



Adult life strategy affects distribution patterns in abyssal isopods – implications for conservation in Pacific nodule areas

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Abstract

Aim of our study is to gain a better knowledge about the isopod crustacean fauna of the abyssal Clarion Clipperton Fracture Zone (CCZ) located in the central Pacific Ocean. In total, we examined 22 EBS samples taken at 6 abyssal areas in the central Pacific manganese nodule area (CCZ and DISCOL). The dataset comprised 619 specimens belonging to 187 species of four different isopod families: 91 species (48.6 % of total) belonging to Munnopsidae, 63 (33.6 %) to Desmosomatidae, 24 (12.8%) to Haploniscidae and 9 (4.8 %) to Macrostylidae. The total number of species found was relatively similar between sites ranging from 38 (German Contractor area) to 50 species (French contractor area). 68 species were represented by singletons. The ranges of distribution differ between families. In total 77% of the species were recorded in a single area (and thus being unique for this specific area), 13.9% in 2 areas, 5.3% in 3 areas, 2.6% in 4 areas and 1% in 5 areas. The proportion of species present in a single area increased in this sequence: Munnopsidae (75.8%), Desmosomatidae (77.7%) and Haploniscidae (83%). A total of 6 (66.6%) out of 9 species of Macrostylidae was recorded in a single area contrasted by the most common species being from this family, Macrostylidae *Macrostylis* M05 with 46 specimens (present in all areas besides DISCOL) followed by several species of Munnopsidae with 10 or more specimens in the dataset. The CCZ areas show the highest number of shared species. Generally, the high diversity in each area is reflected by a low similarity between sampling areas. The rarefaction curves indicate that species richness is similar between areas, but the real number of species is still not sampled. The most distant areas from the central CCZ, the APEI3 and DISCOL, are the most different.



1 Introduction

Spanning 60% of the Earth's surface, deep-sea areas (below 200 m water depth) harbour an immense diversity of habitats and species, but also large deposits of metal-rich seafloor minerals (e.g., polymetallic sulphides, cobalt-rich ferromanganesecrusters, phosphorite- and polymetallic (Mn-) nodules). Despite initial endeavours to explore these resources starting in the 1960s, growing economic interests coupled with advancing technologies to extract minerals from the seafloor have now made deep-sea mining becoming quite realistic (Wedding et al. 2015; Jones et al. 2017).

The abyssal Clarion Clipperton Fracture Zone (CCZ, Fig. 1) located in the tropical north-eastern Pacific is commercially the most important area of proposed Mn-nodule mining. Extraction of these mineral resources will inevitably lead to habitat loss and changes at the directly mined sites primarily through removal, blanketing and compaction of the upper sediment layer (5-20 cm) (Miljutin et al. 2011; Ramirez-Llodra et al. 2011; Jones et al. 2017; Gollner et al. 2017). Furthermore, areas beyond the actual mining block may be indirectly affected through the generation of a potentially toxic sediment cloud, as well as discharge water from dewatering processes at the sea surface (Oebius et al. 2001; Hauton et al. 2017). Thus, the scale and magnitude of its ecological footprint and how it is mitigated will determine whether mining operations will be feasible in the long-term (Petersen et al. 2016).

In order to make predictions on the recolonization potential of the deep-sea fauna, an understanding of the modes and drivers of species' geographic distributions is required. That is, species with a broader distribution and better dispersal ability likely have a greater potential to recolonize impacted areas than those with a limited dispersal capacity. In turn, this understanding would contribute to the design and establishment of ecological reserve areas in the CCZ (Baco et al. 2016; Vanreusel et al. 2016; De Smet et al. 2017).

Presumed low levels of environmental variability and absence of obvious dispersal barriers, led to the assumption that deep-sea species have wider horizontal distributions compared to shallow-water representatives (McClain & Hardy 2010). However, molecular studies have shown that morphologically similar, but genetically distinct (cryptic) species are common among deep-sea lineages, fundamentally changing our understandings of deep-sea species distributions (e.g., Vrijenhoek et al. 1994; Pfenninger & Schwenk 2007; Raupach et al. 2007; Havermans et al. 2013; Brix et al. 2014, 2015; Jennings et al. 2018, in press). Conversely, for some species there is morphological and genetic support for wide geographic distributions even across major topographic barriers (Brix et al. 2011; Menzel et al. 2011; Riehl & Kaiser 2012; Janssen et al. 2015; Easton & Thistle 2016; Bober et al. 2018; Brix et al. 2018). However, biological data on dispersal distances of deep-sea species is still fragmentary due to overall low sampling effort compared to the sheer size of deep-sea floor, and the scant knowledge on species' taxonomy.

Marine benthic invertebrates exhibit a range of reproductive strategies, all these strategies are directly linked to their dispersal potential, with decreasing potential dispersal distance from those with pelagic development to those with direct development (brooding). Yet, some species with true wide geographic ranges have ~~with~~ direct development, and some putatively good dispersers have more limited distributions (Johannesson 1988; Shank 2010; Packmor et al. 2015; Janssen et al. 2015). While



65 there  number of ecological and evolutionary factors used to explain differences in range size, including evolutionary history, physiological tolerance and food availability, early life history, nonetheless, range size seems to represent a relatively good proxy of dispersal capacity (Grantham et al 2003; Sherman et al. 2008; Hilario et al. 2015; Janssen et al. 2015; Baco et al. 2016; but see Johannesson 1988; Lester et al. 2007). For benthic taxa with a pelagic larval phase, the time larvae spend in the water column (planktonic larval duration, PLD), is often used to predict dispersal distances (Hilario et al. 2015). For direct
 70 developers that lack planktonic stages, dispersal is limited to active migration and passive drift or floating (rafting) of the adult stage, making estimation of dispersal distances arguably more complicated (Thiel & Haye 2006).

In this study, we assess the role of the adults' lifestyle in determining the large-scale distribution of asellote isopods across the CCZ. Asellote isopods of superfamily Janiroidea are the most numerous and diverse crustacean taxon encountered within abyssal benthic samples (Brandt et al., 2007). With a few exceptions, isopods lack planktonic larvae, and thus levels of gene
 75 flow result from the active and/or passive migration of adults (Brandt, 1992). Asellotes are principally detritivores and foraminiferivores, but different groups show different lifestyles. The Munnopsidae Lilljeborg 1864 are the most diverse and abundant janiroids in the deep sea and their diversity is reflected in numerous morphological and ecological adaptations, most important of which is their paddle-like posterior legs that are highly specialized for swimming or digging. In the Desmosomatidae Sars 1897, usually referred to as an epifaunal family, swimming adaptations are only poorly expressed
 80 compared to the Munnopsidae Lilljeborg 1864, (Hessler 1981; Hessler and Stromberg, 1989). Yet, still desmosomatids bear long natatory setae on their posterior pereopods and are thus considered to be moderate swimmers (Hessler 1981; Svarvasson 1984; Hessler and Strömberg, 1989; Brix et al., 2015, Bober et al. 2018). The Haploniscidae Hansen, 1916 have no modifications for swimming or burrowing. While in situ observations are lacking, information from epibenthic sledge and core sampling suggests haploniscids live at or near the sediment surface (Harrison 1989). Finally, the Macrostylidae Hansen, 1916,
 85 due to their infaunal tubicolous mode of life, likely have the least dispersal potential and thus distributional ranges may be very limited. Their sexual dimorphism may allow males of some species to be more mobile on the suprabenthos compared to the females however (Harrison 1989; Hessler and Strömberg, 1989; Riehl & Kaiser, 2012; Bober et al. 2018).

In a previous molecular assessment of wide-spread isopod species across the Mid-Atlantic Ridge (MAR), Bober et al. (2018) found lifestyle to have a profound effect on dispersal distances, with munnopsid species maintaining gene flow across the
 90 MAR, while distributional ranges in desmosomatids, nannoniscids (Brix et al. 2018) and macrostylids were much more restricted (but see Riehl et al. 2017). Thus, we expect munnopsid species to exhibit the widest geographic distributions compared to other families. Furthermore, we expect to find the correlation between geographic and genetic distance to be more pronounced in lineages with limited dispersal ability (Haye et al. 2012; Janssen et al. 2015; Riehl et al. 2018). In the absence of detailed information on species' distributional ranges in the CCZ, and the abyss in general, using lifestyle as a dispersal
 95 ability proxy would be highly beneficial to forecasting faunal recolonization potential following disturbance events and related environmental changes. This information would be essential for conservation planning.

The objective of this study is to identify the distributional ranges of four different deep-sea janiroid families (Munnopsidae, Desmosomatidae, Haploniscidae, and Macrostylidae) with varying lifestyles and to determine if these can be used as a proxy



to estimate dispersal distances. Samples were collected during two expeditions in the course of the JPI Oceans Pilot Action
 100 "Ecological Aspects of Deep-Sea Mining" (JPIO) to the CCZ and DISCOL Experimental Area (DEA) area in the northeastern
 and southeastern Pacific respectively. We carried out a molecular analysis of two mitochondrial DNA markers (COI and 16S)
 backed up by morphological means, to delineate species in an integrative approach. Based on this species delimitation, we test
 several statistical parameters to gain more knowledge about the species richness and similarity of the different areas.

1.1 Material and Methods

105 Isopod specimens were collected with an epibenthic sledge (EBS) on the CCZ (SO239 cruise, 13 EBS deployments, Table 1)
 and the Peru Basin (SO242-1 cruise, 9 EBS deployments, Table 1) from the RV Sonne in 2015. In the CCZ the samples were
 taken in 4 contractor areas, from east to west: BGR (German contractor), IOM (Interoceanmetal Joint Organization), GSR
 (Belgian contractor), IFREMER (French contractor). In addition, the APEI3 (Area of Particular Environmental Interest number
 3) was sampled. The sediment samples were immediately fixed on deck in pre-chilled 96% non-denatured ethanol and kept
 110 cool throughout the sorting process according to Riehl et al. (2014). One to three posterior legs (natapods) of each isopod
 specimen were dissected and used for DNA extraction. Before DNA extraction all isopod specimens were morphologically
 determined to family level and given individual voucher numbers. All voucher specimens are stored at the Center of Natural
 History, Hamburg (CeNak) or the crustacean collection Senckenberg, Frankfurt (Table 1). After DNA extraction, all isopod
 specimens were identified morphologically to species level using a LEICA MZ 12.5 stereomicroscope by SB, NB, MM. All
 115 determinations were entered into the excel spreadsheet (table 1) using this as baseline for creating maps in QGIS, as well as
 for statistical analysis. All specimen information and molecular data are managed via the Barcode of Life database (BoLD) in
 the projects "CCZ - Clarion and Clipperton Fracture Zones biodiversity" and "DISCO - DISturbance and reCOLonization
 experiment in a manganese nodule area of the SE Pacific Ocean". For this publication we created a dataset "Dataset - DS-
 LOCOM Locomotion of adult isopods influences distribution" holding a subset of 619 specimens for GenBank submission
 120 and making the sequences visible after publication. All data are stored in the BoLD along with a project OECID, which contains
 all available data and is made publicly available via GenBank submission. The BIN system in BoLD compares newly submitted
 sequences with all already available sequences in BoLD clustering them according to their molecular divergence using
 clustering algorithms. Each cluster receives a unique and specific BIN (barcode identity number as stated for each specimen
 with COI sequence in table1).

125 Outgroups for each family tree consisted of the following: Macrostylidae = *Thaumastosoma diva* KY951731, *Thaumastosoma*
platycarpus IDesm10, *Ketosoma vema* VTDes013 (16S only), KM14-Iso261 *Ketosoma* sp. 2, KY951731, and *Ketosoma*
hessleri KY951729. Haploniscidae = *Ianiropsis epilittoralis* AF260835, AF260836, AF260858, and AF260859.
 Desmosomatids = *Betamorphia fusiformis* EF116524, EF116525, EF116527, EF116528, and *Betamorphia africana* EF682292.
 Munnopsidae = *Thaumastosoma platycarpus* IDesm10, *Ketosoma vema* VTDes013, *Ketosoma werner* D3D60 (COI only),



130 and *Thaumastosoma diva* D3D64 (16S only). Outgroups were chosen based on the most recent evidence for likely sister groups and available sequences.

Molecular Methods

A fragment of the mitochondrial gene Cytochrome Oxidase Subunit 1 (COI) was amplified and sequenced using the primers
 135 jgHCO2198 and jgLCO1490 (Geller et al., 2013) following the protocol of Riehl et al. (2014). Ribosomal 16S sequences were amplified and sequenced using the primers 16Sar and 16Sbr (Palumbi, 1992). The sequences were processed using Geneious 11.1.3 and compared against the GenBank nucleotide database. Sequences were aligned using MAFFT 7.388 (Katoh and Standley, 2013) implemented within Geneious v. 10.1.3. COI sequences were translated into amino-acid sequences within Geneious and checked for stop codons to prevent the inclusion of pseudogenes (Buhay, 2009). COI and 16S datasets were
 140 used individually for VSearch and ABGD species delimitation analyses and both individually and concatenated as a singled mitochondrial dataset for phylogenetic tree reconstruction and PTP/mPTP species delimitation analyses. Tree estimations for each family were run in RAxML (Katoh and Standley, 2013) using the GTRGAMMA model and 1000 bootstrap replicates. Multiple species delimitation methods were applied to the four datasets and results varied based on the amount of within clade sampling, occurrence of singletons, and within and between clade variation. VSearch (Rognes et al., 2016) applies a pairwise
 145 identity threshold and generates clusters of sequences that fall within a specified percent identity, thus assuming a barcode gap, though these can be hard to identify in some cases. VSearch was performed on individual genes without an outgroup. ABGD was performed through the online ABGD webserver (<http://wwwabi.snv.jussieu.fr/public/abgd/abgdweb.html>, 08/18/2018; X = 0.5) on COI and 16S alignments by family. ABGD was performed on uncorrected p-distances using entire datasets under the assumption that the smallest gap in the pairwise distance histogram reflected the boundary between
 150 intraspecific variation (smaller values) and interspecific variation (larger values). Poisson tree processes (PTP) and multi-rate PTP were run using the stand alone mPTP software implementing -single and -multi switch commands on the fully bifurcated trees generated above. Our data contained multiple individuals with the sample haplotypes but the replicate haplotypes can confound delimitation analyses and lead to over-splitting (Marki et al., 2018) so we calculated the minimum branch length for each sequence and used the minimum branch threshold option in order to ignore these replicate branches in subsequent
 155 PTP/mPTP analyses. MCMC analyses were run for 100 million generations, sampling every 10,000 and discarding the first 2 million generations as burn-in. Analyses were initiated using a random delimitation as starting point. We ran 3 MCMC chains for each analysis and assessed chain convergence by checking average standard deviation of delimitation support values (ASDDSV) across the 3 independent MCMC runs, accepting values near zero and below 0.05 as individual MCMC chains appearing to converge on the same distribution of delimitations (Ronquist et al., 2012, Kapli et al., 2017). We inspected the
 160 MCMC output trees and collapsed all putative species clades that had support below 0.70, which resulted in number of supported clades being within the credible range of delimited species (CCI) and the range across CCI where probability is 0.95 (HPD). The ML estimate, on the other hand, was not always within these intervals, meaning that this ML point estimate delimitation was not supported by MCMC analyses (the estimate may instead represent a local maximum or random solution



derived across the ML likelihood surface) and demonstrates the importance of running MCMC analyses. Singletons greatly
 165 affected mPTP analyses but not PTP or ABGD so were removed from mPTP and retained for PTP and ABGD.

