

Biologic Environmental Survey Pty Ltd
PO Box 179 Floreat
Western Australia

6 April 2017
Carly Nixon
Rio Tinto Iron Ore – Central Park
152-158 St Georges Tce
PERTH WA 6000

RE: Results of DNA analysis of subterranean fauna collected at West Angelas Deposits C, D, and G

Dear Carly,

Rio Tinto Iron Ore requested genetic identification of certain troglofauna and stygofauna taxa sampled throughout West Angelas Deposits C, D and G, and comparisons with pre-existing regional sequences to determine whether the species found at West Angelas matched others from elsewhere in the region.

- Based on the results of the West Angelas Deposits C, D and G subterranean fauna survey (Biologic 2016), as requested and approved by RTIO, 26 specimens from 10 taxonomic groups were chosen for sequencing, comprising Bathynellacea (4), Amphipoda (5), Haplotaxida (Enchytraeidae) (6), Oligochaeta (3), Isopoda (2), Hemiptera (Meenoplidae) (2), Thysanura (1), and Symphyla (3) (Table 1).
- Specimens and species were chosen based on the following criteria: A) taxa that have a broad regional context available in the form of multiple previous regional sequences throughout the Pilbara region, B) taxa that were only found within potential impact areas (pits and/ or potential drawdown areas), or taxa that were found both inside and outside of potential impact areas at West Angelas, and C) taxa that had some degree of taxonomic uncertainty regarding their morphological identifications at the species level.
- Analyses/ comparisons were limited to those that would most quickly and adequately address the following hypotheses: 1) does the material from West Angelas represent a single species or multiple different species; and 2) does the material from West Angelas match any previously recorded species from the Pilbara region (based on available sequences). Deeper phylogenetic relationships between material recorded at West Angelas and previous regional material were not investigated and cannot be inferred from the types of neighbour-joining cluster analysis used.

Table 1. Details of specimens sent for DNA analysis (1 specimen per record)

Specimen code	HIGHER TAXON Family	Preliminary ID	Bore/hole name	UTM E z50 GDA94	UTM N z50 GDA94
	BATHYNELLACEA				
BES:1900	Parabathynellidae	Atopobathynella sp. 'WA'	RC15WAC0416	668584.57	7439798.37
BES:2297	Parabathynellidae	Atopobathynella sp. 'WA'	RC15WAC0413	669436.13	7439804.66
BES:1996	Bathynellidae	Bathynellidae sp. 'WA'	RC15WAC0413	669436.13	7439804.66
BES:2054	Bathynellidae	Bathynellidae sp. 'WA'	RC15WAC0384	667401.98	7440199.63
	AMPHIPODA				
BES:1812	Paramelitidae	Kruptus sp. 'WA'	RC13WAD0287	667339.68	7436249.24
BES:1910	Paramelitidae	Kruptus sp. 'WA'	RC15WAC0387	666231.13	7439987.54
BES:1966	Paramelitidae	Kruptus sp. 'WA'	RC14WAD0346	664939.59	7436650.84
BES:1971	Paramelitidae	Kruptus sp. 'WA'	RC15WAC0276	672654.61	7438949.45
BES:2352	Paramelitidae	Maarrka sp. 'WA'	RC12WAD0295	664742.89	7437505.38
	HAPLOTAXIDA				
BES:1844	Enchytraeidae	Enchytraeidae sp. indet.	RC12WAD0189	671538.78	7436245.02
BES:1936	Enchytraeidae	Enchytraeidae sp. indet.	RC15WAC0387	666231.13	7439987.54
BES:2035	Enchytraeidae	Enchytraeidae sp. indet.	RD14WAF0003	689191.74	7433400.35
BES:2039	Enchytraeidae	Enchytraeidae sp. indet.	RC14WAF0066	689286	7433433.84
BES:2114	Enchytraeidae	Enchytraeidae sp. indet.	RC14WAD0350	665336.97	7437144.78
BES:2355	Enchytraeidae	Enchytraeidae sp. indet.	RC15WAC0380	671570.22	7439796.36
	OLIGOCHAETA				
BES:1849		Oligochaeta sp. indet.	RC14WAD0346	664939.59	7436650.84
BES:2030		Oligochaeta sp. indet.	RC15WAC0384	667401.98	7440199.63
BES:2031		Oligochaeta sp. indet.	RC15WAC0413	669436.13	7439804.66
	ISOPODA				
BES:1876	Armadillidae	Armadillidae sp. indet.	RC12WAD0295	664742.89	7437505.38
BES:2199		Isopoda sp. indet.	RC12WAD0295	664742.89	7437505.38
	HEMIPTERA				
BES:2139	Meenoplidae	Meenoplidae sp. indet.	RC15WAC0377	667347.98	7439303.55
BES:2356	Meenoplidae	Meenoplidae sp. indet.	RC14WAD0217	665792.22	7436703.79
	THYSANURA				
BES:1823	Nicoletiidae	Atelurinae sp. indet.	RC14WAD0350	665336.97	7437144.78
	SYMPHYLA				
BES:2112	Scutigerellidae	Scutigerellidae sp. indet.	RC14WAF0072	692251.8	7434505.65
BES:2117	Scutigerellidae	Scutigerellidae sp. indet.	RC15WAC0276	672654.61	7438949.45
BES:2055		Symphyla sp. indet.	RC15WAC0197	668634.6	7439014.15

METHODS

The DNA sequencing and comparisons were conducted by Helix Molecular Solutions. A full account of the methods and detailed results can be found in Appendix I. The following details are provided in summary (from Helix 2016):

 Sequencing of the mitochondrial gene cytochrome oxidase subunit 1 (COI) and the nuclear gene 12s was conducted using multiple primers.



- Sequences were edited using GENEIOUS software, while alignments were conducted using CLUSTAL W software.
- Genetic distances were calculated using uncorrected p-distances (total percentage of nucleotide differences between sequences) and trees were constructed using neighbour-joining in MEGA 6.0 software.
- Based on published data, lineages were defined as haplotypes (or groups of haplotypes) differing by >3% sequence divergence (COI), while the thresholds for species-level divergence were defined on a taxon-by taxon basis, acknowledging that a vast majority of species- pairs differ from each other by >8% (COI), following Hebert et al. (2003). For this reason, divergences <3% (COI) were regarded as the same lineage within a species, and >8% (COI) were regarded as likely to be different species, however divergences between 3% 8% were generally regarded as an intermediate zone between interspecific and intraspecific variability.

RESULTS

Table 2 shows the results of the genetic analyses within each of the groups of taxa. Overall, the analyses found that:

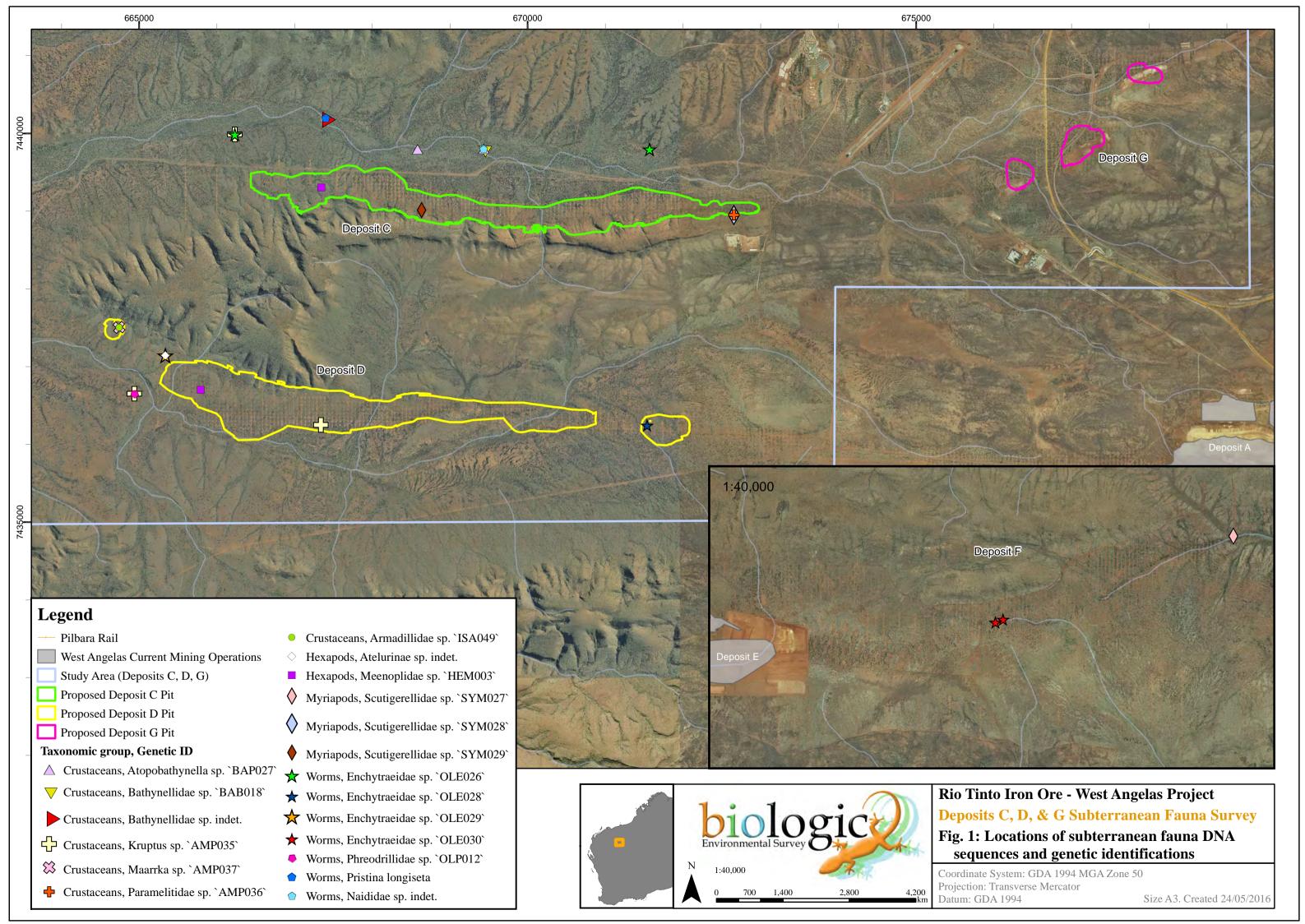
- Several sequences in the Oligochaeta (*Pristina longiseta* and Phreodrillidae `OLP012`), Haplotaxida (Enchytraeidae `OLE026`), and Hemiptera (Meenoplidae `HEM003`) aligned to previously recorded species or lineages that are known to occur widely in the Pilbara;
- 2. Sequences of the Bathynellidae, Parabathynellidae, Amphipoda, Isopoda, and Symphyla were all unique regionally, with high levels of genetic divergence between any of the available regional material from these taxonomic groups and the samples from West Angelas;
- Three specimens, respectively from the Bathynellidae, Oligochaeta, and Thysanura did not sequence successfully, therefore the identifications of these specimens have not changed; and
- 4. Additional putative species were revealed within the Amphipoda (*Kruptus* `AMP045`, Paramelitidae `AMP036`, and *Maarka* `AMP037`), Haplotaxida (Enchytraeidae `OLE026`, `OLE028`, `OLE029`, and `OLE030`), Oligochaeta (*Pristina longiseta* and Phreodrillidae `OLP012`), and Symphyla (Scutigerellidae `SYM027`, `SYM028`, and `SYM029`). The implications for the remaining specimens within these groups that have not been sequenced are discussed in further detail below.

Figure 1 shows the locations of subterranean fauna sequences from Deposits C, D, and G, and the resulting genetic identifications of the taxa.

Table 2: Summary of local and regional genetic alignment results.

Specimen code	HIGHER TAXON Family	Preliminary ID	Bore/hole name	Local match	% div. COI	Regional match	% div. COI	Nominal species- level ID	Comment
BATHYNELL	ACEA								
BES:1900	Parabathynellidae	Atopobathynella sp. 'WA'	RC15WAC0416	BES:2297	0.3%	No	>10%	Atopobathynella	Regionally distinct species of Parabathynellidae. Likely <i>Atopobathynella</i> following G. Perina
BES:2297	Parabathynellidae	Atopobathynella sp. 'WA'	RC15WAC0413	BES:1900	0.376	NO	>1076	`BAP027`	morphological ID, August 2016.
BES:1996	Bathynellidae	Bathynellidae sp. 'WA'	RC15WAC0413	No		No	>19%	Bathynellidae `BAB018`	Regionally distinct species of Bathynellidae
BES:2054	Bathynellidae	Bathynellidae sp. 'WA'	RC15WAC0384						Sequence failed
AMPHIPODA									
BES:1812	Paramelitidae	Kruptus sp. 'WA'	RC13WAD0287	BES: 1910, 1966					Regionally distinct species of Paramelitidae.
BES:1910	Paramelitidae	Kruptus sp. 'WA'	RC15WAC0387	BES: 1812, 1966	0.3 - 0.9%	No	>15%	Kruptus `AMP035`	Likely Kruptus following G. Perina morphological
BES:1966	Paramelitidae	Kruptus sp. 'WA'	RC14WAD0346	BES: 1812, 1910	0.976				ID, August 2016.
BES:1971	Paramelitidae	Kruptus sp. 'WA'	RC15WAC0276	No	>17%	No	>15%	Paramelitidae `AMP036`	Regionally distinct species of Paramelitidae. Juvenile specimens only, uncertain morphological ID. Unable to be placed to genus on current information.
BES:2352	Paramelitidae	Maarrka sp. 'WA'	RC12WAD0295	No	>17%	No	>15%	Maarka`AMP037`	Regionally distinct species of Paramelitidae. Likely <i>Maarka</i> following G. Perina morphological ID, August 2016.
HAPLOTAXII	DA								
BES:1936	Enchytraeidae	Enchytraeidae sp. indet.	RC15WAC0387	BES:2355	1.2%	OLE26	2.8% -	Enchytraeidae	Genetic alignment to a species (OLE26) previously sampled elsewhere in the Pilbara
BES:2355	Enchytraeidae	Enchytraeidae sp. indet.	RC15WAC0380	BES:1936	1.2 /0	OLLZO	3.4%	`OLE026`	(Helix 2016).
BES:1844	Enchytraeidae	Enchytraeidae sp. indet.	RC12WAD0189	No	>16%	No	>12%	Enchytraeidae `OLE028`	Regionally distinct species of Enchytraeidae.
BES:2114	Enchytraeidae	Enchytraeidae sp. indet.	RC14WAD0350	No	>7.5%	Possibly	5.7%	Enchytraeidae `OLE029`	Potentially distinct, but moderate divergences indicate more information required to separate distinct species. Occurs in a large species complex found across a wide area and multiple catchment boundaries (Helix 2016).
BES:2035	Enchytraeidae	Enchytraeidae sp. indet.	RD14WAF0003	BES:2039	1.6%	Possibly	7.8%	Enchytraeidae	Potentially distinct, but moderate divergences indicate more information required to separate distinct species. Occurs in a large species
BES:2039	Enchytraeidae	Enchytraeidae sp. indet.	RC14WAF0066	BES:2035	1.070	1 Ossibiy	7.070	`OLE030`	complex found across a wide area and multiple catchment boundaries (Helix 2016).

Specimen code	HIGHER TAXON Family	Preliminary ID	Bore/hole name	Local match	% div. COI	Regional match	% div. COI	Nominal species- level ID	Comment
OLIGOCHAE	TA								
BES:1849		Oligochaeta sp. indet.	RC14WAD0346	No		OLP12	<2.8%	Phreodrillidae `OLP12`	Genetic alignment to a species (OLP12) previously sampled widely across four catchments in the Pilbara (Helix 2016).
BES:2030		Oligochaeta sp. indet.	RC15WAC0384	No		Pristina Iongiseta	1.7%	Pristina longiseta	Genetic alignment to a cosmopolitan species previously sampled worldwide (Helix 2016).
BES:2031		Oligochaeta sp. indet.	RC15WAC0413						Sequence failed
ISOPODA									
BES:1876		Armadillidae sp. indet.	RC12WAD0295	BES:2199	0.3%	No	>18%	Armadillidae `ISA049`	Regionally distinct species of Armadillidae.
BES:2199		Isopoda sp. indet.	RC12WAD0295	BES:1876	0.3%	INO	>10%	Aimaumuae 13A049	Regionally distinct species of Affiliaulilidae.
HEMIPTERA									
BES:2139	Meenoplidae	Meenoplidae sp. indet.	RC15WAC0377	BES:2356	Identical	HEM003	1.6 -	Meenoplidae	Genetic alignment to a widespread species previously sampled at Murrays Hill, Hardy River,
BES:2356	Meenoplidae	Meenoplidae sp. indet.	RC14WAD0217	BES:2139	identical	TILIVIOUS	2.3%	`HEM003`	and Upper South Fortescue (Helix 2016).
THYSANURA									
BES:1823	Nicoletiidae	Atelurinae sp. indet.	RC14WAD0350						Sequence failed
SYMPHYLA									
BES:2112	Scutigerellidae	Scutigerellidae sp. indet.	RC14WAF0072	No	>16%	No	>16%	Scutigerellidae `SYM027`	Regionally distinct species of Scutigerellidae
BES:2117	Scutigerellidae	Scutigerellidae sp. indet.	RC15WAC0276	Possibly 2055	4.9%	No	>16%	Scutigerellidae `SYM028`	Potentially distinct, but moderate divergence from local specimens indicates more information required to separate distinct species.
BES:2055		Symphyla sp. indet.	RC15WAC0197	Possibly 2117	4.9%	No	>16%	Scutigerellidae `SYM029`	Potentially distinct, but moderate divergence from local specimens indicates more information required to separate distinct species.





CHANGES TO RISK ASSESSMENT

The risk assessment has not changed for any of the taxa that were not sequenced (or not successfully sequenced), including the beetles *Hydrobiomorpha* sp. indet., and Anillini sp. indet., the silverfish Atelurinae sp. indet., the springtail Cyphoderidae sp. indet., the copepods *Australocamptus* sp. `B13` and *Parastenocaris* sp. indet., and *Thermocyclops* sp. `WA`, and the worms Aeolosomatidae sp. indet., and Turbellaria sp. indet. Biologic (2016) contains relevant details for each of these taxa.

Table 2 provides a summary of changes to the risk assessment following the results of the DNA analysis. Figure 2 shows the locations of taxa now considered to be at risk, in the context of the subterranean habitats assessed by Biologic (2016). Four taxa were found to align genetically to widespread taxa, and therefore are now considered to be at negligible risk of impact, comprising:

- The phreodrillid worm Phreodrillidae `OLP12`, found near Deposit C;
- The cosmopolitan naidid worm *Pristina longiseta*, found near Deposit C;
- The enchytraeid worm Enchytraeidae `OLE026`, found near Deposit C; and
- The meenoplid bug Meenoplidae sp. `HEM003`, found within Deposits C and D.

The remaining 13 taxa shown in Table 3 are considered to range from high to moderate low risk based on what is known about the regional occurrence of the taxon from the genetic comparisons, and whether or not the taxon occurs locally outside of the direct impact area (comprising the pit boundaries for troglofauna, and the likely extent of drawdown for stygofauna).

The genetically determined identifications were applied to specimens from the same sample and the same bore/ hole where it was reasonable to do so (such as samples where there were 17 'Enchytraeidae sp. indet.' collected and one was sent for sequencing, or bores/ holes where there were 5 'Enchytraeidae sp. indet.' from the first trip and 2 from the second trip). Nevertheless, not all of the `sp. indet.` taxa were able to be treated this way, owing to the presence of multiple genetically determined species co-occurring in the same habitat/ deposit (particularly in the Enchytraeidae and Paramelitidae). Where a specimen from a different bore/ hole was unable to be reasonably allocated to either of multiple genetically determined species, it remained `sp. indet.` and the risk level did not change materially.

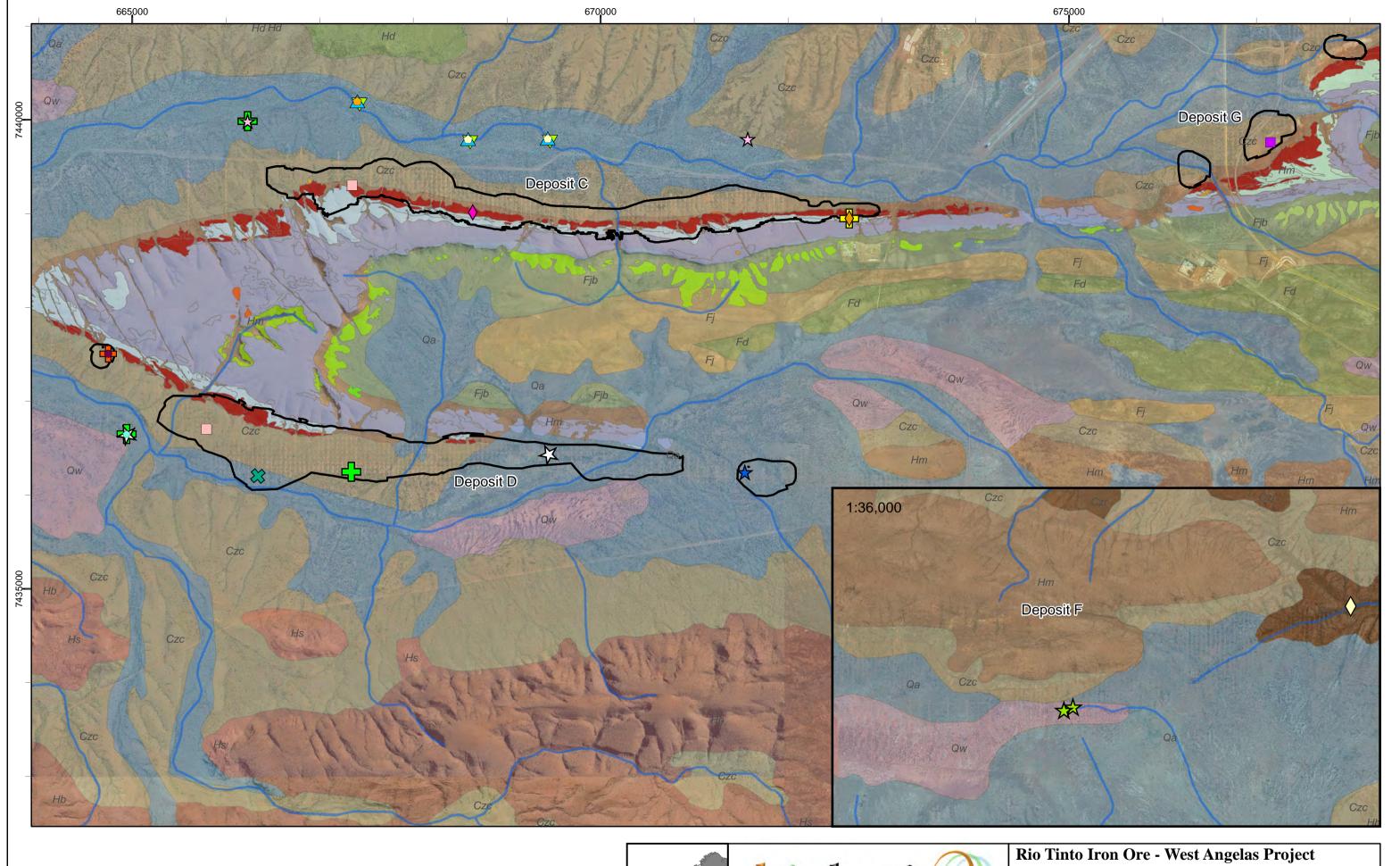
Note also that enchytraeids were assessed herein as stygofauna, because it was assumed that groundwater drawdown may possibly result in desiccation of the air-filled subterranean habitat as well as the loss of groundwater habitat within the drawdown zone.

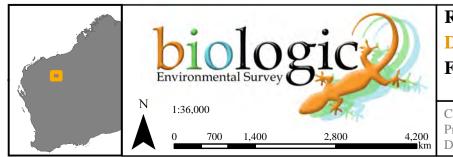
Table 3: Changes to risk assessment of subterranean taxa following DNA analysis.

Morphospecies	Current SRE status	Previous taxon	Within deposit/ impact	Out of deposit/impact	Extent of habitat beyond deposit/ likely impact area	Risk of direct impacts
Worms						
Enchytraeidae `OLE026`	Widespread	Enchytraeidae sp. indet.		Near Dep. C (29)	Regional	Negligible. Regionally widespread species
Enchytraeidae `OLE028`	Confirmed SRE (D)	Enchytraeidae sp. indet.	Dep. D (2)		Likely beyond deposit within Calcrete/ Orebody/ Mt Newman Member, but within likely drawdown	High. Direct impacts may include mining and drawdown.
Enchytraeidae `OLE029`	Potential SRE (A&D)	Enchytraeidae sp. indet.		Near Dep. D (11)	Beyond deposit within Orebody/ Mt Newman Member, but within likely drawdown	High. Direct impacts may include mining and drawdown.
Enchytraeidae `OLE030`	Potential SRE (A&D)	Enchytraeidae sp. indet.	Dep. F (26)		Likely beyond deposit within Alluvials/ Mt Newman Member	$\mbox{\bf Negligible}.$ Unlikely to be affected by mining at Dep. C, D, G
Enchytraeidae sp. indet.	Potential SRE (A)	Enchytraeidae sp. indet.	Dep. D (75), F (38)	Near Dep D (1), C (6)	Likely beyond Deposit D within Calcrete/ Orebody/ Mt Newman Member, but within likely drawdown	Mod / High . Specimens cannot be allocated on current information. Records in/ near Dep. C and D may be at risk from mining or drawdown
Phreodrillidae `OLP12`	Widespread	Oligochaeta sp. indet.	Near Dep. D (1)		Regional	Negligible. Regionally widespread species
Pristina longiseta	Widespread	Oligochaeta sp. indet.	Near Dep. C (6)		Worldwide	Negligible. Cosmopolitan widespread species
c.f. Pristina longiseta	Widespread	Oligochaeta sp. indet.	Near Dep. C (22)		Worldwide	Negligible . Likely to represent <i>P. longiseta</i> owing to location and broad morphology. Widespread.
Crustaceans						
Kruptus sp. `AMP035`	Confirmed SRE (D&E)	Kruptus sp. `WA`	Near Dep. C (6), Dep D (3)		Beyond Deposit C/ D within Calcrete/ Alluvials, but all current records within drawdown	High . Species currently known only from within likely drawdown extent
Maarrka sp. `AMP037`	Confirmed SRE (D&E)	Maarka sp. `WA`	Dep. D (1)		Likely beyond deposit within Orebody/ Mt Newman, but all current records within drawdown	High . Species currently known only from within likely drawdown extent
Paramelitidae sp. `AMP036`	Confirmed SRE (D&E)	Kruptus sp. `WA`	Dep. C (1)		Likely beyond deposit within Orebody/ Mt Newman Member, but all current records within drawdown	High . Species currently known only from within likely drawdown extent
Paramelitidae sp. indet.	Potential SRE (A&E)	Kruptus sp. `WA`	Near Dep. C (1)		Likely beyond Deposit D within Calcrete/ Orebody/ Mt Newman Member, but within likely drawdown	Mod / High . Likely to be the same as <i>K</i> . AMP035, but would not extend range beyond likely drawdown
Atopobathynella sp. `BAP027`	Confirmed SRE (D&E)	Atopobathynella sp. `WA`	Near Dep. C (200)		Unknown, but all current records within likely drawdown	High . Species currently known only from within likely drawdown extent
Bathynellidae sp. `BAB018`	Confirmed SRE (D&E)	Bathynellidae sp. `WA`	Near Dep. C (87)		Unknown, but all current records within likely drawdown	High . Species currently known only from within likely drawdown extent
Armadillidae sp. `ISA049`	Confirmed SRE (D&E)	Armadillidae sp. indet., Isopoda sp. indet.	Dep. D (2)		Recorded close to boundary, habitat likely beyond Dep. D throughout Orebody/ Mt Newman Member	Mod . Current records only just within pit, habitat likely to extend beyond.



