87	26.65	24.89	25.50	25.34	23.36	24.89	23.36	24.58	22.90	22.29	22.60	28.62	26.57	24.73	23.73	4.58	4.58		0.44	0.44	8.24	8.40	8.40	8.59	8.37	8.37	9.03	15.42	15.42	15.27	17.84	19.82	16.95	17.10	20.57	26.43	22.29	23.97	24.46	24.28	22.75	24.16	25.04	20.76	24.66
WAM_Indolpium PSE123_T139701	25.99	25.55	24.67	24.67	25.55	24.01	25.99	25.55	25.99	27.31	26.65	26.43	27.09	26.65	27.97	27.31	26.21	26.43	28.41	28.86	28.86	28.63	28.41	28.19	26.87	26.65	24.45	25.33	26.65	23.13	25.77	23.13	25.33	23.79	22.69	24.23	30.12	27.31	26.65	25.77	3.97	3.97	0.44		0.88	8.15	8.15	8.15	8.15	8.37	8.37	8.59	17.18	17.18	16.52	17.84	19.38	17.62	18.94	20.65	25.99	23.57	25.55	25.66	25.99	24.67	24.49	27.31	22.03	26.38
WAM_Indolpium PSE123_T139705	26.43	25.99	25.11	24.89	25.77	24.23	26.21	25.33	26.21	27.09	26.43	26.21	26.87	26.43	27.75	27.53	26.43	26.65	28.63	29.08	29.08	28.86	28.63	28.41	27.09	26.87	24.67	25.55	26.87	22.91	26.21	23.57	25.33	23.79	22.69	23.79	30.12	27.09	26.65	25.99	4.85	4.85	0.44	0.88		9.03	9.03	9.03	9.03	8.37	8.37	9.03	17.40	17.40	16.52	18.28	19.82	18.06	19.60	21.09	26.65	24.23	25.33	25.44	25.77	24.01	24.74	27.75	22.69	26.16
BMR01754_1860_Xenolpium `sp. MNY01`	23.36	23.35	21.99	22.21	22.75	22.44	26.41	27.09	26.21	26.21	24.89	24.67	24.45	24.45	25.77	25.33	25.11	25.55	25.80	26.11	26.26	26.11	25.95	25.80	25.11	26.65	23.97	24.43	25.19	25.04	23.82	22.75	23.51	22.44	21.68	22.75	29.34	27.48	25.65	23.08	8.09	8.09	8.24	8.15	9.03		0.92	0.61	0.66	2.20	2.20	2.42	16.49	16.49	17.56	18.06	20.26	15.12	16.64	20.73	25.11	22.75	22.90	23.99	23.82	22.29	23.98	24.73	21.53	24.66
BMR01756_1860_Xenolpium `sp. MNY02`	23.66	23.79	22.29	22.52	23.05	22.29	26.41	26.87	25.99	25.99	24.67	24.45	24.23	24.23	25.55	25.55	24.89	25.33	25.80	26.11	26.26	26.11	25.95	25.80	24.89	26.43	23.82	24.28	25.19	24.89	23.66	22.90	23.66	22.29	21.83	22.90	29.57	27.33	25.95	22.91	8.24	8.24	8.40	8.15	9.03	0.92		0.31	0.44	2.86	2.86	3.08	16.49	16.49	17.71	18.28	19.82	15.12	16.64	21.03	24.67	22.29	22.60	23.68	23.66	21.99	23.62	24.58	21.07	24.66
BMR01757_1860_Xenolpium `sp. MNY02`	23.51	23.57	22.14	22.37	22.90	22.14	26.41	26.87	25.99	25.99	24.67	24.45	24.23	24.23	25.55	25.55	24.89	25.33	25.80	26.11	26.26	26.11	25.95	25.80	24.89	26.43	23.82	24.28	25.04	24.89	23.66	22.75	23.51	22.14	21.68	22.75	29.34	27.18	25.80	22.91	8.24	8.24	8.40	8.15	9.03	0.61	0.31		0.00	2.42	2.42	2.64	16.49	16.49	17.71	18.28	19.82	15.12	16.49	21.03	24.89	22.44	22.90	23.99	23.82	22.29	23.98	24.89	21.37	24.96
WAM_Indolpium PSE123_T139683	24.45	23.57	22.69	22.69	24.01	21.37	25.77	26.87	25.99	25.99	24.67	24.45	24.23	24.23	25.55	25.55	24.89	25.33	25.99	26.43	26.43	26.21	25.99	25.77	24.89	26.43	23.35	24.01	25.33	23.57	23.57	21.81	22.91	22.03	22.25	23.35	30.12	27.31	26.87	24.67	8.37	8.37	8.59	8.15	9.03	0.66	0.44	0.00		2.42	2.42	2.64	18.28	18.28	18.50	18.28	19.82	14.98	18.72	21.53	24.89	23.57	23.35	24.56	24.89	23.57	23.97	27.31	22.03	26.16
WAM_Indolpium PSE123_T139675	25.11	24.23	23.79	23.35	24.45	22.91	25.99	26.21	26.21	26.65	25.33	25.11	24.67	24.67	25.99	26.65	25.99	26.43	27.09	27.53	27.53	27.31	27.09	26.87	25.99	27.97	23.79	24.89	26.21	24.01	24.23	22.47	23.57	22.91	23.13	24.01	30.42	27.97	26.87	25.77	8.15	8.15	8.37	8.37	8.37	2.20	2.86	2.42	2.42		0.00	2.42	18.72	18.72	17.84	19.38	20.04	15.86	19.60	21.75	25.99	24.23	24.01	25.00	25.33	24.01	25.00	27.75	23.35	26.60