Isopod Communities and diversity analyses

Analysis of community similarity between areas and their diversity was performed in R using package ‘vegan’ (Oksanen et al
 2008). The sampling effort, expressed as the number of Epibenthic Sledge (EBS) deployments per area was uneven ranging
 from 2 to 8 deployments, therefore the similarity between communities was done using relative abundance (Chord distance,
 170 see Legendre & Gallagher 2001) and using ‘presence-absence’ to explore faunistic differences. Ordination was done using
 nMDS. The community table (Appendix_supplement1) shows the number of specimens from each species found adding up
 all EBS samples for a given area. As the number of specimens found differs between areas, diversity comparison was achieved
 using rarefaction curves, together with standard diversity indices Shannon, Simpson and Jaccard’s Evenness. The expected
 number of species per area was inferred using extrapolation methods. Chao1 (Chao 1994, Colwell & Coddington 1994) uses
 175 the proportions of singletons and doubletons in the sample to estimate expected species richness, while ACE (Chazdon et al
 1998) is an abundance-base coverage estimator. For the analysis of beta (regional) diversity, the total multiple-site beta
 diversity β_{SOR} was calculated using the modified Sørensen Index (Sørensen 1948, Balseaga & Orme 2012), and β_{SOR} was
 decomposed into its additive components “multiple-site species turnover” β_{SIM} (Simpson Index, Simpson 1943) and “multiple-
 site nestedness” β_{SNE} using R package ‘betapart’ (Balseaga 2010, Balseaga & Orme 2012). In order to explore the relative
 180 contribution of every area to species turnover and nestedness, these values were calculated taking one area out each time in a
 jackknife approach. Changes in turnover and nestedness are attributable to the area each time excluded from the analysis.

1.2 Results

In total, we examined 22 EBS samples taken at six abyssal areas. The dataset comprised 619 specimens belonging to 168
 putative species (Table 1). The Munnopsidae accounted for 51 % of the species (congruent) and 48 % of the specimens,
 185 Desmosomatidae accounted for 30 % of the species and 23 % of the specimens, Haploniscidae accounted for 23 % of the
 species and 14 % of the specimens, while the Macrostylidae accounted for only 5 % of the species and 15 % of the specimens
 (Table 4). Desmosomatids were the most diverse group with 0.36 species per specimen (congruent). Haploniscids and
 munnopsids were nearly as diverse as the desmosomatids with 0.26 and 0.29 species per specimen, while macrostylids were
 the least diverse with only 0.09 species per specimen. If you remove species represented by a single specimen (singletons)
 190 from the species counts and compare total species numbers to number of species represented in more than one collection
 location, you see that 52 % of desmosomatid species were found in more than one collection location, while only 38 and 37 %
 of macrostylid and munnopsid species, respectively, and only 26 % of haploniscid species were found in more than one
 collection location.

Molecular data



195 All isopod families were reciprocally monophyletic (Figs. 2-5). As expected with fast evolving genes such as COI and 16S,
 good resolution is given at the tips of the tree and most recent relationships such as species and sometimes even generic level.
 However, no resolution of relationships deeper in the trees was obtained. Given that the research question here is one of species
 delimitation, we did not attempt to find markers that would resolve deeper nodes in the trees. It is notable that the percentage
 of species new to science is quite high and reaches more than 87 % in our dataset. In total, as many as seven of the 187
 200 delimited species were described either previously from other deep-sea locations or even based on CCZ material (Malyutina
 et al. submitted; two new spp. within the new genus *Pirinetes* Malyutina & Brix gen. nov., Riehl & De Smet in press for
Macrostyli cf. *metallicola*, Brix et al. 2018 for *Eugerdella* cf. *egoni*). Emphasis is put here on “m”, because the assigned
 species names are indicated with a “cf.” and need more detailed taxonomic verification.

The congruent species delimitation resulted in 86 munnopsid species OTUs (Table 1, Figure 2). Putative species clade
 205 definition based on genetic data suggests there is substantial cryptic diversity within the Munnopsidae. Specimens identified
 as belonging to *Disconectes* belonged to 14 different putative species, of which those putative species formed 7 clades. Only
 the singleton and clades with fewer samples came from a single collection region. Specimens identified as belonging to the
 “catch-all” genus *Eurycope* belonged to 22 different putative species, of which those putative species formed nine higher level
 clades. One putative *Paramunnopsis* species was collected from three different region while another was collected from two
 210 different regions and was found to be within the same putative species clade as a specimen identified as *Munnopsis abyssalis*.
 Of the six putative *Betamorph* species, four were singletons and one contained specimens collected from three different
 regions. All collected *Bellibos*, belonging to two putative species, were collected from a single region.

The congruent species delimitation resulted in 51 desmosomatid species OTUs (Table 1, Figure 3). The genera *Chelator*
 Hessler, 1970 (6 spp.), *Oecidibranchus* Hessler, 1970 (1 sp.), *Mirabilicoxa* Hessler, 1970 (12 spp.), *Eugerdella* (kussakin,
 215 1965) (18 spp.), *Disparella* Hessler, 1970 (5 spp.), *Prochelator* Hessler, 1970 (4 spp.) and *Eugerd* Meinert, 1895 (3 spp.)
 were present in our dataset. Genetically defined clade composition closely mirrored the morphological identification (Figure
 3).

The congruent species delimitation resulted in 23 haploniscid species OTUs (Table 1, Fig. 4). The clades represent the genera
 220 *Mastigoniscus* (9 spp.), *Haploniscus* (9 spp.) and *Chauliodoniscus* (5 spp.). In Haploniscidae, 100 % of species collected a
 new to science.

The congruent species delimitation resulted in eight macrostyliid species in this monogeneric family (Table 1, Fig. 5). Putative
 species “*Macrostyli* sp. 1”, collected from both GC area and adjacent to IOM area, was strongly supported as sister to the rest
 of the available macrostyliids. The remainder of the macrostyliids formed a single clade that was differentiated into seven
 individual putative species clades (Fig. 5). Only two of these putative species clades can be easily distinguished from the others
 225 based on morphology, while the rest have yet to have morphological apomorphies identified for them. All eight putative species
 clades were supported by a minimum bootstrap value of 97 % in the maximum likelihood-based phylogenetic estimations.
 These eight species are the same that were stable across both COI/16S species delimitation analyses (Osborn et al. in prep. for
 detailed species delimitation analyses comparing methods and challenges with each family’s dataset). It may be possible with



additional sampling to separate the putative species further but based on this dataset, there was not consistent evidence for further splitting so we chose to be conservative with regard to splitting putative species. Four species clades were geographically isolated within a single CCZ region (Fig. 1, clades 4, 6, 7 and 8), the rest contained members from two to five regions. There was genetic signal that suggested genetic differentiation between regions within the largest putative species clade with representatives collected from five regions, but this differentiation, or perhaps our sample size, was not sufficient to support further species level splits.

235 *Community and Diversity comparison by area*

The community table (supplement 1) shows the counts of each species by area. The diversity values are summarized in Table 2. A total of 22 sites (EBS deployments) were sampled at 6 areas. Sampling effort was uneven, with most samples taken in the DISCOL area in the Peru Basin (8). For all other areas 2-4 sites were sampled. A total of 619 specimens could be assigned to 168 species. None of the species was recorded in all 6 areas, while the most common species was *Macrostylidae_Macrostylis_M05* with 46 specimens (present in all areas besides DISCOL). Other species (see Appendix supplement 1) with 10 or more specimens were the munnopsids *Disconectes_Mu11* (22 specimens), *Eurycope_Mu37*, *Disconectes_Mu08* (both with 18 specimens), *Munneurycope_Mu67*, the haploniscids *Haploniscus_H10* (13 specimens each) *Mastigoniscus_H22* (with 12 specimens) and with 10 specimens the desmosomatid *Eugerdella_D39*, the macrostylids *Macrostylis_M03* and *Macrostylis_M04*. The reminding 177 species had less than 10 records, 68 species were represented by singletons.

The total number of species found was relatively similar between sites ranging from 38 (GSR) to 50 species (IFREMER). Remarkably the number of species neither correlates with number of specimens (pearson correlation 0.34, $p=0.49$), nor with number of sites per area (pearson correlation -0.02, $p=0.95$). IOM presented the highest number of unique species (species recorded only in one area) with 36 species (90 % of the species present in the area were unique), followed by DISCOL (31 species, 76 %) and FC (Ifremer; 34 species 68 %). All other areas had less unique species. The extrapolated number of species present per area ranged between 49 (GC: BGR) and 80 (BC: GSR) according to Chao1, and 53 (GC: BGR) and 80 (FC: Ifremer) according to ACE. Between 50 % and 12 % of the species remained unrecorded as predicted by Chao1 and ACE. Diversity values (Shannon, Simpson and Jaccard) are high at all areas. Nevertheless, lowest diversity values were recorded at BGR area (evenness 0.88, Simpson 0.94, Shannon 3.34) while all other area show similar higher values.

Half of the EBS deployments (11) were in the core CCZ area (all areas excluding APEI3 and DISCOL), but these accounted for (not half, but) 2/3 of the specimens (425) and 2/3 of the species (117) recorded. A total of 99 species (84% of all species) were found exclusively in the CCZ area. Chao1 and ACE predicted 137-146 species for the CCZ and 235-252 species for all areas together.

CCZ areas show highest number of shared species

Table 3 shows the faunistic similarity between areas. The greatest number of shared species are between CCZ areas. For instance, GSR shares 16 species with each of BGR and IOM areas, and 11 species with IFREMER. While GSR shares only 4 species with DISCOL and 2 with APEI3. The highest numbers of non-shared species (mean 80.4 ± 4.3) are found between



APEI3 and any other area, followed by DISCOL (mean 78.4 ± 6.5) although t-test shows no significant difference between them ($p=0.58$).

265 *High diversity in each area is reflected by low similarity between sampling areas*

Total multi-site beta diversity was high (total β SOR 0.885, Table 2), meaning that the similarity between areas was low. The beta diversity between CCZ only areas was lower (total β SOR 0.767) revealing slightly higher congruence between areas in the CCZ. In both cases the highest proportion of beta diversity is due to species turnover (β SIM) with only a small proportion accounting for nestedness (β SNE), but the nestedness proportion is 3 times greater within CCZ areas (β SNE = 0.021) than 270 when considering all areas together (β SNE = 0.007). This is also evidenced by removing the areas one by one and calculating beta diversity with the reminding areas only. Removal of APEI3 and DISCOL results in the highest increase in nestedness (β SNE goes from 0.007 to 0.011), while the removal of any of the CCZ areas either does not change β SNE or it decreases up to β SNE = 0.004.

The known unknown: real number of species still not sampled

285 Rarefaction analysis (Figs. 6, 7) shows that all areas are similar in terms of species richness. The lowest curve being BGR (slightly lower diversity) and the highest being IOM. Neither curves show signs of having reached an asymptote.

Distance matters: APEI and DISCOL more different than central CCZ claims

Community analysis using Chord distance was ordinated in an nMDS diagram (Fig. 8), showing the more similar CCZ areas clustering together and the more different DISCOL and APEI3 distinctly apart from each other and from the CCZ areas. Not 280 so evident is the pattern in the presence/absence ordination (Fig. 9) because of the high dissimilarity between areas. The ordination is highly influenced by the number of unique species, highest at IOM, lowest at BGR along the y-axis and other areas spread along the x-axis. The box-plot shows highest median presence/absence dissimilarity to other areas at APEI3, DISCOL and IFREMER areas. The boxplot (Fig. 10) shows that the median Chord distance of the area to any other areas is greater at APEI3 and DISCOL and smaller at any of the CCZ areas.

285 *Comparison by family, species ranges and beta-diversity*

The species abundance diversity greatly differs between families (Table 4). Munnopsidae was the most abundant and diverse family with 294 specimens (199 in CCZ) belonging to 91 species (55 in CCZ), followed by Desmosomatidae with 143 specimens (193 in CCZ) belonging to 63 species (43 in CCZ). These latter families have a similar diversity as evidenced by the by-family rarefaction curve (Fig. 6). Differences in diversity between these families are due to differences in abundance 290 rather than species richness.

The family Haploniscidae is less diverse and was present with 88 specimens (53 in CCZ) belonging to 24 species (14 in CCZ). The family Macrostylidae, although relatively common, is much less diverse, 94 specimens (70 in CCZ) belonged to only 9 species (5 in CCZ). The rarefaction curves of these two families show signs of saturation. This is also indicated by the predicted number of species by Chao1. No additional (unseen) species of Haploniscidae and Macrostylidae are expected in the present 295 dataset, while the expected number of Munnopsidae and Desmosomatidae is 110 and 98 respectively.



Total beta diversity (β SOR) and species turnover (β SIM) increases in this sequence Munnopsidae (β SOR = 0.873; β SIM = 0.860), Desmosomatidae (β SOR = 0.904; β SIM = 0.895) and Haploniscidae (β SOR = 0.916; β SIM = 0.898). This pattern is not evident when comparing within the CCZ (see Table 4). Macrostylidae has lower beta diversity and species turnover (β SOR = 0.809; β SIM = 0.777) mainly due to a single species that shows a large distribution range (see discussion).

300 The ranges of distribution differ between families (Table 5). No species of either family was present in all six studies areas. While **one** species belonging to Munnopsidae was present in five areas (absent in DISCOL). The most widely distributed species of Desmosomatidae was present in all four CCZ areas (no desmosomatid was present in five or six areas). The proportion of species present in a single area increased in this sequence Munnopsidae (75.8%), Desmosomatidae (77.7%) and Haploniscidae (83%). A total of 6 (66.6%) out of 9 species of Macrostylidae was recorded in a single area. In total 77% of the
 305 species were recorded in a single area, 13.9% in 2 areas, 5.3% in 3 areas, 2.6% in 4 areas and 1% in 5 areas.

1.3 Discussion

The most common biological unit is the “species”. A general public understanding of a healthy ecosystem is to have many species living in it. The definition of “**what is a species**” is tricky, and often discussed, more than 20 species definitions exist (summary in Fišer et al. 2017). With our **S** analysis, we provide a stable system to define a species in the deep sea as baseline
 310 for a more closer ecological view on the samples.

Our results indicate, that life-style, and more precisely the locomotion (dispersal) capabilities of deep-sea asellotes are structuring their biodiversity patterns at medium and large scales. The family Munnopsidae is the most mobile of the four families studied here. They possess large swimming legs and can be observe swimming in the deep-sea water layers on ROV videos (citations). The second most mobile family is the Desmosomatidae. They live on the surface of the sediments, but
 315 have appendages modified for swimming (not as pronounced as Munnopsidae). On contrary there is no evidence that Haploniscidae can swim. These asellotes live on or in the sediments and have short legs that they use for crawling. Macrostylidae **live most probably** in tubes into the sediment, although some males of this family are good swimmers.