Morphospecies	Current SRE status	Previous taxon	Within deposit/ impact	Out of deposit/impact	Extent of habitat beyond deposit/ likely impact area	Risk of direct impacts
Myriapods						
Scutigerellidae sp. `SYM027`	Confirmed SRE (D&E)	Scutigerellidae sp. indet.		Outside Dep. F (1)	Locally beyond Deposit F	Negligible . Unlikely to be affected by mining at Dep. C, D, G
Scutigerellidae sp. `SYM028`	Confirmed SRE (D&E)	Scutigerellidae sp. indet.	Dep. C (17)		Recorded close to boundary, habitat likely beyond Dep. C throughout Orebody/ Mt Newman Member	Mod . Current records only just within pit, habitat likely to extend beyond. Moderate genetic similarities to S. SYM029
Scutigerellidae sp. `SYM029`	Confirmed SRE (D&E)	Symphyla sp. indet.	Dep. C (1)		Likely beyond Deposit C throughout Orebody/ Mt Newman Member	Mod . Current records within pit, but habitat may extend beyond. Moderate genetic similarities to S. SYM028
Hexapods						
Meenoplidae sp. `HEM003`	Widespread	Meenoplidae sp. indet. (Biologic)	Dep. C (2), Dep. D (1)	Regional	Regional	Negligible. Regionally widespread species
Meenoplidae sp. indet. (Ecologia 2013)	Potential SRE (A)	Meenoplidae sp. indet. (Ecologia)	Dep. G (1)	Dep. H (1)	Likely beyond Deposit G throughout Orebody/ Mt Newman Member	Mod / Low . Possibly be the same as <i>M</i> . HEM003, which is regionally widespread
Atelurinae sp. indet. (Biologic 2016)	Potential troglobite	Atelurinae sp. indet. (Biologic)		Outside Dep. D (1)	Habitat outside of Dep D throughout Orebody/ Mt Newman Member	Low . Specimen does not occur within pit. Possibly be the same as Ecologia species, owing to proximity and connected habitats
Atelurinae sp. indet. (Ecologia 2013)	Potential troglobite	Atelurinae sp. indet. (Ecologia)	Dep D (1)		Habitat likely beyond Dep D throughout Orebody/ Mt Newman Member	Mod. Possibly same as Biologic species, owing to proximity and connected habitats.





Project

Deposits C, D, & G Subterranean Fauna Survey

Fig. 2: Subterranean fauna risk assessment changes following DNA analysis

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

Datum: GDA 1994 Size A3. Created 24/10/2016

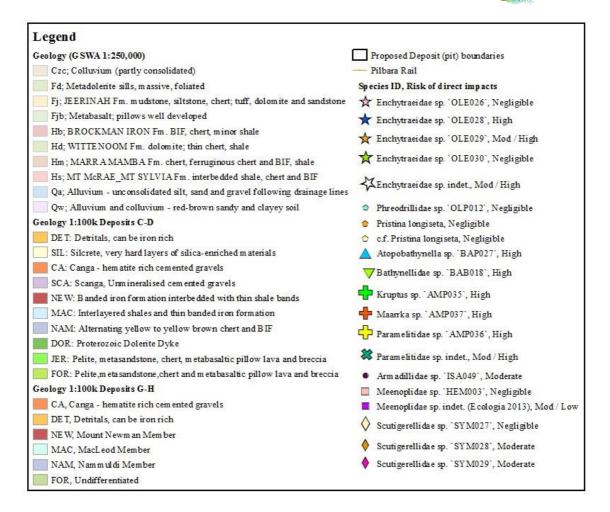


Figure 2 Legend.

OVERALL RISK ASSESSMENT

This assessment considers the risk of direct impacts to subterranean fauna from the development of West Angelas Deposits C, D, and G. As defined in Biologic (2016), direct impacts on troglofauna occur as a result of the removal of habitat within the pit boundaries, while direct impacts on stygofauna include both direct removal of habitat within the pit and the associated drawdown of groundwater throughout permeable hydrogeological layers nearby (which is yet to be modelled precisely).

Including all survey results to date, the following eight troglofauna taxa were regarded to be potentially at risk from mining at Deposits C, D, and G (Figure 3):

Moderate risk of direct impact:

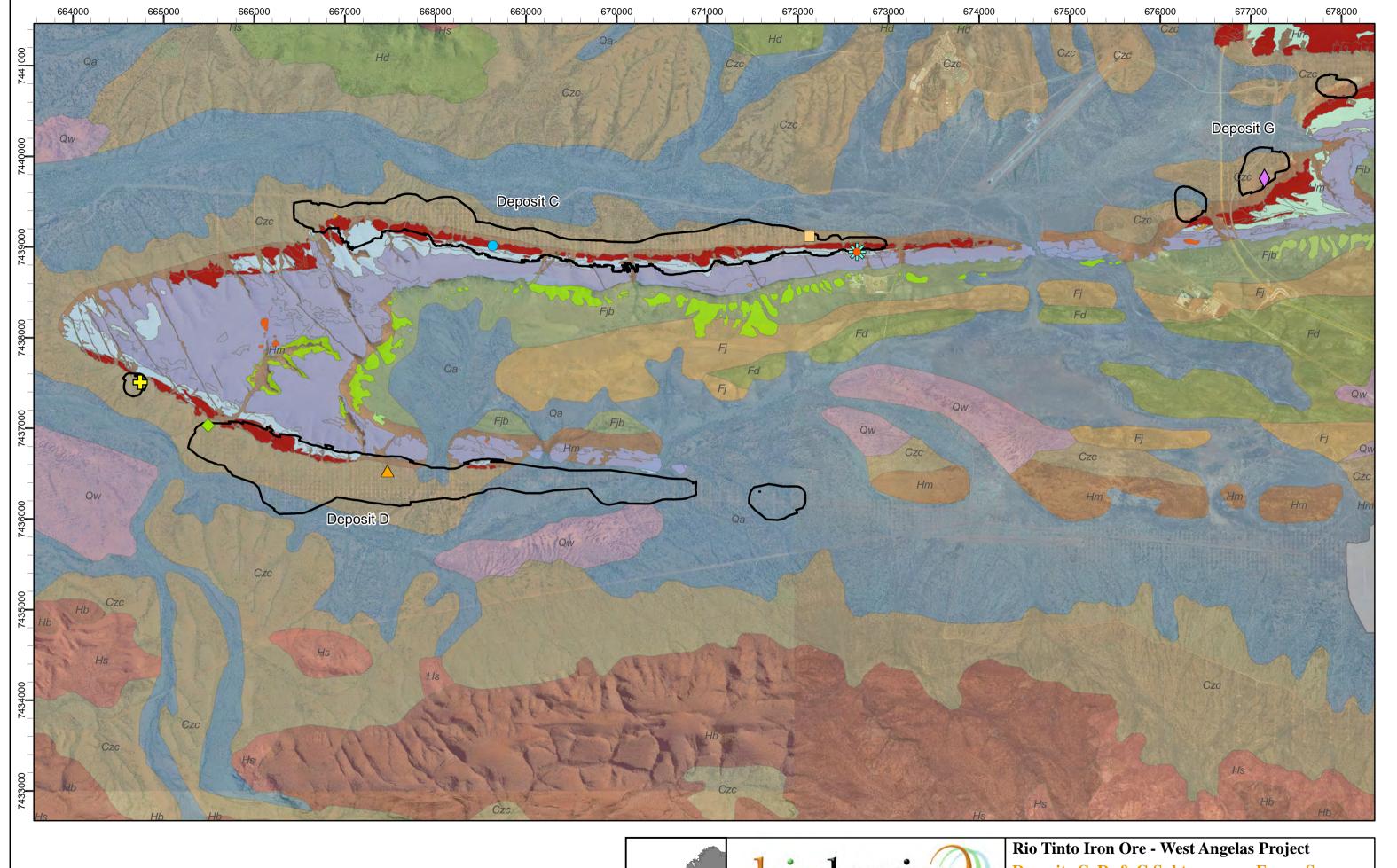
- Isopoda: Armadillidae sp. `ISA049` (Deposit D);
- Symphyla: Scutigerellidae sp. `SYM028` (Deposit C);
- Symphyla: Scutigerellidae sp. `SYM029` (Deposit C);
- Coleoptera: Anillini `sp. indet.` (Ecologia 2013) (Deposit C);
- Coleoptera: Hydrobiomorpha `sp. indet.` (Ecologia 2013) (Deposit D);
- Thysanura: Atelurinae `sp. indet.` (Ecologia 2013) (Deposit D);

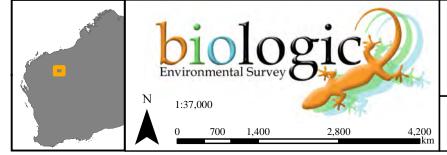
Moderate / Low risk of direct impact:

- Collembola: Cyphoderidae `sp. indet.` (Deposit C); and
- Hemiptera: Meenoplidae 'sp. indet.' (Ecologia 2013) (Deposit G).

Each of these taxa are known only from locations within the proposed mining deposits, and were therefore regarded as being potentially at risk. The potential risk level was moderated by the location of many of the records (particularly Armadillidae sp. `ISA049`, Scutigerellidae sp. `SYM028`, Cyphoderidae `sp. indet.`, Anillini `sp. indet.`, and *Hydrobiomorpha* `sp. indet.`) very close to the deposit boundaries and the lack of any clear geological or geomorphological barriers between suitable habitat layers inside and outside of the deposits (as detailed in Biologic 2016). The current records of these taxa are likely to underestimate the actual distributions of these species throughout the subterranean habitat, owing to both the inherent difficulties in sampling rarely occurring fauna with limited means of dispersal, as well as the physical limitations of accessing the wider subterranean habitat using only suitable and available drill holes.

The potential risk level for Atelurinae `sp. indet.` and Meenoplidae `sp. indet.` was moderated by the likelihood that these taxa (originally collected by Ecologia, and unable to be compared with current specimens) could represent the same species as other representatives of these taxa found to occur outside of the deposits in the current survey. There also remains some doubt as to the likelihood that Cyphoderidae `sp. indet.` and Meenoplidae `sp. indet.` represent obligate (troglobitic) subterranean fauna or potentially facultative subterranean fauna, which may be less likely to be restricted to habitats within the deposits.





Deposits C, D, & G Subterranean Fauna Survey

Fig. 3: Troglofauna taxa overall risk assessment

Coordinate System: GDA 1994 MGA Zone 50

Projection: Transverse Mercator Datum: GDA 1994

Size A3. Created 24/10/2016

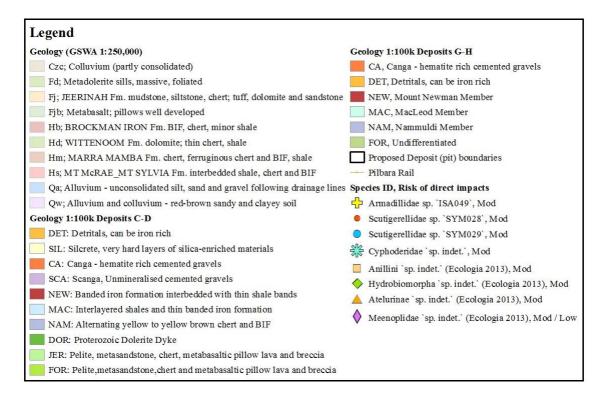


Figure 3 Legend.

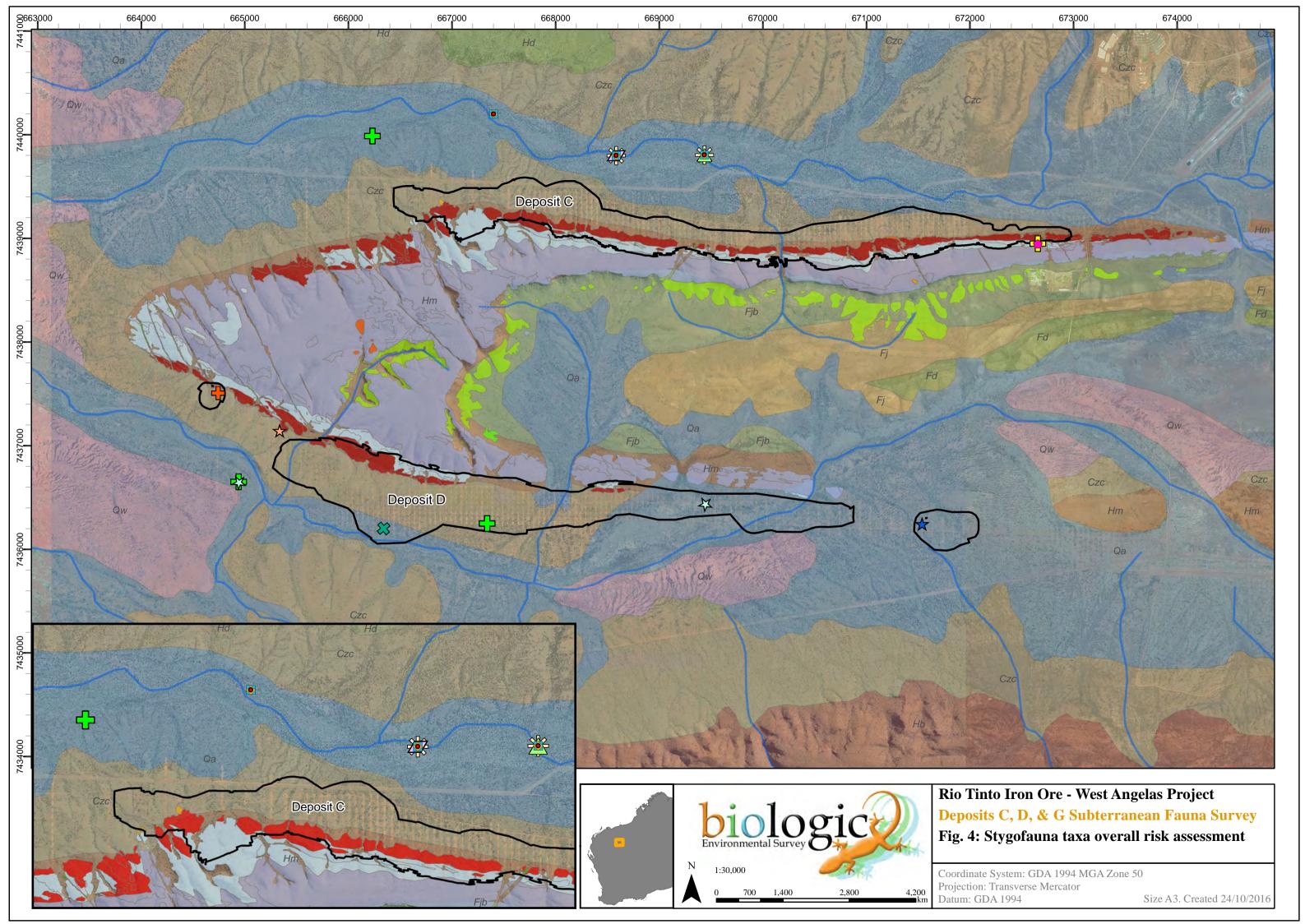
The following 14 stygofauna taxa were regarded to be potentially at risk from mining and the associated groundwater drawdown at Deposits C and D (Figure 4):

High risk of direct impact:

- Haplotaxida: Enchytraeidae sp. `OLE028` (Deposit D);
- Haplotaxida: Enchytraeidae sp. `OLE029` (near Deposit D);
- Amphipoda: Kruptus sp. `AMP035`(near Deposit C and D);
- Amphipoda: Maarrka sp. `AMP037` (Deposit D);
- Amphipoda: Paramelitidae sp. `AMP036` (Deposit C);
- Bathynellacea: Atopobathynella sp. `BAP027` (near Deposit C);
- Bathynellacea: Bathynellidae sp. `BAB018` (near Deposit C);
- Harpacticoida: Australocamptus sp. `B13`(near Deposit C); and

Moderate / High risk of direct impact:

- Haplotaxida: Enchytraeidae `sp. indet.` (near Deposit D);
- Turbellaria: Turbellaria `sp. indet.` (near Deposit C);
- Polychaeta: Aeolosomatidae `sp. indet.` (Deposit C);
- Amphipoda: Paramelitidae `sp. indet.` (Deposit D);
- Cyclopoida: Thermocyclops sp. `WA` (near Deposit C); and
- Harpacticoida: Parastenocaris `sp. indet.` (near Deposit C).



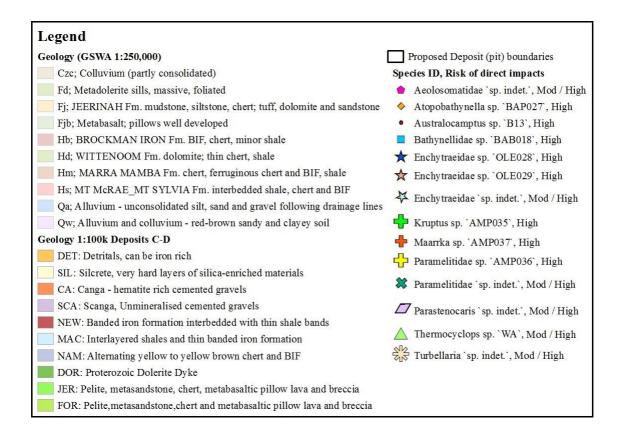


Figure 4 Legend.

The risk level for the five indeterminate taxa (identified as `sp. indet.`) was moderated by the taxonomic uncertainties regarding these taxa (or groups of specimens). Each of these nominal taxa was unable to be allocated to other existing morphospecies (or genetically determined species) on current information, and the possibility remains that they could occur more widely than the other 'high' risk taxa, as some widely occurring members of these groups are known regionally. Nevertheless, for Enchytraeidae `sp. indet.` and Paramelitidae `sp. indet.` in particular, it is also reasonably likely that some of the specimens could represent one of the other existing 'high' risk taxa in their respective groups.

The risk level for the 'high' risk stygofauna was primarily dependent upon the magnitude and extent of groundwater drawdown, which is yet to be modelled in detail, but which is inferred to extend throughout the orebody aquifers within the deposits and the alluvial/ detrital aquifers of the flanking valleys nearby (Biologic 2016). This is inferred to include all of the locations of stygofauna records from the current survey (which are all within 1 km of the deposit boundaries), on the basis of the available hydrogeological information. Nevertheless, it is possible that the risk of direct impact for stygofauna species may be subject to change with further information regarding groundwater drawdown.

It is also possible that the current species distributions may be partly attributed to sampling artefacts, as there has been no sampling for subterranean fauna to the immediate west of the current deposits within the same hydrogeological catchment (Turee Creek East Branch). Previous



stygofauna collected further afield (approximately 15 km to the south west at Turee Creek Borefield), and to the immediate east within the Central Plateau area of West Angelas are not able to be compared with current specimens due to old/ incomplete identifications, incompatible specimen preservation, and a lack of genetic information.

Owing to the position of the deposits within the local catchment and the direction of flow from the Central Plateau to the northern flanking valley between Deposits C and G (as discussed in Biologic 2016), there is a reasonable likelihood that some of the current stygofauna species could also occur in the Central Plateau, and/or further downstream to the west within the Turee Creek East sub-catchment.

Yours sincerely,

Brad Durrant

Principal Zoologist / Managing Director

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- Helix Molecular Solutions (2017) Report on the molecular systematics of subfauna. Unpublished report prepared for Biologic Environmental Survey c/o Alacran Environmental (Appendix I to this document)



Appendix I – Helix Molecular Solutions DNA Report



Helix Molecular Solutions

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2 April, 2017

Frich Volschenk

Via email

Re. Report on the molecular systematics of subfauna

Dear Erich,

Following is a summary of the results of the subfauna study we have completed on eight taxonomic groups. Sixteen distinct genetic lineages were detected among the seven groups for which sequences were obtained. We did not obtain a sequence from the one Thysanura specimen. Four of the 16 lineages have been detected previously (one each of Enchytraeidae, Naididae, Phreodrilidae and Meenoplidae), whereas the remainder appear to be new or require further investigation.

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

Sincerely,

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



Background and Objective

Twenty-six specimens of subfauna (troglofauna and stygofauna) belonging to eight taxonomic groups were sequenced for variation at the mitochondrial COXI or 12s genes. The molecular data were assessed in order to determine the number of species present in each group and compare the results to those obtained during previous surveys that have been undertaken for the these groups elsewhere in the Pilbara.

Methods

Twenty-six specimens of subfauna were sequenced for variation at the mitochondrial cytochrome oxidase subunit I gene (COXI) using multiple pairs of primers (LCOI/HCO2, LCOI-long/HCO2-long, NemF1/NemR1 and LCOI/CIN2341. The 12s region was amplified and sequenced using primers 12-ai and 12s-bi (Simon et al., 1994).

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

Genetic distances were calculated using p-distances, and neighbour-joining trees were constructed from those distances using MEGA 6.0 (Tamura et al., 2013).

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

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

Results and Conclusions

Amphipoda

Neighbour-joining analysis - Reference sequences and outgroups

Five specimens of amphipods, identified on the basis of morphology as belonging to the Paramelitidae, were sequenced for COI. A search of similar sequences on Genbank indicated that the specimens were most similar to sequences of Paramelitidae, thus the sequences were analysed with reference specimens representing 49 distinct genetic lineages of Paramelitidae from the Pilbara. Two specimens of Niphargidae, Niphargus fontanus (Genbank accession #KC315635) and Niphargus glenniei (Genbank accession # KC315646) were used as outgroups. In order reduce analysis time and simplify the presentation of results, a sub-set of reference lineages were selected based on the criteria that they were placed in clades containing the five target sequences in a preliminary NJ analysis.

The neighbour-joining analysis placed the five specimens into three lineages, which did not contain any reference lineages, therefore they were assigned to the new lineages AMP035 – AMP037 (Figure 1). Lineage AMP035 contained three specimens, whereas the remaining two lineages, AMP036 and AMP037, each contained a single specimen (Figure 1).

Differentiation within and between lineages

The three lineages of Paramelitidae detected in the present study differed from one another by between 17.5 and 18.7% sequence divergence (Table 1). Individuals within lineage AMP035 differed from one another by between 0.3 and 0.9% sequence divergence (Table 1).

All three lineages differed from the closest reference lineages by >15% sequence divergence (Table 1).

Conclusions

Three lineages of amphipods were detected in the present study, belonging to the family Paramelitidae. The three lineages differed from one another and from the reference specimens by >15% sequence divergence, indicating that the three lineages represent three species that have so far not been detected in the Pilbara, based on the material available for comparison.

Paramelitidae

AMP035 = one species, new Paramelitidae AMP036 = one species, new Paramelitidae AMP037 = one species, new Paramelitidae

Bathynellacea

Neighbour-joining analysis - Reference sequences and outgroups
Three specimens of Bathynellacea, assigned to the families Bathynellidae and
Parabathynellidae on the basis of morphology, were sequenced for COI. The sequences were
analysed with 47 reference lineages of Bathynellacea from the Pilbara, representing 65
specimens. Two species of Amphipoda were used as outgroups: Chydaekata acuminata
Genbank accession #DQ838024 and Maarka etheli GenBank accession #DQ838031.

The neighbour-joining analysis placed the three specimens into two lineages, which did not contain any reference lineages, therefore they were assigned to the new lineages BAB018 and BAP027 (Figure 2). Lineage BAB018 contained a single specimen, whereas lineage BAP027 each contained two specimens (Figure 2). Lineage BAP027 was placed in a large clade containing reference specimens of Parabathynellidae, and lineage BAB018 was placed in a clade containing reference lineages of Bathynellidae.

Differentiation within and between lineages

Individuals within lineage BAP027 differed from one another by 0.3% sequence divergence (Table 2). Lineage BAP027 differed from the closest reference lineage (CA0084 from Callawa) by 10.8% sequence divergence (Table 2). Lineage BAB018 differed from the closest reference lineage (G456 from the Central Pilbara) by 19.6% sequence divergence (Table 2).

Conclusions

Two lineages of Bathynellacea were detected in the present study, one each belonging to the families Bathynellidae and Parabathynellidae. The two lineages differed from the reference specimens by >10% sequence divergence, indicating that the two lineages represent two species that have so far not been detected in the Pilbara, based on the material available for comparison.

Bathynellidae

BAB018 = one species, new Bathynellidae Parabathynellidae BAP027 = one species, new Parabathynellidae

Enchytraeidae

Neighbour-joining analysis - Reference sequences

Six specimens of Enchytraeidae were sequenced for COI. The sequences were analysed with 55 reference specimens of Enchytraeidae from Genbank and the Pilbara, representing 26 lineages.

The neighbour-joining analysis placed the six specimens into four lineages, three of which did not contain any reference lineages, therefore the three were assigned to new lineages OLE028 – OLE030 (Figure 3). One lineage also contained reference specimens from a previous survey in the Pilbara, and therefore was assigned to the existing lineage OLE026 (Figure 3). Lineages OLE028 and OLE029 each contained a single specimen, whereas lineage OLE030 contained two specimens (Figure 3).

Differentiation within and between lineages

The four lineages of Enchytraeidae detected in the present study differed from one another by between 7.4 and 17.1% sequence divergence (Table 3.) Individuals within lineage OLE026, which contained the two specimens from this study as well as two specimens from a previous survey, differed from one another by between 1.2 and 3.4%, and individuals within lineage OLE030 differed from one another by 1.6% sequence divergence (Table 3). Lineage OLE028 differed from the closest reference lineage (382 from Robe River) by 12.9% sequence divergence (Table 3). Lineage OLE029 differed from the closest reference lineage (EQ15) by 5.7% sequence divergence and OLE differed from the nearest reference specimen (EQ7 and GD10) by 7.8% (Table 3).

Conclusions

Four lineages of Enchytraeidae were detected in the present study. They differed from one another by >7% sequence divergence. One of the lineages (OLE026) has been detected previously in the Pilbara. One lineage, OLE028, differed from the reference specimens by >approximately 13% indicating that it likely represents a species that has so far not been detected in the Pilbara, based on the material available for comparison. The remaining two lineages require further consideration. Lineages OLE029 and OLE030 were placed in a large clade including lineage OLE026 and containing specimens of the morphologically-defined species PST1 (Brown et al., 2015). Haplotypes within the lineage averaged 7.4% sequence divergence and cover a large geographical area covering six creek catchments and three river basins (Brown et al. 2015). Further investigation is required to resolve relationships among members of this group.

Enchytraeidae

OLE028 = one species, new

OLE026 + OLE029 + OLE030 = species complex requiring further investigation; lineage OLE026 has been detected previously

Naididae and Phreodrilidae

Neighbour-joining analysis - Reference sequences

Three additional specimens of Oligochaeta, which were not assigned to a taxonomic group, were sequenced for COI. A search of similar sequences on Genbank indicated that two belonged to the Naididae and one to the Phreodrilidae. For this reason, the sequences were analysed with 15 reference lineages of Naididae, representing five lineages from the Pilbara and Genbank, and 52 specimens of Phreodrilidae, representing 22 lineages from the Pilbara.

The neighbour-joining analysis placed the three specimens into two lineages, both of which also contained reference specimens (Figure 4). Two specimens were genetically identical and were placed in a lineage containing the reference specimen of *Pristina longiseta*, in the family Naididae (Figure 4). The second lineage was placed within Phreodrilidae lineage OLP012, which contained specimens from four drainage basins in the Pilbara (Brown et al., 2015).

Differentiation within and between lineages

The two specimens of Naididae from the present study were genetically identical, and differed from the reference specimen of *Pristina longiseta* by 1.7% sequence divergence (Table 4). The specimen of Phreodrilidae from the present study differed from the remaining specimens within lineage OLP012 by between 1.9 and 2.8% sequence divergence (Table 4).

Conclusions

One lineage each of Naididae and Phreodrilidae were detected in the present study, each corresponding to a single species. Both belong to species that have been detected previously, one to the widespread Naididae species *Pristina longiseta*, and the second to the Phreodrilidae lineage OLP012, distributed widely in the Pilbara (Brown et al., 2015). The genus *Pristina* is known from North America, Central America, Europe, Asia and Australia (Rodrigues et al., 2015).

Naididae

Pristina longiseta, world-wide distribution Phreodrilidae OLP012 = one species, previously detected

Hemiptera (Meenoplidae)

Neighbour-joining analysis - Reference sequences

Two specimens of Hemiptera, assigned to the family Meenoplidae, were sequenced for COI. The sequences were analysed with 26 reference specimens of Meenoplidae from the Pilbara.

The neighbour-joining analysis placed the two specimens in a single genetic lineage, which also contained reference specimens from previous surveys at Murrays Hill, Hardy River and Upper South Fortescue (Figure 5). Therefore the specimens from the present study were assigned to the existing lineage HEM003 (Figure 5).