WAM_Indolpium PSE123_T139696	25.11	24.23	23.79	23.35	24.45	22.91	25.99	26.21	26.21	26.65	25.33	25.11	24.67	24.67	25.99	26.65	25.99	26.43	27.09	27.53	27.53	27.31	27.09	26.87	25.99	27.97	23.79	24.89	26.21	24.01	24.23	22.47	23.57	22.91	23.13	24.01	30.42	27.97	26.87	25.77	8.15	8.15	8.37	8.37	8.37	2.20	2.86	2.42	2.42	0.00		2.42	18.72	18.72	17.84	19.38	20.04	15.86	19.60	21.75	25.99	24.23	24.01	25.00	25.33	24.01	25.00	27.75	23.35	26.60
WAM_Indolpium PSE123_T139678	24.45	23.57	23.35	22.69	24.23	22.91	26.65	26.87	26.65	27.31	25.99	25.77	25.55	25.55	26.87	26.43	25.55	26.65	27.53	27.97	27.97	27.75	27.53	27.31	26.43	27.31	24.45	25.11	26.43	23.57	24.45	22.47	23.79	23.13	23.13	23.79	28.93	27.53	27.31	25.77	7.93	7.93	9.03	8.59	9.03	2.42	3.08	2.64	2.64	2.42	2.42		18.94	18.94	18.72	18.28	20.04	15.64	19.38	22.19	25.99	24.23	24.01	25.22	26.21	24.45	25.00	28.41	23.13	25.94
BMR01748_1860_Olpiidae sp. indet.	23.21	24.67	23.97	23.59	23.66	21.99	26.11	26.21	27.97	27.97	27.75	27.31	29.30	28.19	28.86	27.97	29.08	28.41	25.95	26.26	26.26	26.41	26.26	26.11	27.97	29.08	23.05	23.82	23.36	22.29	23.97	22.29	22.90	23.66	22.44	22.90	26.37	25.95	24.43	22.91	14.81	14.81	15.42	17.18	17.40	16.49	16.49	16.49	18.28	18.72	18.72	18.94		0.00	12.82	14.54	14.32	17.10	16.79	21.49	25.55	19.85	22.44	23.84	22.29	21.07	22.56	21.22	21.83	23.28
BMR01755_1860_Xenolpium `sp. MNY01`	23.21	24.67	23.97	23.59	23.66	21.99	26.11	26.21	27.97	27.97	27.75	27.31	29.30	28.19	28.86	27.97	29.08	28.41	25.95	26.26	26.26	26.41	26.26	26.11	27.97	29.08	23.05	23.82	23.36	22.29	23.97	22.29	22.90	23.66	22.44	22.90	26.37	25.95	24.43	22.91	14.81	14.81	15.42	17.18	17.40	16.49	16.49	16.49	18.28	18.72	18.72	18.94	0.00		12.82	14.54	14.32	17.10	16.79	21.49	25.55	19.85	22.44	23.84	22.29	21.07	22.56	21.22	21.83	23.28
MT044589_Indolpium sp. WAM T149362	24.58	25.33	25.04	23.59	24.89	22.90	25.65	25.55	26.65	25.77	26.21	25.77	27.53	27.09	27.75	26.65	27.09	25.99	26.11	26.57	26.41	26.57	26.41	25.95	26.43	26.21	25.04	25.95	23.51	22.90	23.05	23.21	24.12	22.14	22.29	22.60	28.74	26.41	25.04	23.24	15.57	15.57	15.27	16.52	16.52	17.56	17.71	17.71	18.50	17.84	17.84	18.72	12.82	12.82		12.34	13.22	18.02	16.95	20.27	25.77	21.07	23.36	23.99	23.21	20.76	23.98	24.73	23.05	23.89
WAM_Indolpium PSE125_T105066	24.45	24.45	25.11	23.57	25.55	21.15	24.45	24.67	24.67	27.09	24.67	24.23	26.65	25.77	26.43	25.33	25.99	25.33	26.21	26.43	26.43	26.65	26.43	26.21	24.67	26.21	24.23	24.45	22.91	21.37	24.23	22.69	22.47	23.79	23.13	24.01	28.78	27.53	26.21	22.47	17.84	17.84	17.84	17.84	18.28	18.06	18.28	18.28	18.28	19.38	19.38	18.28	14.54	14.54	12.34		15.86	18.72	18.28	20.87	23.35	22.03	24.01	24.78	25.11	23.57	24.49	26.87	22.91	25.94
WAM_Indolpium PSE124_T136334	26.43	25.99	25.77	24.45	26.21	23.35	27.31	26.87	26.87	27.75	26.87	26.43	27.09	26.87	27.75	27.53	27.75	26.87	28.63	28.86	28.86	29.08	28.86	29.52	28.86	27.75	27.09	26.65	26.65	23.57	24.67	23.79	25.77	25.33	26.43	26.87	30.86	29.08	29.52	27.53	18.50	18.50	19.82	19.38	19.82	20.26	19.82	19.82	19.82	20.04	20.04	20.04	14.32	14.32	13.22	15.86		19.82	19.60	22.63	26.43	25.55	26.21	25.44	27.09	25.55	26.03	28.41	24.45	25.72