The diversity patterns seems to correspond with these differences in locomotory capabilities. Munnopsidae is the most abundant and diverse family. We do not believe that this perception is biased by the sampling gear, because Munnopsidae are
 320 nevertheless most of the time sitting on the sediments were they feed on foraminifera and only swim occasionally (citations). The enhanced locomotory capabilities of Munnopsidae will result in an enhance connectivity between areas in the CCZ. It may well be that the species have large distribution ranges and therefore the probability of finding them in the EBS samples is higher. Desmosomatidae are less abundant and therefore also diversity is a bit lower. But species richness of Desmosomatidae is as large as Munnopsidae as shown in Figure 6. Finally, the families with reduced dispersal capability have remarkably less
 325 species diversity in the area and the species have much more restricted distributions. Haploniscidae have 83% of the species present in a single area, while this percentage is lower for Desmosomatidae (77%) and Munnopsidae (75%). Macrostylidae deserves as special mention. This sediment dwelling family displayed an unusual low diversity. Only nine species were



recorded although 94 specimens were analysed (more specimens than Haploniscidae). And these species had a remarkably small range of distribution, as 6 out of 9 species were found in a single area and two species in two contiguous areas. This pattern would have reinforced our hypothesis. But one of the species is present in as much as five areas, the so-called “sp. M” (OTU M04-M07, see Table 1, Fig. 5). In our study, low morphological variation is contrasted by genetic differentiation in *Macrostylis* sp. M (cf. *metallicola*), which belongs to at minimum three different species according to our SD. If a real affiliation to *metallicola* can be provided for clade 5 this would follow the wide distribution of this species across the CCZ according to Riehl and De Smet (in review). The authors state that also in their distribution data, they find molecular hints of *metallicola* being a complex of more (cryptic) species and thus, the morphological uniform appearance leads to underestimating biodiversity or we may observe ongoing radiation processes. However, as a result any mining impact on the populations of this species would disturb this process or limit the genetic potential of the population and thus, cause changes in the radiation and distribution pattern of this species.

Genetic differentiation in Macrostylidae: Riehl & Kühne (in review) state that two species from the North Pacific Ocean are indicated to be one in reality: *Macrostylis ovata* and *M. grandis* specimens were genetically not distinct but identical or highly similar. Differences of below 1 % uncorrected p distance and single mutational differences in the 16S marker provided a clear indication that *M. ovata* is a junior synonym of *M. grandis*. This range of intraspecific variability is supported by previous studies on Macrostylidae, which reported up to 8 % p- distance of intraspecific variation (Bober et al., 2018b, 2018a; Kniesz et al., 2018; Riehl and De Smet, under review; Riehl and Kaiser, 2012).

It is important to remark that our result cannot be extrapolated to understanding the global diversity of the families. Even the global species pool of all four families would be the same, it would be easier to collect more species of Munnopsidae and Desmosomatidae because they have larger distributional ranges than species with smaller distribution ranges like Haploniscidae and Macrostylidae, just because our sampling is limited in space. We only visited a few areas in the abyssal Eastern Pacific.

Little is known about the behaviour of deep-sea asellotes (Hessler and Strömberg, 1989) and most observations come from the morphological descriptions of dead specimens. Especially Macrostylidae, a change to a more epifaunal lifestyle with sexually mature males reproducing with probably stationary females was discussed in species descriptions of strongly sexual dimorphic species (Bober et al., 2017; Kniesz et al., 2017). Sex-specific differences in dispersal capacities are known more from Macrostylidae than from Munnopsidae for which, to our knowledge, no dispersal effecting sexual dimorphisms are apparent.

In desmosomatids and nannoniscids, sexual dimorphism is more pronounced than in munnopsids, for example, males show more adaptations to swimming than females in various species. The species delimitation done on the KuramBIO II dataset for desmosomatids and nannoniscids (Jennings et al. in press) revealed that a strong sexual dimorphism, especially the genus *Mirabilicoxa*, limits morphological species determination and only the integrated approach made a clear assignment to species possible. Thus, determination based on morphological features may underestimate true species richness, which became evident for macrostylids in our data set. The wide distribution of M05 would have been easily explained if the males would have showed a strong sexual dimorphism, but this was not the case in the individuals available in our dataset.



Haplomiscidae show a sexual dimorphism, which is strongly visible in males, while females of different species may have a similar morphological appearance. Thus, species determination sometimes depends on the male specimens and is also not possible in juvenile stages (Brökeland 2010a,b, Brix et al. 2011).

365 Brandt et al. (2011) considered the distribution of isopod families sorted by mobility types: walking, swimming, burrowing, walking-swimming, walking-burrowing. There is a similarity of the Isopoda found on the Maud Rise seamount compared to the other deep-sea stations in the Weddell Sea: especially the comparably “lower mobile” families Macrostylidae and Haplomunnidae were highly abundant. To find two isopod families with comparably restricted active distribution abilities in such high abundances on a seamount top was regarded by Brandt et al. (2011) as unusual.

370 Bober et al. (2018) used only one munnopsid species with a known pan-ocean distribution, *Acanthocope galathea* Wolff, 1962 (Malyutina et al. 2018) while for desmosomatids, nannoniscids and macrostylids the complete amount of available species and specimens (>400 specimens for both families, nannoniscids and desmosomatids, resulted in 72 species for COI and 45 for 16S by species delimitation according to Brix et al. 2018) was used. Our dataset used the complete set of specimens available in the family Munnopsidae and revealed that this swimming family is the only one showing potential species with

375 atlantic-pacific distribution (in case of *Acanthocope* cf. *galathea*) and also showing the distribution over the largest distances. On genus level, pacific-atlantic distribution has been reported also within the nannoniscids for species of two genera possessing swimming legs in a strong sexual dimorphism (Kaiser et al. 2017). Due to their prevailing reproduction mode (brooding) coupled with putatively poor swimming abilities most of species within the sister-family of Desmosomatidae, the Nannoniscidae (most species of this family have walking legs), we expected to find strong population divergence or even

380 presence of cryptic lineages in relation to distance. Kaiser et al. (unpublished, personal communication) show that two *Nannoniscus* lineages show wide geographic distribution (>1400 km apart), but there is also evidence for cryptic lineages in close vicinity (same licence area); some evidence that geographic distance is important, but also heterogeneity and oceanographic currents (Taboada et al. 2018).

Although we are dealing with a brooding taxon here and may not discuss larval distribution, adult forms of these small faunal species (2 – 10 mm average size), will be influenced by currents when moving actively in the water column. Etter & Bower

385 (2015) tested the distance of distribution during the PIP in the North Atlantic Ocean using physical particles as models. This experiment resulted in a possible distribution over hundreds of kilometres and even through current systems with a strong temperature gradient. Thus, actively swimming taxa are more likely not depending on any watermass or current system as already indicated by Schnurr et al. (2014, 2018) for the subarctic region around Iceland. For other ascellote families in the

390 present dataset, water masses did play a major role shaping distribution patterns, more than benthic surface structure (Brix & Svavarsson 2010) while for other, sediment types are most important as outlined by Stransky & Svavarsson (2010).

Based on two separately treated genetic datasets of Macrostylidae and Desmosomatidae/Nannoniscidae from the central Atlantic Ocean, Bober et al. (2018) found most species at only one side of the Mid Atlantic Ridge (MAR). The MAR seems to be a dispersal barrier for the non-swimming Macrostylidae and weakly-swimming Desmosomatidae and Nannoniscidae.

395 However, four species of Macrostylidae and Desmosomatidae did cross the MAR, but evidence for regular unrestricted gene



flow is lacking. Brix et al. (2018) observed from SD data for desomatids and nannoniscids of the VEMA fracture zone in the North Atlantic Ocean that even robustly-sampled species exhibit “small” ranges of around 500 km, and three species were distributed on the order of 1000–2500 km. Interestingly Wilson (2017), for the Pacific abyss, measured the rate of species turnover. Isopods change at a rate of 0.012 species per km, this gives an approximate linear species range of 84 km. Assuming circular distribution this gives an isopod species range of 2,228 km².

Some deep-sea taxa are reported to have broader ranges compared to the shallow-water taxa (Costello and Chaudhary, 2017). Either this might be an artefact of species misidentification or a result of the evolutionary history of these deep-sea species. Another hypothesis to explain the broad horizontal ranges of some deep-sea species was the “thought to be homogeneity” of seafloor habitats and stable abiotic conditions in temperature, salinity and pressure (McClain & Hardy 2010). The suggestion of Carney (2005) that abiotic and biotic factors vary greatly with depth and this restricts vertical ranges of many species despite the potential for broad horizontal distribution ranges as also discussed for isopods along the Kuril–Kamchatka Trench (Bober et al. in review, Jennings et al. in press) as well as in polar regions (Brix et al. 2014).

Nearly half of the deep-sea bivalve and gastropod that have a larval stage in the North Atlantic Ocean have wide distribution ranges along an entire basin (Rex 1981) or even show a pan-Atlantic distribution (Jennings & Etter 2014). The same pattern is observed for cirriped crustaceans distributing along currents in the South Pacific/Indian Ocean along the hydrothermal vent chains (Suzuki et al 2018) or along currents in the North Atlantic underwater mountain chains (like the acorn barnacle *Bathylasma* cf. *hirsutum*, Brix pers. observation). On the other hand, these unique deep-sea habitats such as vent sites, seamounts, hard rocks or cold-water coral reefs may limit the distribution ranges of species because their geochemical cycles and biological activity promotes restricted ranges and isolation, generating highly endemic faunas (McClain & Hardy 2010).

Endemism in the deep-sea habitats is known and describes as “rare” species (Brandt et al. 2007) those species occurring at only one sampling point with only one individual. This phenomenon is also observed in our dataset in each of the four families. It has been discussed as sampling bias due to patchiness of distribution by Kaiser et al. (2009) for EBS samples from the Southern Ocean. Therefore, it is not clear whether the high number of so called “singletons” in our dataset is true endemism or a result of sampling bias. Pelagic species and pelagic life stages of many benthic species can drift and swim across and/or between oceans during their lifetime. Benthic species, however, spend most of their life on the seabed, and thus may be dispersing shorter distances (Costello et al., 2017). However, it has to be noted that there is – even more than in the VEMA dataset – a large distance between the sampling locations (inside CCZ/DISCOL) and the likely patchiness (Kaiser et al., 2009) cannot be sufficiently inferred based on our analysis – especially because in the CCZ dataset not every specimen was sequenced (in the DISCOL dataset yes, but with a lower success rate than in CCZ). Nevertheless, our dataset represents the most comprehensive dataset for the deep sea so far. Nevertheless, we are still facing the problem of undersampling the real number of species (Fig. 6, 7), may be except for Macrostylidae (Fig. 6).

Compared to all other asellotan isopod families, munnopsids are highly specialized for swimming and accordingly, some species have moved towards a benthopelagic (e.g., in *Munnopsoides* Tattersall, 1905) or even holobenthic (e.g., in *Paramunnopsis* Hansen, 1916) mode, while others follow a burrowing (e.g., in *Ilyarachna* Sars 1869, or *Bellibos* Haugness



430 & Hessler, 1979), or epibenthic (e.g., in *Rectisura* Malyutina, 2003 or *Vanhoeffenura* Malyutina, 2004) life style (reviewed in Osborn 2009).

For the swimming Munnopsidae Bober et al. (2018) were able to detect persistent gene flow across the MAR in the example species *Acanthocope galathea* Wolff, 1962. Specimens were collected along a latitudinal transect crossing the tropical abyssal North Atlantic during the Vema-TRANSIT expedition (Malyutina et al. 2018). For *Acanthocope galathea* a persistent gene
 435 flow over a vast geographic distance of 1,843 km is assumed in the VEMA fracture zone. This species is also available in the Pacific dataset and may be regarded as world-wide distributed (as indicated from the genetic data in our Pacific dataset) or alternatively as putative cryptic species due to the large genetic distances in the Atlantic and Pacific datasets.

Malyutina et al. (submitted) described a new genus and two new species of the munnopsid subfamily Eurycopinae from the CCZ material. The new genus was revealed by the molecular SD independent from the taxonomic investigation and
 440 morphological analysis and was independently confirmed by the molecular SD approach. In previous SDs for Desmosomatidae (Brix et al. 2018, Jennings et al. in press), the genera clustered well together, representing most probable relationships (Hessler 1970) as well as showing the taxonomic problem in the case of *Eugerdella* (Brix et al. 2018) and *Mirabilicoxa* (Jennings et al. in press). In the case of desmosomatids and nannoniscids, most comparable to the present dataset is the VEMA dataset in a horizontal distribution calculating species ranges, while the KuramBio II dataset is limited by a vertical distribution of species
 445 showing a strong bathymetric influence (factor depth) on species distribution as already stated for several peracarid taxa in other regions of the world (Brix et al. 2014 for *Chelator insignis*, Havermann et al. 2013 for *Eurythenes gryllus*).

Conclusion

Cardoso et al. (2011) list seven reasons why invertebrates are rarely included in present-day conservation. We focus on the most common and most fundamental drawback: taxonomic incompleteness. Our study of a community where over 87 % of
 450 the isopod species are new to science or described within the last two years, indicates the need for quick assessment tools like species elimination in the deep-sea environment. Additionally, taxonomic expertise is needed, which can lead to a description of the key species even though it is not possible to describe every species due to time constraints (Brix et al. 2018). If no SD or other rapid assessment method is possible due to constraints in the sampling method or fixation of the samples, the taxonomic incompleteness leads to incomplete knowledge of species distributions, ecology, population dynamics, but also
 455 lower public interest in those species. Even though taxonomic incompleteness is an old and well-known problem in conservation, molecular taxonomy (e.g. Fujita et al. 2012, Fontaneto et al. 2015) has unveiled that the taxonomic impediment may be much deeper than previously thought. Our dataset shows the known “unknown” living in 5000 m depth on the deep-sea floor in an area just awaiting more human impact when extraction of the metal resources here begins.

Geographic distance and locomotion type is most important for connectivity of populations. Exceptions like “sp. M” seem to
 460 underline a rule that natatory capability allows only the munnopsids to occur in five of the six areas samples. Long-distance populations are more diverse than patchy/local populations. Janssen et al. (in press) stated that in the case of polychaetes with



long- and short-distance dispersal capabilities, large populations are continuously distributed over large geographic scales. Although ~~their analyses~~ (Janssen et al. in press) suggest a similar pattern in isopods, spatial genetic structuring of isopod populations do imply weak barriers to gene flow. They conclude that mining-related habitat destruction will most likely impact the continuity of isopod populations. This is based on the assumption that ecosystem recovery after major impacts is predicted to occur slowly at evolutionary time scales. As already stated in Blaczewicz et al. (2019), studies on species richness and distribution patterns of small specimen like peracarid crustaceans are indispensable for the conservation of the abyssal ecosystem and for the development of management strategies for sustained commercial activities in the future.