Differentiation within and between lineages

The two specimens of Meenoplidae from the present study were genetically identical at COI and differed from the reference specimens from Murrays Hill, Hardy River and Upper South Fortescue by between 1.6 and 2.3% sequence divergence (Table 5).

Conclusions

The two specimens of Meenoplidae from the present study belonged to a single species, that has been detected previously at Murrays Hill, Hardy River and Upper South Fortescue.

Meenoplidae

HEM003 = one species, detected previously

Isopoda

Neighbour-joining analysis - Reference sequences

Two specimens of Isopoda were sequenced for COI. The specimens were not further assigned to family. A search of similar sequences on Genbank indicated that the specimens were most similar to sequences of Troglarmadillo, thus the sequences were analysed with reference specimens representing 48 distinct genetic lineages of presumptive Armadillidae from the Pilbara, representing 66 specimens. In order reduce analysis time and simplify the presentation of results, a sub-set of reference lineages were selected based on the criteria that they were placed in clades or near-by clades containing the two target sequences in a preliminary NJ analysis. Thirty-five lineages representing 46 specimens were used in the final NJ analysis.

The neighbour-joining analysis placed the two specimens into a single lineage, which did not contain any reference lineages, therefore it was assigned to the new lineage ISA049 (Figure 6). The lineage was placed in a clade containing reference specimens of Troglarmadillo from the Pilbara (Figure 6).

Differentiation within and between lineages

The two specimens in lineage ISA049 differed from one another by 0.3% sequence divergence (Table 6). Lineage ISA049 differed from the closest reference lineages by >18% sequence divergence (Table 6).

Conclusions

A single lineage of Isopoda was detected in the present study, likely belonging to the family Armadillidae. The lineage differed from the reference specimens by >18% sequence divergence, indicating that it likely represents a new species that has so far not been detected in the Pilbara, based on the material available for comparison.

Armadillidae

ISA049 = one species, new

Symphyla

Neighbour-joining analysis - Reference sequences

Three specimens of Symphyla were sequenced for COI. Two were assigned to the family Scutigerellidae, on the basis of morphology, whereas the third was not further assigned. A search of similar sequences on Genbank and the Helix database indicated that the specimens were most similar to sequences of Scutigerellidae, thus the sequences were analysed with reference specimens representing 26 distinct genetic lineages of presumptive Scutigerellidae from the Pilbara.

The neighbour-joining analysis placed the three specimens into three distinct genetic lineages, which did not contain any reference lineages, and were in fact most similar to one another (Figure 7). The three lineages were therefore assigned to the new lineages SYM027, SYM028 and SYM029 (Figure 7).

Differentiation within and between lineages

The three lineages from the present study differed from one another by between 4.9 and 17.5% sequence divergence (Table 7). The three lineages differed from the closest reference lineages by >16% sequence divergence (Table 7).

Conclusions

Three distinct lineages of Symphyla were detected in the present study, likely belonging to the family Scutigerellidae. Two of the lineages, SYM028 and SYM029, showed moderately low genetic differentiation from one another (approximately 5%), thus require further consideration. The two lineages may represent incipient species, or differentiation within a single species between geographically separate sites, arising from the poor dispersal abilities of the taxon. Sampling of intermediate sites my help resolve their relationshps. The three lineages differed from the reference specimens by >16% sequence divergence, indicating that they are likely to represent new species that have so far not been detected in the Pilbara, based on the material available for comparison.

Scutiaerellidae:

SYM027 = one species, new

SYM028 + SYM029 = one or two new species, requiring further investigation

Thysanura

A DNA sequence was not obtained from the specimen of Thysanura.

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Table 1. (attached). Genetic distances (below diagonal) and standard error (above diagonal, in blue) between specimens of Amphipoda detected in the present study and the reference lineages as shown in Figure 1.

Table 2. (attached). Genetic distances (below diagonal) and standard error (above diagonal, in blue) between specimens of Bathynellacea detected in the present study and the reference lineages as shown in Figure 2.

Table 3. (attached). Genetic distances (below diagonal) and standard error (above diagonal, in blue) between specimens of Enchytraeidae detected in the present study and the reference lineages as shown in Figure 3.

Table 4. (attached). Genetic distances (below diagonal) and standard error (above diagonal, in blue) between specimens of Naididae and Phreodrilidae detected in the present study and the reference lineages as shown in Figure 4.

Table 5. (attached). Genetic distances (below diagonal) and standard error (above diagonal, in blue) between specimens of Meenoplidae detected in the present study and the reference lineages as shown in Figure 5.

Table 6. (attached). Genetic distances (below diagonal) and standard error (above diagonal, in blue) between specimens of Isopoda detected in the present study and the reference lineages as shown in Figure 6.

Table 7. (attached). Genetic distances (below diagonal) and standard error (above diagonal, in blue) between specimens of Symphyla detected in the present study and the reference lineages as shown in Figure 7.

Figure 1. Neighbour-joining analysis of specimens of Amphipoda from the present study. Numbers on major nodes correspond to bootstrap support over 100 iterations. Scale bargenetic distance. The specimens from the present study are highlighted in yellow; Genbank voucher specimens are highlighted in turquoise.

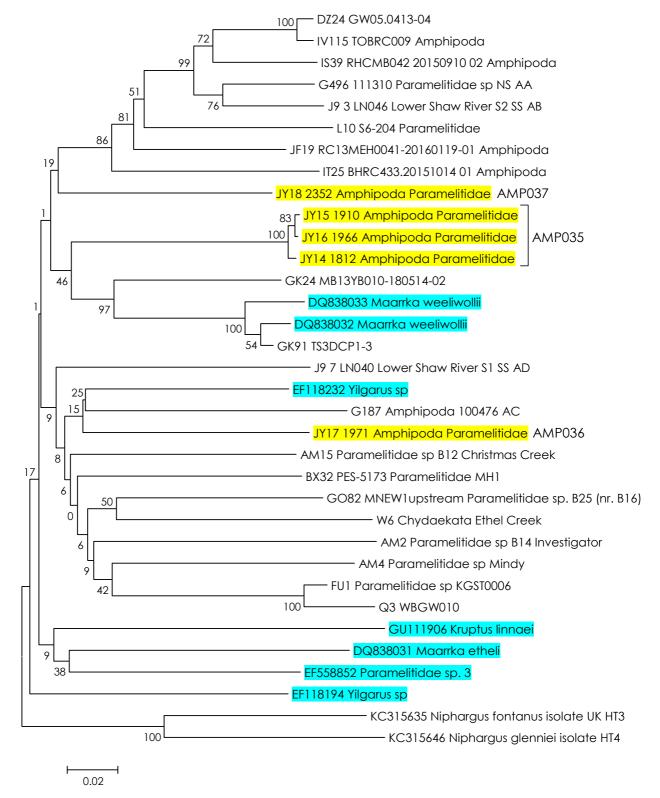


TABLE 1. Amphipod Distance Matrix	1																															
TABLE 1. Amphipod disidnce Mainx																						(9									\neg	
Specimen ID	IY14 1812 Amphipoda Paramelitidae	IY15 1910 Amphipoda Paramelitidae	Y16 1966 Amphipoda Paramelifidae	IY17 1971 Amphipoda Paramelitidae	IY18 2352 Amphipoda Paramelitidae	AM15 Paramelitidae sp B12 Christmas Creek	AM2 Paramelitidae sp B14 Investigator	AM4 Paramelitidae sp Mindy	X32 PES-5173 Paramelitidae MH1	0Q838031 Maarrka etheli	0Q838032 Maarrka weeliwollii	JQ838033 Maarrka weeliwollii	2224 GW05.0413-04	F118194 Yilgarus sp	:F118232 Yilgarus sp	:F558852 Paramelitidae sp. 3	U1 Paramelitidae sp KGST0006	3187 Amphipoda 100476 AC	3496 111310 Paramelitidae sp NS AA	GK24 MB13YB010-180514-02	5K91 TS3DCP1-3	3082 MNEW1 upstream Paramelitidae sp. B25 (nr. B16)	3U111906 Kruptus linnaei	S39 RHCMB042 20150910 02 Amphipoda	125 BHRC433.20151014 01 Amphipoda	V115TOBRC009 Amphipoda	19 3 LN046 Lower Shaw River S2 SS AB	19 7 LN040 Lower Shaw River S1 SS AD	F19 RC13MEH0041-20160119-01 Amphipoda	.10 S6-204 Paramelitidae	Q3 WBGW010	W6 Chykneta Ethel Creek
JY14 1812 Amphipoda Paramelitidae		0.003	0.003	0.015	0.014	0.015	0.015	0.015	0.016	0.016	0.015	0.015	0.016	0.017	0.014	0.016	0.014	0.015	0.015	0.014	0.014	0.015	0.018	0.014	0.019	0.015	0.016	0.016	0.015	0.017	0.019	0.015
JY15 1910 Amphipoda Paramelitidae	0.009		0.002	0.016	0.014	0.016	0.015	0.015	0.015	0.016	0.015	0.016	0.016	0.016	0.015	0.016	0.014	0.015	0.015	0.014	0.014	0.015	0.018	0.014	0.019	0.015	0.016	0.016	0.015	0.017	0.019	0.015
JY16 1966 Amphipoda Paramelitidae	0.006	0.003		0.016	0.014	0.015	0.015	0.015	0.015	0.016	0.015	0.016	0.016	0.016	0.015	0.016	0.014	0.015	0.015	0.014	0.014	0.015	0.018	0.014	0.019	0.015	0.016	0.016	0.015	0.017	0.019	0.015
JY17 1971 Amphipoda Paramelitidae	0.181	0.181	0.181		0.014	0.015	0.015	0.015	0.015	0.016	0.015	0.015	0.015	0.015	0.014	0.015	0.015	0.015	0.015	0.014	0.014	0.015	0.016	0.014	0.019	0.015	0.016	0.017	0.014	0.015	0.020	0.014
JY18 2352 Amphipoda Paramelitidae	0.177	0.178	0.175	0.187		0.014	0.015	0.015	0.015	0.015	0.015	0.015	0.014	0.014	0.015	0.014	0.016	0.014	0.013	0.013	0.014	0.013	0.016	0.013	0.018	0.014	0.014	0.017	0.013	0.016	0.021	0.015
AM15 Paramelitidae sp B12 Christmas Creek	0.207	0.208	0.205	0.180	0.188		0.013	0.016	0.016	0.016	0.014	0.016	0.016	0.015	0.016	0.016	0.014	0.015	0.015	0.012	0.013	0.014	0.018	0.016	0.020	0.016	0.018	0.016	0.013	0.017	0.021	0.016
AM2 Paramelitidae sp B14 Investigator	0.219	0.223	0.220	0.219	0.226	0.214		0.016	0.015	0.017	0.016	0.015	0.015	0.018	0.015	0.018	0.015	0.017	0.015	0.014	0.015	0.015	0.017	0.015	0.020	0.015	0.017	0.018	0.015	0.015	0.021	0.016
AM4 Paramelitidae sp Mindy	0.226	0.228	0.225	0.207	0.222	0.193	0.211		0.016	0.015	0.014	0.015	0.017	0.017	0.017	0.015	0.016	0.017	0.017	0.016	0.014	0.016	0.019	0.015	0.019	0.017	0.016	0.017	0.017	0.018	0.020	0.017
BX32 PES-5173 Paramelitidae MH1	0.202	0.199	0.201	0.194	0.191	0.178	0.204	0.195		0.014	0.016	0.016	0.018	0.017	0.016	0.015	0.018	0.015	0.017	0.016	0.015	0.015	0.016	0.017	0.019	0.018	0.017	0.017	0.014	0.015	0.020	0.016
DQ838031 Maarrka etheli	0.233	0.236	0.236	0.245	0.214	0.231	0.229	0.231	0.233		0.017	0.018	0.018	0.014	0.015	0.014	0.016	0.016	0.015	0.015	0.017	0.015	0.017	0.017	0.022	0.018	0.018	0.017	0.017	0.019	0.024	0.016
DQ838032 Maarrka weeliwollii	0.170	0.173	0.173	0.205	0.184	0.199	0.234		0.216	0.194		0.006	0.014	0.015	0.015	0.016	0.013	0.017	0.015	0.013	0.005	0.015	0.019	0.015	0.021	0.015	0.016	0.016	0.013	0.018	0.021	0.014
DQ838033 Maarrka weeliwollii	0.178		0.182	0.219	0.190	0.201	0.234	0.229	0.224	0.201	0.030		0.015	0.016	0.015	0.016	0.015	0.017	0.015	0.013	0.007	0.016	0.018	0.015	0.021	0.015	0.017	0.016	0.014	0.018	0.021	0.015
DZ24 GW05.0413-04	0.206	0.209	0.209	0.206	0.201	0.212	0.239	0.237	0.224	0.230	0.214	0.218		0.016	0.015	0.017	0.015	0.014	0.011	0.016	0.014	0.016	0.019	0.011	0.017	0.005	0.010	0.017	0.012	0.014		0.016
EF118194 Yilgarus sp	0.197	_	0.199	0.217	0.191	0.216	0.254	0.243	0.202	0.236	0.211	0.221	0.209		0.016	0.015	0.017	0.015	0.017	0.014	0.014	0.016	0.019	0.016	0.019	0.016	0.016	0.018	0.016	0.016	0.021	0.016
EF118232 Yilgarus sp	0.212	0.213	0.212	0.172	0.190	0.194	0.223	0.212	0.176	0.238	0.200	0.205	0.209	0.197		0.015	0.015	0.014	0.017	0.015	0.015	0.015	0.017	0.015	0.021	0.015	0.018	0.015	0.017	0.016	0.020	0.016
EF558852 Paramelitidae sp. 3	0.199	0.196	0.198	0.222	0.191	0.213	0.242	0.236	0.219	0.202	0.194	0.203	0.207	0.211	0.202		0.018	0.015	0.015	0.016	0.015	0.014	0.018	0.015	0.022	0.017	0.016	0.015	0.017	0.017	0.025	0.014
FU1 Paramelitidae sp KGST0006	0.204	0.202	0.202	0.210	0.223	0.175	0.217	0.184	0.194	0.226	0.217	0.224	0.225	0.233	0.197	0.211		0.016	0.015	0.015	0.012	0.014	0.019	0.017	0.021	0.015	0.017	0.014	0.015	0.019	0.010	0.016
G187 Amphipoda 100476 AC	0.219	0.223	0.221	0.192	0.215	0.203	0.227	0.210	0.222	0.244	0.224	0.224	0.208	0.213	0.184	0.212	0.213		0.014	0.018	0.016	0.015	0.017	0.014	0.021	0.014	0.015	0.017	0.015	0.017	0.021	0.015
G496 111310 Paramelitidae sp NS AA	0.208	0.211	0.210	0.208	0.205	0.212	0.233	0.215	0.212	0.226	0.220	0.226	0.079	0.219	0.205	0.211	0.229	0.208		0.015	0.015	0.015	0.018	0.011	0.020	0.011	0.009	0.016	0.013	0.014	0.023	0.015
GK24 MB13YB010-180514-02	0.178		0.175	0.208	0.183	0.190	0.218	0.221	0.204	0.205	0.140	0.145	0.208	0.202	0.187	0.179	0.212	0.207	0.212		0.011	0.014	0.019	0.014	0.019	0.016	0.016	0.016	0.014	0.019	0.023	0.016
GK91 TS3DCP1-3	0.158	0.161	0.161	0.199	0.174	0.193	0.224	0.218	0.205	0.193	0.017	0.046	0.210	0.205	0.197	0.184	0.210	0.219	0.211	0.117		0.013	0.019	0.014	0.021	0.014	0.016	0.014	0.013	0.018	0.021	0.014
GO82 MNEW1upstream Paramelitidae sp. B25 (nr. B16)	0.222	0.219	0.221	0.190	0.199	0.178			0.172	0.225	0.198	0.198		0.227		0.208		0.218		0.191			0.018	0.015	0.020	0.016	0.018	0.016				0.015
GU111906 Kruptus linnaei	0.242			0.230	0.248	0.253			0.234	0.250	0.240	0.240		0.244				0.253		0.238				0.018	0.024	0.018	0.018	0.019		0.019		0.016
IS39 RHCMB042 20150910 02 Amphipoda	0.207	0.211	0.210	0.196	0.189	0.217	0.228		0.219	0.236	0.220	0.223	0.081	0.216	0.186		0.241	0.203	0.089	0.219	0.211		0.244		0.016	0.011	0.013	0.016	0.012	0.014	0.023	0.015
IT25 BHRC433.20151014 01 Amphipoda	0.195	_	0.195	0.200	0.173	0.238	0.240	0.228	0.209	0.214	0.183	0.195	1	0.195	0.224	0.214	0.231	0.244	0.173	0.195	0.180	0.221	0.244	0.166		0.017	0.017	0.023	0.016	0.017	0.022	0.023
IV115 TOBRC009 Amphipoda	0.199	0.202	0.202	0.209	0.204	0.218	0.232	0.240	0.220	0.229	0.213	0.217	0.013	0.218	0.208	0.208	0.218	0.209	0.083	0.213	0.210	0.219	0.228	0.081	0.149		0.011	0.017	0.012	0.014	0.022	0.016
J9 3 LN046 Lower Shaw River S2 SS AB	0.215	0.217	0.217	0.204	0.219	0.230	0.245	0.206	0.220	0.228	0.217	0.217		0.221		0.200	0.226	0.223	0.076	0.228		0.199	0.239	0.111	0.173			0.016	0.013	0.014		0.015
J9 7 LN040 Lower Shaw River S1 SS AD	0.219	_	0.219	0.210	0.200	0.191	0.245		0.192	0.213	0.195	0.204		0.215		0.208	0.182	0.219	0.221	0.193		0.213	0.243	0.232	0.223		0.224		0.017	0.018		0.018
JF19 RC13MEH0041-20160119-01 Amphipoda	0.206	0.211	0.208	0.203	0.183	0.205	0.221	0.201	0.189	0.223	0.201	0.201		0.199	0.174	0.217	0.210	0.207	0.125	0.204	0.191	0.203	0.217	0.128	0.151	0.130	0.134			0.013		0.016
L10 S6-204 Paramelitidae	0.231	0.233	0.233	0.212	0.219	0.234	0.238	0.217	0.222	0.228	0.210	0.207		0.236	0.193	0.228	0.240	0.202	0.143	0.214		0.219	0.236	0.136	0.166	0.133	0.158	0.232	0.143		0.022	0.017
Q3 WBGW010	0.231	0.231	0.228	0.225	0.255	0.210	0.218		0.225	0.236	0.231	0.241		0.241			0.037	0.223		0.252	0.231	0.204	0.239	0.268	0.228		0.240	0.191		0.255		0.022
W6 Chykaeta Ethel Creek	0.240	0.238	0.240	0.219	0.211	0.232	0.218	0.215	0.217	0.237	0.220	0.233	0.221	0.233	0.205	0.205	0.220	0.213	0.223	0.214	0.208	0.183	0.263	0.222	0.243	0.224	0.210	0.236	0.223	0.226	0.239	

Estimates of Evolutionary Divergence between Sequences

The number of base differences per site from between sequences are shown. Standard error estimate(s) are shown above the diagonal. The analysis involved 34 nucleotide sequences. Codon positions included were 1st+2nd+3rd+Noncoding. All ambiguous positions were removed for [1.] Tamura K., Stecher G., Peterson D., Filipski A., and Kumar S. (2013). MEGA6: Molecular Evolutionary Genetics Analysis version 6.0. Molecular Biology and Evolution 30: 2725-2729.

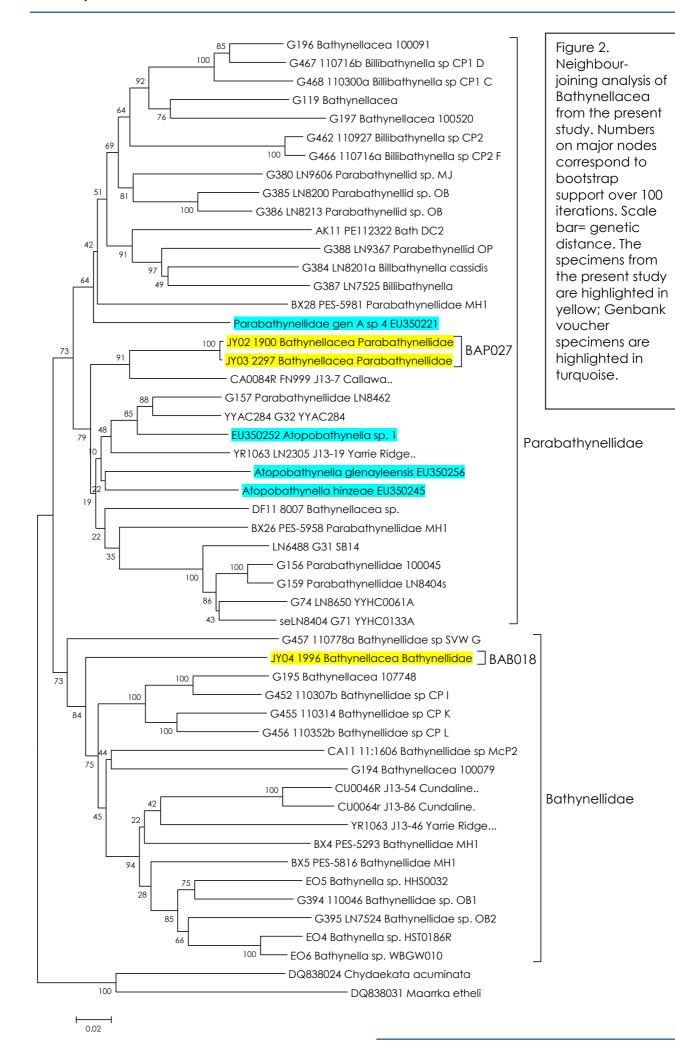
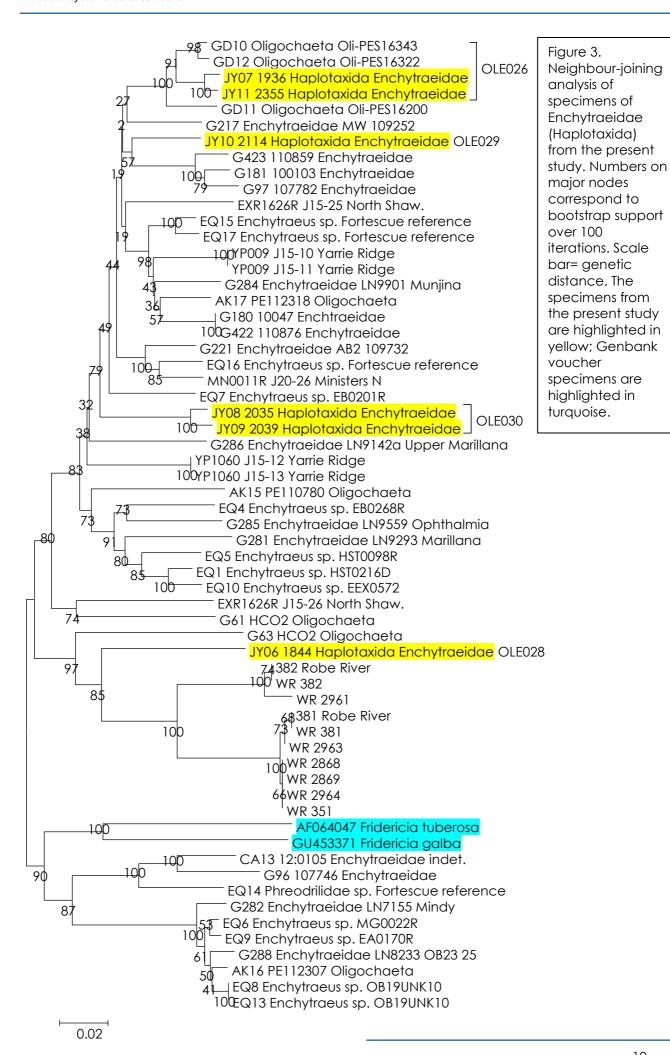