MN058683_Indolpium sp. WAM T136397	21.53	22.03	22.60	23.44	23.05	21.37	25.65	27.31	26.87	27.09	26.43	26.21	27.31	27.31	27.97	27.31	25.99	25.55	25.65	25.95	25.80	26.26	26.11	25.80	26.65	29.52	23.82	24.28	25.04	23.51	22.90	22.90	23.51	22.44	23.21	22.90	26.72	26.41	24.12	23.57	15.27	15.27	16.95	17.62	18.06	15.12	15.12	15.12	14.98	15.86	15.86	15.64	17.10	17.10	18.02	18.72	19.82		17.86	20.27	24.89	21.53	23.05	22.76	22.44	20.92	21.49	23.51	21.37	23.89
MT052860_Indolpium sp. WAM T149297	21.53	22.47	20.61	20.99	21.22	21.22	26.41	26.87	25.99	28.19	26.21	25.33	25.55	25.55	26.43	25.99	26.43	25.33	24.28	24.73	24.73	24.58	24.43	24.58	24.45	25.55	24.12	24.58	23.21	23.66	22.14	22.14	21.68	23.36	22.14	21.68	29.69	27.63	25.65	23.73	15.57	15.57	17.10	18.94	19.60	16.64	16.64	16.49	18.72	19.60	19.60	19.38	16.79	16.79	16.95	18.28	19.60	17.86		20.73	23.57	20.46	25.04	23.38	23.51	21.68	22.56	22.44	20.31	23.89
EU559544_Calocheiridius termitophilus	21.03	22.85	21.18	20.95	18.28	20.57	24.85	25.50	24.17	26.16	25.50	25.50	26.38	26.16	26.38	25.50	25.06	25.50	23.63	24.08	24.54	24.24	24.24	23.93	24.17	24.84	19.96	20.57	22.71	21.18	21.03	20.88	20.88	22.10	22.41	21.49	24.23	25.76	23.02	22.71	19.66	19.66	20.57	20.65	21.09	20.73	21.03	21.03	21.53	21.75	21.75	22.19	21.49	21.49	20.27	20.87	22.63	20.27	20.73		18.89	17.98	22.10	20.24	23.02	20.42	21.67	21.64	19.81	24.31
WAM_Beierolpium_"PSE126"_T139688	25.11	25.11	24.01	23.13	22.91	22.47	26.43	25.11	24.45	27.09	25.33	25.11	25.77	25.55	25.77	25.55	24.89	25.55	24.67	24.89	25.11	25.11	25.11	24.67	22.91	25.99	22.91	23.35	24.67	22.25	23.13	22.03	21.37	23.57	25.11	23.35	31.45	26.43	27.75	26.65	25.33	25.33	26.43	25.99	26.65	25.11	24.67	24.89	24.89	25.99	25.99	25.99	25.55	25.55	25.77	23.35	26.43	24.89	23.57	18.89		18.94	22.03	21.26	24.01	22.91	24.23	24.45	22.03	22.19
EU559545_Beierolpium bornemisszai	22.14	23.35	21.22	22.67	21.68	20.92	24.28	25.33	23.79	26.65	25.77	25.55	26.87	26.65	26.87	25.55	25.11	25.33	25.34	25.19	25.50	25.34	25.19	25.34	24.89	27.09	23.21	23.66	24.28	22.75	23.51	23.66	23.36	23.05	23.51	22.75	25.53	26.41	26.41	23.57	21.53	21.53	22.29	23.57	24.23	22.75	22.29	22.44	23.57	24.23	24.23	24.23	19.85	19.85	21.07	22.03	25.55	21.53	20.46	17.98	18.94		18.78	19.81	22.29	18.93	21.49	20.00	20.46	21.30
MN058684_Beierolpium sp. WAM T136468	25.04	25.55	23.36	24.66	25.04	23.66	25.65	25.11	25.11	26.21	24.67	24.23	25.77	25.55	25.55	25.99	25.33	25.11	25.80	25.80	26.11	25.80	25.80	25.50	25.99	28.41	23.66	24.12	25.50	25.04	24.89	24.58	24.58	23.97	24.73	23.66	27.08	27.48	27.63	24.06	23.66	23.66	23.97	25.55	25.33	22.90	22.60	22.90	23.35	24.01	24.01	24.01	22.44	22.44	23.36	24.01	26.21	23.05	25.04	22.10	22.03	18.78		19.97	22.44	19.39	21.85	20.92	23.82	23.28
KX263396_Antillolpium sp. 783047	24.77	26.76	24.77	23.92	23.22	22.60	24.30	25.44	23.90	26.10	24.34	24.34	25.44	25.88	25.66	24.78	24.56	25.22	23.84	23.99	23.84	23.99	23.68	23.84	25.00	26.54	22.91	23.07	24.61	25.23	23.38	24.61	24.77	24.61	23.99	25.54	27.20	28.33	26.47	25.13	23.99	23.99	24.46	25.66	25.44	23.99	23.68	23.99	24.56	25.00	25.00	25.22	23.84	23.84	23.99	24.78	25.44	22.76	23.38	20.24	21.26	19.81	19.97		21.83	21.67	22.03	21.67	22.76	21.32