Author contributions

Saskia Brix: Manuscript writing, coordination and management of sequence data (in BoLD), quality check, morphological identification, discussing the species delimitations, figures and manuscript writing, preparing the voucher specimens for museum storage.
 Karen J. Osborn: Data quality assessment/control, alignments, supervision of species delimitation analyses, tree/species delimitation figures, portions to the manuscript, editing.
 Sarah Schnurr: preparing specimens for genetics and sampling on board as well as lab work at the Smithsonian producing the raw data and providing preliminary trees.
 Sarit B. Truskey: performing the species delimitation and phylogenetic analyses and preliminary trees.
 Stefanie Kaiser: sorting and preparing specimens on board, helping with the morphological species delimitation, discussing the idea and providing ideas in manuscript writing, adding important parts to the text.
 Nils Brenke: species determination of DISCOL Isopoda and morphological comparison to the JPIO dataset together with Saskia Brix.
 Marina Malyutina: Identification of the Munnopsidae and linking the manuscript to the description of a new genus.
 Pedro Martinez: Paper idea and statistical analyses, manuscript writing and statistical figures.

Sample availability

No geoscientific samples which are registered as International Geo Sample Number (IGSN) have been used for the manuscript.

Competing interests

The authors declare that they have no conflict of interest.



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Figures

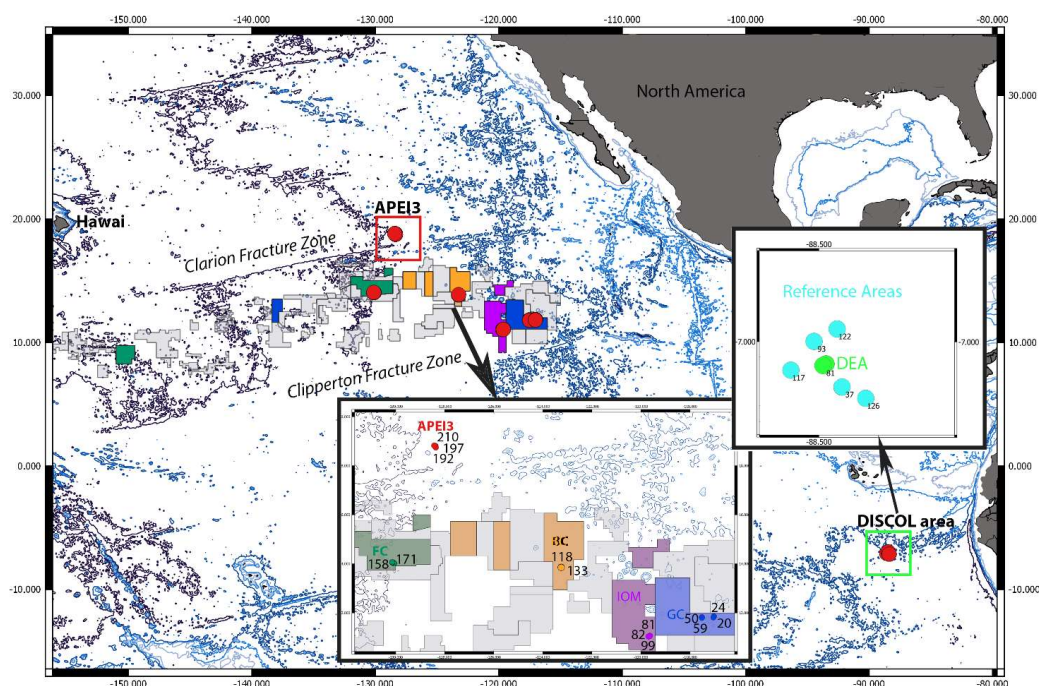


Fig. 1: Map of the locations of the EBS sampling sites (red dots) within the manganese nodule contractor and the DISCOL Experimental Area (DEA) areas in the north- and south-eastern Pacific. The colourcode in this map reflects the colourcode given in the circle trees (Fig.s 2 – 5), but is not reflected in the statistical graphs (Fig.s 6 – 10). In the CCZ the samples were taken in four contractor areas, from east to west: GC (dark blue - German contractor: BGR), IOM (violet - InterOceanmetal Joint Organization), BC (orange - Belgian contractor: GSR), FC (dark green - French contractor: IFREMER). In addition, the APEI3 (red - Area of Particular Environmental Interest number 3) and DISCOL Experimental Area (light green/blue – DEA and Reference Areas).

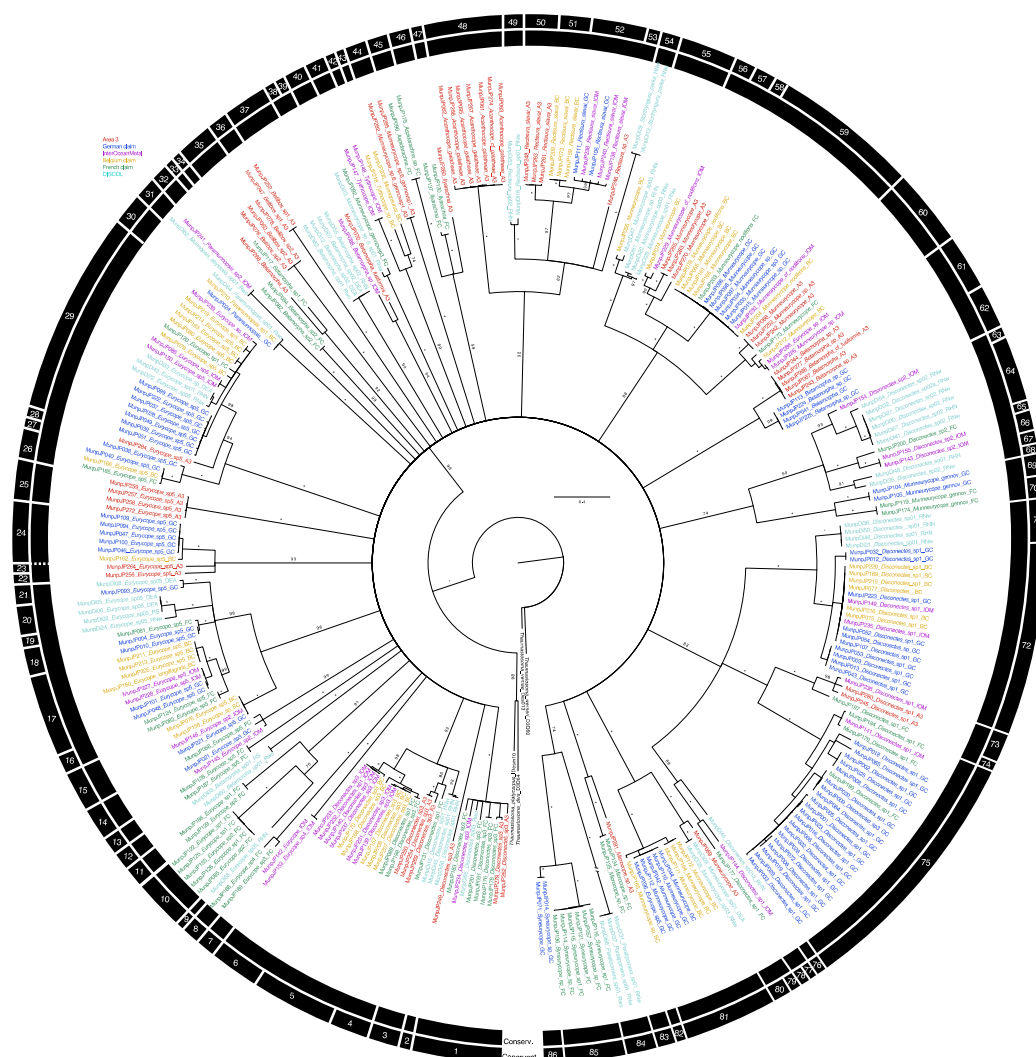


Figure 2. Phylogenetic tree of all munnopsid samples based on 16S and COI sequences for 294 specimens. Colours indicate collection location, with black indicating outgroups. All unsupported branches were collapsed and bootstrap support indicated with asterisks indicating 100 % bootstrap support. The outer two bars summarize the results of the species delimitation analyses which included morphological determination, Vsearch for individual genes, ABGD for individual genes, PTP and mPTP for both individual genes and the concatenated datasets. The conservative bar indicates that all SD analyses supported that split, while the congruent bar indicates that the majority of SD analyses indicated that split. Numbers on congruent bars are arbitrary and provided to allow a way to refer to specific supported clades.

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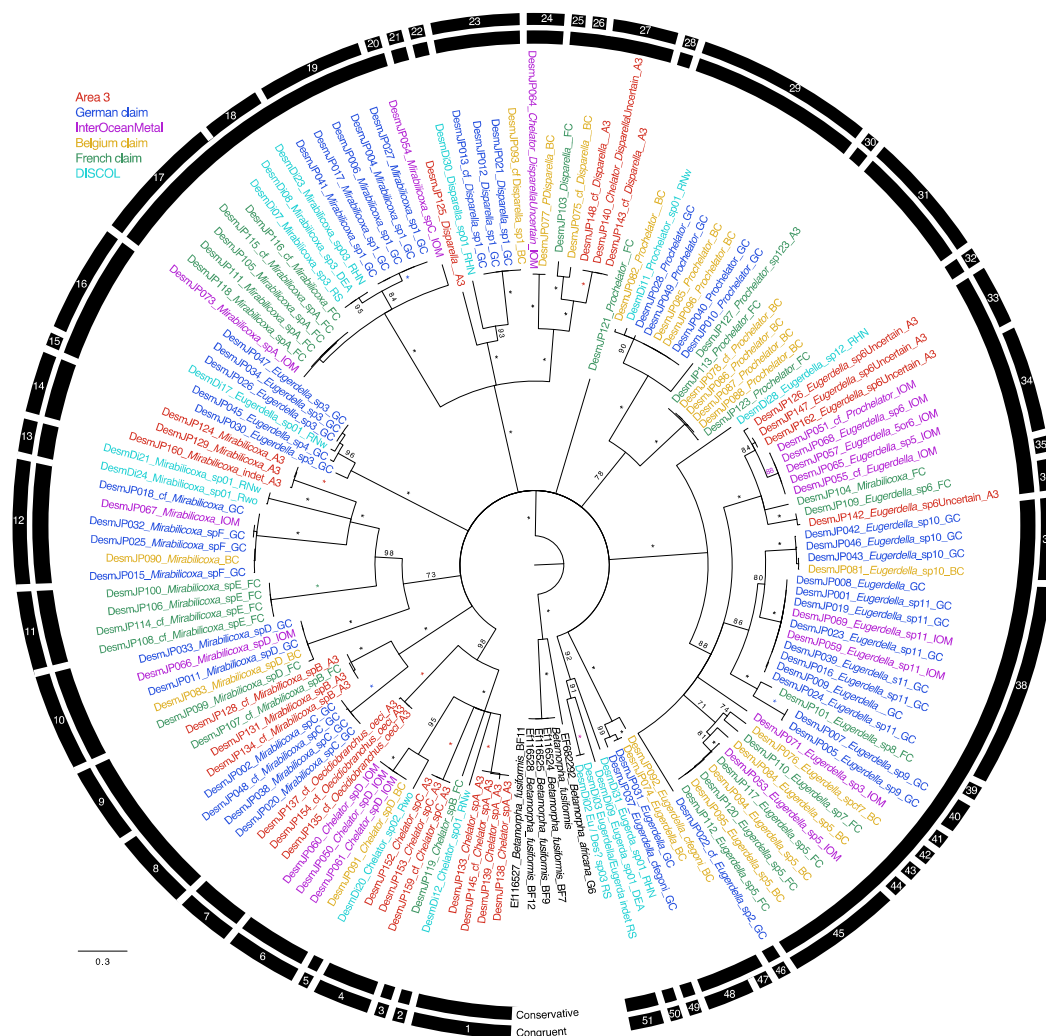


Figure 3: Phylogenetic tree of all desmosomatid samples based on 16S and COI sequences for 143 specimens. Colors indicate collection location, with black indicating outgroups. All unsupported branches were collapsed and bootstrap support indicated with asterisks indicating 100 % bootstrap support. The outer two bars summarize the results of the species delimitation analyses which included morphological determination, Vsearch for individual genes, ABGD for individual genes, PTP and mPTP for both individual genes and the concatenated datasets. The conservative bar indicates that all SD analyses supported that split, while the congruent bar indicates that the majority of SD analyses indicated that split. Numbers on congruent bars are arbitrary and provided to allow a way to refer to specific supported clades.



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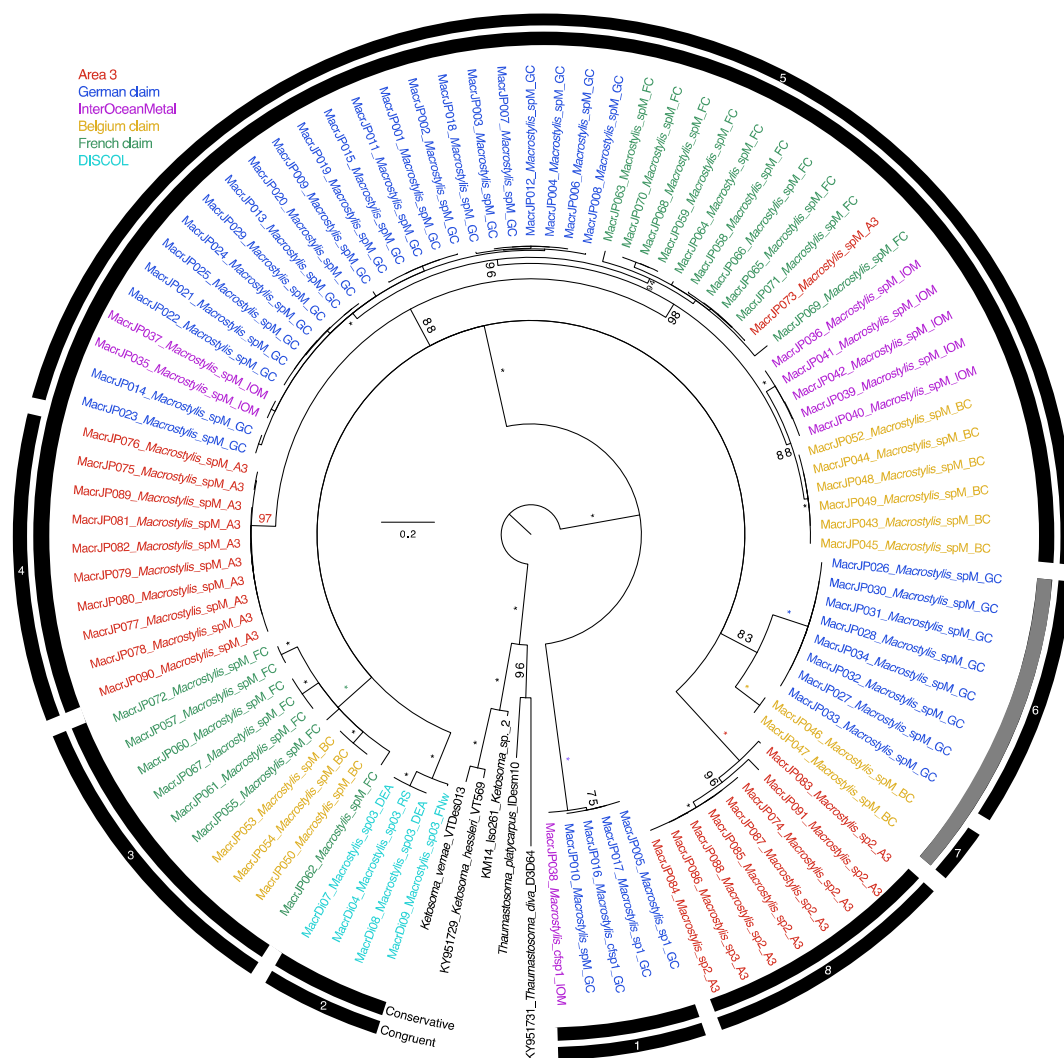


Figure 5: Phylogenetic tree of all macrotylid samples based on 16S and COI sequences for 94 specimens. Colors indicate collection location, with black indicating outgroups. All unsupported branches were collapsed and bootstrap support indicated with asterisks indicating 100 % bootstrap support. The outer two bars summarize the results of the species delimitation analyses which included morphological determination, Vsearch for individual genes, ABGD for individual genes, PTP and mPTP for both individual genes and the concatenated datasets. The conservative bar indicates that all SD analyses supported that split, while the congruent bar indicates that the majority of SD analyses indicated that split. Numbers on congruent bars are arbitrary and provided to allow a way to refer to specific supported clades.