TABLE 2. Bathynellacea Distance Matrix																																											
	nellacea Parabathynellida nellacea Parabathynellida	neliacea Bathynelliaae	glenayleensis EU350256	n hinzeae EU350245	arabathynellidae MH1	arabathynellidae MH1	hynellidae MH1	<	79 JIS-/ Callawa Bathynellidae sp McP2	daline	Cundaline.	nellacea sp.	sp. HST0186R	sp. HHS0032	sp. WBGW010	bathynella sp. 1	1C4	ynellidae 100045	de LN84	cea 100079	cea 107748	cea 100091	cea 100520	abathynellid sp. MJ	Billbathynella cassidis	abathynellid sp. OB	abathynellid sp. OB bathynella	abethynellid OP	hynellidae sp. OB1	thynellidae sp. OB2	nellida	nynellidae sp.C.P.R. athynellidae sp.C.P.L.		Billibathynella sp CP2	nella sp CP2	bathynella sp CP1	llibathynella sp CP1 C	C0061A	4 co 4 Eli35021	20133A	nnie Ridge	J13-19 Yame Ridge	AC284
Specimen ID	JY02 1900 Bathyr JY03 2297 Bathyr	JY04 1996 Bathyr AK11 PE112322 B	Atopobathynello	Atopobathynellc	P.ES-	BX28 PES-5981 Par	BX4 PES-5293 Bat	BX5 PES-5816 Bathynellidae	CAU084R FN999 JIS-7 CA11 11:1606 Bathyn	CU0046R J13-54	CU0064r J13-86 C	DF11 8007 Bathyr	EO4 Bathynella s	EO5 Bathynella s	nella	EU350252 Atopob	G119 LCOI Plate	G156 Parabathy	Parabath	G194 Bathynella	G195 Bathynella	G196 Bathynella	G197 Bathynella	G380 LN9606 Parabat	G384 LN8201a Bi	G385 LN8200 P or	G386 LN8213 Por G387 LN7525 Billi	G388 LN9367 Par	G394 110046 Bat	G395 LN7524 Bai	G452 110307b Bc	G455 110314 BGI G456 110352b Bc	G457 110778aBc	G462 110927 Billi	G466 110716a Billibathyr		G468 110300a Billibathyr		EN6488 G31 SB14	Sell/8404 G71 YY	YR1063 J13-46 Yarrie	305	YY AC284 G32 YY
JY02 1900 Bathynellacea Parabathynellidae JY03 2297 Bathynellacea Parabathynellidae	0.002 0.	016 0.	019 0.0	17 0.015	0.014	0.016	0.018	0.016	0.013 0.0	0.0	23 0.0	24 0.01	8 0.017	0.016	0.017	0.016	0.018	0.020 0.	.017 0.0	020 0.02	0.0	17 0.018	0.019	0.017	0.015	0.016	0.015 0.0	17 0.01	8 0.016	0.015	0.017 0	.015 0.0	0.01	5 0.016	0.016	0.016	0.016	0.017 0	0.018 0.	017 0.0	018 0.01	18 0.0	7 0.016
	0.236 0.236	0.016	018 0.0	17 0.012	0.014	0.016	0.016	0.016	0.015 0.0	0.0	20 0.0	19 0.02	0.017	7 0.016	0.017	0.018	0.018 (0.019 0.	.017 0.0	020 0.0	8 0.0	14 0.018	3 0.019	0.016	0.015	0.015	0.016 0.0	16 0.01	7 0.015	0.016	0.017 0	0.015 0.0	014 0.01	5 0.016	0.016	0.018	0.017	0.017 0	0.019 0.	017 0.0	018 0.0	17 0.0	5 0.018
AK11 PE112322 Bath DC2	0.233 0.231 0.	.261	0.0	19 0.021	0.016	0.017	0.020	0.021	0.018	0.0	24 0.0	24 0.02	4 0.02	0.019	0.021	0.019	0.020	0.021 0.	.019 0.0	020 0.02	1 0.0	19 0.02	1 0.020	0.017	0.017	0.015	0.016	16 0.01	7 0.020	0.019	0.020 0	.020 0.0	0.01	8 0.01	0.016	0.020	0.019	0.019 0	0.019 0.	020 0.0	019 0.02	21 0.0	7 0.019
Atopobathynella glenayleensis EU350256	0.177 0.175 0.		224	0.016	0.016	0.018	0.017	0.024	0.019	0.0	21 0.0	21 0.01	8 0.02	0.021	0.021	0.016	0.020	0.018 0.	.016 0.0	0.02	3 0.0	23 0.017	7 0.018	0.018	0.019	0.017	0.017	20 0.02	0.020	0.020	0.023 0	.019 0.0	0.02	0.018	0.018	0.018	0.019	0.016 0	.018 0.	017 0.0	0.02	21 0.0	5 0.015
Atopobathynella hinzeae EU350245	0.144 0.142 0.		240 0.15	59	0.017	0.020	0.022	0.023	0.019 0.0	020 0.0	24 0.0	24 0.02	1 0.022	2 0.022	0.022	0.016	0.018	0.021 0.	.016 0.0	020 0.02	5 0.0	24 0.019	9 0.021	0.017	0.019	0.017	0.019 0.0	19 0.02	0.022	0.022	0.022 0	.021 0.0	0.01	8 0.018	0.019	0.019	0.019	0.019 0	0.018	016 0.0	019 0.02	25 0.02	0.015
BX26 PES-5958 Parabathynellidae MH1 BX28 PES-5981 Parabathynellidae MH1	0.168 0.168 0.	.LLO U.	236 0.18 241 0.2	10 0.178	7 0.216	0.015	0.017 (0.017 (0.015 0.0	0.0	21 0.0	21 0.01	0.018	0.017	0.018	0.016	0.017 (0.016 0.	017 0.0	015 0.0	8 0.0	16 0.01	0.020	0.014	0.015	0.016	0.015 0.0	14 0.01	6 0.017	0.017	0.015 0	0.016	0.01	5 0.014	0.015	0.015	0.016	0.015 0	0.015 0.	017 0.0	015 0.01	18 0.0	4 0.016
BX4 PES-5293 Bathynellidae MH1	0.259 0.258 0		241 0.2 265 0.2	67 0.263		0.296	0.018	0.017	0.018 0.0	0.0	19 0.0	20 0.02	1 0.014	4 0.013	0.017	0.018	0.020 0	0.020 0.	.020 0.0	017 0.03	0.0	18 0.07	1 0.021	0.018	0.013	0.013	0.018 0.0	19 0.01	9 0.014	0.017	0.017 0	.016 0.0	0.01	6 0.018	0.018	0.018	0.016	0.020 0	0.020 0.	020 0.0	020 0.01	17 0.0	8 0.020
BX5 PES-5816 Bathynellidae MH1	0.236 0.236 0.		266 0.25				0.180	C	0.018 0.0	0.0	21 0.0	21 0.02	4 0.013	3 0.014	0.014	0.020	0.021	0.021 0.	.021 0.0	021 0.0	8 0.0	18 0.02	1 0.021	0.019	0.018	0.019	0.018 0.0	19 0.01	9 0.015	0.013	0.016 0	.016 0.0	0.01	6 0.018	0.018	0.017	0.016	0.022 0	0.021 0.	021 0.0	022 0.01	14 0.02	0.022
CA0084R FN999 J13-7 Callawa	0.108 0.108 0.	.200	220 0.17	74 0.171	0.152	0.219	0.261	0.243	0.0	0.0	21 0.0	22 0.02	0.019	0.017	0.019	0.020	0.021	0.020 0.	.019 0.0	020 0.0	9 0.0	16 0.018	0.021	0.015	0.016	0.016	0.016	17 0.01	7 0.017	0.017	0.017 0	.017 0.0	0.01	5 0.017	0.017	0.015	0.016	0.017 0	0.020 0.	017 0.0	020 0.01	16 0.0	5 0.020
CA11 11:1606 Bathynellidae sp McP2	0.264 0.264 0.		295 0.25	59 0.253	0.263	0.274	0.234	0.235).279	0.0	23 0.0	24 0.02	4 0.017	7 0.018	0.016	0.019	0.022	0.020 0.	.018 0.0	019 0.02	0.0	19 0.02	0.021	0.017	0.017	0.017	0.017	18 0.01	9 0.016	0.019	0.017 0	.017 0.0	0.01	9 0.017	0.016	0.017	0.018	0.021 0	0.019	020 0.0	021 0.01	18 0.0	7 0.019
CU0046R J13-54 Cundaline	0.274 0.271 0.	.226 0.	273 0.2	60 0.279	0.267	0.307		0.214 0	0.245 0.2	264 262 0.0	0.0	10 0.02	5 0.02	0.020	0.021	0.021	0.023 (0.024 0.	.022 0.0	022 0.02	5 0.0	21 0.022	2 0.023	0.023	0.023	0.022	0.023 0.02	24 0.02	3 0.020	0.019	0.023 0	.022 0.0	020 0.02	2 0.023	0.023	0.023	0.024	0.023 0	0.022 0.	023 0.0	023 0.02	21 0.02	3 0.021
CU0064r J13-86 Cundaline. DF11 8007 Bathynellacea sp.	0.283 0.281 0.	224 0.	282 0.26 252 0.17	6∠ U.2/5 78 ∩ 1∠3	0.265	0.312		0.219 0		0.0	66 0.2	69	0.020	5 0.019	0.021	0.021	0.022 (0.022 0. 0.019 0	0.022 0.0	021 0.02 018 0.04	4 0.0	22 0.02	1 0.025	0.024	0.023	0.022	0.023 0.02	21 0.02	∠ 0.020 4 0.025	0.019	0.023 0	.021 0.0	0.02 120 0.02	4 0.023	0.022	0.023	0.025	0.022 0	1.021 0. 1.014 0	023 0.0	022 0.02 017 0.04	20 0.02 26 0.01	0.021
EO4 Bathynella sp. HST0186R	0.252 0.253 0		275 0.2	0.100	0.176	0.243		0.157 (247 0.2	02 0.2	07 0.26	9	0.012	0.007	0.021	0.021	0.022 0	.020 0.0	021 0.01	8 0.0	17 0.02	0.020	0.018	0.018	0.018	0.018 0.0	18 0.01	9 0.012	0.014	0.017 0	.018 0.0	0.02	5 0.018	3 0.019	0.018	0.017	0.021 0	.022 0.	022 0.0	020 0.01	16 0.0	9 0.020
EO5 Bathynella sp. HHS0032	0.246 0.244 0.			44 0.255	0.233	0.291	0.197	0.168	0.249 0.2	251 0.2	05 0.2	02 0.27	2 0.130)	0.013	0.020	0.020	0.021 0.	.021 0.0	021 0.0	9 0.0	16 0.020	0.023	0.017	0.018	0.018	0.017 0.0	18 0.01	8 0.011	0.013	0.016 0	.017 0.0	0.01	6 0.01	0.016	0.017	0.016	0.020 0	0.022 0.	020 0.0	021 0.01	14 0.0	8 0.022
EO6 Bathynella sp. WBGW010	0.237 0.239 0.		268 0.23		0.236				0.248 0.2	235 0.1		93 0.25	5 0.039	0.133		0.021	0.020	0.022 0.	.020 0.0	021 0.0	8 0.0	16 0.02	0.022	0.017	0.018	0.017	0.018	18 0.01	8 0.014	0.013	0.016	.017 0.0	0.01	5 0.017	0.017	0.018	0.017	0.021 0	0.021 0.	022 0.0	019 0.01	16 0.0	9 0.022
EU350252 Atopobathynella sp. 1	0.154 0.152 0.	.210 0.	231 0.13	07 0.1 1	0.100			0.232	0.150 0.2	-00 0.2	.00 0.2	64 0.16	1 0.24	. 0.200	0.232		0.018	0.019 0.	.013 0.0	0.02	5 0.0	20 0.017	7 0.017	0.018	0.018	0.018	0.018	19 0.01	8 0.021	0.020	0.021 0	.019 0.0	0.01	9 0.020	0.020	0.018	0.018	0.017 0	.017 0.	019 0.0	0.02	22 0.0	7 0.013
G119 LCOI Plate1C4	0.208 0.205 0.		223 0.22	LO O.LL				0.268	_	299 0.2		94 0.21		7 0.290	0.268	0.214	0.041	0.020 0.	.018 0.0	020 0.02	5 0.0	21 0.019	9 0.017	0.016	0.020	0.015	0.016 0.02	21 0.01	9 0.022	0.019	0.021 0	0.020 0.0	0.01	8 0.019	0.020	0.018	0.018	0.020 0	0.019 0.	016 0.0	019 0.02	25 0.0	9 0.019
G156 Parabathynellidae 100045 G157 Parabathynellidae LN8462	0.200 0.198 0.		242 0.18	75 0.140	0.161		0.276	0.230 0	1.195 0.2	253 0.2	., 0 0.2	67 0.16 74 0.16	8 0.248 3 0.24	0.238	0.238	0.182	0.241	0.	.015 0.0	014 0.02	2 0.0	22 0.019	0.019	0.020	0.020	0.018	0.019 0.02	21 0.02	0.022	0.021	0.021 0	020 0.0	0.02	0.017	0.017	0.017	0.020	0.013 0	0.015	020 0.0	012 0.02	22 0.0	9 0.018
G157 Farabathynellidae LN8404s	0.167 0.163 0.		249 0.18	82 0.142	0.147	0.242	0.233 (0.238 0	200 0 3	251 0.2		64 0.16	3 0.24	6 0.242	0.232	0.104	0.212	0.029 0.	169	0.02	2 0.0	22 0.01	9 0.017	0.017	0.016	0.018	0.018 0.0	21 0.01	0.021	0.021	0.017 0	020 0.0	119 0.02	1 0.017	7 0.020	0.017	0.020	0.017 0	0.013 0.	017 0.0	018 0.02	23 0.0	9 0.012
G194 Bathynellacea 100079	0.265 0.262 0.		299 0.29	98 0.293	3 0.281	0.300		0.246		256 0.2		69 0.30		6 0.249	0.256	0.290		0.298 0.	.281 0.:	290	0.0	18 0.02	4 0.022	0.016	0.017	0.017	0.018 0.02	20 0.01	8 0.019	0.017	0.018 0	.018 0.0	0.01	8 0.017	0.017	0.021	0.019	0.022 0	0.023 0.	023 0.0	023 0.01	18 0.0	7 0.024
G195 Bathynellacea 107748	0.225 0.225 0.	.219 0.	253 0.26	62 0.231	0.221	0.261	0.216	0.209	0.219 0.2	219 0.2	19 0.2	14 0.22	3 0.230	0.235	0.215	0.226	0.269	0.221 0.	.207 0.:	229 0.23	15	0.020	0.022	0.016	0.016	0.016	0.017 0.0	18 0.01	7 0.017	0.018	0.010 0	.014 0.0	0.01	7 0.020	0.020	0.018	0.018	0.022 0	.022 0.	020 0.0	022 0.01	19 0.0	6 0.022
G196 Bathynellacea 100091	0.198 0.196 0.	. <mark>253</mark> 0.	235 0.20	00 0.211	0.234	0.190	0.276	0.259	0.214 0.2	273 0.2	86 0.2	90 0.23	8 0.278	0.278	0.271	0.228	0.143	0.242 0.	.230 0.:	236 0.30	0.2	71	0.019	0.016	0.018	0.015	0.018	20 0.01	8 0.020	0.020	0.022 0	.020 0.0	0.01	9 0.01	0.016	0.010	0.012	0.018 0	0.018	0.0	0.02	23 0.0	9 0.020
G197 Bathynellacea 100520	0.228 0.225 0.	.2,000.	247 0.23	0.1 0.2 12	0.245	0.232	0.282	0.305	0.255 0.3	303 0.3	0.0	31 0.26	4 0.305	5 0.311	0.292	0.253	0.156	0.259 0.	.2 12 0	242 0.32	9 0.2		4	0.015	0.018	0.016	0.01	20 0.01	8 0.022	0.022	0.021 0	.019 0.0	0.01	9 0.020	0.020	0.021	0.019	0.021 0	0.019 0.	017 0.0	020 0.02	24 0.0	9 0.019
G380 LN9606 Parabathynellid sp. MJ	0.199 0.199 0.	.236 0.	219 0.2	11 0.200	0.200	0.216		0.254 0	0.200 0.2	284 0.2	83 0.2	98 0.20 79 0.24	9 0.25	0.267	0.236	0.213	0.190 (0.213 0.	200 0.:	211 0.27	4 0.2	0.100	0.170	0 170	0.015	0.013	0.012 0.0	15 0.01	5 0.017	0.017	0.017 0	.018 0.0	0.01	/ 0.015	0.015	0.015	0.015	0.020 0	0.019 0.	016 0.0	019 0.01	17 0.0	6 0.017
G384 LN8201 a Billbathynella cassidis G385 LN8200 Parabathynellid sp. OB	0.222 0.222 0.	257 0	212 0.19	OO O.LLC	0.231	0.211				277 0.2 271 0.2	95 0.2	00 0.24	1 0.26	7 0.260	0.245	0.225		0.248 0.	190 0	255 0.29			3 0.217 6 0.205	0.179	0 192	0.014	0.014 0.0	15 0.01	4 U.UI/	0.01/	0.016 0	0.0	114 0.01	5 0.013	0.015	0.016	0.013	0.019 0	1.017 0.	014 0.0	0.0 0.0	1/ 0.0	6 0.018
G386 LN8213 Parabathynellid sp. OB	0.191 0.191 0	_	197 0.20	, O 0.200				0.245		268 0.2	_	93 0.20	7 0.26		0.257	0.205	0.172	0.219 0	,0 0		9 0.2	_			0.172	0.066	0.0	16 0.01	6 0.017	0.016	0.016 0	.018 0.0	0.01	6 0.015	0.015	0.015	0.015	0.016 0	0.016 0	016 0.0	016 0.01	18 0.0	6 0.017
G387 LN7525 Billibathynella	0.230 0.233 0.	.246 0.	204 0.25	55 0.242	0.218	0.212	0.256			281 0.3	02 0.3	00 0.25	2 0.250	0.260		0.251	0.212	0.248 0.	.234 0.:				5 0.238	0.195	0.155	0.198	0.191	0.01	4 0.017	0.019	0.017 0	.016 0.0	0.01	5 0.01	0.016	0.016	0.016	0.020 0	.022 0.	019 0.0	020 0.01	19 0.0	8 0.018
Cood E147507 T drabelity ficilia Of	0.244 0.243 0.	.272 0.	212 0.24	46 0.255	0.240	0.235		0.268	0.226 0.2	286 0.2	81 0.2	74 0.26		0.261	0.258	0.244		J. 200 0.	.242 0.:	259 0.27	3 0.2	53 0.19	. 0.200	0.202	0.164	0.216	0.17	79	0.018	0.017	0.017 0	.016 0.0	0.01	8 0.017	0.017	0.015	0.016	0.021 0	0.020 0.	0.0	021 0.01	19 0.0	6 0.019
G394 110046 Bathynellidae sp. OB1	0.246 0.244 0.	.221 0.	282 0.23	32 0.238	0.231	0.275		0.166	0.241 0.2	238 0.1	86 0.2	00 0.26	4 0.142	2 0.118	0.137	0.244		0.244 0.	238 0.:	244 0.25	6 0.2	28 0.263	0.288	0.258	0.250	0.257	0.258 0.25	0.25	8	0.013	0.016 0	.016 0.0	0.01	6 0.016	0.015	0.017	0.017	0.022 0	0.020 0.	021 0.0	021 0.01	14 0.0	9 0.021
G395 LN7524 Bathynellidae sp. OB2	0.261 0.262 0.		277 0.26		0.243	0.288		0.164	0.261 0.2	246 0.2		98 0.27	4 0.13	0.139	0.130	0.265		0.255 0.		253 0.26	0.2		0.288		0.265	0.276	0.257 0.26	52 0.25 35 0.24	8 0.150	0.000	0.019 0	.017 0.0	0.01	6 0.017	0.017	0.018	0.017	0.021 0	0.021 0.	020 0.0	020 0.01	14 0.0	8 0.020
G452 110307b Bathynellidae sp CP I G455 110314 Bathynellidae sp CP K	0.214 0.214 0.	.∠18 0. 209 ∩	253 0 2	51 N 239	3 0.224	0.239	0.210	J. 199 C	1.221 0.2	212 0.2	24 0.2	21 0.23	6 0.216	0.222	0.209	0.215	0.263 ().ZZ3 ().) 213 ()	217 0.	225 0.23	7 0.0	35 0.25	7 0.290	0.226	0.233	0.22/ 0	0.229 0.20	29 0.24	2 0.216	0.238	0.136	0.U 0.C	0.01 0.01	5 0.018	3 0.019	0.018	0.019	0.020 0	1020 0	021 0.0	020 U.U 021 0.01	19 0.0	8 0.022
G456 110352b Bathynellidae sp CP L	0.227 0.227 0.	.196 0.	253 0.23	38 0.228	3 0.221	0.247	0.215	0.199 0	0.229 0.2	212 0.2	21 0.2	14 0.22	6 0.222	2 0.229	0.209	0.213	0.259	0.219 0.	.215 0.:	219 0.24	3 0.1	32 0.240	0.280	0.226	0.245	0.240 (0.246 0.22	25 0.23	3 0.226	0.226	0.137 0	1.098	0.01	5 0.016	0.016	0.015	0.016	0.019 0	0.017 0.	020 0.0	019 0.01	18 0.0	6 0.019
G457 110778a Bathynellidae sp SVW G	0.237 0.236 0.	.243 0.	256 0.24	44 0.223	3 0.231	0.267	0.253	0.241	0.242 0.2	272 0.2	62 0.2	69 0.25	7 0.238	3 0.246	0.231	0.211	0.246	0.236 0.	.217 0.:	232 0.27	1 0.2	24 0.24	2 0.263	0.238	0.258	0.245	0.243 0.24	47 0.26	4 0.238	3 0.255	0.217 0	.224 0.2	214	0.01	0.016	0.016	0.017	0.020 0	0.021 0.	021 0.0	022 0.01	18 0.0	7 0.020
G462 110927 Billibathynella sp CP2	0.211 0.211 0.	. <mark>253</mark> 0.	231 0.23	32 0.240	0.209	0.222	0.267	0.269	0.213 0.2	272 0.3	0.0	05 0.24	8 0.279	0.259	0.275			J.LUL U.	.244 0.:	215 0.26	9 0.2	0, 0.10	. 0.2	0.179	0.221	0.185	0.199 0.2	12 0.23	0.262				246 0.27	0	0.006	0.014	0.015	0.018 0	.017 0.	0.0	0.01	19 0.0	7 0.019
G466 110716a Billibathynella sp CP2 F	0.209 0.209 0.		233 0.23			0.228			0.216 0.2			93 0.25		0.262			0.192		.246 0.:				. 0.2.0	0.182	0.216		0.204 0.2	10 0.23					248 0.27		2	0.015	0.015	0.017 0	.017 0.	017 0.0	016 0.01	19 0.0	8 0.020
G467 110716b Billibathynella sp CP1 D	0.202 0.202 0.		231 0.20	09 0.215		0.201	0.267 (0.247	0.206 0.2	279 0.2		86 0.23	0.20	0.268		0.238		0.228 0.	244 0.:	232 0.28	0.2		3 0.211	0.180	0.211	0.166	0.163 0.2	0.20	9 0.266		0.254 0	.243 0.2	245 0.25	7 0.107	0.188	0.000	0.011	0.018 0	0.017 0.	017 0.0	018 0.02	20 0.0	7 0.021
G468 110300a Billibathynella sp CP1 C G74 LN8650 YYHC0061A	0.206 0.203 0.	.200 0.	233 0.2 236 0.18	13 U.219	0.237	0.226	0.263 (0.250	1.219 0.2	279 0.2	0.2	86 0.23	8 U.26	0.272	0.254	0.248	0.143 (0.234 0.	172 0.	238 U.29	0.2		0.194		0.223	0.163 (0.179 0.22	22 0.20	9 0.262	0.2//	0.259 0	234 0.2	259 0.25	0.192	0.194	0.089	0.241	0.019 0	1.019 0.	018 0.0	0.0 010	14 0.0	9 0.021
LN6488 G31 SB14	0.207 0.205 0.	218 0	255 D 1	72 N 183	0.100	0.232	0.20/ 0).231 C	201 0.2	264 0.2	61 0.2	54 0 14	3 0.23	7 0.262	0.249	0.106	0.233 0	0.077 U.	164 0	0/3 U.Z	7 0.2	25 0.23	3 0.249	0.220	0.233	0.20/ 0	208 0.20	52 U.25 50 0.25	2 0.2/2	0.204	0.243 0	224 0.2	204 0.23	6 0.23	1 0.241	0.230	0.241	n n88	n.013 ().	019 0.0	012 0.02	22 D.U.	9 0.015
Parabathynellidae gen A sp 4 EU350221	0.165 0.163 0.	.209 0.	200 0.17	75 0.171	0.197	0.190	0.265	0.242 0	0.157 0.2	265 0.2	48 0.2	62 0.19	7 0.26	0.248	0.248	0.178	0.170	0.219 0.	.167 0.:	213 0.3	4 0.2	38 0.16	7 0.207	0.167	0.200	0.167	0.154 0.22	21 0.20	5 0.246	0.259	0.236 0	.248 0.2	234 0.23	4 0.209	0.209	0.177	0.184	0.220 0	1.222	0.0	018 0.02	23 0.0	9 0.018
seLN8404 G71 YYHC0133A	0.195 0.192 0.	.218 0.	240 0.17	72 0.188	0.161	0.228		0.243	0.207 0.2	266 0.2	81 0.2	74 0.16	1 0.249	0.251	0.243	0.165	0.246		.161 0.0	065 0.30	5 0.2	36 0.23	4 0.259	0.220	0.262	0.215	0.213 0.20	66 0.26	4 0.249	0.259	0.238 0	.226 0.2	222 0.23	4 0.234	0.243	0.234	0.236	0.071 0	.071 0.	222	0.02	23 0.03	0 0.014
YR1063 J13-46 Yarrie Ridge	0.286 0.290 0.		294 0.27	7 0 0.000	0.279	0.298	0.203	0.195	0.272 0.2	253 0.2	02 0.2	07 0.29	8 0.202	2 0.186	0.207	0.295	0.307	0.298 0.	.302 0.:	298 0.24	8 0.2	56 0.283	3 0.314	0.296	0.282	0.293	0.283 0.27	77 0.28	1 0.176		0.240 0	.254 0.2	251 0.28	5 0.285	0.282	0.282	0.283	0.327 0	.304 0.	286 0.3	314	0.0	6 0.022
YR1063 LN2305 J13-19 Yarrie Ridge YYAC284 G32 YYAC284	0.165 0.165 0.		208 0.15		0.148			J.2 10 C			60 0.2					0.150	0.220			179 0.27	1 0.2		9 0.236			0.195	0.184		2 0.257		0.222 0	.232 0.2	217 0.24			0.216	0.237	0.1010	1.189 0.	171 0.	181 0.27	72	0.018
	0.150 0.152 0.							2 247 0	1 47 0 4	274 In 2	10 In 2	55 IO 17	ALO OF	EIO OFT								27 0 22	410 042	10 207	0.213	0 100 0	0.184 0.23	001004	010 243	010010	0 215 0	22/10/	220 0 22		10001					1/5/0		94 0.1	01

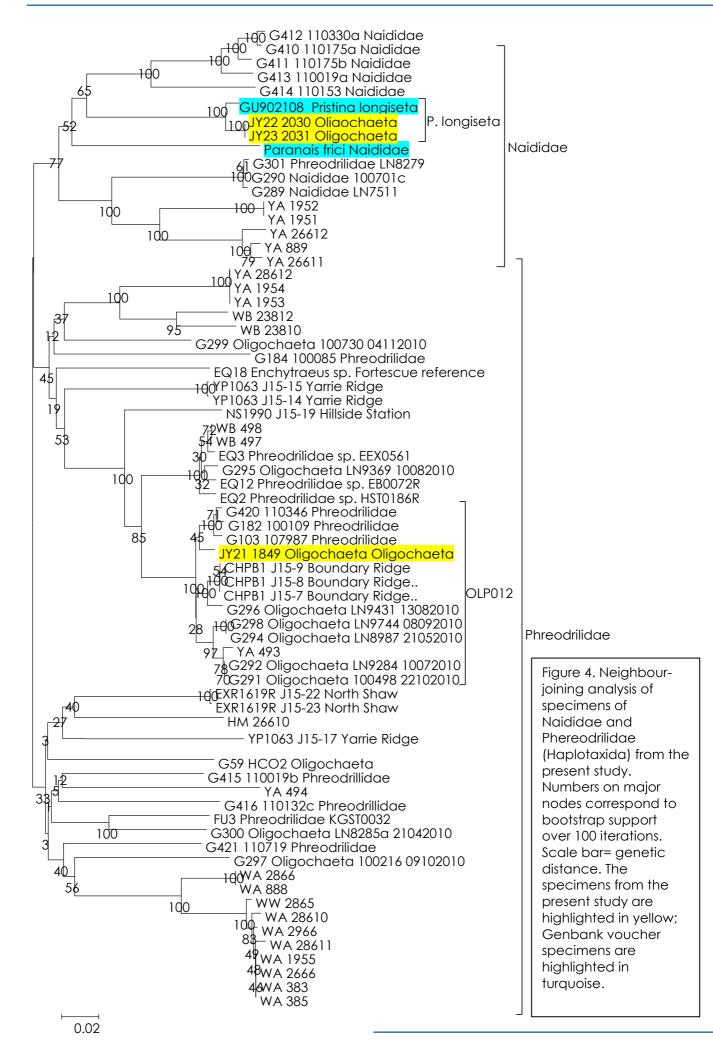
Estimates of Evolutionary Divergence between Sequences
The number of base differences per site from between sequences are shown. Standard error estimate(s) are shown above the diagonal. The analysis involved 52 nucleotide sequences concerning the sequence pair. There were a total of 834 positions in the final dataset. Evolutionary analyses were concerning the sequence pair. There were a total of 834 positions in the final dataset. Evolutionary Genetics Analysis version 6.0. Molecular Biology and Evolution 30: 2725-2729.