EU559546_Euryolpium sp. JM-2008	23.82	24.67	21.37	21.76	22.75	21.68	22.75	23.79	24.23	22.69	21.37	22.25	22.47	21.59	21.81	22.69	22.69	22.03	22.75	22.44	22.14	22.75	22.75	22.60	22.25	23.57	22.29	22.75	22.60	23.36	21.22	23.21	22.90	21.07	21.37	22.14	26.37	25.19	24.28	24.71	24.28	24.28	24.28	25.99	25.77	23.82	23.66	23.82	24.89	25.33	25.33	26.21	22.29	22.29	23.21	25.11	27.09	22.44	23.51	23.02	24.01	22.29	22.44	21.83		13.89	15.99	16.10	22.44	25.42
MN058685_Euryolpium sp. WAM T136709	20.46	21.37	18.93	19.47	20.61	20.31	23.66	25.55	24.45	26.43	24.01	23.79	25.11	25.33	25.33	24.01	25.33	24.67	22.29	22.60	22.75	22.90	22.90	22.14	23.13	26.21	19.85	20.46	20.76	22.14	20.15	21.37	21.07	20.76	21.37	21.07	24.47	23.21	23.51	20.30	22.29	22.29	22.75	24.67	24.01	22.29	21.99	22.29	23.57	24.01	24.01	24.45	21.07	21.07	20.76	23.57	25.55	20.92	21.68	20.42	22.91	18.93	19.39	21.67	13.89		12.26	15.42	18.93	22.67
MN436737_Euryolpium sp. BMR00041	22.03	22.17	21.67	21.23	20.07	20.25	21.85	23.20	21.39	25.00	22.42	22.42	23.97	23.71	23.71	22.94	22.68	21.91	22.03	22.38	22.38	23.09	22.91	22.03	21.13	23.71	22.38	22.20	22.56	22.56	21.14	21.67	22.56	21.49	21.31	21.67	25.30	28.06	23.80	24.28	22.74	22.74	24.16	24.49	24.74	23.98	23.62	23.98	23.97	25.00	25.00	25.00	22.56	22.56	23.98	24.49	26.03	21.49	22.56	21.67	24.23	21.49	21.85	22.03	15.99	12.26		16.70	20.07	24.60
MN058681_Austrohorus sp. WAM T135388	23.51	24.89	21.07	22.21	22.14	21.07	24.43	27.09	24.67	25.55	25.33	25.11	25.77	25.55	26.21	25.33	25.33	24.67	23.51	23.51	23.36	23.36	23.05	23.21	25.33	24.67	21.53	21.37	22.90	23.82	23.05	22.75	23.05	22.44	23.21	22.29	28.62	26.41	23.66	24.55	24.73	24.73	25.04	27.31	27.75	24.73	24.58	24.89	27.31	27.75	27.75	28.41	21.22	21.22	24.73	26.87	28.41	23.51	22.44	21.64	24.45	20.00	20.92	21.67	16.10	15.42	16.70		21.68	24.20
KX054242_Olipiidae sp. sc_02343	24.58	25.55	23.21	23.59	22.14	21.83	25.65	26.65	24.45	26.65	25.99	24.89	26.43	26.87	27.31	25.55	25.33	25.99	25.19	25.34	25.50	25.19	25.19	24.73	25.11	26.21	23.66	23.05	24.43	21.99	21.99	21.83	22.44	22.29	22.75	20.76	28.03	26.41	23.51	24.88	20.46	20.46	20.76	22.03	22.69	21.53	21.07	21.37	22.03	23.35	23.35	23.13	21.83	21.83	23.05	22.91	24.45	21.37	20.31	19.81	22.03	20.46	23.82	22.76	22.44	18.93	20.07	21.68		25.12
KX263395_Antillolpium sp. 772A	26.49	27.48	26.03	26.72	25.27	25.88	28.63	29.02	28.80	28.14	27.48	27.04	27.70	27.26	27.48	26.82	28.36	27.92	26.49	26.49	26.64	26.64	26.64	26.34	28.58	30.12	26.34	26.49	28.17	27.56	26.79	27.71	27.56	27.25	26.79	25.73	31.53	30.46	29.39	28.07	24.96	24.96	24.66	26.38	26.16	24.66	24.66	24.96	26.16	26.60	26.60	25.94	23.28	23.28	23.89	25.94	25.72	23.89	23.89	24.31	22.19	21.30	23.28	21.32	25.42	22.67	24.60	24.20	25.12	

3.3 Scorpiones

The four scorpion specimens were all identified as belonging to the buthid genus *Lychas*. The specimens formed a single OTU, *Lychas* `sp. Biologic-SCOR001`, which included five specimens found outside of the Study Area (Fig. 3.3.1). Within this OTU, genetic distances were as high as 4.87%, and the closest specimen from another OTU was 12.5% (Table 3.3.1). This OTU has a linear distance of over 60km (Table 3.1).