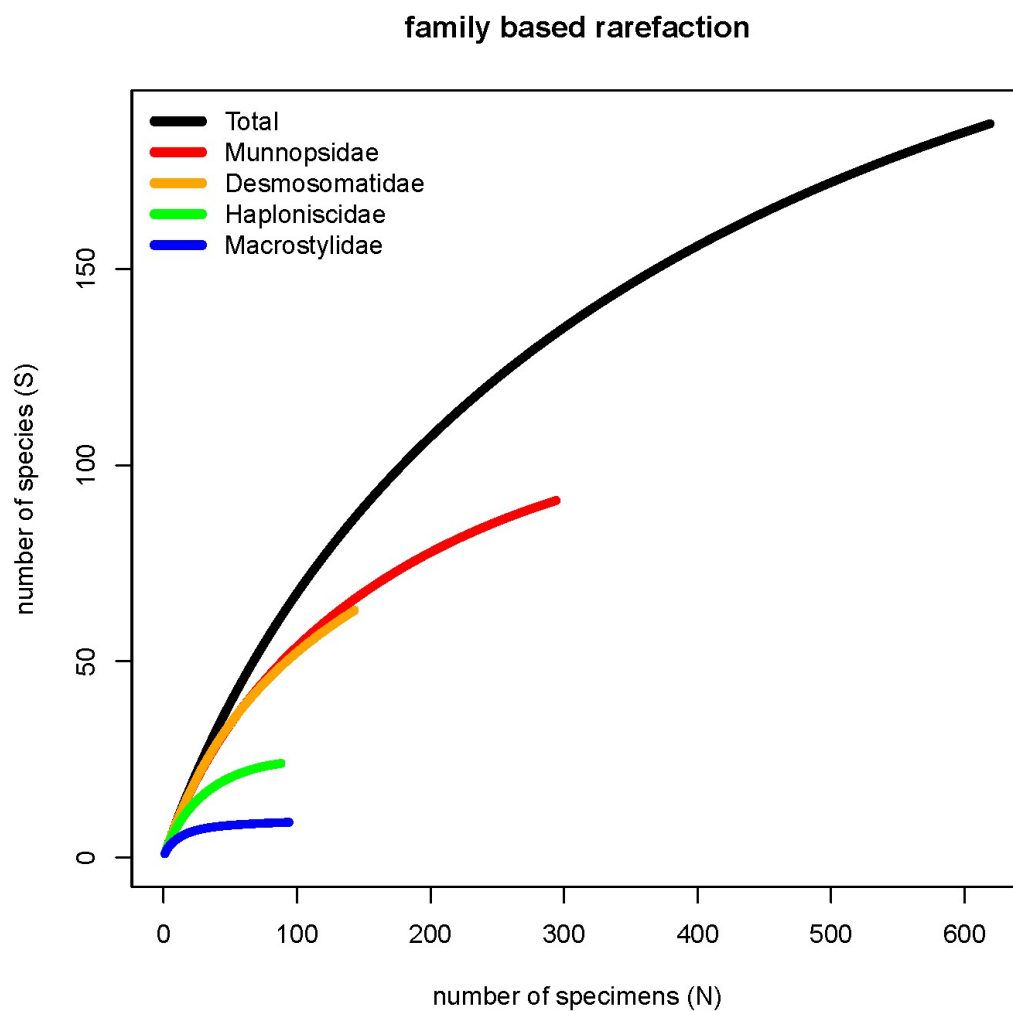
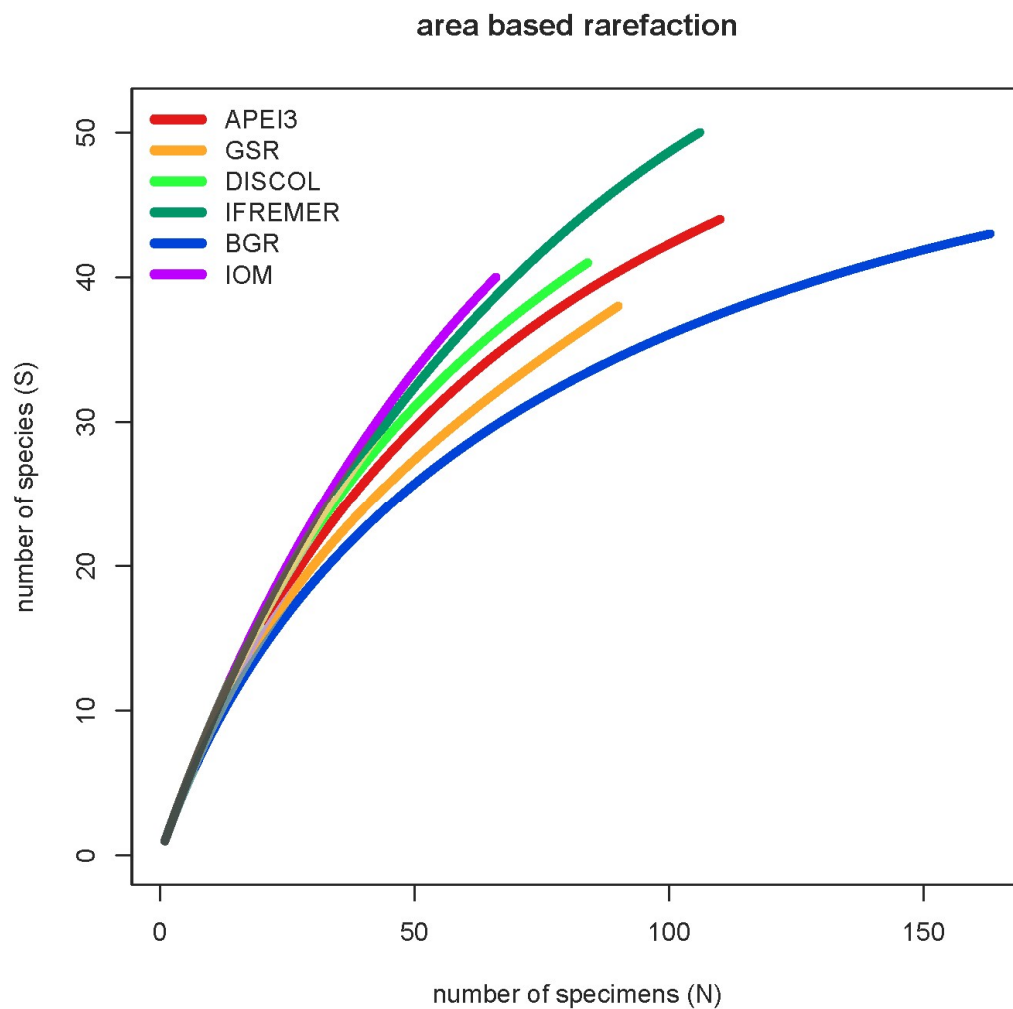


Fig. 6: Rarefaction analysis by isopod family, considering all areas together.



740 Fig. 7: Rarefaction analysis by area, considering all families together.

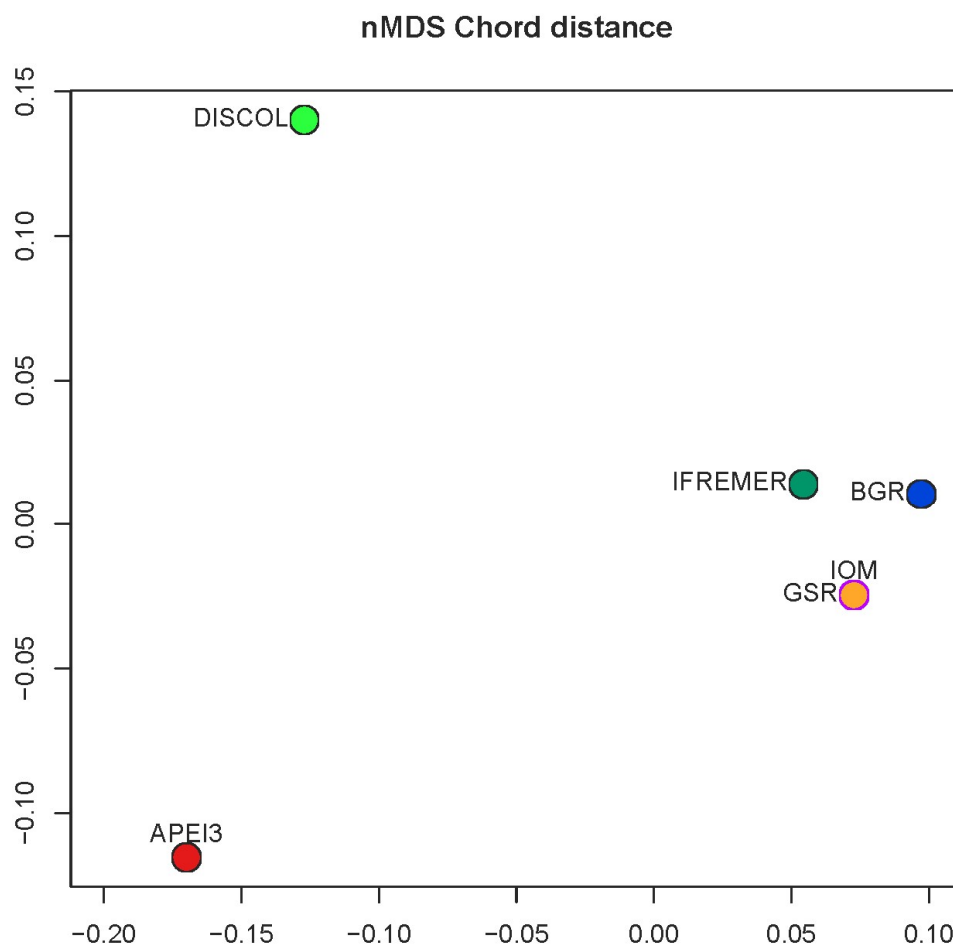
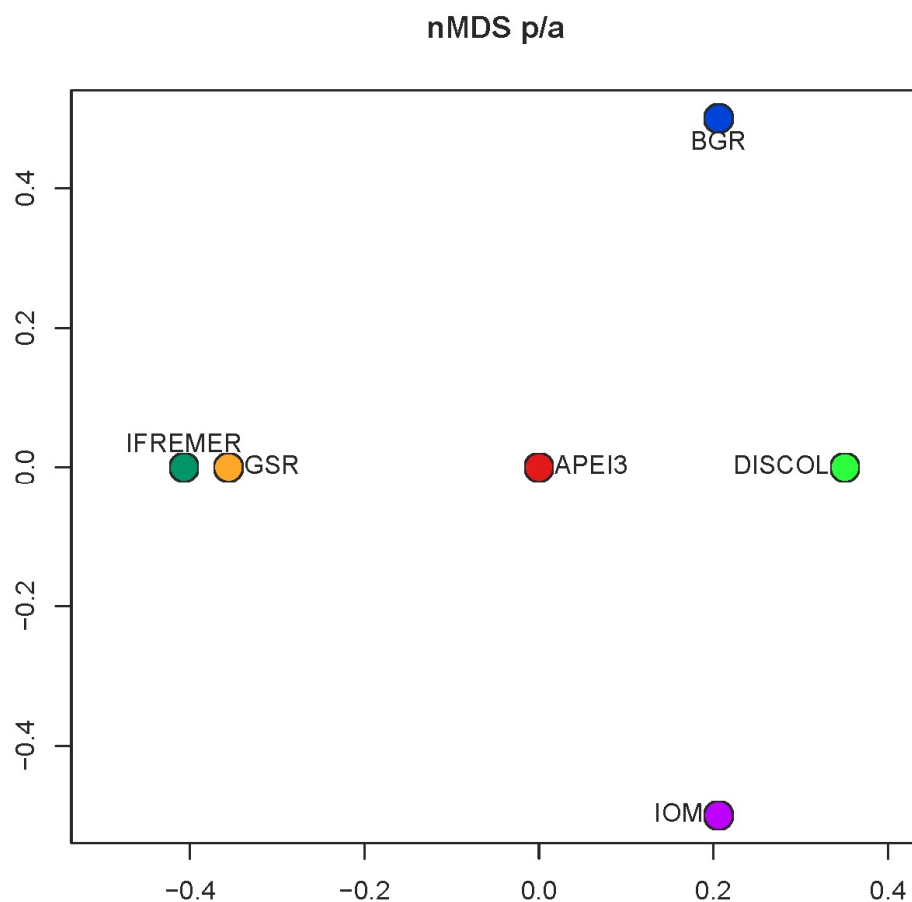


Fig. 8: nMDS ordination plot of Chord-distance between areas.



745 Fig. 9: nMDS ordination plot of Euclidean-distance between areas of presence-absence transformed data.

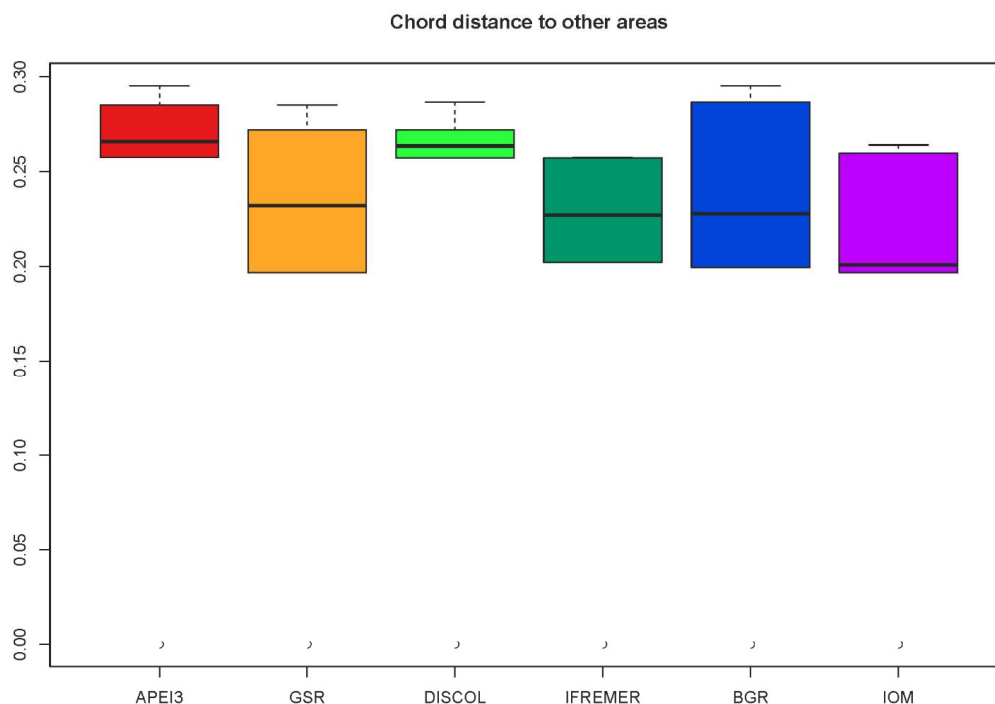


Fig. 10: Box and whiskers plot showing the median and range of the Chord distance of every area to other areas.