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TABLE 3. Enchytraeidae Distance Matrix		1 1	т т																	т .		T 1											
Specimen ID	Y06 1844 Hapiolaxida Enchytraeidae Y07 1936 Hapiolaxida Enchytraeidae	708 2035 Haplotaxida Enchytraeidae 709 2039 Haplotaxida Enchytraeidae	Y 10 21 14 Haplotaxida Enchytraeidae	Y I I 2355 Haplotaxida Enchyltaeidae 81 Robe River	82. Robe River LF064047 Fridericia Iuberosa	.K15 PE110780 Oligochaeta	K16 PE112307 Oligochaeta K17 PE112318 Oligochaeta	CA13 12:0105 Enchytraeldae Indet. Q1 Enchytraeus sp. HST0216D		Q5 Enchytraeus sp. HST0098R Q6 Enchytraeus sp. MG0022R	Q7 Enchytraeus sp. 680201 R Q8 Enchytraeus sp. O819UnK10 Q9 Enchytraeus sp. EA0170R	Q10 Enchytraeus sp. EEX0572 Q13 Enchytraeus sp. OB19UNK10	Q14 Phreodilidae sp. Fartescue reference Q15 Enchytraeus sp. Fortescue reference	Q16 Enchytraeus sp. Fortescue reference	Q17 Enchytraeus sp. Fortescue reference XR1 626R J15-25 North Shaw.	XR1626R J15-26 North Shaw. S61 HCO2 Oligochaeta	5180 10047 Enchtraeidae	3181 100103 Enchytraeidae	5217 Enchytraeidae MW 109252 5221 Enchytraeidae AB2 109732	2281 Enchytraeidae LN9293 Marillana 2282 Enchytraeidae LN7155 Mindy Coondine	2284 Enchytraeidae LN9901 Munjina	2285 Enchytraeldae LN9559 Ophthalmia 2286 Enchytraeldae LN9142a Upper Manillano	5288 Enchytraeidae LN8233 OB23 25 5422 1 1087 & Enchytraeidae	5423 1 10859 Enchytraeidae	59 & 1077 4& Enchytraeidae 597 107782 Enchytraeidae	5D 10 Oligochaeta Oli-PES 1 63 43 5D 11 Oligochaeta Oli-PES 1 6200	5D12 Oligochaeta Oli-PES1 6322 5U453371 Fridericia galba	AN0011R J20-26 Ministers N	VR 2869 VR 2869	VR 2961 NR 2963	VR 2964	NR 351 PDO9-J15-10 Yorrie Ridge PDO9-J15-11 Yorrie Ridge	P1060 J15-12 Yarrie Ridge P1060 J15-13 Yarrie Ridge
JY06 1844 Haplotaxida Enchytraeidae	0.014	0.014 0.014	0.014	0.014 0.014	0.017 0.01	4 0.013	0.014 0.014	0.016 0.013	0.014	0.014 0.014	0.013 0.014 0.014	1 0 013 0 014	0.015 0.013	3 0.013	0.014 0.014	0.015 0.013 0	013 0.0	14 0.013 0	0 0 0	2 0.014 0.0	14 0.015	0.012 0.013	0.015 0.014	0.013	0.015 0.013	0.014 0.013	0.014 0.0	014 0 014	0014 0014	0.017 0.0	014 0.014	0.014 0.013 0.013	3 0 0 1 4 0 0 1 4
JY07 1936 Haplotaxida Enchytraeidae	0.163	0.011 0.010	0.010	0.004 0.019	0.016 0.01	7 0.011	0.014 0.010	0.014 0.011	0.014	0.011 0.014	0.010 0.014 0.01-	0.011 0.014	0.015 0.010	0.009	0.010 0.012	0.014 0.015 0.	014 0.0	09 0.011 0	0.009 0.010	0.011 0.0	14 0.010	0.013 0.011	0.014 0.009	0.011	0.015 0.012	0.006 0.007	0.007 0.0	0.009	0.018 0.018	0.016 0.0	018 0.018	0.018 0.010 0.010	0.010 0.010
JY08 2035 Haplotaxida Enchytraeidae	0.167 0.080		0.011	0.010 0.019	0.017 0.013	5 0.012	0.013 0.011	0.015 0.011	0.012	0.012 0.012	0.010 0.013 0.013	0.011 0.013	0.015 0.011	0.010	0.011 0.012	0.012 0.014 0.	0.0	10 0.011 0	0.010	0.013 0.0	13 0.011	0.011 0.011	0.013 0.010	0.011	0.015 0.011	0.011 0.010	0.010 0.0	0.009	0.019 0.019	0.017 0.0	019 0.019	0.019 0.011 0.011	0.010 0.010
JY09 2039 Haplotaxida Enchytraeidae	0.167 0.087		0.009	0.010 0.019	0.017 0.01:	5 0.011	0.012 0.011	0.013 0.010	0.012	0.011 0.011	0.009 0.012 0.013	0.010 0.012	0.014 0.011	0.010	0.011 0.012	0.012 0.013 0.	0.0	10 0.011 0	0.010	0.013 0.0	12 0.011	0.011 0.010	0.012 0.010	0.011	0.014 0.011	0.011 0.010	0.011 0.0	0.010	0.018 0.018	0.017 0.0	0.018	0.018 0.011 0.011	0.009 0.009
JY10 2114 Haplotaxida Enchytraeidae		0.089 0.090		0.010 0.018	0.018 0.01	6 0.011	0.013 0.009	0.013 0.010	0.012	0.011 0.013	0.009 0.013 0.013	0.011 0.013	0.014 0.008	8 0.009	0.010 0.011	0.013 0.013 0.	0.0	10 0.009 0	0.009 0.009	0.012 0.0	14 0.010	0.011 0.010	0.014 0.010	0.009	0.014 0.009	0.009 0.009	0.009 0.0	0.009	0.017 0.017	0.017 0.0	0.017	0.017 0.009 0.009	0.010 0.010
JY11 2355 Haplotaxida Enchytraeidae 381 Robe River	0.140 0.179	0.080 0.085	0.0/4	0.019	0.016 0.018	0.012	0.014 0.009	0.014 0.011	0.013	0.011 0.014	0.010 0.014 0.01	0.011 0.014	0.015 0.010	0.009	0.010 0.012	0.014 0.015 0.	014 0.0	19 0.011 0	0.009	0.012 0.0	114 0.010	0.013 0.010	0.014 0.009	0.011	0.015 0.011	0.006 0.007	0.006 0.0	114 0.009	0.018 0.018	0.016 0.0	0.018	0.004 0.009 0.009	0.010 0.010
381 Robe River 382 Robe River	0.140 0.178	0.183 0.175	0.186	0.183	0.015 0.01	1 0.017	0.019 0.018	0.020 0.020	0.020	0.019 0.019	0.018 0.019 0.01	0.019 0.019	0.019 0.013	7 0.017	0.018 0.019	0.017 0.016 0.	0.0 0.0	18 0.020 0	0.019 0.018	0.019 0.0	20 0.019	0.021 0.021	0.019 0.019	0.020	0.020 0.019	0.019 0.019	0.017 0.0	123 0.016	0.004 0.004	0.015 0.0	0.004	0.004 0.018 0.018	0.017 0.017
AF064047 Fridericia tuberosa		0.189 0.187	0.183	0.197 0.190	0.02	0.017	0.016 0.017	0.015 0.016	0.016	0.017 0.020	0.016 0.016 0.01	7 0.016 0.017	0.015 0.015	5 0.015	0.015 0.014	0.016 0.016 0	016 0.0	16 0.015	0.015 0.016	5 0.017 0.0	16 0.015	0.015 0.020	0.017 0.016	0.015	0.016 0.015	0.017 0.017	0.016 0.0	115 0.017	0.019 0.019	0.020 0.0	019 0.019	0.019 0.016 0.016	0.016 0.016
AK15 PE110780 Oligochgeta		0.124 0.124		0.113 0.192 0.161 0.195	0.192 0.18	8	0.013 0.010	0.014 0.010	0.011	0.010 0.013	0.010 0.013 0.01	0.010 0.013	0.015 0.010	0.011	0.011 0.011	0.012 0.011 0.	012 0.0	11 0.011 0	0.010	0.012 0.0	13 0.011	0.010 0.011	0.014 0.011	0.010	0.014 0.011	0.011 0.011	0.011 0.0	0.011	0.017 0.017	0.018 0.0	017 0.017	0.017 0.011 0.011	0.010 0.010
AK16 PE112307 Oligochaeta	0.184 0.163	0.144 0.141	0.150	0.161 0.195	0.198 0.193	2 0.171	0.014	0.012 0.013	0.014	0.014 0.006	0.012 0.004 0.003	0.013 0.004	0.012 0.014	4 0.013	0.014 0.015	0.014 0.013 0.	0.0	14 0.013 0	0.013 0.013	3 0.015 0.0	05 0.014	0.013 0.014	0.005 0.014	0.013	0.013 0.013	0.014 0.013	0.013 0.0	0.013	0.018 0.018	0.020 0.0	019 0.018	0.018 0.013 0.013	0.014 0.014
AK17 PE112318 Oligochaeta		0.089 0.096			0.158 0.183		0.162	0.013 0.011	0.012	0.011 0.014	0.009 0.014 0.014	0.011 0.014	0.014 0.009	9 0.009	0.008 0.010	0.013 0.013 0.	0.0	07 0.011 0	0.009 0.009	0.012 0.0	14 0.008	0.011 0.011	0.014 0.007	0.010	0.014 0.010	0.010 0.010	0.009 0.0	0.009	0.017 0.017	0.017 0.0	017 0.017	0.017 0.008 0.008	0.010 0.010
CA13 12:0105 Enchytraeidae indet.		0.152 0.143					0.126 0.155		0.014	0.013 0.011	0.013 0.012 0.01	0.013 0.012	0.009 0.015	5 0.011	0.015 0.015	0.015 0.013 0.	0.0	14 0.013 0	0.013	3 0.016 0.0	0.013	0.014 0.014	0.012 0.014	0.013	0.009 0.013	0.013 0.014	0.014 0.0	0.012	0.019 0.019	0.019 0.0	019 0.019	0.019 0.014 0.014	0.013 0.013
EQ1 Enchytraeus sp. HST0216D		0.105 0.106					0.162 0.106		0.010	0.008 0.013	0.010 0.012 0.013	0.005 0.012	0.014 0.009	9 0.010	0.010 0.011	0.013 0.013 0.	0.0	11 0.010 0	0.009 0.010	0.009 0.0	13 0.011	0.009 0.011	0.013 0.011	0.010	0.013 0.010	0.011 0.010	0.010 0.0	0.010	0.019 0.019	0.017 0.0	019 0.019	0.019 0.010 0.010	0.010 0.010
EQ4 Enchytraeus sp. EB0268R	0.171 0.109	0.104 0.110						0.171 0.073		0.010 0.014	0.011 0.013 0.01	0.010 0.013	0.014 0.010	0.011	0.011 0.012	0.013 0.013 0.	014 0.0	11 0.010 0	0.010 0.012	2 0.010 0.0	14 0.011	0.009 0.010	0.015 0.011	0.010	0.013 0.011	0.012 0.012	0.012 0.0	0.011	0.020 0.020	0.018 0.0	020 0.020	0.020 0.010 0.010	0.010 0.010
EQ5 Enchytraeus sp. HST0098R	0.158 0.110	0.113 0.108			0.209 0.183		0.166 0.112			0.013	0.011 0.013 0.014	0.008 0.013	0.013 0.010	0.010	0.010 0.011	0.013 0.012 0.	013 0.0	10 0.010 0	0.009 0.011	0.011 0.0	0.010	0.010 0.010	0.014 0.011	0.011	0.013 0.011	0.010 0.010	0.010 0.0	0.010	0.019 0.019	0.018 0.0	019 0.019	0.019 0.010 0.010	0.009 0.009
EQ6 Enchytraeus sp. MG0022R EQ7 Enchytraeus sp. EB0201R	0.186 0.138	0.144 0.141					0.019 0.156	0.125 0.138	0.169 (0.012 0.005 0.00	0.013 0.003	0.012 0.013	0.000	0.013 0.014	0.014 0.013 0.	014 0.0	00 0.010 0	0.013 0.013	0.013 0.0	12 0.014	0.014 0.013	0.005 0.014	0.013	0.012 0.013	0.013 0.013	0.013 0.0	13 0.013	0.019 0.019	0.020 0.0	019 0.019	0.019 0.013 0.013	0.013 0.013
EQ8 Enchytraeus sp. OB19UNK10		0.078 0.081		0.163 0.198		4 0 169		0.137 0.087			0.011 0.01	0.010 0.011	0.014 0.000	3 0.007	0.007 0.010	0.014 0.012 0.	013 0.0	14 0.013 0	0.010 0.007	0.013 0.0	0.010	0.011 0.012	0.012 0.010	0.007	0.014 0.010	0.010 0.007	0.010 0.0	14 0.013	0.018 0.018	0.017 0.0	010 0.010	0.018 0.007 0.007	0.010 0.010
EQ9 Enchytraeus sp. EA0170R	0.183 0.159	0.142 0.140	0.100	0.156 0.201	0.212 0.18	5 0 166	0.016 0.162	0.122 0.156	0.165	0.158 0.008	0.137 0.014	0.013 0.004	0.012 0.013	3 0.013	0.013 0.014	0.014 0.013 0	014 0.0	14 0.013 0	0.013 0.014	0.015 0.0	05 0.015	0.014 0.014	0.004 0.014	0.014	0.013 0.013	0.013 0.013	0.013 0.0	13 0.014	0.019 0.019	0.020 0.0	019 0.019	0.019 0.013 0.013	0.013 0.013
EQ10 Enchytraeus sp. EEX0572	0.160 0.113	0.102 0.106	0.109	0.110 0.198	0.198 0.18	5 0.101	0.159 0.112	0.160 0.024	0.082	0.050 0.155	0.092 0.155 0.15	0.012	0.013 0.010	0.010	0.010 0.011	0.012 0.013 0.	013 0.0	11 0.011 0	0.010 0.010	0.010 0.0	13 0.010	0.009 0.011	0.014 0.011	0.011	0.013 0.011	0.010 0.010	0.010 0.0	0.010	0.019 0.019	0.018 0.0	019 0.019	0.019 0.010 0.010	0.010 0.010
EQ13 Enchytraeus sp. OB19UNK10	0.186 0.166	0.144 0.141	0.153	0.163 0.198	0.209 0.194	4 0.169	0.013 0.166	0.127 0.158	0.169	0.159 0.017	0.141 0.000 0.01	0.155	0.012 0.013	3 0.013	0.013 0.014	0.014 0.013 0.	0.0	14 0.013 0	0.013	3 0.014 0.0	0.014	0.013 0.013	0.005 0.014	0.013	0.013 0.013	0.013 0.013	0.013 0.0	0.013	0.018 0.018	0.019 0.0	0.018	0.018 0.013 0.013	0.013 0.013
EQ14 Phreodrilidae sp. Fortescue reference	0.180 0.165	0.148 0.144	0.172	0.163 0.175	0.183 0.16	7 0.181	0.128 0.153	0.079 0.149		0.159 0.124		0.148 0.126	0.013	3 0.012	0.014 0.015	0.015 0.014 0.	0.0	14 0.014 0	0.014	0.017 0.0	12 0.015	0.014 0.015	0.013 0.014	0.014	0.009 0.015	0.014 0.014	0.014 0.0	0.014	0.018 0.018	0.018 0.0	0.018	0.018 0.013 0.013	0.014 0.014
EQ15 Enchytraeus sp. Fortescue reference	0.153 0.082	0.096 0.103	0.057	0.080 0.178			0.153 0.048			0.099 0.147		0.099 0.152		0.008	0.005 0.010	0.013 0.012 0.	0.0	07 0.010 0	0.009 0.009	0.012 0.0	14 0.008	0.010 0.010	0.014 0.007	0.009	0.014 0.009	0.009 0.009	0.009 0.0	0.008	0.018 0.018	0.017 0.0	0.018	0.018 0.008 0.008	0.010 0.010
EQ16 Enchytraeus sp. Fortescue reference	0.153 0.074	0.089 0.085	0.075				0.162 0.079			0.092 0.152		0.099 0.158		1 0 070	0.008 0.011	0.013 0.012 0.	013 0.0	09 0.010 0	0.008 0.007	0.012 0.0	14 0.009	0.011 0.012	0.014 0.009	0.010	0.013 0.010	0.008 0.008	0.008 0.0	0.006	0.016 0.016	0.017 0.0	0.016	0.016 0.009 0.009	0.009 0.009
EQ17 Enchytraeus sp. Fortescue reference EXR1626R J15-25 North Shaw.	0.137 0.078	0.093 0.099		0.075 0.195 0.093 0.181	0.178 0.19		0.153 0.045 0.162 0.082			0.105 0.145 0.106 0.159		0.101 0.152	0.149 0.018	4 0.082	0.010	0.012 0.013 0.	014 0.0	10 0 010 0	0.009	0.012 0.0	15 0.008	0.010 0.011	0.014 0.008	0.010	0.014 0.010	0.009 0.010	0.009 0.0	15 0.008	0.017 0.017	0.017 0.0	017 0.017	0.017 0.008 0.008	0.011 0.011
EXR1626R J15-26 North Shaw.	0.166 0.142	0.070 0.100			0.178 0.18		0.174 0.136			0.139 0.174		0.129 0.174		1 0.124	0.0.0	0.012 0.012 0	015 0.0	13 0.012 0	0.014 0.013	3 0.014 0.0	14 0.014	0.012 0.013	0.014 0.013	0.012	0.016 0.013	0.013 0.013	0.014 0.0	116 0.007	0.018 0.018	0.019 0.0	018 0.018	0.019 0.012 0.012	3 0.011 0.011
G61 HCO2 Oligochaeta	0.150 0.139	0.146 0.144	0.136	0.140 0.155	0.155 0.18	5 0.128	0.159 0.147	0.170 0.117	0.126	0.120 0.158	0.131 0.161 0.15	0.117 0.161	0.162 0.134	4 0.133	0.139 0.145	0.114	0.0	12 0.014 0	0.013 0.012	2 0.013 0.0	13 0.013	0.012 0.014	0.013 0.012	0.013	0.014 0.014	0.014 0.014	0.014 0.0	0.013	0.016 0.016	0.016 0.0	016 0.016	0.016 0.013 0.013	0.012 0.012
G63 HCO2 Oligochaeta	0.140 0.170	0.148 0.147	0.164	0.166 0.158	0.152 0.193	7 0.178	0.192 0.158	0.173 0.154	0.175	0.156 0.197	0.152 0.193 0.20	0.156 0.193	0.173 0.166	6 0.152	0.159 0.164	0.162 0.158	0.0	13 0.013 0	0.013 0.012	2 0.013 0.0	13 0.013	0.013 0.014	0.013 0.013	0.012	0.015 0.013	0.013 0.014	0.013 0.0	0.012	0.017 0.017	0.020 0.0	0.017	0.017 0.014 0.014	0.013 0.013
G180 10047 Enchtraeidae	0.161 0.081	0.105 0.108	0.074		0.172 0.18			0.163 0.105								0.142 0.144 0.		0.010	0.009	0.013 0.0	14 0.008	0.011 0.011	0.015 0.000	0.008	0.015 0.010	0.009 0.009	0.009 0.0	0.009	0.019 0.019	0.017 0.0	0.019	0.019 0.008 0.008	0.010 0.010
G181 100103 Enchytraeidae	0.171 0.090	0.099 0.097	0.068	0.087 0.201 0.068 0.178	0.178 0.19	0 0.117	0.162 0.090		0.102	0.104 0.156		7 0.114 0.161			0.076 0.093		156 0.0	84 (0.009 0.010	0.011 0.0	0.010	0.010 0.011	0.013 0.010	0.006	0.015 0.005	0.010 0.010	0.010 0.0	0.010	0.020 0.020	0.020 0.0	020 0.020	0.020 0.011 0.011	0.012 0.012
G217 Enchytraeidae MW 109252 G221 Enchytraeidae AB2 109732	0.163 0.068	0.080 0.082	0.065			5 0.111		0.169 0.106	0.107	0.112 0.155	0.075 0.164 0.15	0.110 0.164			0.064 0.080	0.140 0.137 0.	1/3 0.0	71 0.078	0.009	0.011 0.0	13 0.009	0.010 0.011	0.014 0.008	0.008	0.014 0.009	0.009 0.009	0.009 0.0	13 0.008	0.018 0.018	0.018 0.0	017 0.018	0.018 0.009 0.009	0.011 0.011
G281 Enchytraeidae LN9293 Marillana	0.148 0.074	0.000 0.002	0.000	0.118 0.195			0.132 0.067	0.133 0.101	0.113	0.078 0.130	0.070 0.136 0.13	7 0.101 0.136	0.174 0.087		0.119 0.123		173 0.0	25 0 122 0	1122 0 112	0.012 0.0	14 0.010	0.011 0.011	0.014 0.007	0.010	0.014 0.010	0.007 0.007	0.008 0.0	15 0.006	0.017 0.017	0.018 0.0	010 0.017	0.017 0.007 0.007	0.010 0.010
G282 Enchytraeidae LN7155 Mindy Coondiner	0.184 0.164	0.140 0.139	0.149	0.161 0.192	0.198 0 18	1 0.167	0.022 0.165	0.124 0.161	0.176	0.168 0.024	0.143 0.024 0.02	0.159 0.024	0.128 0.154	6 0.167	0.158 0.160	0.165 0.151 0	193 0 1	64 0.159 0	0.158 0.152	2 0.177	0.015	0.013 0.014	0.005 0.014	0.013	0.013 0.013	0.014 0.013	0.014 0.0	0.014	0.019 0.019	0.020 0.0	020 0.019	0.019 0.014 0.014	0.013 0.013
G284 Enchytraeidae LN9901 Munjina	0.163 0.086	0.103 0.106	0.075	0.083 0.178		2 0.118	0.171 0.054	0.165 0.106	0.122	0.109 0.167	0.088 0.174 0.170	0.109 0.174	0.162 0.052	2 0.079	0.054 0.086	0.139 0.147 0.	164 0.0	49 0.083 0	0.067 0.072	0.125 0.1	68	0.010 0.011	0.015 0.008	0.010	0.014 0.010	0.009 0.010	0.009 0.0	0.009	0.018 0.018	0.018 0.0	0.018	0.018 0.008 0.008	0.011 0.011
G285 Enchytraeidae LN9559 Ophthalmia	0.173 0.110	0.101 0.103	0.119	0.109 0.181	0.181 0.173	3 0.109	0.174 0.118	0.173 0.073	0.076	0.077 0.171	0.112 0.171 0.170	0.079 0.171	0.161 0.119	9 0.112	0.122 0.128	0.135 0.123 0.	166 0.1	16 0.118 0	0.106 0.104	0.097 0.1	70 0.118	0.011	0.014 0.011	0.011	0.013 0.011	0.012 0.011	0.012 0.0	0.011	0.021 0.021	0.019 0.0	0.021	0.021 0.011 0.011	0.010 0.010
G286 Enchytraeidae LN9142a Upper Marillana		0.098 0.098		0.089 0.201			0.149 0.107	0.170 0.092		0.086 0.151		0.088 0.148		0.071	0.097 0.109			98 0.100 0			49 0.103		0.014 0.011	0.012	0.015 0.012	0.012 0.011	0.012 0.0	0.011	0.021 0.021	0.020 0.0	021 0.021	0.021 0.012 0.012	0.010 0.010
G288 Enchytraeidae LN8233 OB23 25 G422 110876 Enchytraeidae	0.185 0.162	0.148 0.146	0.152					0.130 0.167				0.162 0.016				0.174 0.156 0.			J. 165 0.156			0.167 0.152		0.014	0.014 0.013	0.014 0.014	0.014 0.0	0.014	0.019 0.019	0.020 0.0	0.019	0.019 0.014 0.014	0.013 0.013
G422 1108/6 Enchytraeidae G423 110859 Enchytraeidae	0.161 0.081	0.105 0.108	0.074		0.172 0.18			0.164 0.106		0.106 0.155	0.087 0.159 0.15				0.047 0.085			00 0.085 0 74 0.031 0	0.073 0.071	0.125 0.1 3 0.119 0.1		0.116 0.098 0.118 0.104		0.008	0.013 0.010	0.007 0.009	0.007 10.0	114 0.008	0.019 0.019	0.017 0.0	017 0.019	0.017 0.008 0.008	0.010 0.010
G96 107746 Enchytraeidae	0.181 0.174	0.152 0.147	0.180	0.178 0.189	0.198 0 17	4 0.187	0.149 0.168	0.162 0.111 0.058 0.175	0.176	0.175 0.143	0.173 0.147 0.14	0.118 0.165 0.176 0.147	0.082 0.180	0.157	0.074 0.096 0.182 0.181	0.196 0.192 0.	187 0 1	79 0.167	0.172 0.169	0.185 0.1	45 0.174	0.182 0.183	0.149 0.180	0.172	0.014	0.014 0.014	0.015 0.0	0.014	0.020 0.020	0.021 0.0	020 0.020	0.020 0.014 0.014	0.014 0.014
G97 107782 Enchytraeidae		0.099 0.100					0.171 0.092			0.114 0.166		0.119 0.173			0.083 0.093						68 0.091			0.029	0.178	0.011 0.010	0.010 0.0	0.010	0.019 0.019	0.019 0.0	019 0.019	0.019 0.011 0.011	0.012 0.012
GD10 Oligochaeta Oli-PES16343		0.078 0.084					0.155 0.070		0.102	0.103 0.144		0.103 0.152		0.067	0.067 0.082					0.116 0.1	58 0.073	0.119 0.091	0.159 0.073	0.083	0.170 0.083	0.007	0.004 0.0	0.008	0.018 0.018	0.017 0.0	0.018	0.018 0.010 0.010	0.010 0.010
GD11 Oligochaeta Oli-PES16200		0.085 0.085					0.157 0.074		0.100	0.108 0.142		0.110 0.151			0.075 0.080					0.124 0.1		0.110 0.107			0.164 0.089		0.007 0.0	0.009	0.019 0.019	0.018 0.0	019 0.019	0.019 0.010 0.010	0.010 0.010
GD12 Oligochaeta Oli-PES16322	0.164 0.034	0.081 0.087	0.066				0.156 0.073			0.106 0.145		7 0.106 0.154	0.163 0.068	0.070	0.067 0.085	0.139 0.144 0.	159 0.0	72 0.076 0	0.065 0.069	0.113 0.1	59 0.076	0.121 0.094	0.161 0.073	0.074	0.172 0.077	0.008 0.040	0.0	0.008	0.019 0.019	0.017 0.0	019 0.019	0.019 0.010 0.010	0.009 0.009
GU453371 Fridericia galba MN0011R J20-26 Ministers N	0.194 0.183	0.189 0.184	0.1//	0.189 0.189	0.195 0.15		0.186 0.178 0.169 0.073		0.199 (0.172 0.187 0.18	3 0.190 0.187	0.1/6 0.179	2 0.181	0.1/9 0.192	0.194 0.186 0.	195 0.1	90 0.191 0 73 0.084 0	0.182 0.181	0.186 0.1	8U U.190	0.196 0.193	0.185 0.192	0.189	0.183 0.188 0.176 0.091	0.191 0.191	0.189	0.013	0.020 0.020	0.022 0.0	0.020 0.020	0.020 0.013 0.013	0.014 0.014
WR 2868	0.161 0.074	0.081 0.093	0.068					0.174 0.108				0.195 0.192		5 0.036	0.192 0.178			86 0 198 0	172 0.046	5 0.113 0.1	86 0 175	0.119 0.093						83 0.166	0.016	0.017 0.0	010 0.016	0.000 0.010 0.010	0.010 0.010
WR 2869	0.135 0.175	0.181 0.172	0.183	0.181 0.006	0.083 0.18	7 0.189	0.189 0.169	0.183 0.183		0.172 0.186	0.175 0.192 0.19	0.195 0.192	0.169 0.175	5 0.163	0.192 0.178	0.181 0.149 0	152 0.1	86 0.198 0	0.172 0.175	5 0.192 0.1	86 0.175	0.178 0.198	0.186 0.186	0.183	0.183 0.186	0.183 0.169	0.181 0.1	83 0.166	0.000	0.015 0.0	0.000	0.000 0.018 0.018	0.017 0.017
WR 2961	0.138 0.158	0.178 0.172	0.192	0.175 0.095	0.014 0.21	8 0.201	0.206 0.166	0.192 0.198	0.198	0.218 0.212	0.178 0.218 0.22	0.206 0.218	0.192 0.181	1 0.163	0.186 0.183	0.186 0.163 0.	160 0.1	81 0.186 0	0.169 0.178	3 0.201 0.2	06 0.183	0.189 0.189	0.212 0.181	0.175	0.206 0.181	0.172 0.166	0.169 0.2	203 0.175	0.092 0.092	0.0	015 0.015	0.015 0.017 0.017	0.017 0.017
WR 2963	0.138 0.175	0.181 0.172	0.183	0.181 0.003	0.083 0.18	7 0.189	0.192 0.169	0.186 0.183	0.198	0.192 0.189	0.178 0.195 0.198	0.195 0.195	0.172 0.175	5 0.163	0.192 0.178	0.181 0.152 0.	155 0.1	86 0.198 0	0.175 0.178	3 0.192 0.1	89 0.175	0.178 0.198	0.189 0.186	0.183	0.186 0.186	0.183 0.169	0.181 0.1	86 0.166	0.003 0.003	0.092	0.003	0.003 0.018 0.018	0.017 0.017
WR 2964	0.135 0.175	0.181 0.172	0.183	0.006		7 0.189		0.183 0.183	0.198	0.192 0.186	0.175 0.192 0.193	0.195 0.192	0.169 0.175	5 0.163	0.192 0.178	0.181 0.149 0.	152 0.1	86 0.198 0	0.172 0.175	0.192 0.1	86 0.175	0.178 0.198	0.186 0.186	0.183	0.183 0.186	0.183 0.169	0.181 0.1	83 0.166	0.000 0.000	0.092 0.0	003	0.000 0.018 0.018	0.017 0.017
WR 351	0.135 0.175	0.181 0.172	0.183		0.083 0.18	7 0.107	0.189 0.169	0.100 0.100		0.192 0.186		0.195 0.192	0.169 0.175	5 0.163	0.192 0.178	0.181 0.149 0.	152 0.1	86 0.198 0	0.172 0.175	5 0.192 0.1	86 0.175	0.178 0.198	0.186 0.186	0.183	0.183 0.186	0.183 0.169		83 0.166			0.000	0.018 0.018	0.017 0.017
YP009 J15-10 Yarrie Ridge	0.160 0.085	0.100 0.106	0.077		0.160 0.19		0.160 0.056			0.115 0.157		0.115 0.165			0.052 0.085			57 0.094 0				0.121 0.101		0.088	0.177 0.094			80 0.082			175 0.175		0.010 0.010
YP009 J15-11 Yarrie Ridge YP1060 J15-12 Yarrie Ridge	0.158 0.085	0.100 0.106	0.077	0.082 0.1/8	0.160 0.19	5 0 115	0.160 0.056	0.16/ 0.10/	0.113	0.113 0.15/	0.092 0.165 0.16	3 0.113 0.165	0.133 0.052	2 0.079	0.032 0.085	0.136 0.130 0.	151 0.0	99 0.094 0	105 0.0/8	0.121 0.1	46 0 100	0.121 0.101	0.164 0.056	0.088	0.1// 0.094	0.079 0.086	0.078 0.1	98 0.082	0.1/3 0.1/5	0.169 0.	1/3 0.1/5	0.173 0.000	0.010 0.010
YP1060 J15-13 Yarrie Ridge	0.158 0.094	0.089 0.094	0.073	0.000 0.100	0.166 0.18	5 0.115	0.150 0.070	0.160 0.071	0.104	0.075 0.155	0.094 0.153 0.153 0.094 0.153 0.153	3 0 094 0 153	0.149 0.072	2 0.070	0.070 0.076	0.112 0.114 0	151 0.0	99 0.111	105 0.085	5 0 109 0 1	46 0.100	0.101 0.073	0.154 0.077	0.106	0.179 0.109	0.074 0.072	0.074 0.1	98 0 089	0.163 0.163	0.175 0.	163 0.163	0.163 0.098 0.098	3 0 000
Table Estimates of Evolutionary Divergence between		12.007 10.074	3.070		12.100 10.10	- 10.1.10	200 0.070	12.100 10.071	15.104		1	12.07-10.100	1-1-7 10.072	- 0.070							10.100	12.101 10.070	12.704 0.077	, 5		1						10.070 10.070	12.300

[27] 1503 [10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.