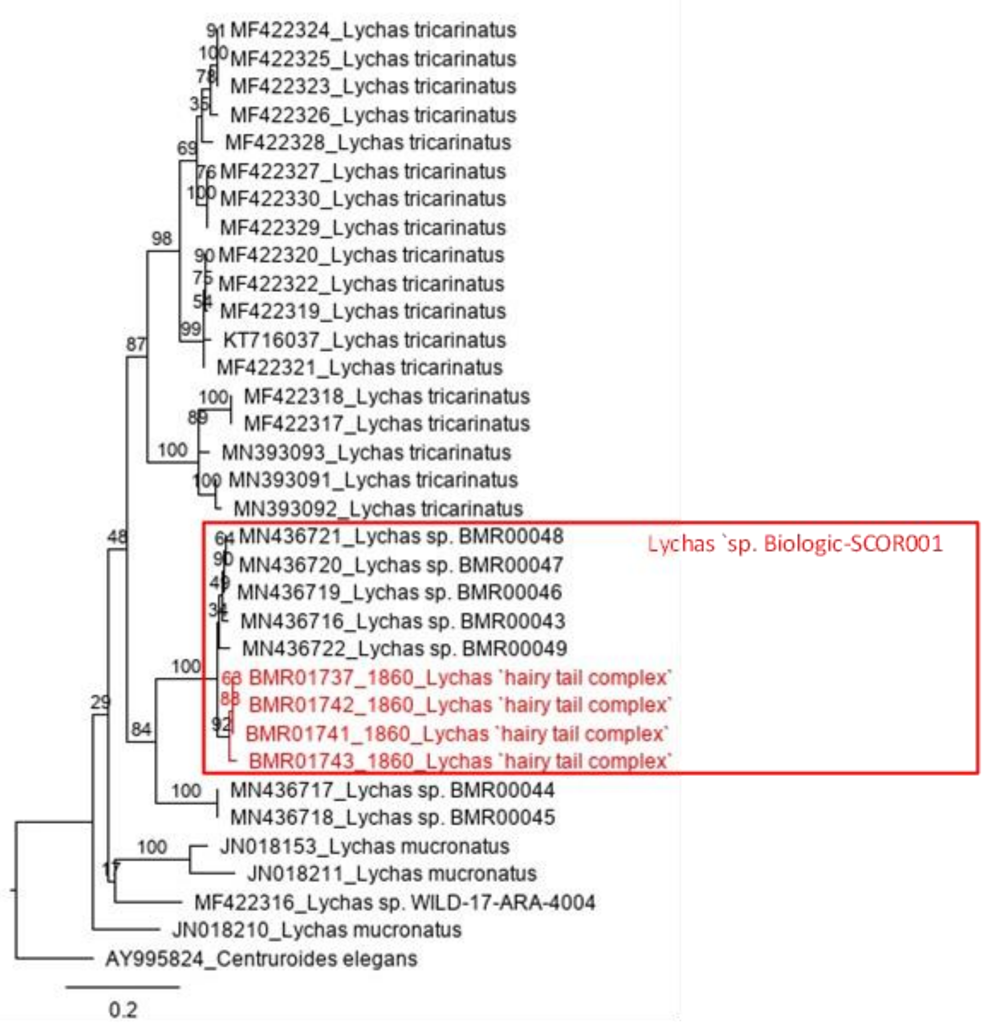

Figure 3.3.1: Maximum Likelihood phylogeny showing relationships among specimens. Numbers are bootstrap values.

Table 3.3.1: Genetic distances among specimens. Colours correspond to OTUs in Fig 3.3.1, and grey boxes indicate intraspecific genetic distances.

COI pairwise distance (%)	AY995824	BMR01737	BMR01741	BMR01742	BMR01743	MN436716	MN436719	MN436720	MN436721	MN436722	MN436717	MN436718	KT716037	MF422319	MF422320	MF422322	MF422321	MF422323	MF422324	MF422325	MF422326	MF422327	MF422330	MF422329	MF422328	MF422317	MF422318	MN393091	MN393092	MN393093	MF422316	JN018210	JN018153	JN018211
AY995824_Centruroides elegans		18.09	18.39	19.36	18.47	19.00	20.30	19.45	19.87	20.94	21.14	21.00	16.82	17.04	16.74	16.74	16.74	16.29	16.51	16.51	16.44	16.59	16.59	16.74	17.04	20.97	20.97	21.40	22.40	20.40	16.98	19.20	17.90	18.78
BMR01737_1860_Lychas `hairy tail complex`	18.09		0.76	1.05	2.36	4.26	4.13	3.95	3.88	4.71	13.66	13.71	12.91	13.62	13.62	13.62	13.62	15.02	15.09	15.09	15.02	15.02	15.02	15.17	14.40	17.34	17.34	15.00	16.00	15.00	16.82	14.60	14.59	15.26
BMR01741_1860_Lychas `hairy tail complex`	18.39	0.76		0.46	1.60	3.80	3.63	3.50	3.39	4.22	13.66	13.71	12.98	13.47	13.47	13.47	13.47	14.55	14.62	14.62	14.55	14.55	14.55	14.71	14.24	17.03	17.03	14.40	15.40	14.40	16.35	14.00	14.83	15.37
BMR01742_1860_Lychas `hairy tail complex`	19.36	1.05	0.46		2.05	4.26	3.80	3.65	3.55	4.71	13.66	13.71	13.08	13.62	13.62	13.62	13.62	14.71	14.62	14.62	14.71	14.71	14.71	14.86	14.40	17.49	17.49	14.40	15.40	14.40	16.67	14.40	15.63	16.36
BMR01743_1860_Lychas `hairy tail complex`	18.47	2.36	1.60	2.05		3.57	4.29	4.18	4.04	4.87	13.50	13.55	13.38	13.85	13.85	13.85	13.85	14.32	14.39	14.39	14.32	14.78	14.78	14.94	14.47	17.26	17.26	15.00	16.00	15.00	16.59	14.20	15.52	15.29
MN436716_Lychas sp. BMR00043	19.00	4.26	3.80	4.26	3.57		1.32	1.52	1.45	2.92	13.01	13.07	14.42	14.86	14.86	14.86	14.86	14.71	14.78	14.78	14.86	15.79	15.79	15.94	15.17	17.65	17.65	14.40	15.40	15.20	16.04	14.20	15.14	15.21
MN436719_Lychas sp. BMR00046	20.30	4.13	3.63	3.80	4.29	1.32		0.17	0.17	2.64	12.54	12.50	14.51	15.02	15.02	15.02	15.02	15.02	15.10	15.10	15.35	16.17	16.17	16.34	15.02	17.99	17.99	14.40	15.40	15.20	16.78	14.60	14.95	16.08
MN436720_Lychas sp. BMR00047	19.45	3.95	3.50	3.65	4.18	1.52	0.17		0.00	2.76	12.68	12.74	14.26	14.71	14.71	14.71	14.71	14.55	14.62	14.62	14.86	15.48	15.48	15.64	14.55	17.96	17.96	14.60	15.60	15.40	15.88	14.40	14.68	15.37
MN436721_Lychas sp. BMR00048	19.87	3.88	3.39	3.55	4.04	1.45	0.17	0.00		2.76	12.68	12.74	14.19	14.70	14.70	14.70	14.70	14.54	14.61	14.61	14.86	15.67	15.67	15.83	14.54	18.26	18.26	14.60	15.60	15.40	16.26	14.40	14.63	15.54
MN436722_Lychas sp. BMR00049	20.94	4.71	4.22	4.71	4.87	2.92	2.64	2.76	2.76		13.33	13.43	14.95	15.26	15.26	15.26	15.26	15.58	15.51	15.51	16.07	15.91	15.91	15.75	15.26	18.02	18.02	14.80	15.80	15.20	17.00	15.40	15.69	15.45
MN436717_Lychas sp. BMR00044	21.14	13.66	13.66	13.66	13.50	13.01	12.54	12.68	12.68	13.33		0.28	14.80	15.45	15.29	15.29	14.96	15.29	15.37	15.37	15.29	15.45	15.45	15.61	15.45	16.75	16.75	14.40	15.40	15.40	15.54	17.20	15.88	15.30