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Tables

Table 1: List of specimens used for this study including all information about station, species identification from morphology and molecular species delimitation (OTUs), museum storage and associated database numbers in BoLD and GenBank.

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original Field_ID (used in circle trees)	BOLD sample ID	genus	morphospecies	OTU (congruent)	BIN (BOLD)	database_ID DZM HH	museum catalogue number	family	loco type	RegionCode	station	GenBank no COI	GenBank no 16S
DesmD102	DSB_1214	cf. <i>Eugenda</i>	sp.03	052	BOLD:ADL4889	50277	ZMH K-56556	Desmosomatidae	WS	DISCOL	37	X	
DesmD103	DSB_1215	cf. <i>Eugenda</i>	indet	052	BOLD:ADL4889	50278	ZMH K-57490	Desmosomatidae	WS	DISCOL	45	X	
DesmD107	DSB_1219	<i>Mirabilicoxa</i>	sp.3	019	BOLD:ADL2574	50382	ZMH K-57491	Desmosomatidae	WS	DISCOL	37	X	X
DesmD108	DSB_1292	<i>Mirabilicoxa</i>	sp.3	019	BOLD:ADL2574	50357	ZMH K-57492	Desmosomatidae	WS	DISCOL	81	X	X
DesmD109	DSB_1293	<i>Eugenda</i>	sp.01	051	BOLD:ADL2893	50358	ZMH K-57493	Desmosomatidae	WS	DISCOL	85	X	X
DesmD111	DSB_1295	<i>Prochelator</i>	sp.01	030	BOLD:ADL2576	50360	ZMH K-57494	Desmosomatidae	WS	DISCOL	93	X	
DesmD112	DSB_1296	<i>Chelator</i>	sp.01	003	BOLD:ADM1410	50361	ZMH K-57495	Desmosomatidae	WS	DISCOL	93	X	X
DesmD117	DSB_1301	<i>Eugerdella</i>	sp.01	017	BOLD:ADL5038	50366	ZMH K-57496	Desmosomatidae	WS	DISCOL	93	X	
DesmD120	DSB_1345	<i>Chelator</i>	sp.02	006	BOLD:ADL9249	50410	ZMH K-57497	Desmosomatidae	WS	DISCOL	126	X	X
DesmD121	DSB_1346	<i>Mirabilicoxa</i>	sp.01	015	BOLD:ADL5368	50411	ZMH K-57498	Desmosomatidae	WS	DISCOL	117	X	X
DesmD123	DSB_1348	<i>Mirabilicoxa</i>	sp.03	019	BOLD:ADL2574	50413	ZMH K-57499	Desmosomatidae	WS	DISCOL	122	X	X
DesmD124	DSB_1349	<i>Mirabilicoxa</i>	sp.01	015	BOLD:ADL5368	50414	ZMH K-57500	Desmosomatidae	WS	DISCOL	126	X	X
DesmD128	DSB_1353	<i>Eugerdella</i>	sp.12	033	BOLD:ADL4885	50418	ZMH K-57501	Desmosomatidae	WS	DISCOL	122	X	X
DesmD130	DSB_1355	<i>Disparella</i>	sp.01	023	BOLD:ADL5538	50420	ZMH K-57502	Desmosomatidae	WS	DISCOL	122	X	X
DesmD131	DSB_1356	<i>Eugenda</i>	sp.01	050		50421	ZMH K-57503	Desmosomatidae	WS	DISCOL	122	X	X
DesmD1001	DSB_1762	<i>Eugerdella</i>	sp.11	039	BOLD:ADW6372	50827	ZMH K-57504	Desmosomatidae	WS	GC	20	X	
DesmD1002	DSB_1763	<i>Mirabilicoxa</i>	sp.C	009	BOLD:ADL5035	50828	ZMH K-57505	Desmosomatidae	WS	GC	20	X	X
DesmD1004	DSB_1765	<i>Mirabilicoxa</i>	sp.1	020	BOLD:ADL5037	50830	ZMH K-57506	Desmosomatidae	WS	GC	20	X	X
DesmD1005	DSB_1766	<i>Eugerdella</i>	sp.9	041	BOLD:ADG0134	50831	ZMH K-57507	Desmosomatidae	WS	GC	20	X	
DesmD1006	DSB_1767	<i>Mirabilicoxa</i>	sp.1	020	BOLD:ADL5037	50832	ZMH K-57508	Desmosomatidae	WS	GC	20	X	X
DesmD1007	DSB_1768	<i>Eugerdella</i>	sp.9	041	BOLD:ADG0134	50833	ZMH K-57509	Desmosomatidae	WS	GC	20	X	
DesmD1008	DSB_1769	<i>Eugerdella</i>	indet	039		50834	ZMH K-57510	Desmosomatidae	WS	GC	20	X	X
DesmD1009	DSB_1770	<i>Eugerdella</i>	indet	039	BOLD:ADW6372	50835	ZMH K-57511	Desmosomatidae	WS	GC	20	X	X
DesmD1010	DSB_1771	<i>Prochelator</i>	indet	030	BOLD:ADP9936	50836	ZMH K-57512	Desmosomatidae	WS	GC	20	X	
DesmD1011	DSB_1772	<i>Mirabilicoxa</i>	sp.D	011	BOLD:ADL5366	50837	ZMH K-57513	Desmosomatidae	WS	GC	20	X	
DesmD1012	DSB_1773	<i>Disparella</i>	sp.1	024	BOLD:ADL4887	50838	ZMH K-57514	Desmosomatidae	WS	GC	20	X	X
DesmD1013	DSB_1774	cf. <i>Disparella</i>	sp.1	024	BOLD:ADL4887	50839	ZMH K-57515	Desmosomatidae	WS	GC	20	X	X
DesmD1015	DSB_1776	<i>Mirabilicoxa</i>	sp.F	013	BOLD:ACY9838	50841	ZMH K-57516	Desmosomatidae	WS	GC	24	X	X
DesmD1016	DSB_1777	<i>Eugerdella</i>	sp.11	039	BOLD:ADW6372	50842	ZMH K-57517	Desmosomatidae	WS	GC	24	X	
DesmD1017	DSB_1778	<i>Mirabilicoxa</i>	sp.1	020	BOLD:ADL5037	50843	ZMH K-57518	Desmosomatidae	WS	GC	24	X	X
DesmD1018	DSB_1779	cf. <i>Mirabilicoxa</i>	indet	013	BOLD:ACY9838	50844	ZMH K-57519	Desmosomatidae	WS	GC	24	X	
DesmD1019	DSB_1780	<i>Eugerdella</i>	sp.11	039	BOLD:ADW6372	50845	ZMH K-57520	Desmosomatidae	WS	GC	24	X	X
DesmD1020	DSB_1781	<i>Mirabilicoxa</i>	sp.C	009	BOLD:ADL5035	50846	ZMH K-57521	Desmosomatidae	WS	GC	24	X	X
DesmD1021	DSB_1782	<i>Disparella</i>	sp.1	024	BOLD:ADL4887	50847	ZMH K-57522	Desmosomatidae	WS	GC	24	X	X
DesmD1022	DSB_1783	cf. <i>Eugerdella</i>	sp.2	047	BOLD:ADL4886	50848	ZMH K-57523	Desmosomatidae	WS	GC	24	X	
DesmD1023	DSB_1784	<i>Eugerdella</i>	sp.11	039	BOLD:ADW6372	50849	ZMH K-57524	Desmosomatidae	WS	GC	24	X	X
DesmD1024	DSB_1785	<i>Eugerdella</i>	sp.11	039	BOLD:ADW6372	50850	ZMH K-57525	Desmosomatidae	WS	GC	24	X	X
DesmD1025	DSB_1786	<i>Mirabilicoxa</i>	sp.F	013	BOLD:ACY9838	50851	ZMH K-57526	Desmosomatidae	WS	GC	24	X	X
DesmD1026	DSB_1787	<i>Eugerdella</i>	sp.3	017	BOLD:ADL5370	50852	ZMH K-57527	Desmosomatidae	WS	GC	50	X	
DesmD1027	DSB_1788	<i>Mirabilicoxa</i>	sp.1	020	BOLD:ADL5037	50853	ZMH K-57528	Desmosomatidae	WS	GC	50	X	X
DesmD1028	DSB_1789	<i>Prochelator</i>	indet	030	BOLD:ADP9936	50854	ZMH K-57529	Desmosomatidae	WS	GC	50	X	
DesmD1030	DSB_1791	<i>Eugerdella</i>	sp.3	016	BOLD:ADM0377	50856	ZMH K-57530	Desmosomatidae	WS	GC	50	X	
DesmD1031	DSB_1792	<i>Eugerdella</i>	indet	049	BOLD:ADL2572	50857	ZMH K-57531	Desmosomatidae	WS	GC	50	X	
DesmD1032	DSB_1793	<i>Mirabilicoxa</i>	sp.F	013	BOLD:ACY9838	50858	ZMH K-57532	Desmosomatidae	WS	GC	50	X	X
DesmD1033	DSB_1794	<i>Mirabilicoxa</i>	sp.D	011	BOLD:ADL5366	50859	ZMH K-57533	Desmosomatidae	WS	GC	50	X	X
DesmD1034	DSB_1795	<i>Eugerdella</i>	sp.3	017	BOLD:ADL5370	50860	ZMH K-57534	Desmosomatidae	WS	GC	50	X	
DesmD1037	DSB_1798	<i>Eugerdella</i>	cf. <i>egoni</i>	049	BOLD:ADL5536	50863	ZMH K-57535	Desmosomatidae	WS	GC	50	X	
DesmD1038	DSB_1799	<i>Mirabilicoxa</i>	sp.C	009	BOLD:ADL5035	50864	ZMH K-57536	Desmosomatidae	WS	GC	59	X	X
DesmD1039	DSB_1800	<i>Eugerdella</i>	sp.11	039	BOLD:ADW6372	50865	ZMH K-57537	Desmosomatidae	WS	GC	59	X	X
DesmD1040	DSB_1801	<i>Prochelator</i>	indet	030	BOLD:ADP9936	50866	ZMH K-57538	Desmosomatidae	WS	GC	59	X	
DesmD1041	DSB_1802	<i>Mirabilicoxa</i>	sp.1	020	BOLD:ADL5037	50867	ZMH K-57539	Desmosomatidae	WS	GC	59	X	X
DesmD1042	DSB_1803	<i>Eugerdella</i>	sp.10	038	BOLD:ADL5031	50868	ZMH K-57540	Desmosomatidae	WS	GC	59	X	X
DesmD1043	DSB_1804	<i>Eugerdella</i>	sp.10	038	BOLD:ADL5031	50869	ZMH K-57541	Desmosomatidae	WS	GC	59	X	X
DesmD1045	DSB_1806	<i>Eugerdella</i>	sp.4	017	BOLD:ACY6387	50871	ZMH K-57542	Desmosomatidae	WS	GC	59	X	
DesmD1046	DSB_1807	<i>Eugerdella</i>	sp.10	038	BOLD:ADL5031	50872	ZMH K-57543	Desmosomatidae	WS	GC	59	X	X
DesmD1047	DSB_1808	<i>Eugerdella</i>	sp.3	017	BOLD:ADL5370	50873	ZMH K-57544	Desmosomatidae	WS	GC	59	X	
DesmD1048	DSB_1809	cf. <i>Mirabilicoxa</i>	sp.C	009	BOLD:ADL5035	50874	ZMH K-57545	Desmosomatidae	WS	GC	59	X	X
DesmD1049	DSB_1810	<i>Prochelator</i>	indet	030	BOLD:ADP9936	50875	ZMH K-57546	Desmosomatidae	WS	GC	59	X	
DesmD1050	DSB_1811	<i>Chelator</i>	sp.D	007	BOLD:ADL5034	50876	ZMH K-57547	Desmosomatidae	WS	IOM	81	X	X
DesmD1051	DSB_1812	cf. <i>Eugerdella</i>	indet	036	BOLD:ADG1796	50877	ZMH K-57548	Desmosomatidae	WS	IOM	81	X	