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TABLE 4. Naididae Distance Matrix						1 1	1 1		1 1		T T	1 1		1 1		1 1		1 1	1	1 1			1 1	1 1	1 1			т т		1 1						T = T	$\neg \neg$
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JY21 1849 Oligochaeta Oligochaeta	0.017 0.006 0.006 0.006 0.010 0.014	0.010 0.01	0.015 0.015 0.024 0.	.014 0.005 0.00	6 0.014 0.01	0.000 0.000	6 0.006 0.007	0.011 0.00	0.016 0.	007 0.014	0.015 0.0	0.016	0.017 0.0	16 0.016	0.015 0	0.015 0.014 0	0.005	6 0.016 0.02	0.011	0.023 0.0	018 0.023	0.023 0.023	0.023 0.02	2 0.023 0.0	23 0.023 0	0.022 0.021	0.023 0.012	2 0.012 0.	.023 0.02	0.021 0.	022 0.022 0	.022 0.022	0.022 0.	0.008	0.022 0.0	22 0.015 02	.015 0.015
JY22 2030 Oligochaeta Oligochaeta	0.235 0.016 0.017 0.017 0.016 0.015	0.017 0.01	6 0.017 0.018 0.020 0.	.016 0.017 0.01	6 0.016 0.01	13 0.012 0.018	8 0.018 0.017	0.016 0.013	0.016 0.0	017 0.015	0.016 0.0	013 0.015	0.015 0.0	16 0.016	0.015 0	0.013 0.014	0.01	4 0.019 0.02	2 0.015	0.018 0.0	005 0.022	0.022 0.022	0.022 0.02	2 0.022 0.0	22 0.022 0	0.022 0.021	0.020 0.02	1 0.021 0.	.022 0.02	0.021 0.	022 0.022 0	.021 0.022	0.022 0.	022 0.024	0.021 0.0	21 0.013 0.0	.013 0.017
CHPB1 J15-7 Boundary Ridge CHPB1 J15-8 Boundary Ridge	0.025 0.229 0.000 0.000 0.011 0.014	0.011 0.01	0 0.016 0.015 0.024 0.	.015 0.007 0.00	6 0.014 0.01	16 0.017 0.00	6 0.006 0.007	0.011 0.00	0.016 0.0	007 0.014	0.014 0.0	017 0.016	0.016 0.0	16 0.016	0.015 0	0.015 0.013 0	0.006 0.01	6 0.016 0.02	0.011	0.022 0.0	017 0.023	0.023 0.024	0.024 0.02	3 0.023 0.0	23 0.023 0	0.023 0.021	0.023 0.014	4 0.014 0.	.024 0.02	0.021 0.	021 0.021 0	.022 0.022	0.021 0.	021 0.009	0.022 0.0	.2 0.014 0.0	.014 0.015
CHPB1 J15-9 Boundary Ridge	0.022 0.230 0.000 0.000 0.011 0.015	0.012 0.01	11 0.016 0.016 0.024 0.	0.15 0.007 0.00	7 0.015 0.01	17 0.017 0.007	7 0.007 0.007	0.012 0.00	0.017 0.	007 0.014	0.015 0.	017 0.016	0.017 0.0	17 0.017	0.015 0	0.013 0.014 0	0.007 0.01	7 0.016 0.02	2 0.011	0.022 0.0	017 0.023	0.023 0.024	0.024 0.02	3 0.023 0.0	23 0.023 0	0.023 0.021	0.023 0.014	4 0.014 0.	0.024 0.02	1 0.021 0.	021 0.021 0	022 0.022	0.021 0.	0.007	0.022 0.0	22 0.015 0.0	1015 0.015
EQ12 Phreodrilidae sp. EB0072R	0.074 0.241 0.088 0.087 0.088 0.013	0.004 0.00	04 0.015 0.015 0.022 0.	.014 0.011 0.01	1 0.016 0.01	15 0.016 0.01	1 0.011 0.012	0.005 0.01	0.016 0.	012 0.015	0.015 0.0	016 0.015	0.016 0.0	15 0.015	0.015 0	0.013 0.014 0	0.011 0.01	5 0.017 0.02	3 0.012	0.021 0.0	017 0.022	0.022 0.022	0.022 0.02	1 0.022 0.0	22 0.022 0	0.021 0.021	0.021 0.007	7 0.007 0.	022 0.020	0.020 0.	022 0.022 0	021 0.021	0.022 0.	022 0.015	0.022 0.0	21 0.016 0.	016 0.016
EQ18 Enchytraeus sp. Fortescue	0.165 0.191 0.172 0.174 0.176 0.158	0.014 0.01	3 0.016 0.017 0.022 0.	.015 0.014 0.01	4 0.015 0.01	16 0.016 0.015	5 0.015 0.015	0.014 0.013	0.017 0.	015 0.014	0.016 0.0	016 0.015	0.017 0.0	16 0.016	0.015 0	0.014 0.016	0.014 0.01	5 0.016 0.02	0.014	0.021 0.0	016 0.021	0.021 0.021	0.021 0.02	1 0.021 0.0	21 0.021 0	0.021 0.020	0.021 0.018	8 0.018 0.	.021 0.023	3 0.023 0.	021 0.021 0	.020 0.020	0.021 0.	021 0.020	0.022 0.0	20 0.014 0./	.014 0.018
EQ2 Phreodrilidae sp. HST0186R	0.076 0.240 0.089 0.087 0.088 0.015 0.156		05 0.015 0.015 0.022 0.	.014 0.010 0.01	1 0.016 0.01	15 0.015 0.01	1 0.011 0.012	0.005 0.01	0.015 0.	0.015	0.015 0.0	015 0.015	0.015 0.0	15 0.015	0.015 0	0.013 0.014 0	0.01	5 0.017 0.02	0.012	0.021 0.0	017 0.022	0.022 0.022	0.023 0.02	2 0.022 0.0	22 0.022 0	0.022 0.021	0.021 0.007	7 0.007 0.	.022 0.020	0.020 0.	022 0.022 0	.020 0.020	0.022 0.	0.016	0.022 0.0	21 0.016 0.0	.016 0.016
EQ3 Phreodrilidae sp. EEX0561 EXR1619R 115-22 North Shaw	0.070 0.244 0.084 0.082 0.083 0.013 0.161 0.193 0.218 0.192 0.192 0.185 0.197 0.197		0.015 0.015 0.022 0.	.014 0.010 0.01	1 0.015 0.01	16 0.016 0.01	1 0.011 0.011	0.006 0.01	0.015 0.0	011 0.014	0.015 0.0	016 0.015	0.016 0.0	15 0.015	0.015 0	0.013 0.014 0	0.011 0.01	5 0.016 0.02	2 0.013	0.021 0.0	017 0.022	0.022 0.022	0.023 0.02	0.022 0.0	22 0.022 0	0.021 0.020	0.020 0.004	4 0.004 0.	.022 0.019	0.019 0.	021 0.021 0	020 0.020	0.021 0.	021 0.014	0.022 0.0	0.016 0.0	.016 0.016
EXR1619R J15-22 North Shaw EXR1619R J15-23 North Shaw	0.193 0.218 0.192 0.192 0.185 0.197 0.197			0.01 0.016 0.01	6 0.017 0.01	16 0.017 0.01	5 0.015 0.015	0.015 0.01	0.017 0	015 0.015	0.016 0.0	016 0.017	0.016 0.0	17 0.016	0.017.0	0.014 0.014 0	10.0 010.0	6 0.017 0.02	0.015	0.023 0.0	0.022	0.022 0.022	0.022 0.02	0.022 0.0	22 0.022 0	0.020 0.020	0.020 0.019	0.019 0.	0.024	4 0.024 0.	021 0.021 0	023 0.023	0.021 0.	021 0.020	0.020 0.0	23 0.017 0	1014 0.015
Fridericia tuberosa Enchytraeidae	0.221 0.201 0.216 0.216 0.216 0.198 0.207			.022 0.025 0.02	4 0.023 0.02	23 0.023 0.025	5 0.025 0.025	0.023 0.02	0.023 0.	025 0.023	0.021 0.0	023 0.024	0.024 0.0	24 0.024	0.023 0	0.023 0.024 0	0.025 0.02	1 0.023 0.02	3 0.022	0.023 0.0	020 0.024	0.024 0.024	0.025 0.02	2 0.024 0.0	24 0.024 0	0.022 0.023	0.023 0.02	2 0.022 0.	.024 0.023	3 0.023 0.	023 0.023 0	.025 0.025	0.023 0.	023 0.025	0.024 0.0	24 0.023 0.	.023 0.024
FU3 Phreodrilidae KGST0032	0.179 0.225 0.191 0.189 0.191 0.180 0.187			0.014 0.01	4 0.017 0.01	16 0.016 0.015	5 0.015 0.015	0.015 0.01	0.015 0.	015 0.014	0.013 0.0	016 0.016	0.017 0.0	17 0.016	0.017 0	0.014 0.013	0.014 0.01	4 0.017 0.02	2 0.015	0.023 0.0	017 0.020	0.020 0.020	0.020 0.01	8 0.020 0.0	20 0.020	0.018 0.022	0.021 0.02	2 0.022 0.	.020 0.019	9 0.019 0.	022 0.022 0	.021 0.021	0.022 0.	022 0.022	0.021 0.0	20 0.016 0/	.016 0.017
G103 107987 Phreodrilidae	0.019 0.237 0.028 0.025 0.026 0.086 0.169	0.087 0.08	33 0.194 0.197 0.221 0.		0.014 0.01	0.00 0.000	7 0.007 0.008	0.011 0.00	0.016 0.	0.014	0.014 0.0	016 0.016	0.016 0.0	16 0.016	0.015 0	0.015 0.013 0	0.003	7 0.016 0.02	2 0.012	0.023 0.0	018 0.023	0.023 0.023	0.024 0.02	3 0.023 0.0	23 0.023 0	0.023	0.023 0.014	4 0.014 0.	.024 0.022	2 0.022 0.	022 0.022 0	.022 0.022	0.022 0.	022 0.009	0.022 0.0	22 0.015 0.0	.015 0.015
G182 100109 Phreodrilidae	0.025 0.234 0.026 0.025 0.026 0.094 0.170				0.014 0.01	16 0.016 0.007	7 0.007 0.008	0.012 0.00	0.016 0.	008 0.014	0.014 0.0	016 0.016	0.016 0.0	16 0.016	0.015 0	0.015 0.014 0	0.003 0.01	7 0.015 0.02	0.011	0.022 0.0	017 0.023	0.023 0.023	0.023 0.02	2 0.023 0.0	23 0.023	0.022 0.022	0.023 0.014	4 0.014 0.	023 0.022	2 0.022 0.	022 0.022 0	.022 0.023	0.022 0.	022 0.010	0.022 0.0	.2 0.014 0.0	.014 0.015
G184 100085 Phreodrilidae G289 Naididae LN7511	0.191 0.236 0.202 0.200 0.202 0.182 0.193 0.224 0.183 0.230 0.234 0.234 0.213 0.221					0.016 0.015	6 0.016 0.015	0.016 0.01	0.014 0.	0.015	0.016 0.0	016 0.016	0.017 0.0	14 0.015	0.017 0	0.014 0.016 0	10.0 210.0	5 0.017 0.02	2 0.014	0.021 0.0	014 0.022	0.022 0.022	0.022 0.02	2 0.022 0.0	22 0.022 0	0.022 0.021	0.023 0.023	3 0.023 0.	0.022	2 0.022 0.	021 0.021 0	019 0.012	0.021 0.	0.023	0.020 0.0	2 0.015 0.0	U15 0.016
G290 Naididae 100701c	0.227 0.180 0.232 0.237 0.237 0.213 0.221					14 0.003	6 0.016 0.017	0.015 0.016	0.014 0	017 0.016	0.016 0.	002 0.015	0.015 0.0	14 0.015	0.017 0	0.013 0.014 0	0.016 0.01	5 0.017 0.02	2 0.017	0.020 0.0	013 0.022	0.022 0.022	0.022 0.02	9 0.022 0.0	21 0.021 0	0.020 0.021	0.021 0.02	2 0.022 0	021 0.018	8 0.018 0	022 0.022 0	019 0.019	0.022 0	0.020	0.022 0.0	19 0.016 0.	1016 0.018
G291 Oligachaeta 100498 22102010	0.024 0.244 0.028 0.027 0.027 0.086 0.170						0.000 0.004	0.011 0.00	0.015 0.	004 0.015	0.015 0.0	016 0.017	0.017 0.0	17 0.017	0.016 0	0.016 0.014	0.007 0.01	7 0.015 0.02	3 0.011	0.023 0.0	018 0.023	0.023 0.023	0.024 0.02	3 0.023 0.0	23 0.023 0	0.023 0.022	0.023 0.014	4 0.014 0.	024 0.022	2 0.022 0.	023 0.023 0	.022 0.022	0.023 0.	023 0.004	0.022 0.0	23 0.015 0/	.015 0.015
G292 Oligochaeta LN9284 10072010	0.024 0.244 0.028 0.027 0.027 0.086 0.170							0.011 0.00	0.015 0.	0.015	0.015 0.0	016 0.017	0.017 0.0	17 0.017	0.016 0	0.016 0.014	0.007 0.01	7 0.015 0.02	3 0.011	0.023 0.0	018 0.023	0.023 0.023	0.024 0.02	3 0.023 0.0	23 0.023 0	0.023 0.022	0.023 0.014	4 0.014 0.	.024 0.022	2 0.022 0.	023 0.023 0	.022 0.022	0.023 0.	023 0.004	0.022 0.0	23 0.015 0.0	.015 0.015
G294 Oligochaeta LN8987 21052010	0.028 0.243 0.033 0.030 0.030 0.089 0.174	0.089 0.08	33 0.183 0.182 0.233 0.	.192 0.037 0.04	2 0.198 0.22	28 0.228 0.013	3 0.013	0.012 0.00	0.016 0.0	000 0.015	0.015 0.0	016 0.017	0.017 0.0	17 0.017	0.016 0	0.016 0.014	0.007	7 0.016 0.02	2 0.011	0.023 0.0	018 0.023	0.023 0.024	0.024 0.02	3 0.023 0.0	23 0.023 0	0.023	0.023 0.014	4 0.014 0.	.024 0.022	2 0.022 0.	023 0.023 0	.022 0.022	0.023 0.	023 0.007	0.022 0.0	Z2 0.015 0.0	.015 0.015
G295 Oligochaeta LN9369 10082010	0.075 0.246 0.083 0.087 0.087 0.013 0.164 0.025 0.240 0.015 0.014 0.014 0.091 0.173							0.013	0.015 0.0	007 0.014	0.015 0.0	015 0.015	0.015 0.0	15 0.015	0.016.0	0.014 0.014 0	0.012 0.01	6 0.017 0.02	0.012	0.021 0.0	017 0.022	0.022 0.023	0.023 0.02	2 0.022 0.0	22 0.022 0	0.022 0.021	0.021 0.000	0.006 0.	022 0.020	0.020 0.	021 0.021 0	020 0.021	0.021 0.	021 0.015	0.023 0.0	.1 0.017 0.0	.017 0.016
G296 Oligochaeta LN9431 13082010 G297 Oligochaeta 100216 09102010	0.201 0.222 0.210 0.215 0.215 0.218 0.218								0.016 0.	016 0.016	0.013 0.	014 0.017	0.017 0.0	18 0.018	0.013 0	0.016 0.014 0	10.0 810.0	5 0.016 0.02	0.016	0.022 0.0	016 0.023	0.023 0.023	0.024 0.02	1 0.023 0.0	21 0.023 0	0.022 0.021	0.023 0.013	1 0.021 0	024 0.02	1 0 0 2 1 0 1	022 0.022 0	022 0.022	0.022 0.	022 0.008	0.022 0.0	21 0.015 0.0	1015 0.017
G298 Oligochaeta LN9744 08092010	0.028 0.243 0.033 0.030 0.030 0.089 0.174								0.207	0.015	0.015 0.0	016 0.017	0.017 0.0	17 0.017	0.016 0	0.016 0.014	0.007 0.01	7 0.016 0.02	2 0.011	0.023 0.0	018 0.023	0.023 0.024	0.024 0.02	3 0.023 0.0	23 0.023	0.023 0.022	0.023 0.014	4 0.014 0.	024 0.022	2 0.022 0.	023 0.023 0	.022 0.022	0.023 0.	023 0.007	0.022 0.0	22 0.015 0/	.015 0.015
G299 Oligochaeta 100730 04112010	0.165 0.215 0.165 0.170 0.170 0.158 0.148									167	0.015 0.0	016 0.015	0.016 0.0	16 0.016	0.016 0	0.014 0.015 0	0.01	6 0.016 0.02	0.016	0.021 0.0	016 0.022	0.022 0.022	0.022 0.02	0.022 0.0	22 0.022 0	0.020 0.019	0.017 0.020	0.020 0.	.021 0.020	0.020 0.0	020 0.020 0	.023 0.023	0.020 0.	020 0.024	0.019 0.0	22 0.014 0.0	.014 0.018
G300 Oligochaeta LN8285a 21042010	0.177 0.219 0.180 0.186 0.186 0.180 0.194									176 0.186	0.1	0.016	0.016 0.0	17 0.016	0.017 0	0.015 0.012	0.014 0.01	6 0.017 0.02	0.015	0.021 0.0	017 0.023	0.023 0.023	0.022 0.02	0.023 0.0	23 0.023 0	0.020 0.023	0.021 0.020	0.020 0.	.023 0.022	2 0.022 0.	021 0.021 0	.022 0.023	0.021 0.	021 0.021	0.022 0.0	.2 0.014 0.0	.014 0.017
G301 Phreodrilidae LN8279 G410 110175a Naididae	0.228 0.183 0.234 0.239 0.239 0.215 0.222 0.216 0.173 0.213 0.220 0.223 0.210 0.209									230 0.215	0.207	0.015	0.015 0.0	0.014	0.017 0	0.013 0.015 0	0.016 0.01	5 0.017 0.02	2 0.016	0.020 0.0	014 0.021	0.021 0.021	0.022 0.01	9 0.022 0.0	21 0.021 0	0.019 0.021	0.020 0.02	0.022 0.	021 0.018	0.018 0.	022 0.022 0	019 0.019	0.022 0.	022 0.021	0.022 0.0	9 0.016 0.0	.016 0.018
G411 110175b Naididae	0.214 0.176 0.213 0.220 0.220 0.209 0.212												0.003	06 0.006	0.011 0	0.015 0.015 0	0.017 0.01	7 0.017 0.02	3 0.016	0.021 0.0	016 0.023	0.023 0.023	0.023 0.02	3 0.023 0.0	22 0.023 0	0.023 0.020	0.022 0.020	0.020 0	023 0.02	1 0.021 0	020 0.021 0	022 0.022	0.021 0.	0.022	0.022 0.0	23 0.016 0	1016 0.018
G412 110330a Naididae	0.220 0.177 0.216 0.222 0.222 0.215 0.213	0.212 0.21	3 0.218 0.219 0.218 0.	.235 0.226 0.22	5 0.228 0.20	03 0.204 0.224	4 0.224 0.220	0.215 0.223	0.241 0.	220 0.214	0.224 0.3	203 0.007	0.023	0.007	0.012 0	0.015 0.015	0.017 0.01	7 0.018 0.02	3 0.015	0.021 0.0	016 0.024	0.024 0.024	0.023 0.02	4 0.024 0.0	24 0.024 0	0.024 0.021	0.021 0.020	0.020 0.	.023 0.02	0.021 0.	020 0.020 0	.022 0.022	0.020 0.	020 0.021	0.021 0.0	22 0.016 0./	.016 0.018
G413 110019a Naididae	0.215 0.178 0.217 0.225 0.225 0.203 0.210												0.034 0.0	143	0.011 0	0.015 0.016	0.01	7 0.018 0.02	0.016	0.021 0.0	016 0.021	0.021 0.021	0.021 0.02	2 0.021 0.0	21 0.021 0	0.022 0.021	0.021 0.020	0.020 0.	.021 0.021	0.021 0.	021 0.021 0	.022 0.022	0.021 0.	0.021	0.018 0.0	23 0.015 0.0	.015 0.019
G414 110153 Naididae G415 110019b Phreodrillidae	0.207 0.172 0.204 0.209 0.212 0.215 0.210												0.110 0.1	17 0.114	0	0.014 0.013 0	0.015	6 0.018 0.02	3 0.016	0.021 0.0	016 0.023	0.023 0.023	0.023 0.02	4 0.023 0.0	23 0.023 0	0.024 0.021	0.022 0.02	1 0.021 0.	.023 0.024	4 0.024 0.	019 0.019 0	.024 0.024	0.019 0.	019 0.022	0.022 0.0	24 0.015 0.0	.015 0.019
G415 110019b Phreodrillidae	0.190 0.195 0.190 0.190 0.192 0.177 0.183 0.201 0.212 0.203 0.204 0.207 0.199 0.190										0.171 0.			16 0.205	0.212	0.013	0.014 0.01	4 0.015 0.02	310.0	0.021 0.0	014 0.021	0.021 0.020	0.021 0.02	2 0.021 0.0	21 0.021 0	0.021 0.022	0.022 0.02	0.020 0.	020 0.020	0.020 03	020 0.020 0	022 0.022	0.020 0.	020 0.023	0.019 0.0	21 0.014 0.0	014 0.018
G420 110346 Phreodrilidae	0.020 0.236 0.028 0.027 0.027 0.090 0.166	0.092 0.08	37 0.198 0.197 0.224 0.	.179 0.007 0.00	7 0.206 0.22	21 0.224 0.03	1 0.031 0.039	0.091 0.03	0.102 0.	039 0.172	0.180 0.1	225 0.219	0.217 0.2			0.200 0.200	0.01	6 0.015 0.02	2 0.011	0.023 0.0	018 0.023	0.023 0.023	0.024 0.02	3 0.023 0.0	23 0.023 0	0.022 0.021	0.024 0.015	5 0.015 0.	.023 0.022	2 0.022 0.0	023 0.023 0	.022 0.022	0.021 0.	023 0.010	0.021 0.0	22 0.014 0.	0.014 0.015
G421 110719 Phreodrilidae	0.185 0.201 0.197 0.198 0.200 0.192 0.197															0.168 0.169 0	0.192	0.017 0.01	9 0.015	0.022 0.0	015 0.021	0.021 0.021	0.020 0.01	9 0.021 0.0	21 0.021 0	0.019 0.025	0.023 0.023	2 0.022 0.	.020 0.022	2 0.022 0.	022 0.022 0	.024 0.024	0.022 0.	022 0.024	0.019 0.0	23 0.014 0./	.014 0.017
G59 HCO2 Oligochaeta	0.182 0.216 0.184 0.187 0.187 0.188 0.195															0.174 0.187 0			0.015	0.021 0.0	019 0.021	0.021 0.020	0.020 0.01	8 0.021 0.0	21 0.021 0	0.021	0.021 0.02	1 0.021 0.	.020 0.024	4 0.024 0.	019 0.019 0	.022 0.023	0.019 0.	0.020	0.019 0.0	23 0.016 0.0	.016 0.018
HM 26610	0.218 0.226 0.218 0.218 0.218 0.226 0.206																		0.022	0.023 0.0	023 0.023	0.023 0.024	0.024 0.02	2 0.023 0.0	23 0.023 0	0.022 0.025	0.025 0.02	2 0.022 0.	.023 0.020	0.020 0.	022 0.022 0	.021 0.022	0.022 0.	022 0.023	0.021 0.0	21 0.023 0.0	.023 0.021
NS 1990 J15-19 Hillside Station Paranais frici Naididae	0.096 0.237 0.099 0.099 0.099 0.111 0.171 0.246 0.192 0.232 0.232 0.232 0.232 0.232 0.223	0.111 0.10	9 0.194 0.192 0.227 0.	223 0 235 0 23	5 0.194 0.22	26 0.226 0.099	4 0.099 0.101	0.109 0.10	0.215 0.	244 0 198	0.188 0.3	228 0.226	0.219 0.2	18 0.222	0.229 0 0.195 0	0.197 0.208 0	0.096 0.20	9 0.192 0.23	19 0 221	0.024 0.0	015 0.022	0.022 0.022	0.022 0.02	3 0.022 0.0	22 0.022 0	0.022 0.019	0.021 0.016	0.016 0.	022 0.022	0.022 0.0	021 0.021 0	023 0.023	0.021 0.	021 0.015	0.021 0.0	22 0.015 0.0	015 0.015
Pristina longiseta	0.232 0.017 0.229 0.229 0.229 0.238 0.194	0.237 0.24	11 0.213 0.211 0.187 0.	.224 0.235 0.23	2 0.245 0.18	35 0.182 0.23	5 0.235 0.234	0.240 0.23	0.216 0.	234 0.221	0.215 0.	185 0.177	0.179 0.1	74 0.180	0.174 0	0.196 0.216 0	0.234 0.20	2 0.210 0.22	0.224	0.186	0.023	0.023 0.023	0.023 0.02	2 0.023 0.0	23 0.023 0	0.022 0.021	0.020 0.02	1 0.021 0.	.022 0.02	0.021 0.0	021 0.021 0	.021 0.022	0.021 0.	021 0.024	0.022 0.0	21 0.015 0.	.015 0.016
WA 1955	0.244 0.241 0.249 0.249 0.249 0.252 0.212															0.201 0.215				0.252 0.3	235	0.000 0.004	0.004 0.01	3 0.003 0.0	000.0	0.013 0.022	0.022 0.023	2 0.022 0.	.004 0.023	3 0.023 0.	022 0.022 0	.023 0.023	0.022 0.	022 0.023	0.020 0.0	23 0.020 0.	.020 0.020
WA 2666	0.244 0.241 0.249 0.249 0.249 0.252 0.212	0.261 0.26	1 0.209 0.209 0.233 0.	.192 0.244 0.23	8 0.258 0.22	21 0.218 0.24	4 0.244 0.246	0.264 0.24	0.178 0.	246 0.221	0.218 0.3	218 0.266	0.255 0.2	72 0.252	0.255 0	0.201 0.215	0.18	6 0.192 0.19	8 0.229	0.252 0.3	235 0.000	0.004	0.004 0.01	3 0.003 0.0	000.0	0.013 0.022	0.022 0.023	2 0.022 0.	.004 0.023	3 0.023 0.	022 0.022 0	.023 0.023	0.022 0.	022 0.023	0.020 0.0	Z3 0.020 0.0	.020 0.020
WA 28610 WA 28611	0.246 0.244 0.252 0.252 0.252 0.255 0.212 0.249 0.241 0.255 0.255 0.255 0.258 0.218	0.264 0.26	4 0.212 0.212 0.236 0.	195 0.246 0.24	0.261 0.22	23 0.221 0.24	6 0.246 0.249	0.266 0.249	0.183 0.	249 0.223	0.221 0.3	221 0.269	0.258 0.2	75 0.255	0.258 0	0.203 0.215 0	0.18	9 0.198 0.20	0.232	0.255 0.3	238 0.006	0.006	0.005 0.01	3 0.005 0.0	0.004	0.013 0.023	0.023 0.023	2 0.022 0.	005 0.023	3 0.023 0.	022 0.022 0	023 0.023	0.022 0.	0.024	0.020 0.0	.3 0.021 0.0	.021 0.020
WA 28611 WA 2866	0.241 0.238 0.246 0.246 0.246 0.232 0.195	0.244 0.24	11 0.198 0.198 0.201 0	178 0.241 0.24	5 0.249 0.22	01 0.198 0.24	4 0.244 0.246	0.244 0.24	0.172 0	246 0.206	0.206 0	201 0.246	0.241 0.2	52 0.235	0.252 0	0.178 0.201 0	0.238 0.16	0.166 0.19	2 0.221	0.246 0	232 0.069	0.069 0.049	0.074	0.013 0.0	13 0.013	0.000 0.021	0.022 0.02	1 0.021 0	.013 0.023	2 0.022 0	020 0.020 0	.023 0.023	0.022 0.	020 0.029	0.020 0.0	23 0.020 0	0.020 0.021
WA 2966	0.246 0.241 0.252 0.252 0.252 0.252 0.212	0.261 0.26	1 0.212 0.212 0.233 0.	.195 0.246 0.24	1 0.258 0.22	23 0.221 0.24	6 0.246 0.249	0.264 0.249	0.178 0.	249 0.221	0.221 0.3	221 0.266	0.255 0.2	72 0.252 0	0.252 0	0.201 0.215	0.18	9 0.192 0.19	8 0.226	0.252 0.3	235 0.003	0.003 0.009	0.009 0.07	2 0.0	0.003	0.013 0.022	0.022 0.02	2 0.022 0.	.005 0.023	3 0.023 0	022 0.022 0	.023 0.023	0.022 0.	022 0.023	0.020 0.0	23 0.020 0.	.020 0.020
WA 383	0.244 0.241 0.249 0.249 0.249 0.252 0.212	0.261 0.26	1 0.209 0.209 0.233 0.	.192 0.244 0.23	8 0.258 0.22	21 0.218 0.24	4 0.244 0.246	0.264 0.24	0.178 0.	246 0.221	0.218 0.3	218 0.266	0.255 0.2	72 0.252	0.255 0	0.201 0.215	0.18	6 0.192 0.19	8 0.229	0.252 0.3	235 0.000	0.000 0.006	0.006 0.06	9 0.003	0.000	0.013 0.022	0.022 0.023	2 0.022 0.	.004 0.023	3 0.023 0.	022 0.022 0	.023 0.023	0.022 0.	022 0.023	0.020 0.0	23 0.020 0.0	.020 0.020
WA 385	0.244 0.241 0.249 0.249 0.249 0.252 0.212	0.261 0.26	0.209 0.209 0.233 0.	192 0.244 0.23	8 0.258 0.22	21 0.218 0.24	4 0.244 0.246	0.264 0.24	0.178 0.	246 0.221	0.218 0.:	218 0.266	0.255 0.2	72 0.252	0.255 0	0.201 0.215 0	0.241 0.18	6 0.192 0.19	8 0.229	0.252 0.3	235 0.000	0.000 0.006	0.006 0.06			0.013 0.022	0.022 0.02	2 0.022 0.	.004 0.023	3 0.023 0.	022 0.022 0	023 0.023	0.022 0.	022 0.023	0.020 0.0	/3 0.020 0.0	.020 0.020
WA 888 WB 23810	0.241 0.238 0.246 0.246 0.246 0.232 0.195 0.212 0.223 0.206 0.206 0.206 0.209 0.198	0.244 0.24	11 0.198 0.198 0.201 0.	224 0.241 0.23	15 0.249 0.20	0.198 0.24	6 0.244 0.246	0.244 0.24	0.172 0.	246 0.206	0.206 0.3	201 0.246	0.241 0.2	20 0.235	0.252 0	0.178 0.201 0	0.238 0.16	0 0.166 0.19	0.221	0.246 0.3	232 0.069	0.069 0.069	0.074 0.00	0 0.072 0.0		0.021	0.021 0.02	0.021 0.	013 0.022	2 0.022 0.0	020 0.020 0	022 0.024	0.020 0.	020 0.022	0.021 0.0	3 0.020 0.0	.020 0.021
WB 23812	0.209 0.206 0.209 0.209 0.209 0.201 0.201																						0.223 0.20				0.012 0.020	0.020 0	022 0.020	0.020 0	018 0.018 0	021 0.022	0.014 0.	0.022	0.021 0.0	21 0.020 0	1020 0.024
WB 497	0.063 0.252 0.074 0.074 0.074 0.017 0.183	0.020 0.00	06 0.186 0.186 0.193 0.	.201 0.077 0.08	0 0.221 0.22	26 0.226 0.072	2 0.072 0.077	0.011 0.07	0.229 0.	077 0.181	0.186 0.:	229 0.229	0.218 0.2	29 0.215	0.226 0	0.175 0.192 0	0.080 0.20	3 0.186 0.21					0.266 0.24				0.192	0.000 0.	022 0.020	0.020 0.	021 0.021 0	.021 0.021	0.021 0.	021 0.014	0.022 0.0	21 0.022 0.	.022 0.020
WB 498	0.063 0.252 0.074 0.074 0.074 0.017 0.183																									0.241 0.201			.022 0.020	0.020 0.	021 0.021 0	.021 0.021	0.021 0.	021 0.014	0.022 0.0	21 0.022 0/	.022 0.020
WW 2865	0.244 0.235 0.249 0.249 0.249 0.246 0.206	0.255 0.25	55 0.203 0.203 0.227 0.	.192 0.244 0.23	8 0.252 0.22	23 0.221 0.24	4 0.244 0.246	0.258 0.24	0.181 0.	246 0.215	0.215 0.:	221 0.264	0.252 0.2								229 0.006					0.069 0.223			0.023	3 0.023 0.	021 0.021 0	.023 0.023	0.021 0.	021 0.024	0.020 0.0	.2 0.020 O.0	.020 0.020
YA 1951 YA 1952	0.246 0.218 0.244 0.244 0.244 0.244 0.244 0.226 0.246 0.218 0.244 0.244 0.244 0.244 0.244 0.226	0.241 0.23	88 0.218 0.218 0.216 0.	201 0.246 0.24	9 0.232 0.15	58 0.155 0.24	6 0.246 0.255	0.238 0.24	0.209 0.	255 0.198	0.221 0.	155 0.192	0.195 0.1			0.212 0.238 0					221 0.258					0.238 0.206				0.000 0.	023 0.023 0	016 0.017	0.023 0.	023 0.021	0.021 0.0	7 0.022 0.0	.022 0.019
YA 1953	0.209 0.218 0.198 0.198 0.198 0.212 0.181	0.241 0.23	12 0 201 0 201 0 207 0	215 0 212 0 21	5 0 183 0 23	38 0.238 0.210	2 0 212 0 218	0.238 0.24	0.207 0.	218 0 155	0.221 0.	241 0 215	0.173 0.1	15 0.187	0.221 0	0.212 0.238 0	215 0 18	9 0 183 0 22	0.238	0.209 0.	221 0.238	0.238 0.261	0.264 0.23	3 0 235 0 2	38 0 238 0	0.238 0.208	0.140 0.23	6 0 206 0	238 0.000	9 0 209	0.000 0	023 0.017	0.023 0.	000 0.021	0.021 0.0	23 0 020 0	1020 0.017
YA 1954	0.209 0.218 0.198 0.198 0.198 0.212 0.181																		0.198	0.218 0.3	221 0.238	0.238 0.241	0.241 0.22	3 0.235 0.2	38 0.238 0	0.223 0.100					000 0	.023 0.022	0.000 0.	000 0.023	0.021 0.0	23 0.020 0/	.020 0.023
YA 26611	0.235 0.226 0.235 0.235 0.235 0.232 0.215	0.229 0.23	32 0.232 0.232 0.224 0.	.215 0.235 0.23	5 0.238 0.14	49 0.149 0.23	5 0.235 0.235	0.232 0.23	0.221 0.	235 0.203	0.218 0.	149 0.198	0.192 0.1	98 0.195	0.221 0	0.212 0.232 0	0.235 0.23	2 0.229 0.22	9 0.229	0.223 0.3	223 0.238	0.238 0.241	0.244 0.22	1 0.238 0.2	38 0.238 0	0.221 0.221	0.201 0.232	2 0.232 0.	235 0.10	6 0.106 0.	229 0.229	0.008	0.023 0.	023 0.022	0.023 0.0	ıs 0.022 0.º	.022 0.021
YA 26612	0.241 0.226 0.241 0.241 0.241 0.235 0.215															0.215 0.232 0																	0.022 0.	022 0.022	0.023 0.0	J7 0.023 0.0	.023 0.021
YA 28612	0.209 0.218 0.198 0.198 0.198 0.212 0.181	0.215 0.21	2 0.201 0.201 0.207 0.	215 0.212 0.21	5 0.183 0.23	38 0.238 0.212	2 0.212 0.218	0.218 0.20	0.195 0.	218 0.155	0.198 0.1	241 0.215	0.218 0.2	15 0.218	0.201 0	0.201 0.232 0	0.215 0.18	9 0.183 0.22	0.198	0.218 0.3	221 0.238	0.238 0.241	0.241 0.22	3 0.235 0.2	38 0.238 0	0.223 0.100	0.140 0.20	6 0.206 0.	238 0.209	9 0.209 0.	0 000.0 000	229 0.226		0.023	0.021 0.0	.3 0.020 0.0	.020 0.023
YA 386 YA 493	0.209 0.218 0.198 0.198 0.198 0.212 0.181 0.020 0.264 0.026 0.026 0.026 0.083 0.183	0.213 0.21	77 0 186 0 186 0 201 0	201 0.023 0.03	2 0.163 0.23	32 0 232 0 00	6 0.006 0.017	0.216 0.20	0.173 0.	017 0 201	0.176 0.	235 0 244	0.210 0.2	44 0 235	0.201 0	0.201 0.232 0	0.18	3 0 189 0 22	9 0.095	0.218 0.	249 0.238	0.236 0.241	0.241 0.22	8 0 246 0 2	44 0 244 0	0.223 0.100	0.140 0.200	2 0.72 0	244 0 244	6 0 246 0	209 0.000 0	232 0.226	0.000	209	0.021 0.0	22 0.022 0.0	1022 0.021
YA 494	0.213 0.251 0.216 0.216 0.216 0.224 0.213	0.216 0.22	24 0.201 0.201 0.246 0.	.195 0.219 0.22	2 0.248 0.24	45 0.242 0.214	6 0.216 0.219	0.224 0.21	0.230 0.	219 0.187	0.210 0.3	245 0.236	0.222 0.2	39 0.207	0.257 0	0.184 0.198 0	0.219 0.19	5 0.201 0.19	2 0.219	0.219 0.3	245 0.224	0.224 0.222	0.230 0.21	6 0.224 0.2	24 0.224 0	0.216 0.233	0.230 0.219	9 0.219 0.	222 0.248	8 0.248 0.	227 0.227 0	265 0.268	0.227 0.	227 0.222	0.0	23 0.022 0.	.022 0.020
YA 889	0.241 0.221 0.235 0.235 0.235 0.232 0.212	0.229 0.23	32 0.229 0.229 0.218 0.	.212 0.241 0.23	5 0.235 0.15	52 0.152 0.24	1 0.241 0.241	0.232 0.23	0.226 0.	241 0.201	0.215 0.	152 0.195	0.189 0.1	95 0.192	0.221 0	0.209 0.229 0	0.241 0.22	9 0.232 0.22	0.235	0.221 0.3	218 0.232	0.232 0.235	0.238 0.22	1 0.232 0.2	32 0.232 0	0.221 0.215	0.195 0.232	2 0.232 0.	229 0.115	5 0.115 0.	223 0.223 0	.011 0.020	0.223 0.	223 0.238		0.023 0/	.023 0.021
YP1063 J15-14 Yarrie Ridge	0.167 0.184 0.165 0.162 0.163 0.170 0.169	0.166 0.17	0 0.189 0.189 0.204 0.	.191 0.165 0.17	0 0.206 0.20	0.206 0.174	4 0.174 0.174	0.170 0.173	0.203 0.	174 0.161	0.171 0.3	204 0.207	0.205 0.2	0.204	0.213 0	0.168 0.190 0	0.167 0.18	2 0.195 0.21	2 0.155	0.218 0.	191 0.226	0.226 0.229	0.232 0.20	9 0.226 0.2	26 0.226 0	0.209 0.209	0.195 0.178	8 0.178 0.	.221 0.203	3 0.203 0.	203 0.203 0	.212 0.215	0.203 0.	203 0.178	0.233 0.2	.5 0.0	.001 0.017
YP1063 J15-15 Yarrie Ridge YP1063 J15-17 Yarrie Ridge	0.167 0.186 0.165 0.162 0.163 0.170 0.169 0.193 0.225 0.197 0.197 0.189 0.198 0.217																																				0.017
Table. Estimates of Evolutionary Divergence		0.170 0.20			10.22/ 10.23	Ju.zu6 Ju.188	U 10.100 U.168	0.170 0.19	J.207 U.	. 30 0.207	10.173 [0.	2.00 U.Z36	U.Z 14 U.Z	±∪ U.∠13 (0.442 U	U.ZUG U.ZUG L	∠∪+ U.ZU	- JU.ZU4 U.I/	JU.176	U.ZZ0 U.	. 10 U.ZUI	U.ZU1 U.ZU3	, v.zvô v.ZV	. 10.201 [0.2	J. [U.ZU]	v.201 U.212	U.172 U.16.	J 10.163 U.	70 U.Z 2	- JU-E 12 U.	z U.Z I Z U	U.U.ZZ3	U.Z 1 Z U.	U.109	U.Z	U.ZUZ U.	202