MN436718_Lychas sp. BMR00045	21.00	13.71	13.71	13.71	13.55	13.07	12.50	12.74	12.74	13.43	0.28		15.03	15.66	15.49	15.49	15.17	15.33	15.42	15.42	15.33	15.82	15.82	15.98	15.49	16.95	16.95	14.60	15.60	15.60	15.91	17.40	15.76	15.36
KT716037_Lychas tricarinatus	16.82	12.91	12.98	13.08	13.38	14.42	14.51	14.26	14.19	14.95	14.80	15.03		1.63	1.47	1.47	1.31	8.66	8.66	8.66	8.17	7.52	7.52	7.68	8.01	15.69	15.69	13.40	14.40	13.20	14.38	15.60	16.36	15.72
MF422319_Lychas tricarinatus	17.04	13.62	13.47	13.62	13.85	14.86	15.02	14.71	14.70	15.26	15.45	15.66	1.63		0.45	0.45	0.60	8.15	8.33	8.33	7.54	6.94	6.94	7.09	7.54	15.84	15.84	13.20	14.20	13.40	14.15	16.20	16.20	14.85
MF422320_Lychas tricarinatus	16.74	13.62	13.47	13.62	13.85	14.86	15.02	14.71	14.70	15.26	15.29	15.49	1.47	0.45		0.00	0.45	7.99	8.18	8.18	7.09	6.79	6.79	6.94	7.69	15.54	15.54	13.20	14.20	13.40	14.31	16.40	16.20	14.85
MF422322_Lychas tricarinatus	16.74	13.62	13.47	13.62	13.85	14.86	15.02	14.71	14.70	15.26	15.29	15.49	1.47	0.45	0.00		0.45	7.99	8.18	8.18	7.09	6.79	6.79	6.94	7.69	15.54	15.54	13.20	14.20	13.40	14.31	16.40	16.20	14.85
MF422321_Lychas tricarinatus	16.74	13.62	13.47	13.62	13.85	14.86	15.02	14.71	14.70	15.26	14.96	15.17	1.31	0.60	0.45	0.45		7.84	8.02	8.02	7.24	6.33	6.33	6.49	7.54	15.23	15.23	13.00	14.00	13.20	14.15	16.00	15.73	15.02
MF422323_Lychas tricarinatus	16.29	15.02	14.55	14.71	14.32	14.71	15.02	14.55	14.54	15.58	15.29	15.33	8.66	8.15	7.99	7.99	7.84		0.00	0.00	2.11	4.37	4.37	4.53	3.47	14.78	14.78	13.80	14.80	13.60	14.15	16.40	15.42	16.67
MF422324_Lychas tricarinatus	16.51	15.09	14.62	14.62	14.39	14.78	15.10	14.62	14.61	15.51	15.37	15.42	8.66	8.33	8.18	8.18	8.02	0.00		0.00	2.04	4.56	4.56	4.72	3.62	15.09	15.09	13.80	14.80	13.60	14.15	16.40	15.41	16.67
MF422325_Lychas tricarinatus	16.51	15.09	14.62	14.62	14.39	14.78	15.10	14.62	14.61	15.51	15.37	15.42	8.66	8.33	8.18	8.18	8.02	0.00	0.00		2.04	4.56	4.56	4.72	3.62	15.09	15.09	13.80	14.80	13.60	14.15	16.40	15.41	16.67
MF422326_Lychas tricarinatus	16.44	15.02	14.55	14.71	14.32	14.86	15.35	14.86	14.86	16.07	15.29	15.33	8.17	7.54	7.09	7.09	7.24	2.11	2.04	2.04		4.37	4.37	4.53	3.92	14.33	14.33	13.60	14.60	13.80	14.62	15.80	15.58	16.17
MF422327_Lychas tricarinatus	16.59	15.02	14.55	14.71	14.78	15.79	16.17	15.48	15.67	15.91	15.45	15.82	7.52	6.94	6.79	6.79	6.33	4.37	4.56	4.56	4.37		0.00	0.15	3.47	15.08	15.08	13.80	14.80	13.80	13.99	15.40	15.73	16.67
MF422330_Lychas tricarinatus	16.59	15.02	14.55	14.71	14.78	15.79	16.17	15.48	15.67	15.91	15.45	15.82	7.52	6.94	6.79	6.79	6.33	4.37	4.56	4.56	4.37	0.00		0.15	3.47	15.08	15.08	13.80	14.80	13.80	13.99	15.40	15.73	16.67
MF422329_Lychas tricarinatus	16.74	15.17	14.71	14.86	14.94	15.94	16.34	15.64	15.83	15.75	15.61	15.98	7.68	7.09	6.94	6.94	6.49	4.53	4.72	4.72	4.53	0.15	0.15		3.62	15.23	15.23	14.00	15.00	14.00	14.15	15.60	15.58	16.83
MF422328_Lychas tricarinatus	17.04	14.40	14.24	14.40	14.47	15.17	15.02	14.55	14.54	15.26	15.45	15.49	8.01	7.54	7.69	7.69	7.54	3.47	3.62	3.62	3.92	3.47	3.47	3.62		15.08	15.08	13.60	14.60	13.80	13.99	15.60	15.58	17.16