DesmP053	DSB_1814	<i>Eugerdella</i>	sp.5	D44	BOLD-ADL5216	S0879 ZMH K-57549	Desmosomatidae	WS	IOM	81 X
DesmP054	DSB_1815	<i>Mirabilicixa</i>	sp.C	D06	BOLD-ADG12900	S0880 ZMH K-57550	Desmosomatidae	WS	IOM	81 X
DesmP055	DSB_1816	<i>d. Eugerdella</i>	indef	D36	BOLD-ADG1796	S0881 ZMH K-57551	Desmosomatidae	WS	IOM	81 X
DesmP057	DSB_1818	<i>Eugerdella</i>	S or 6	D36	BOLD-ADG1796	S0883 ZMH K-57552	Desmosomatidae	WS	IOM	81 X
DesmP059	DSB_1820	<i>Eugerdella</i>	sp.11	D39	BOLD-ADW6372	S0885 ZMH K-57553	Desmosomatidae	WS	IOM	81 X
DesmP060	DSB_1821	<i>Cheator</i>	sp.D	D07	BOLD-ADL5034	S0886 ZMH K-57554	Desmosomatidae	WS	IOM	81 X
DesmP061	DSB_1822	<i>Cheator</i>	sp.D	D07	BOLD-ADL5034	S0887 ZMH K-57555	Desmosomatidae	WS	IOM	81 X
DesmP064	DSB_1825	<i>d. Disparella</i>	indef	D25	BOLD-ADL5032	S0890 ZMH K-57556	Desmosomatidae	WS	IOM	99 X
DesmP065	DSB_1826	<i>Eugerdella</i>	sp.5	D36	BOLD-ADG1796	S0891 ZMH K-57557	Desmosomatidae	WS	IOM	99 X
DesmP066	DSB_1827	<i>Mirabilicixa</i>	sp.D	D11	BOLD-BSL5366	S0892 ZMH K-57558	Desmosomatidae	WS	IOM	99 X
DesmP067	DSB_1828	<i>Mirabilicixa</i>	indef	D13	BOLD-AC9838	S0893 ZMH K-57559	Desmosomatidae	WS	IOM	99 X
DesmP068	DSB_1829	<i>Eugerdella</i>	sp.6	D39	BOLD-ADG1796	S0894 ZMH K-57560	Desmosomatidae	WS	IOM	99 X
DesmP069	DSB_1830	<i>Eugerdella</i>	sp.11	D39	BOLD-ADW6372	S0895 ZMH K-57561	Desmosomatidae	WS	IOM	99 X
DesmP071	DSB_1832	<i>Eugerdella</i>	sp.3	D42	BOLD-ADML1411	S0897 ZMH K-57562	Desmosomatidae	WS	IOM	99 X
DesmP073	DSB_1834	<i>Mirabilicixa</i>	sp.A	D18	BOLD-AC9585	S0899 ZMH K-57563	Desmosomatidae	WS	IOM	99 X
DesmP074	DSB_1835	<i>Eugerdella</i>	indef	D49	BOLD-ADL2572	S0900 ZMH K-57564	Desmosomatidae	WS	BC	118 X
DesmP075	DSB_1836	<i>d. Disparella</i>	indef	D27	BOLD-ADL5535	S0901 ZMH K-57565	Desmosomatidae	WS	BC	118 X
DesmP076	DSB_1837	<i>Eugerdella</i>	sp. cf.7	D45	BOLD-ADL2895	S0902 ZMH K-57566	Desmosomatidae	WS	BC	118 X
DesmP077	DSB_1838	<i>Disparella</i>	indef	D25	BOLD-ADL5032	S0903 ZMH K-57567	Desmosomatidae	WS	BC	118 X
DesmP078	DSB_1839	<i>d. Prochelator</i>	sp.1	D32	BOLD-ADL3300	S0904 ZMH K-57568	Desmosomatidae	WS	BC	118 X
DesmP081	DSB_1842	<i>Eugerdella</i>	sp.10	D38	BOLD-ADL5031	S0907 ZMH K-57569	Desmosomatidae	WS	BC	118 X
DesmP082	DSB_1843	<i>d. Prochelator</i>	indef	D10	BOLD-ADG936	S0908 ZMH K-57570	Desmosomatidae	WS	BC	118 X
DesmP083	DSB_1844	<i>Mirabilicixa</i>	sp.D	D11	BOLD-BSL5366	S0909 ZMH K-57571	Desmosomatidae	WS	BC	118 X
DesmP084	DSB_1845	<i>Eugerdella</i>	sp.5	D43	BOLD-BSL5372	S0910 ZMH K-57572	Desmosomatidae	WS	BC	118 X
DesmP085	DSB_1846	<i>Prochelator</i>	indef	D30	BOLD-ADG9936	S0911 ZMH K-57573	Desmosomatidae	WS	BC	118 X
DesmP086	DSB_1847	<i>Prochelator</i>	sp.1	D32	BOLD-ADL3300	S0912 ZMH K-57574	Desmosomatidae	WS	BC	118 X
DesmP087	DSB_1848	<i>Prochelator</i>	sp.1	D32	BOLD-ADL3300	S0913 ZMH K-57575	Desmosomatidae	WS	BC	133 X
DesmP088	DSB_1849	<i>Prochelator</i>	sp.1	D32	BOLD-ADL3300	S0914 ZMH K-57576	Desmosomatidae	WS	BC	133 X
DesmP090	DSB_1851	<i>Mirabilicixa</i>	indef	D13	BOLD-AC9838	S0916 ZMH K-57577	Desmosomatidae	WS	BC	133 X
DesmP091	DSB_1852	<i>Cheator</i>	sp.D	D07	BOLD-ADL5034	S0917 ZMH K-57578	Desmosomatidae	WS	BC	133 X
DesmP092	DSB_1853	<i>Eugerdella</i>	cf. egoni	D48	BOLD-BSL5371	S0918 ZMH K-57579	Desmosomatidae	WS	BC	133 X
DesmP093	DSB_1854	<i>d. Disparella</i>	sp.5	D44	BOLD-BSL5367	S0919 ZMH K-57580	Desmosomatidae	WS	BC	133 X
DesmP094	DSB_1855	<i>Eugerdella</i>	sp.5	D44	BOLD-BSL5216	S0920 ZMH K-57581	Desmosomatidae	WS	BC	133 X
DesmP095	DSB_1856	<i>Eugerdella</i>	sp.5	D44	BOLD-BSL5216	S0921 ZMH K-57582	Desmosomatidae	WS	BC	133 X
DesmP096	DSB_1857	<i>Prochelator</i>	indef	D30	BOLD-ADG9936	S0922 ZMH K-57583	Desmosomatidae	WS	BC	133 X
DesmP099	DSB_1860	<i>Mirabilicixa</i>	sp.D	D11	BOLD-ADL5215	S0925 ZMH K-57584	Desmosomatidae	WS	FC	158 X
DesmP100	DSB_1861	<i>Mirabilicixa</i>	sp.E	D12	BOLD-ADL5213	S0926 ZMH K-57585	Desmosomatidae	WS	FC	158 X
DesmP101	DSB_1862	<i>Eugerdella</i>	sp.8	D40	BOLD-ADL2751	S0927 ZMH K-57586	Desmosomatidae	WS	FC	158 X
DesmP103	DSB_1864	<i>Disparella</i>	indef	D26	BOLD-ADL2577	S0929 ZMH K-57587	Desmosomatidae	WS	FC	158 X
DesmP104	DSB_1865	<i>Mirabilicixa</i>	indef	D37	BOLD-ADL5211	S0930 ZMH K-57588	Desmosomatidae	WS	FC	158 X
DesmP105	DSB_1866	<i>Mirabilicixa</i>	sp.A	D18	BOLD-AC9585	S0931 ZMH K-57589	Desmosomatidae	WS	FC	158 X
DesmP106	DSB_1867	<i>Mirabilicixa</i>	sp.E	D13	BOLD-ADL5213	S0932 ZMH K-57590	Desmosomatidae	WS	FC	158 X
DesmP107	DSB_1868	<i>d. Mirabilicixa</i>	sp.B	D10	BOLD-ADL4888	S0933 ZMH K-57591	Desmosomatidae	WS	FC	158 X
DesmP108	DSB_1869	<i>d. Mirabilicixa</i>	sp.E	D12	BOLD-ADL5213	S0934 ZMH K-57592	Desmosomatidae	WS	FC	158 X
DesmP109	DSB_1870	<i>Eugerdella</i>	sp.6	D34	BOLD-ADL5033	S0935 ZMH K-57593	Desmosomatidae	WS	FC	158 X
DesmP110	DSB_1871	<i>Eugerdella</i>	sp.7	D46	BOLD-ADL2578	S0936 ZMH K-57594	Desmosomatidae	WS	FC	158 X
DesmP111	DSB_1872	<i>Mirabilicixa</i>	sp.A	D18	BOLD-AC9585	S0937 ZMH K-57595	Desmosomatidae	WS	FC	171 X
DesmP112	DSB_1873	<i>Eugerdella</i>	sp.5	D44	BOLD-BSL5216	S0938 ZMH K-57596	Desmosomatidae	WS	FC	171 X
DesmP113	DSB_1874	<i>Prochelator</i>	indef	D32	BOLD-ADL3300	S0939 ZMH K-57597	Desmosomatidae	WS	FC	171 X
DesmP114	DSB_1875	<i>d. Mirabilicixa</i>	sp.E	D12	BOLD-ADL5213	S0940 ZMH K-57598	Desmosomatidae	WS	FC	171 X
DesmP115	DSB_1876	<i>d. Mirabilicixa</i>	sp.A	D18	BOLD-AC9585	S0941 ZMH K-57599	Desmosomatidae	WS	FC	171 X
DesmP116	DSB_1877	<i>Cheator</i>	indef	D12	BOLD-ADL5035	S0942 ZMH K-57600	Desmosomatidae	WS	FC	171 X
DesmP117	DSB_1878	<i>Eugerdella</i>	sp.5	D44	BOLD-BSL5216	S0943 ZMH K-57601	Desmosomatidae	WS	FC	171 X
DesmP118	DSB_1879	<i>Mirabilicixa</i>	sp.A	D18	BOLD-AC9585	S0944 ZMH K-57602	Desmosomatidae	WS	FC	171 X
DesmP119	DSB_1880	<i>Cheator</i>	sp.B	D40	BOLD-ADL5212	S0945 ZMH K-57603	Desmosomatidae	WS	FC	171 X
DesmP120	DSB_1881	<i>Eugerdella</i>	sp.5	D44	BOLD-BSL5216	S0946 ZMH K-57604	Desmosomatidae	WS	FC	171 X
DesmP121	DSB_1882	<i>Prochelator</i>	indef	D29	BOLD-ADL2573	S0947 ZMH K-57605	Desmosomatidae	WS	FC	171 X
DesmP123	DSB_1884	<i>Prochelator</i>	sp.1	D32	BOLD-ADL3300	S0949 ZMH K-57606	Desmosomatidae	WS	FC	171 X
DesmP124	DSB_1885	<i>Mirabilicixa</i>	indef	A3	BOLD-ADL5365	S0950 ZMH K-57607	Desmosomatidae	WS	A3	192 X
DesmP125	DSB_1886	<i>Disparella</i>	indef	D22	BOLD-ADL2753	S0951 ZMH K-57608	Desmosomatidae	WS	A3	192 X
DesmP126	DSB_1887	<i>Eugerdella</i>	sp.6	D35	BOLD-ADL5217	S0952 ZMH K-57609	Desmosomatidae	WS	A3	192 X
DesmP127	DSB_1888	<i>Prochelator</i>	sp.13	D39	BOLD-ADL5217	S0953 ZMH K-57610	Desmosomatidae	WS	A3	192 X
DesmP128	DSB_1889	<i>d. Mirabilicixa</i>	sp.B	D10	BOLD-ADL4888	S0954 ZMH K-57611	Desmosomatidae	WS	A3	192 X
DesmP129	DSB_1890	<i>Mirabilicixa</i>	indef	D14	BOLD-BSL5365	S0955 ZMH K-57612	Desmosomatidae	WS	A3	192 X