Table. Estimates of Evolutionary Divergence between Sequence pair. There were a total of 851 positions in the final dataset. Evolutionary analyses were conducted in MEGA6 [1].

Tamura K, Stefander G, Peterson D, Filipidik A, and futures 2,(2013), MEGA6: Molecular Evolutionary Genetics Analysis version 6.0. Molecular Biology and Evolution30: 2725-2729.

Declarater Ahough urnorst care has been taken be sensure the correctness of the caption, test operations in the final dataset. Evolutionary analyses were conducted in MEGA6 [1].

Tamura K, Stefander G, Peterson D, Filipidik A, and futures 2,(2013), MEGA6: Molecular Evolutionary Genetics Analysis version 6.0. Molecular Biology and Evolution30: 2725-2729.

Declarater Ahough urnorst care has been taken to ensure the correctness of the caption, test opprovider is at "who days warranty of any larts" days in the final dataset. Evolutionary analyses were conducted in MEGA6 [1].

Tamura K, Stefander G, Peterson D, Filipidik A, and futures 3. (2013), MEGA6: Molecular Evolutionary analyses were conducted in MEGA6 [1].

Tamura K, Stefander G, Peterson D, Filipidik A, and futures 3. (2013), MEGA6: Molecular Evolutionary densities of the supplementary of the stefander of the supplementary of t

Figure 5. Neighbour-joining analysis of specimens of Meenoplidae (Hempitera) from the present study. Numbers on major nodes correspond to bootstrap support over 100 iterations. Scale bargenetic distance. The specimens from the present study are highlighted in yellow; Genbank voucher specimens are highlighted in turquoise.

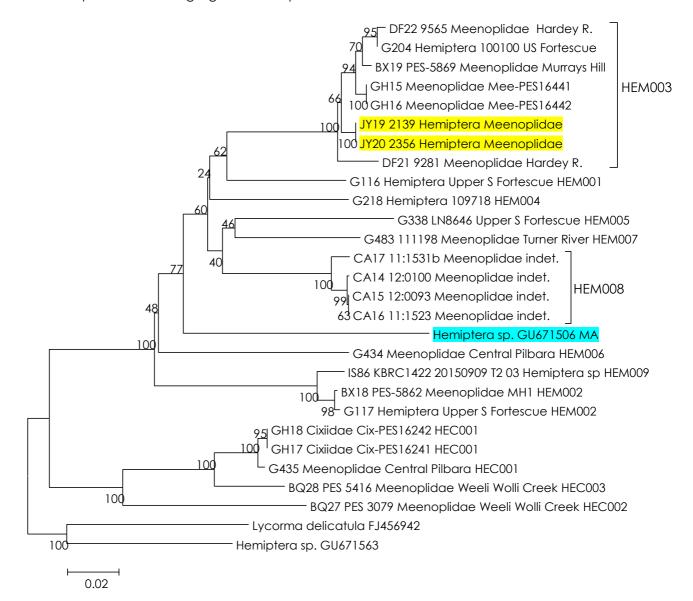


TABLE 5. Meenoplidae Distance Matrix	1																									
	IY19 2139 Hemiptera Meenoplidae	/20 2356 Hemiptera Meenoplidae	Q27 PES 3079 Meenoplidae Weeli Wolli Creek MH	BQ28 PES 5416 Meenopiidae Weeli Wolli Creek MI	BX18 PES-5862 Meenoplidae MH1 MG	BX19 PES-58 <i>69</i> Meenoplidae MH1 MB	A14 12:0100 Meenoplidae indet.	CA1512:0093 Meenoplidae indet.	.2A16 11:1523 Meenoplidae indet.	CA17 11:1531b Meenoplidae indet.	DF21 9281 Meenoplidae sp.	DF22 9565 Meenoplidae sp.	3116 Hemiptera Upper S Fortescue MC(2)	3117 Hemiptera Upper S Fortescue MG(2)	5204 Hemiptera 100100 widespread MB(2)	5218 Hemiptera 109718(2)	5338 Hemiptera LN8646 Upper S Fortescue ME(2)	3434 Meenopiidae Central Pilbara MF	5435 Meenoplidae Central Pilbara MJ	5483 111198 Meenoplidae Turner River MD	GH15 Meenoplidae Mee-PES16441	GH16 Meenoplidae Mee-PES16442	SH17 Cixiidae Cix-PES1 6241	ЭН18 Сіхії dae Сіх-РЕS16242	emiptera sp. GU671506 MA	S86 KBRC 1422 201 50909 T2 03 Hemiptera sp
Specimen ID JY19 2139 Hemiptera Meenoplidae	5	0.000	0.014	0.016	0.013	0.005	0.012	0.012	0.012	0.012	0.005	0.008	0.010	0.013	0.006	0.012	0.014	0.014	0.015	0.014	0.005	0.005	0.016	0.016	0.015	<u>∽</u>
JY20 2356 Hemiptera Meenoplidae	0.000	0.000	0.014	0.016	0.013	0.005	0.012	0.012	0.012	0.012	0.005	0.008	0.010	0.013	0.006	0.012	0.014	0.014	0.015	0.014	0.005	0.005	0.016	0.016	0.015	0.014
BQ27 PES 3079 Meenoplidae Weeli Wolli Creek MH	0.220	0.221		0.012	0.016	0.014	0.015	0.015	0.015	0.015	0.014	0.019	0.015	0.016	0.015	0.015	0.017	0.014	0.013	0.017	0.014	0.014	0.014	0.014	0.019	0.017
BQ28 PES 5416 Meenoplidae Weeli Wolli Creek MI	0.217	0.216	0.127		0.015	0.016	0.016	0.016	0.016	0.015	0.016	0.020	0.016	0.015	0.016	0.016	0.015	0.015	0.008	0.017	0.016	0.016	0.008	0.008	0.017	0.017
BX18 PES-5862 Meenoplidae MH1 MG	0.146	0.146	0.216	0.206		0.014	0.015	0.015	0.015	0.015	0.014	0.018	0.015	0.002	0.014	0.015	0.015	0.014	0.015	0.016	0.014	0.014	0.016	0.016	0.015	0.005
BX19 PES-5869 Meenoplidae MH1 MB	0.016	0.016	0.226	0.224	0.149		0.012	0.012	0.012	0.012	0.007	0.005	0.010	0.014	0.004	0.012	0.015	0.014	0.015	0.014	0.004	0.004	0.016	0.016	0.015	0.015
CA14 12:0100 Meenoplidae indet.	0.115	0.115	0.210	0.211	0.149	0.120		0.001	0.001	0.004	0.012	0.015	0.012	0.015	0.012	0.012	0.013	0.014	0.015	0.014	0.010	0.010	0.016	0.016	0.015	0.014
CA15 12:0093 Meenoplidae indet.	0.115	0.115	0.210	0.211	0.147	0.120	0.001		0.000	0.004	0.012	0.015	0.012	0.015	0.012	0.012	0.013	0.013	0.015	0.014	0.010	0.010	0.016	0.016	0.015	0.014
CA16 11:1523 Meenoplidae indet.	0.115	0.115	0.210	0.211	0.147	0.120	0.001	0.000		0.004	0.012	0.015	0.012	0.015	0.012	0.012	0.013	0.013	0.015	0.014	0.010	0.010	0.016	0.016	0.015	0.015
CA17 11:1531b Meenoplidae indet.	0.115	0.115	0.209	0.207	0.144	0.118	0.015	0.013	0.013		0.012	0.014	0.012	0.016	0.012	0.013	0.012	0.013	0.015	0.013	0.012	0.012	0.016	0.016	0.015	0.016
DF21 9281 Meenoplidae sp.	0.023	0.023	0.228	0.227	0.153	0.031	0.117	0.117	0.117	0.117		0.010	0.010	0.014	0.007	0.012	0.015	0.014	0.016	0.014	0.006	0.006	0.017	0.017	0.015	0.015
DF22 9565 Meenoplidae sp.	0.022	0.022	0.241	0.226	0.168	0.012	0.130	0.130	0.130	0.135	0.036		0.013	0.018	0.002	0.016	0.018	0.020	0.020	0.019	0.006	0.006	0.020	0.020	0.018	0.019
G116 Hemiptera Upper S Fortescue MC(2)	0.095	0.095	0.221	0.203	0.132	0.101	0.111	0.111	0.111	0.105	0.107	0.111		0.015	0.010	0.012	0.016	0.014	0.014	0.014	0.010	0.010	0.015	0.015	0.014	0.014
G117 Hemiptera Upper S Fortescue MG(2)	0.148	0.148	0.218	0.204	0.003	0.151	0.148	0.150	0.150	0.148	0.156	0.168	0.130		0.014	0.015	0.015	0.014	0.015	0.017	0.014	0.014	0.016	0.016	0.015	0.005
G204 Hemiptera 100100 widespread MB(2)	0.019	0.019	0.231	0.224	0.153	0.009	0.117	0.117	0.117	0.117	0.031	0.002	0.104	0.153		0.012	0.014	0.014	0.016	0.014	0.004	0.004	0.016	0.016	0.015	0.015
G218 Hemiptera 109718(2)	0.110	0.110	0.218	0.209	0.148	0.116	0.107	0.107	0.107	0.108	0.119	0.125	0.110	0.147	0.119		0.014	0.016	0.016	0.015	0.012	0.012	0.016	0.016	0.016	0.015
G338 Hemiptera LN8646 Upper S Fortescue ME(2)	0.136	0.136	0.223	0.189	0.168	0.137	0.112	0.112	0.112	0.114	0.142	0.139	0.128	0.167	0.136	0.127		0.016	0.014	0.014	0.014	0.014	0.014	0.014	0.015	0.015
G434 Meenoplidae Central Pilbara MF	0.153	0.154	0.210	0.207	0.138	0.156	0.152	0.150	0.150	0.146	0.162	0.171	0.138	0.144	0.159	0.147	0.158		0.015	0.015	0.015	0.015	0.016	0.016	0.016	0.014
G435 Meenoplidae Central Pilbara MJ	0.206	0.205	0.137	0.045	0.204	0.216	0.195	0.194	0.194	0.192	0.213	0.204	0.203	0.206	0.213	0.200	0.187	0.208		0.015	0.015	0.015	0.003	0.003	0.018	0.017
G483 111198 Meenoplidae Turner River MD	0.117	0.117	0.227	0.212	0.162	0.120	0.109	0.108	0.108	0.104	0.126	0.135	0.107	0.166	0.121	0.124	0.111	0.142	0.191		0.014	0.014	0.016	0.016	0.016	0.016
GH15 Meenoplidae Mee-PES16441	0.016	0.016	0.229	0.226	0.150	0.012	0.110	0.110	0.112	0.116	0.025	0.014	0.103	0.150	0.010	0.116	0.139	0.163	0.214	0.121		0.000	0.016	0.016	0.015	0.013
GH16 Meenoplidae Mee-PES16442	0.016	0.016	0.229	0.226	0.150	0.012	0.110	0.110	0.112	0.116	0.025	0.014	0.103	0.150	0.010	0.116	0.139	0.163	0.214	0.121	0.000		0.016	0.016	0.015	0.013
GH17 Cixiidae Cix-PES16241	0.204	0.205	0.133	0.050	0.204	0.215	0.200	0.200	0.200	0.190	0.212	0.200	0.202	0.205	0.210	0.202	0.184	0.206	0.006	0.193	0.219	0.219		0.000	0.019	0.017
GH18 Cixiidae Cix-PES16242	0.204	0.205	0.133	0.050	0.204	0.215	0.200	0.200	0.200	0.190	0.212	0.200	0.202	0.205	0.210	0.202	0.184	0.206	0.006	0.193	0.219	0.219	0.000		0.019	0.017
Hemiptera sp. GU671506 MA	0.169	0.169	0.250	0.234	0.191	0.167	0.178	0.178	0.178	0.179	0.170	0.161	0.163	0.193	0.167	0.158	0.163	0.178	0.236	0.157	0.169	0.169	0.234	0.234		0.016
IS86 KBRC1422 20150909 T2 03 Hemiptera sp	0.155	0.154	0.223	0.199	0.020	0.158	0.145	0.143	0.146	0.152	0.166	0.178	0.130	0.017	0.159	0.151	0.169	0.152	0.199	0.166	0.147	0.147	0.212	0.212	0.194	

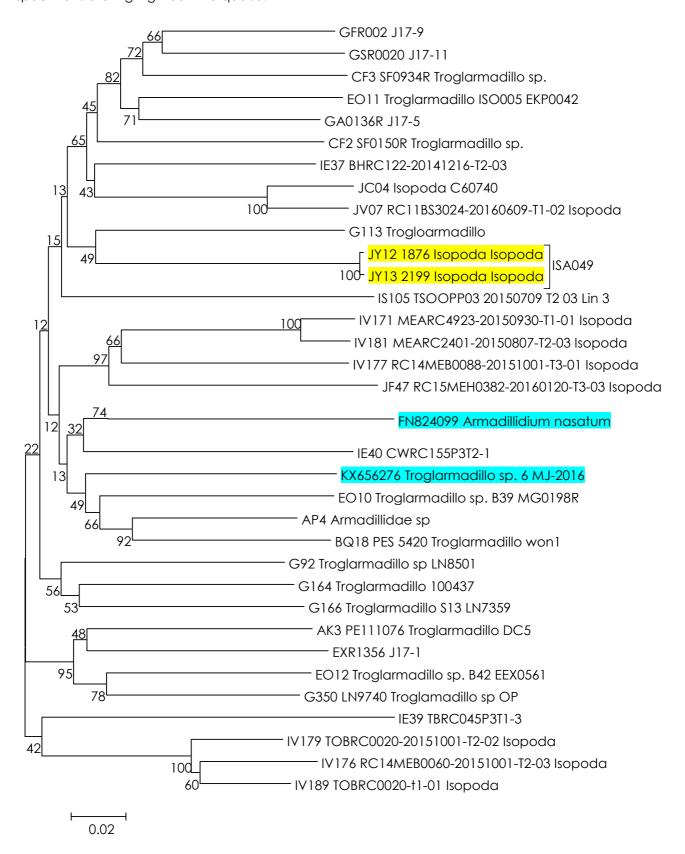
Table. Estimates of Evolutionary Divergence between Sequences

The number of base differences per site from between sequences are shown. Standard error estimate(s) are shown above the diagonal. The analysis involved 28 nucleotide sequences. Codon positions included were 1st+2nd+3rd+Noncoding. All ambiguous positions were removed for each sequence pair. There were a total of 834 positions in the final dataset. Evolutionary analyses were conducted in MEGA6 [1].