MF422317_Lychas tricarinatus	20.97	17.34	17.03	17.49	17.26	17.65	17.99	17.96	18.26	18.02	16.75	16.95	15.69	15.84	15.54	15.54	15.23	14.78	15.09	15.09	14.33	15.08	15.08	15.23	15.08		0.00	8.00	9.00	6.60	17.14	17.00	17.60	17.99
MF422318_Lychas tricarinatus	20.97	17.34	17.03	17.49	17.26	17.65	17.99	17.96	18.26	18.02	16.75	16.95	15.69	15.84	15.54	15.54	15.23	14.78	15.09	15.09	14.33	15.08	15.08	15.23	15.08	0.00		8.00	9.00	6.60	17.14	17.00	17.60	17.99
MN393091_Lychas tricarinatus	21.40	15.00	14.40	14.40	15.00	14.40	14.40	14.60	14.60	14.80	14.40	14.60	13.40	13.20	13.20	13.20	13.00	13.80	13.80	13.80	13.60	13.80	13.80	14.00	13.60	8.00	8.00		1.00	4.60	15.20	14.80	15.60	18.00
MN393092_Lychas tricarinatus	22.40	16.00	15.40	15.40	16.00	15.40	15.40	15.60	15.60	15.80	15.40	15.60	14.40	14.20	14.20	14.20	14.00	14.80	14.80	14.80	14.60	14.80	14.80	15.00	14.60	9.00	9.00	1.00		5.60	16.20	15.80	16.60	19.00
MN393093_Lychas tricarinatus	20.40	15.00	14.40	14.40	15.00	15.20	15.20	15.40	15.40	15.20	15.40	15.60	13.20	13.40	13.40	13.40	13.20	13.60	13.60	13.60	13.80	13.80	13.80	14.00	13.80	6.60	6.60	4.60	5.60		16.80	16.20	17.40	18.80
MF422316_Lychas sp. WILD-17-ARA-4004	16.98	16.82	16.35	16.67	16.59	16.04	16.78	15.88	16.26	17.00	15.54	15.91	14.38	14.15	14.31	14.31	14.15	14.15	14.15	14.15	14.62	13.99	13.99	14.15	13.99	17.14	17.14	15.20	16.20	16.80		14.20	14.94	16.01
JN018210_Lychas mucronatus	19.20	14.60	14.00	14.40	14.20	14.20	14.60	14.40	14.40	15.40	17.20	17.40	15.60	16.20	16.40	16.40	16.00	16.40	16.40	16.40	15.80	15.40	15.40	15.60	15.60	17.00	17.00	14.80	15.80	16.20	14.20		15.40	17.00
JN018153_Lychas mucronatus	17.90	14.59	14.83	15.63	15.52	15.14	14.95	14.68	14.63	15.69	15.88	15.76	16.36	16.20	16.20	16.20	15.73	15.42	15.41	15.41	15.58	15.73	15.73	15.58	15.58	17.60	17.60	15.60	16.60	17.40	14.94	15.40		8.36
JN018211_Lychas mucronatus	18.78	15.26	15.37	16.36	15.29	15.21	16.08	15.37	15.54	15.45	15.30	15.36	15.72	14.85	14.85	14.85	15.02	16.67	16.67	16.67	16.17	16.67	16.67	16.83	17.16	17.99	17.99	18.00	19.00	18.80	16.01	17.00	8.36	

4 SUMMARY

Using well-established DNA extraction and sequencing methods, this molecular systematics analysis designated eight distinct species/ OTUs to 27 high quality sequences from the Study Area. All OTUs, the areas in which they were found, and the specimen numbers per OTU are shown in Appendix A. The following are the key findings at the species/ OTU level:

- Spirobolida (COI): one OTU, matching external sequences beyond the survey areas.
- Pseudoscorpiones (COI): five OTUs, four unique lineages in the 40 km area around the two survey areas, one matching external sequences beyond the survey areas.
- Scorpiones (COI): one OTU, a unique lineage in the 40 km area around the two survey areas.

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Appendix A: All Operational Taxonomic Units (OTUs) found in the Study Area. Reactions states Fail;PCR indicates no DNA product was produced from the extraction and FAIL: low quality sequence indicates DNA product produced was not of the quality threshold set.

BMR	Unique ID code	Site	Latitude	Longitude	Family	Lowest ID Legacy	OTU Name	Reaction State
Spirobolida								
BMR01726	9533	SMNN-100	-22.80923	119.13916	Trigoniulidae	*Austrostrophus* sp. indet.	*Austrostrophus* `sp. clade A NGW-2020`	PASS
BMR01727	9721	SMNN-11	-22.82741	119.14794	Trigoniulidae	*Austrostrophus* sp. indet.	*Austrostrophus* `sp. clade A NGW-2020`	PASS
BMR01728	9687	SMNN-34	-22.82464	119.16626	Trigoniulidae	*Austrostrophus* sp. indet.	*Austrostrophus* `sp. clade A NGW-2020`	PASS
Pseudoscorpiones								
BMR01732	5890	SMNN-33	-22.82589	119.16533	Olpiidae	*Indolpium* `sp. MNY02`	-	FAIL; low quality sequence
BMR01745	9769	SMNN-06	-22.82874	119.14272	Olpiidae	Olpiidae sp. indet.	-	FAIL; PCR
BMR01749	9777	SMNN-87	-22.80994	119.14695	Garypidae	*Synsphronus* `PSE014 (8/2 long Pilbara)`	*Synsphronus* `PSE014 `	PASS
BMR01750	9725	SMNN-98	-22.81131	119.13582	Garypidae	*Synsphronus* `PSE014 (8/2 long Pilbara)`	*Synsphronus* `PSE014 `	PASS
BMR01751	9730	SMNN-99	-22.81051	119.13775	Garypidae	*Synsphronus* `PSE014 (8/2 long Pilbara)`	*Synsphronus* `PSE014 `	PASS
BMR01729	6379	SMNN-40	-22.82382	119.16951	Olpiidae	*Indolpium* `sp. MNY01`	*Indolpium* `sp. PSE118`	PASS
BMR01730	6667	SMNN-43	-22.82561	119.16778	Olpiidae	*Indolpium* `sp. MNY01`	*Indolpium* `sp. PSE118`	PASS
BMR01747	9780	SMNN-23	-22.82482	119.15851	Olpiidae	Olpiidae sp. indet.	*Austrohorus* `sp. PSE121`	PASS
BMR01733	9732	SMNN-40	-22.82382	119.16951	Olpiidae	*Indolpium* `sp. MNY02`	*Austrohorus* `sp. PSE121`	PASS
BMR01734	9734	SMNN-46	-22.81491	119.13616	Olpiidae	*Indolpium* `sp. MNY02`	*Austrohorus* `sp. PSE121`	PASS
BMR01735	9738	SMNN-48	-22.81283	119.14023	Olpiidae	*Indolpium* `sp. MNY02`	*Austrohorus* `sp. PSE121`	PASS
BMR01736	9744	SMNN-80	-22.81367	119.14748	Olpiidae	*Indolpium* `sp. MNY02`	*Austrohorus* `sp. PSE121`	PASS
BMR01744	9735	SMNN-01	-22.82963	119.13847	Olpiidae	Olpiidae sp. indet.	*Austrohorus* `sp. PSE121`	PASS
BMR01731	9743	SMNN-11	-22.82741	119.14794	Olpiidae	*Indolpium* `sp. MNY02`	*Austrohorus* `sp. PSE122`	PASS
BMR01746	9741	SMNN-100	-22.80923	119.13916	Olpiidae	Olpiidae sp. indet.	*Indolpium* `sp. PSE123`	PASS
BMR01752	9773	SMNN-01	-22.82963	119.13847	Olpiidae	*Xenolpium* `sp. MNY01`	*Indolpium* `sp. PSE123`	PASS
BMR01753	9742	SMNN-100	-22.80923	119.13916	Olpiidae	*Xenolpium* `sp. MNY01`	*Indolpium* `sp. PSE123`	PASS
BMR01754	9771	SMNN-33	-22.82589	119.16533	Olpiidae	*Xenolpium* `sp. MNY01`	*Indolpium* `sp. PSE123`	PASS
BMR01756	9768	SMNN-25	-22.82506	119.16050	Olpiidae	*Xenolpium* `sp. MNY02`	*Indolpium* `sp. PSE123`	PASS
BMR01757	7940	SMNN-25	-22.82506	119.16050	Olpiidae	*Xenolpium* `sp. MNY02`	*Indolpium* `sp. PSE123`	PASS
BMR01755	9774	SMNN-87	-22.80994	119.14695	Olpiidae	*Xenolpium* `sp. MNY01`	*Xenolpium* `sp. Biologic-PSEU028`	PASS
BMR01748	9530	SMNN-81	-22.81223	119.14815	Olpiidae	Olpiidae sp. indet.	*Xenolpium* `sp. Biologic-PSEU028`	PASS
Scorpiones								
BMR01737	9503	SMNN-15	-22.82672	119.14984	Buthidae	*Lychas* `hairy tail complex`	*Lychas* `sp. Biologic-SCOR001`	PASS
BMR01741	9665	SMNN-17	-22.82600	119.15296	Buthidae	*Lychas* `hairy tail complex`	*Lychas* `sp. Biologic-SCOR001`	PASS
BMR01742	6594	YAN_1	-22.83081	119.13854	Buthidae	*Lychas* `hairy tail complex`	*Lychas* `sp. Biologic-SCOR001`	PASS
BMR01743	7631	YAN_2	-22.83066	119.14044	Buthidae	*Lychas* `hairy tail complex`	*Lychas* `sp. Biologic-SCOR001`	PASS