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^{1.} Tamura K., Stecher G., Peterson D., Filipski A., and Kumar S. (2013). MEGA6: Molecular Evolutionary Genetics Analysis version 6.0. Molecular Biology and Evolution30: 2725-2729.

Figure 6. Neighbour-joining analysis of specimens of Isopoda from the present study. Numbers on major nodes correspond to bootstrap support over 100 iterations. Scale bar= genetic distance. The specimens from the present study are highlighted in yellow; Genbank voucher specimens are highlighted in turquoise.



## 1	TABLE 6. Isopoda Distance Matrix	Ī																																
Fig. 2 Proposed topocode 0.008 0.007 0.015	Lineage ID	JY12 1876 Isopoda Isopoda	JY13 2199 Isopoda Isopoda	PE111076 Troglarm	Amadilidae		SF0934R Troglam	10 Troglarmadiilo sp. B39 MG01	150005	Troglamadillo sp. 842	EXR1356 J17-1	Amadilidium	G113 Trogloarmadillo			Troglamadillo sp	Sp	GA0136R J17-5	GFR002 J17-9	GSR0020 J17-11	BHRC122-20141216-T2-	C045P3T1	CWRCI	IS 105 TSOOPP03 201 50709 T2 03 Lin 3		IV 176 RC 14MEB0060-20151001-T2-03 Isopod	RC14MEB0088-20151001-T3-01	C0020-20151001-T2-02	MEARC2401-20150807-12-03	IV 189 TOBRC0020-11-01 Isopoda	Isopoda	JF47 RC15MEH0382-20160120-T3-03 Isopod	RC11BS3024-20160609-T1-	KX656276 Troglarmadillo sp. 6 MJ-2016
AS PET LIDIA' Englemen CIS								0.016		0.015	0.016	0.014		0.016	0.016	0.016			0.015	0.017	0.015	0.020	0.015	0.016	0.018		0.014	0.015						
## After September 1,000 1	JY13 2199 Isopoda Isopoda			0.017				0.016		0.015	0.016	0.014	0.015	0.016	0.016	0.016	0.013		0.015	0.017	0.015	0.020	0.015	0.016	0.018	0.015	0.014	0.015	0.018				.016	
East Part Trager Amendation Service 1.7 1.																								0.017	0.015									
EPS PROGREMOGRIUS D. 1.000 1.																			0.015				0.010	0.015							***			
E31 Forglammodilli sp. 839 McG198R 0.225 0.225 0.225 0.225 0.227 0.106 0.016 0.016 0.016 0.016 0.016 0.015 0.015 0.016 0.015 0.016 0.015 0.016 0.015 0.016 0.015 0.016 0.015 0.016 0.015 0.016 0.015 0.016 0.016 0.015 0.016 0.016 0.015 0.016 0.016 0.015 0.016 0.016 0.015 0.016 0.016 0.015 0.016 0.016 0.015 0.016 0.016 0.016 0.015 0.016 0.016 0.016 0.015 0.016 0.016 0.016 0.015 0.016	9													0.016					0.016			0.025												
EQ1 In regishmodillis SC005 EKP0042	,	0.200					0.014				0.016	0.014							0.014		0.012	0.020	0.017	0.015	0.016		0.015	0.015						
EO1 Troglamedillo ISCO05 ERP042						_		0.016			0.016	0.015							0.013		0.014	0.022	0.018	0.015	0.017			0.016					_	
EXPLISAGE JIT-1 FERT ISSG JIT-1 FERT I									0.015		0.016	0.014	0.016	0.013	0.015	0.016	0.015		0.015	0.016	0.015	0.024	0.017	0.015	0.016	0.014	0.016	0.014	0.016					
ERBISSÁIT?-1 0.287 0.287 0.70 0.193 0.20 0.220 0.220 0.220 0.220 0.220 0.230 0.235 0.014 0.017 0.015	EO11 Troglarmadillo ISO005 EKP0042							_		0.015		0.015	0.015	0.015	0.014	0.015	0.014	0.013	0.016	0.015	0.015	0.021	0.018	0.014	0.018	0.017	0.016	0.016	0.018	0.015	0.015	.014 0		
FN8240P9 Armadillidium nosatum 0.242 0.242 0.243 0.242 0.243 0.213 0.277 0.246 0.205 0.277 0.225 0.277 0.225 0.205 0.205 0.014 0.015 0.01								0.190			0.017	0.016	0.014	0.015	0.014	0.014	0.015	0.014	0.014	0.015	0.013	0.023	0.015	0.015	0.014	0.015	0.015	0.014	0.014	0.015	0.015	.014 0	.015	
G113 Troglosmodillo 0.189 0.189 0.215 0.174 0.205 0.179 0.225 0.217 0.225 0.230 0.235 0.016 0.014 0.015 0.015 0.016 0.014 0.016 0.020 0.014 0.017 0.014 0.017 0.014 0.017 0.014 0.017 0.014 0.015 0.015 0.016 0.014 0.015 0.015 0.015 0.014 0.017 0.014 0.017 0.014 0.017 0.014 0.017 0.014 0.015 0.015 0.015 0.014 0.015 0.015 0.014 0.015 0.015 0.014 0.015 0.015 0.014 0.017 0.014 0.017 0.014 0.015 0.015 0.015 0.014 0.015 0.015 0.01			0.120.		0.193 0.2	20 0.220		0.209		_		0.016	0.017	0.016	0.015	0.014	0.017	0.016	0.013	0.016	0.013	0.023	0.014	0.017	0.015	0.015	0.016	0.014	0.016	0.014	0.016	.016 0	.016	
G164 frogiarmacilia 10437	FN824099 Armadillidium nasatum	0.242	0.242	0.245	0.212 0.2	13 0.227	0.236	0.209	0.230	0.235	0.228		0.014	0.012	0.015	0.015	0.015	0.015	0.015	0.015	0.015	0.021	0.015	0.017	0.016	0.014	0.015	0.013	0.016	0.014	0.014	.015 0	.015	0.015
G166 Troglarmacdillo \$13 LN7359	G113 Trogloarmadillo	0.189	0.189	0.215	0.174 0.2	0.197	0.197	0.225	0.217	0.225	0.230	0.235		0.016	0.014	0.016	0.015	0.015	0.016	0.014	0.016	0.020	0.014	0.015	0.017	0.014	0.017	0.014	0.017	0.014	0.015	.016 0	.014	0.015
GSS LN9740 Troglamedillo sp OP	G164 Troglarmadillo 100437	0.216	0.215	0.191	0.203 0.2	00 0.178	0.204	0.199	0.215	0.215	0.220	0.228	0.206		0.014	0.015	0.012	0.015	0.014	0.013	0.016	0.022	0.014	0.017	0.016	0.016	0.014	0.015	0.015	0.015	0.014	.015 0	.015	0.015
G92 Troglarmadilia sp IN8501 0.215 0.215 0.205 0.205 0.205 0.207 0.170 0.120 0.190 0.212 0.196 0.201 0.182 0.215 0.225 0.196 0.192 0.195 0.203 0.182 0.195 0.015	G166 Troglarmadillo S13 LN7359	0.222	0.222	0.197	0.182 0.2	10 0.203	0.203	0.215	0.193	0.201	0.200	0.235	0.210	0.161		0.014	0.013	0.015	0.015	0.014	0.015	0.021	0.014	0.016	0.015	0.013	0.014	0.013	0.016	0.014	0.015	.013 0	.014	ე.015
GA0136R J17-5	G350 LN9740 Troglamadillo sp OP	0.233	0.233	0.173	0.178 0.2	10 0.222	0.216	0.198	0.204	0.145	0.164	0.210	0.222	0.189	0.182		0.016	0.015	0.015	0.015	0.015	0.020	0.015	0.015	0.016	0.014	0.015	0.015	0.016	0.015	0.017	.014 0	.016	0.015
GFR002 J17-9 0.203	G92 Troglarmadillo sp LN8501	0.215	0.215	0.205	0.203 0.1	97 0.190	0.212	0.196	0.201	0.182	0.215	0.234	0.210	0.175	0.162	0.204		0.015	0.014	0.015	0.015	0.021	0.015	0.016	0.015	0.015	0.014	0.015	0.015	0.015	0.014	.013 0	.012	0.013
GSR0020 J17-11 0.205 0.205 0.205 0.219 0.191 0.174 0.174 0.174 0.174 0.174 0.175 0.174 0.174 0.235 0.235 0.251 0.202 0.195 0.186 0.223 0.208 0.150 0.130 0.014 0.014 0.015 0.016 0.016 0.016 0.016 0.016 0.016 0.016 0.016 0.016 0.014 0.014 0.014 0.014 0.014 0.016 0.015 0.016 0.016 0.016 0.016 0.015 0.016 0.	GA0136R J17-5	0.209	0.211	0.213	0.193 0.1	94 0.170	0.148	0.196	0.141	0.203	0.217	0.229	0.213	0.203	0.182	0.193	0.183		0.013	0.013	0.015	0.023	0.017	0.014	0.017	0.016	0.016	0.015	0.017	0.015	0.015	.014 0	.013	0.016
E37 BHRC122-20141216-T2-03 C.249	GFR002 J17-9	0.203	0.205	0.205	0.195 0.2	0.180	0.153	0.203	0.168	0.209	0.217	0.252	0.196	0.195	0.182	0.221	0.194	0.148		0.012	0.015	0.022	0.017	0.015	0.017	0.014	0.017	0.015	0.017	0.013	0.014	.015 0	.015	0.016
E39 FBRC045P3T1-3	GSR0020 J17-11	0.205	0.205	0.219	0.191 0.2	17 0.174	0.140	0.218	0.174	0.235	0.232	0.251	0.202	0.195	0.186	0.223	0.208	0.150	0.130		0.014	0.021	0.016	0.014	0.018	0.017	0.016	0.017	0.017	0.016	0.014	.014 0	.014	0.015
E40 CWRC155P3T2-1 0.217 0.213 0.189 0.20 0.227 0.223 0.189 0.20 0.225 0.192 0.214 0.211 0.212 0.213 0.188 0.224 0.216 0.207 0.225 0.213 0.216 0.207 0.225 0.215 0.	IE37 BHRC122-20141216-T2-03	0.191	0.189	0.207	0.187 0.2	0.169	0.174	0.196	0.170	0.204	0.207	0.227	0.199	0.196	0.182	0.209	0.191	0.167	0.162	0.166		0.022	0.016	0.015	0.016	0.016	0.015	0.015	0.016	0.014	0.014	.014 0	.014	0.016
STOC 10 10 10 10 10 10 10 1	IE39 TBRC045P3T1-3	0.246	0.243	0.245	0.232 0.2	43 0.246	0.262	0.253	0.251	0.243	0.249	0.262	0.243	0.222	0.253	0.236	0.243	0.222	0.262	0.258	0.239		0.018	0.019	0.022	0.019	0.021	0.020	0.022	0.021	0.023	.019 0	.021	0.020
No.	IE40 CWRC155P3T2-1	0.217	0.217	0.213	0.189 0.2	201 0.207	0.225	0.192	0.214	0.211	0.212	0.221	0.188	0.226	0.214	0.204	0.207	0.222	0.227	0.217	0.218	0.243		0.018	0.014	0.014	0.015	0.014	0.014	0.015	0.017	.014 0	.016	0.015
N 176 RC 14MEB0060-20151001-T2-03 1sopoda 0.229 0.231 0.230 0.198 0.210 0.225 0.244 0.215 0.250 0.198 0.225 0.248 0.215 0.250 0.198 0.225 0.248 0.215 0.250 0.215 0.250 0.215 0.215 0.250 0.215 0.215 0.250 0.215 0.215 0.215 0.215 0.215 0.215 0.	IS 105 TSOOPP03 20150709 T2 03 Lin 3	0.227	0.228	0.248	0.228 0.2	236 0.208	0.205	0.231	0.226	0.245	0.238	0.242	0.216	0.207	0.222	0.235	0.201	0.198	0.213	0.213	0.216	0.265	0.258		0.016	0.017	0.017	0.016	0.017	0.016	0.016	.014 0	.015	0.014
	IV171 MEARC4923-20150930-T1-01 Isopoda	0.237	0.237	0.243	0.222 0.2	19 0.217	0.228	0.204	0.219	0.224	0.237	0.215	0.225	0.213	0.203	0.225	0.197	0.206	0.221	0.215	0.223	0.267	0.214	0.216		0.017	0.016	0.014	0.006	0.015	0.015	.014 0	.015	0.015
	IV176 RC14MEB0060-20151001-T2-03 Isopoda	0.229	0.231	0.230	0.198 0.2	10 0.225	0.244	0.215	0.250	0.198	0.209	0.223	0.225	0.188	0.207	0.188	0.201	0.236	0.220	0.234	0.218	0.219	0.223	0.230	0.231		0.015	0.010	0.016	0.010	0.014	.016 0	.015	0.016
	IV177 RC14MEB0088-20151001-T3-01 Isopoda	0.221	0.219	0.235	0.201 0.2	0.207	0.232	0.200	0.223	0.232	0.248	0.219	0.216	0.204	0.207	0.220	0.204	0.217	0.226	0.224	0.214	0.258	0.218	0.232	0.166	0.218		0.013	0.016	0.014	0.014	.015 0	.015	0.017
N 18 18 18 18 18 18 18		0.211	0.211	0.213	0.198 0.2	13 0.204	0.229	0.198	0.227	0.181	0.187	0.212	0.222	0.194	0.191	0.200	0.181	0.216	0.211	0.220	0.195	0.217	0.204	0.218	0.201	0.082	0.207		0.013	0.009	0.015	.015 0	.015	0.015
JC04 Isopoda C60740 0.214 0.215 0.205 0.192 0.195 0.192 0.185 0.214 0.215 0.205 0.192 0.195 0.192 0.185 0.214 0.219 0.185 0.210 0.192 0.210 0.2	IV181 MEARC2401-20150807-T2-03 Isopoda	0.236	0.236	0.232	0.216 0.2	14 0.220	0.237	0.198	0.219	0.219	0.236	0.212	0.225	0.215	0.200	0.216	0.193	0.205	0.218	0.215	0.217	0.267	0.217	0.220	0.038	0.228	0.169	0.207		0.014	0.016	.013 0	.015	0.015
JC04 Isopoda C60740 0.214 0.215 0.205 0.192 0.192 0.195 0.192 0.19 0.192 0.195 0.192 0.192 0.195 0.192 0.195 0.192 0.195 0.195 0.210 0.192 0.195 0.19		0.221	0.221	0.221	0.195 0.2	10 0.207	0.234	0.201				0.212		0.191		0.197		0.214	0.206	0.224	0.202			0.226	0.216				0.207		0.014	.016 0	.013	0.015
JF47 RC15MEH0382-20160120-T3-03 Isopoda	·	0.214	0.215	0.205	0.192 0.2	19 0.192	0.185	0.210	0.192	0.210	0.222	0.252	0.199	0.193	0.212	0.233	0.223	0.200	0.192	0.192	0.180	0.251	0.226	0.213	0.230	0.228	0.224	0.229	0.230	0.213	С	.014 0	.010	0.017
JV07 RC11BS3024-20160609-T1-02 Isopoda 0.212 0.212 0.208 0.195 0.213 0.185 0.183 0.197 0.197 0.223 0.232 0.252 0.193 0.191 0.215 0.231 0.207 0.191 0.188 0.194 0.169 0.258 0.218 0.215 0.229 0.228 0.223 0.229 0.232 0.219 0.061 0.224 0.016		0.246	0.246	0.237	0.211 0.2	16 0.219	-	0.220		0.229		0.236	0.227	0.219	0.219	0.225	0.210	0.219	0.220	0.224	0.220	0.267	0.221	0.231	0.191	0.245	0.185	0.224					_	
		0.212	0.212	0.208	0.195 0.2	13 0.185	0.183	0.197	0.197	0.223	0.232	0.252	0.193	0.191	0.215	0.231	0.207	0.191	0.188	0.194	0.169	0.258	0.218	0.215	0.229	0.228	0.223	0.229	0.232	0.219	0.061 0	.224		0.016
			_			_	-			_		_								0.217	_	_						_				_	.223	

Table. Estimates of Evolutionary Divergence between Sequences

The number of base differences per site from between sequences are shown. Standard error estimate(s) are shown above the diagonal. The analysis involved 35 nucleotide sequences. Codon positions included were 1st+2nd+3rd+Noncoding. All ambiguous positions were removed for each sequence pair. There were a total of 714 positions in the final dataset. Evolutionary analyses were conducted in MEGA6 [1].

1. Tamura K., Stecher G., Peterson D., Filipski A., and Kumar S. (2013). MEGA6: Molecular Evolutionary Genetics Analysis version 6.0. Molecular Biology and Evolution30: 2725-2729.

Figure 7. Neighbour-joining analysis of specimens of Symphyla from the present study. Numbers on major nodes correspond to bootstrap support over 100 iterations. Scale bar= genetic distance. The specimens from the present study are highlighted in yellow; Genbank voucher specimens are highlighted in turquoise.

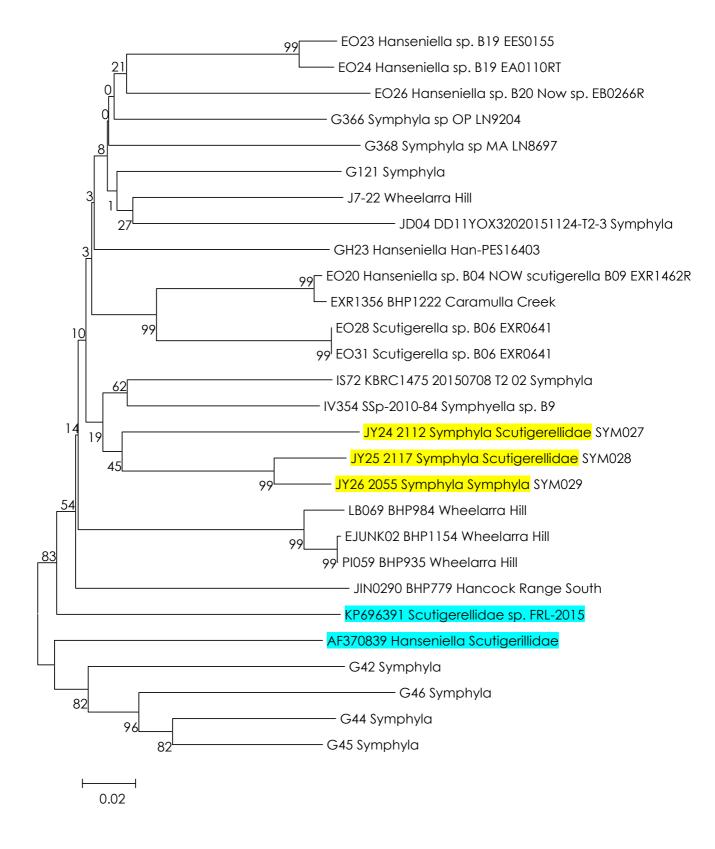


TABLE 7. Symphyla Distance Matrix																												
Specimen ID	1724 2112 Symphyla Scutigerellidae	1725 2117 Symphyla Scutigerellidae	JY26 2055 Symphyla Symphyla	AF370839 Hanseniella Scutigerillidae	EJUNKO2 BHP1154 Jimblebar E	EO20 Hanseniella sp. 804 NOW scutigerella 809 EXR 14628	EO23 Hanseniella sp. B19 EES0155	EO24 Hanseniella sp. B19 EA0110RT	EO26 Hanseniella sp. B20 Now sp. EB0266R	EO28 Scutigerella sp. B06 EXR0641	EO31 Scutigerella sp. B06 EXR0641	EXR1356 BHP1222 Caramulla Creek	3121 Symphyla	3366 Symphyla sp OP LN9204	G368 Symphyla sp MA LN8697	G42 Symphyla	G44 Symphyla	G45 Symphyla	G46 Symphyla	GH23 Hanseniella Han-PES16403	S72 KBRC1475 20150708 T2 02 Symphyla	V354 SSp-2010-84 Symphyella sp. B9	77-22 Wheelarra Hill	JD04 DD11YOX32020151124-12-3 Symphyla	JIN0290 BHP779 Hancock Range South	.P696391 Scutigerellidae sp. FRL-2015	LB069 BHP984 Hashimoto	PIOS9 BHP935 Hashimoto
JY24 2112 Symphyla Scutigerellidae	Ţ	0.014	0.014	0.015	о.012		<u>ш</u> 0.015	о.014	<u>ш</u>	0.017	0.017	<u>ш</u>	0.013	0.012	0.015	0.018	0.017	0.013	0.021	0.015	0.014	0.011	0.012	0.015	0.016	0.018	0.011	0.012
JY25 2117 Symphyla Scutigerellidae	0.175	0.014	0.010		0.012					0.017	0.017	0.016			0.013	0.019		0.013			0.014	0.015	0.012		0.017			0.012
JY26 2055 Symphyla Symphyla		0.049			0.013				0.012	0.013	0.013	0.015	0.013	0.013	0.015	0.018	0.019	0.015	0.025		0.014	0.015	0.012	0.020	0.018	0.018	0.013	0.013
AF370839 Hanseniella Scutigerillidae	0.211	0.224	0.220		0.014		0.015	0.013	0.013	0.016	0.016	0.017		0.014	0.014	0.019	0.017	0.015	0.017	0.011	0.017	0.015	0.015	0.018	0.014	0.016	0.014	0.014
EJUNK02 BHP1154 Wheelarra Hill	0.194	0.192	0.198	0.209		0.013	0.016	0.013	0.014	0.016	0.016	0.014	0.014	0.017	0.016	0.021	0.017	0.016	0.018	0.014	0.016	0.015	0.013	0.017	0.016	0.017	0.006	0.001
EO20 Hanseniella sp. B04 NOW scutigerella B09 EXR1462R	0.172	0.209	0.203	0.226	0.192		0.015	0.015	0.012	0.012	0.012	0.003	0.012	0.014	0.014	0.020	0.019	0.014	0.021	0.013	0.016	0.012	0.015	0.017	0.014	0.018	0.015	0.014
EO23 Hanseniella sp. B19 EES0155	0.202	0.178	0.172	0.223	0.197	0.181		0.005	0.014	0.013	0.013	0.017	0.013	0.012	0.011	0.019	0.017	0.016	0.022	0.015	0.012	0.012	0.014	0.017	0.015	0.018	0.013	0.015
EO24 Hanseniella sp. B19 EA0110RT	0.206	0.175	0.166	0.218	0.194	0.183	0.027		0.013	0.013	0.013	0.017	0.015	0.014	0.012	0.019	0.016	0.014	0.023	0.013	0.013	0.013	0.013	0.016	0.016	0.018	0.012	0.014
EO26 Hanseniella sp. B20 Now sp. EB0266R	0.211	0.195	0.192	0.240	0.228	0.181	0.173	0.168		0.015	0.015	0.013	0.014	0.012	0.014	0.015	0.020	0.011	0.017	0.012	0.012	0.015	0.015	0.015	0.016	0.020	0.014	0.014
EO28 Scutigerella sp. B06 EXR0641	0.203	0.187	0.191	0.217	0.195	0.125	0.176	0.180	0.197		0.000	0.013	0.013	0.011	0.015	0.020	0.016	0.016	0.017	0.013	0.014	0.012	0.012	0.015	0.015	0.020	0.017	0.017
EO31 Scutigerella sp. B06 EXR0641	0.203	0.187	0.191	0.217	0.195	0.125	0.176	0.180	0.197	0.000		0.013	0.013	0.011	0.015	0.020	0.016	0.016	0.017	0.013	0.014	0.012	0.012	0.015	0.015	0.020	0.017	0.017
EXR1356 BHP1222 Caramulla Creek	0.179	0.212	0.206	0.226	0.191	0.008	0.183	0.183	0.180	0.133	0.133		0.012	0.014	0.016	0.022	0.019	0.015	0.021	0.014	0.018	0.014	0.015	0.017	0.013	0.018	0.015	0.014
G121 Symphyla	0.196	0.191	0.176	0.216				0.180			0.177			0.013	0.013	0.020	0.016	0.012	0.021	0.011	0.016	0.012	0.013	0.014	0.016	0.018		0.013
G366 Symphyla sp OP LN9204	0.203		0.190		0.190			0.164			0.171		0.174		0.012	0.020	0.015	0.016			0.015	0.012	0.014		0.015	0.020		0.016
G368 Symphyla sp MA LN8697	0.186	0.211	0.206	0.220	0.202			0.188			0.196		0.185			0.016	0.018	0.016			0.015	0.014	0.014		0.014	0.017	0.016	0.016
G42 Symphyla	0.238	0.216	0.201		0.260			0.212			0.228				0.239		0.017	0.014			0.020	0.022	0.017		0.019	0.017	0.021	0.021
G44 Symphyla	0.241	0.231	0.227	0.208	0.218			_		0.245		0.224			0.224			0.012			0.021	0.019	0.021	0.030	0.021	0.021	0.018	0.017
G45 Symphyla	0.226	0.227	0.224	0.200	0.236					0.231		0.224				0.182	_		0.017		0.015	0.017	0.017	0.020	0.015	0.017	0.017	0.016
G46 Symphyla	0.253	0.267	0.258	0.217	0.240		0.244			0.216	0.216			0.252		0.215	0.178			0.020	0.025	0.023	0.019	0.026	0.018	0.022	0.020	0.018
GH23 Hanseniella Han-PE\$16403	0.191		0.191		0.189			0.179		0.182	0.182					0.224	_	0.227			0.013	0.013	0.015	0.020	0.013	0.018		0.014
IS72 KBRC1475 20150708 T2 02 Symphyla	0.174		0.163		0.205			0.163		0.187	0.187					0.207	0.229			0.181		0.014	0.012	0.020	0.016	0.017	0.015	0.016
IV354 SSp-2010-84 Symphyella sp. B9	0.194		0.163	0.221	0.186			0.185			0.177					0.239	_	0.218		0.186		0.170	0.014	0.017	0.014	0.017	0.015	0.015
J7-22 Wheelarra Hill	0.221		0.191					0.165		0.185	0.185					0.254		0.223			0.197		0.175		0.013	0.017		0.014
JD04 DD11YOX32020151124-T2-3 Symphyla	0.189	0.212	0.210	0.228	0.216			0.195			0.199					0.255	_	0.228			0.210				0.020	0.021	0.017	0.017
JIN0290 BHP779 Hancock Range South	0.221	0.170	0.197	0.229				0.195		0.203	0.203			0.186		0.212		0.224		0.196		0.208	0.205		0.017	0.017		0.016
KP696391 Scutigerellidae sp. FRL-2015	0.237	0.207	0.201	0.220	0.215					0.207		0.195	0.216		-	0.221	0.247	0.238				0.204	0.198	0.241		0.010	0.019	0.017
LB069 BHP984 Wheelarra Hill	0.187	0.196	0.201		0.029			0.192		0.201	0.201	0.192				0.258		0.240			0.199		0.212		0.195		0.000	0.006
PI059 BHP935 Wheelarra Hill	0.192	0.191	0.197	0.209	0.002	0.191	U.195	0.195	0.228	U.194	0.194	0.189	0.203	0.189	0.200	0.260	0.218	0.236	0.240	0.189	0.203	0.185	0.200	0.216	0.209	0.214	0.028	

Table. Estimates of Evolutionary Divergence between Sequences

The number of base differences per site from between sequences are shown. Standard error estimate(s) are shown above the diagonal. The analysis involved 28 nucleotide sequences. Codon positions included were 1st+2nd+3rd+Noncoding. All ambiguous positions were removed for each sequence pair. There were a total of 14667 positions in the final dataset. Evolutionary analyses were conducted in MEGA6 [1].

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^{1.} Tamura K., Stecher G., Peterson D., Filipski A., and Kumar S. (2013). MEGA6: Molecular Evolutionary Genetics Analysis version 6.0. Molecular Biology and Evolution30: 2725-2729.