DesmP131	DSB_1892	<i>Mirabilicoxa</i>	sp.B	D10	BOLD:ADL4888	50957 ZMH K-57613	Desmosomatidae	WS	A3	192	X	X
DesmP133	DSB_1894	<i>Chelator</i>	sp.A	D01	BOLD:ADL5030	50959 ZMH K-57614	Desmosomatidae	WS	A3	192	X	X
DesmP134	DSB_1895	<i>cf. Mirabilicoxa</i>	sp.B	D10	BOLD:ADL4888	50960 ZMH K-57615	Desmosomatidae	WS	A3	192	X	X
DesmP135	DSB_1896	<i>Oecidiobanchus</i>	oeci	D08	BOLD:ADL5367	50961 ZMH K-57616	Desmosomatidae	WS	A3	192	X	X
DesmP137	DSB_1898	<i>Oecidiobanchus</i>	oeci	D08	BOLD:ADL5367	50963 ZMH K-57617	Desmosomatidae	WS	A3	197	X	X
DesmP138	DSB_1899	<i>Chelator</i>	sp.A	D01	BOLD:ADL5030	50964 ZMH K-57618	Desmosomatidae	WS	A3	197	X	X
DesmP139	DSB_1900	<i>Chelator</i>	sp.A	D01	BOLD:ADL5030	50965 ZMH K-57619	Desmosomatidae	WS	A3	197	X	X
DesmP140	DSB_1901	<i>cf. Disparella</i>	indet	D28	BOLD:ADL3347	50966 ZMH K-57620	Desmosomatidae	WS	A3	197	X	X
DesmP142	DSB_1903	<i>Eugerdella</i>	sp. 6 ?	D34	BOLD:ADL5033	50968 ZMH K-57621	Desmosomatidae	WS	A3	197	X	X
DesmP143	DSB_1904	<i>cf. Disparella</i>	indet	D28	BOLD:ADL3347	50969 ZMH K-57622	Desmosomatidae	WS	A3	197	X	X
DesmP145	DSB_1906	<i>cf. Chelator</i>	sp.A	D01	BOLD:ADL5030	50971 ZMH K-57623	Desmosomatidae	WS	A3	197	X	X
DesmP147	DSB_1908	<i>Eugerdella</i>	sp. 6 ?	D35	BOLD:ADL5217	50973 ZMH K-57624	Desmosomatidae	WS	A3	197	X	X
DesmP148	DSB_1909	<i>cf. Disparella</i>	indet	D28	BOLD:ADL3347	50974 ZMH K-57625	Desmosomatidae	WS	A3	210	X	X
DesmP152	DSB_1913	<i>Chelator</i>	sp.C	D05	BOLD:ADL2581	50978 ZMH K-57626	Desmosomatidae	WS	A3	210	X	X
DesmP153	DSB_1914	<i>Chelator</i>	sp.C	D05	BOLD:ADL2581	50979 ZMH K-57627	Desmosomatidae	WS	A3	210	X	X
DesmP154	DSB_1915	<i>Oecidiobanchus</i>	oeci	D08	BOLD:ADL5367	50980 ZMH K-57628	Desmosomatidae	WS	A3	210	X	X
DesmP159	DSB_1920	<i>cf. Chelator</i>	sp.C	D05	BOLD:ADL2581	50985 ZMH K-57629	Desmosomatidae	WS	A3	210	X	X
DesmP160	DSB_1921	<i>Mirabilicoxa</i>	indet	D14	BOLD:ADL5365	50986 ZMH K-57630	Desmosomatidae	WS	A3	210	X	X
DesmP162	DSB_1949	<i>Eugerdella</i>	sp. 6 ?	D35	BOLD:ADL5217	51014 ZMH K-57631	Desmosomatidae	WS	A3	197	X	X
HaplDi02	DSB_1320	<i>Chauiadobiscus</i>	sp. 01	H15	BOLD:ADL2819	50385 ZMH K-57632	Haplonscidae	W	DISCOL	93	X	X
HaplDi03	DSB_1321	<i>Chauiadobiscus</i>	sp. 01	H15	BOLD:ADL2819	50386 ZMH K-57633	Haplonscidae	W	DISCOL	93	X	X
HaplDi04	DSB_1322	<i>Chauiadobiscus</i>	sp. 01	H15	BOLD:ADL2819	50387 ZMH K-57634	Haplonscidae	W	DISCOL	93	X	X
HaplDi05	DSB_1323	<i>cf. Chauiadobiscus</i>	indet	H07	BOLD:ADL3283	50388 ZMH K-57635	Haplonscidae	W	DISCOL	93	X	X
HaplDi07	DSB_1325	<i>Chauiadobiscus</i>	sp. 01	H14	BOLD:ADL2983	50390 ZMH K-57636	Haplonscidae	W	DISCOL	93	X	X
HaplDi08	DSB_1326	<i>Chauiadobiscus</i>	sp. 01	H14	BOLD:ADL2983	50391 ZMH K-57637	Haplonscidae	W	DISCOL	93	X	X
HaplDi09	DSB_1327	<i>Chauiadobiscus</i>	sp. 01	H23	BOLD:ADL3281	50392 ZMH K-57638	Haplonscidae	W	DISCOL	93	X	X
HaplDi11	DSB_1329	<i>Chauiadobiscus</i>	sp. 01	H15	BOLD:ADL2819	50394 ZMH K-57639	Haplonscidae	W	DISCOL	93	X	X
HaplDi12	DSB_1330	<i>cf. Chauiadobiscus</i>	indet	H07	BOLD:ADL3283	50395 ZMH K-57640	Haplonscidae	W	DISCOL	93	X	X
HaplDi13	DSB_1331	<i>Chauiadobiscus</i>	sp. 01	H15	BOLD:ADL2819	50396 ZMH K-57641	Haplonscidae	W	DISCOL	93	X	X
HaplDi14	DSB_1332	<i>cf. Chauiadobiscus</i>	indet	H07	BOLD:ADL3283	50397 ZMH K-57642	Haplonscidae	W	DISCOL	93	X	X
HaplDi15	DSB_1333	<i>Chauiadobiscus</i>	sp. 01	H23	BOLD:ADL2981	50398 ZMH K-57643	Haplonscidae	W	DISCOL	93	X	X
HaplDi16	DSB_1334	<i>cf. Chauiadobiscus</i>	indet	H07	BOLD:ADL3283	50399 ZMH K-57644	Haplonscidae	W	DISCOL	93	X	X
HaplDi17	DSB_1335	<i>Chauiadobiscus</i>	sp. 01	H14	BOLD:ADL2983	50400 ZMH K-57645	Haplonscidae	W	DISCOL	93	X	X
HaplDi18	DSB_1336	<i>Chauiadobiscus</i>	sp. 01	H14	BOLD:ADL2983	50401 ZMH K-57646	Haplonscidae	W	DISCOL	93	X	X
HaplDi19	DSB_1337	<i>cf. Chauiadobiscus</i>	indet	H07	BOLD:ADL3283	50402 ZMH K-57647	Haplonscidae	W	DISCOL	85	X	X
HaplDi24	DSB_1342	<i>Chauiadobiscus</i>	sp. 01	H09	BOLD:ADL6396	50407 ZMH K-57648	Haplonscidae	W	DISCOL	117	X	X
HaplDi25	DSB_1343	<i>Chauiadobiscus</i>	sp. 01	H14	BOLD:ADL2983	50408 ZMH K-57649	Haplonscidae	W	DISCOL	117	X	X
HaplP001	DSB_2044	<i>Mastigoniscus</i>	sp. # 3	H17	BOLD:ADL3127	51109 ZMH K-57650	Haplonscidae	W	GC	20	X	X
HaplP002	DSB_2045	<i>Mastigoniscus</i>	sp. # 3	H17	BOLD:ADL3127	51110 ZMH K-57651	Haplonscidae	W	GC	20	X	X
HaplP003	DSB_2046	<i>Haplonsiscus</i>	sp. # 2	H12	BOLD:ADL3122	51111 ZMH K-57652	Haplonscidae	W	GC	20	X	X
HaplP004	DSB_2047	<i>Mastigoniscus</i>	sp. # 3	H17	BOLD:ADL3127	51112 ZMH K-57653	Haplonscidae	W	GC	20	X	X
HaplP005	DSB_2048	<i>Mastigoniscus</i>	sp. # 3	H17	BOLD:ADL3127	51113 ZMH K-57654	Haplonscidae	W	GC	20	X	X
HaplP006	DSB_2049	<i>Haplonsiscus</i>	sp. # 2	H12	BOLD:ADL3122	51114 ZMH K-57655	Haplonscidae	W	GC	24	X	X
HaplP008	DSB_2051	<i>Haplonsiscus</i>	sp. # 4	H06	BOLD:ADL6761	51116 ZMH K-57656	Haplonscidae	W	GC	24	X	X
HaplP009	DSB_2052	<i>Mastigoniscus</i>	sp. # 3	H17	BOLD:ADL3127	51117 ZMH K-57657	Haplonscidae	W	GC	24	X	X
HaplP010	DSB_2053	<i>Haplonsiscus</i>	sp. # 2	H10	BOLD:ADL3282	51118 ZMH K-57658	Haplonscidae	W	GC	50	X	X
HaplP011	DSB_2054	<i>Mastigoniscus</i>	sp. # 5	H16	BOLD:ADL2988	51119 ZMH K-57659	Haplonscidae	W	GC	50	X	X
HaplP013	DSB_2056	<i>Haplonsiscus</i>	sp. # 2	H10	BOLD:ADL4714	51121 ZMH K-57660	Haplonscidae	W	GC	50	X	X
HaplP014	DSB_2057	<i>Haplonsiscus</i>	sp. # 2	H10	BOLD:ADL3282	51122 ZMH K-57661	Haplonscidae	W	GC	50	X	X
HaplP015	DSB_2058	<i>Haplonsiscus</i>	sp. # 2	H10	BOLD:ADL4714	51123 ZMH K-57662	Haplonscidae	W	GC	50	X	X
HaplP016	DSB_2059	<i>Haplonsiscus</i>	sp. # 2	H10	BOLD:ADL4714	51124 ZMH K-57663	Haplonscidae	W	GC	50	X	X
HaplP017	DSB_2060	<i>Mastigoniscus</i>	sp. # 5	H16	BOLD:ADL2988	51125 ZMH K-57664	Haplonscidae	W	GC	59	X	X
HaplP018	DSB_2061	<i>Mastigoniscus</i>	sp. # 5	H16	BOLD:ADL2988	51126 ZMH K-57665	Haplonscidae	W	IOM	81	X	X
HaplP019	DSB_2062	<i>Haplonsiscus</i>	sp. # 2	H10	BOLD:ADL3123	51127 ZMH K-57666	Haplonscidae	W	IOM	81	X	X
HaplP020	DSB_2063	<i>Mastigoniscus</i>	sp. # 5	H08	BOLD:ADL2984	51128 ZMH K-57667	Haplonscidae	W	IOM	81	X	X
HaplP021	DSB_2064	<i>Mastigoniscus</i>	sp. # 3	H23	BOLD:ADL6395	51129 ZMH K-57668	Haplonscidae	W	IOM	81	X	X
HaplP022	DSB_2065	<i>Haplonsiscus</i>	sp. # 2	H10	BOLD:ADL4710	51130 ZMH K-57669	Haplonscidae	W	IOM	99	X	X
HaplP023	DSB_2066	<i>Mastigoniscus</i>	sp. # 3	H22	BOLD:ADL2982	51131 ZMH K-57670	Haplonscidae	W	BC	118	X	X
HaplP024	DSB_2067	<i>Mastigoniscus</i>	sp. # 3007	H19	BOLD:ADL2985	51132 ZMH K-57671	Haplonscidae	W	BC	118	X	X
HaplP025	DSB_2068	<i>Mastigoniscus</i>	sp. # 3	H22	BOLD:ADL2982	51133 ZMH K-57672	Haplonscidae	W	BC	118	X	X
HaplP026	DSB_2069	<i>Mastigoniscus</i>	sp. # 3	H22	BOLD:ADL2982	51134 ZMH K-57673	Haplonscidae	W	BC	118	X	X
HaplP027	DSB_2070	<i>Mastigoniscus</i>	sp. # 3007	H19	BOLD:ADL2985	51135 ZMH K-57674	Haplonscidae	W	BC	118	X	X
HaplP028	DSB_2071	<i>Mastigoniscus</i>	sp. # 3	H22	BOLD:ADL2982	51136 ZMH K-57675	Haplonscidae	W	BC	118	X	X
HaplP029	DSB_2072	<i>Mastigoniscus</i>	sp. # 3007	H19	BOLD:ADL2985	51137 ZMH K-57676	Haplonscidae	W	BC	118	X	X



HapIP031	DSB_2074	<i>Mastigoniscus</i>	sp. # 3	H22	BOLD:ADL2982	51139 ZMH K-57677	Haplonscidae	W	BC	118	X
HapIP032	DSB_2075	<i>Haplonsiscus</i>	sp. # 2	H10	BOLD:ADL3968	51140 ZMH K-57678	Haplonscidae	W	BC	118	X
HapIP033	DSB_2076	<i>Haplonsiscus</i>	sp. # 2	H10	BOLD:ADL3968	51141 ZMH K-57679	Haplonscidae	W	BC	118	X
HapIP034	DSB_2077	<i>Mastigoniscus</i>	sp. # 3	H22	BOLD:ADL2982	51142 ZMH K-57680	Haplonscidae	W	BC	118	X
HapIP035	DSB_2078	<i>Mastigoniscus</i>	sp. # 3	H22	BOLD:ADL2982	51143 ZMH K-57681	Haplonscidae	W	BC	133	X
HapIP036	DSB_2079	<i>Mastigoniscus</i>	sp. # 3	H22	BOLD:ADL2982	51144 ZMH K-57682	Haplonscidae	W	BC	133	X
HapIP037	DSB_2080	<i>Mastigoniscus</i>	sp. # 3	H22	BOLD:ADL2982	51145 ZMH K-57683	Haplonscidae	W	BC	133	X
HapIP038	DSB_2081	<i>Mastigoniscus</i>	sp. # 3007	H19	BOLD:ADL2985	51146 ZMH K-57684	Haplonscidae	W	BC	133	X
HapIP039	DSB_2082	<i>Mastigoniscus</i>	sp. # 3007	H19	BOLD:ADL2985	51147 ZMH K-57685	Haplonscidae	W	BC	133	X
HapIP040	DSB_2083	<i>Mastigoniscus</i>	sp.	H22	BOLD:ADL2982	51148 ZMH K-57686	Haplonscidae	W	BC	133	X
HapIP041	DSB_2084	<i>Mastigoniscus</i>	sp. # 3	H21	BOLD:ADL3128	51149 ZMH K-57687	Haplonscidae	W	FC	158	X
HapIP042	DSB_2085	<i>Mastigoniscus</i>	sp. # 3007	H18	BOLD:ADL6560	51150 ZMH K-57688	Haplonscidae	W	FC	158	X
HapIP043	DSB_2086	<i>Haplonsiscus</i>	sp. # 2	H10	BOLD:ADL3123	51151 ZMH K-57689	Haplonscidae	W	FC	158	X
HapIP044	DSB_2087	<i>Haplonsiscus</i>	sp. # 1a	H05	BOLD:ADL6397	51152 ZMH K-57690	Haplonscidae	W	FC	158	X
HapIP045	DSB_2088	<i>Haplonsiscus</i>	sp. # 1	H04	BOLD:ADL3129	51153 ZMH K-57691	Haplonscidae	W	FC	158	X
HapIP046	DSB_2089	<i>Haplonsiscus</i>	sp. # 1	H04	BOLD:ADL3129	51154 ZMH K-57692	Haplonscidae	W	FC	158	X
HapIP047	DSB_2090	<i>Mastigoniscus</i>	sp. # 7	H13	BOLD:ADL3125	51155 ZMH K-57693	Haplonscidae	W	FC	171	X
HapIP048	DSB_2091	<i>Mastigoniscus</i>	sp. # 3	H21	BOLD:ADL3128	51156 ZMH K-57694	Haplonscidae	W	FC	171	X
HapIP049	DSB_2092	<i>Haplonsiscus</i>	sp. # 2	H10	BOLD:ADL2986	51157 ZMH K-57695	Haplonscidae	W	FC	171	X
HapIP050	DSB_2093	<i>Haplonsiscus</i>	sp. # 2	H10	BOLD:ADL3123	51158 ZMH K-57696	Haplonscidae	W	FC	171	X
HapIP051	DSB_2094	<i>Mastigoniscus</i>	sp. # 3	H21	BOLD:ADL3128	51159 ZMH K-57697	Haplonscidae	W	FC	171	X
HapIP052	DSB_2095	<i>Haplonsiscus</i>	sp. # 1	H03	BOLD:ADL2989	51160 ZMH K-57698	Haplonscidae	W	FC	171	X
HapIP053	DSB_2096	<i>Mastigoniscus</i>	sp. # 7	H13	BOLD:ADL3125	51161 ZMH K-57699	Haplonscidae	W	FC	171	X
HapIP054	DSB_2097	<i>Haplonsiscus</i>	sp. # 2	H10	BOLD:ADL2986	51162 ZMH K-57700	Haplonscidae	W	FC	171	X
HapIP055	DSB_2098	<i>Haplonsiscus</i>	sp. # 1	H03	BOLD:ADL2989	51163 ZMH K-57701	Haplonscidae	W	FC	171	X
HapIP057	DSB_2100	<i>Mastigoniscus</i>	sp. # 5	H02	BOLD:ADL3126	51165 ZMH K-57702	Haplonscidae	W	A3	210	X
HapIP058	DSB_2101	<i>Haplonsiscus</i>	sp. # 2	H11	BOLD:ADL2820	51166 ZMH K-57703	Haplonscidae	W	A3	210	X
HapIP059	DSB_2102	<i>Mastigoniscus</i>	sp. # 5	H08	BOLD:ADL2984	51167 ZMH K-57704	Haplonscidae	W	A3	210	X
HapIP060	DSB_2103	<i>Haplonsiscus</i>	sp. # 2	H11	BOLD:ADL3124	51168 ZMH K-57705	Haplonscidae	W	A3	210	X
HapIP061	DSB_2104	<i>Mastigoniscus</i>	sp. # 5	H08	BOLD:ADL2984	51169 ZMH K-57706	Haplonscidae	W	A3	210	X
HapIP062	DSB_2105	<i>Haplonsiscus</i>	sp. # 2	H11	BOLD:ADL3124	51170 ZMH K-57707	Haplonscidae	W	A3	210	X
HapIP063	DSB_2106	<i>Mastigoniscus</i>	sp. # 3	H01	BOLD:ADL3280	51171 ZMH K-57708	Haplonscidae	W	A3	210	X
HapIP064	DSB_2107	<i>Mastigoniscus</i>	sp. # 5	H08	BOLD:ADL2984	51172 ZMH K-57709	Haplonscidae	W	A3	210	X
HapIP065	DSB_2108	<i>Haplonsiscus</i>	sp. # 2	H11	BOLD:ADL3124	51173 ZMH K-57710	Haplonscidae	W	A3	197	X
HapIP066	DSB_2109	<i>Mastigoniscus</i>	sp. # 3	H01	BOLD:ADL3130	51174 ZMH K-57711	Haplonscidae	W	A3	197	X
HapIP067	DSB_2110	<i>Haplonsiscus</i>	sp. # 2	H11	BOLD:ADL2820	51175 ZMH K-57712	Haplonscidae	W	A3	192	X
HapIP068	DSB_2111	<i>Mastigoniscus</i>	sp. # 5	H20	BOLD:ADL2987	51176 ZMH K-57713	Haplonscidae	W	A3	192	X
HapIP069	DSB_2112	<i>Mastigoniscus</i>	sp. # 5	H20	BOLD:ADL2987	51177 ZMH K-57714	Haplonscidae	W	A3	192	X
HapIP070	DSB_2113	<i>Haplonsiscus</i>	sp. # 2	H11	BOLD:ADL2820	51178 ZMH K-57715	Haplonscidae	W	A3	192	X
HapIP071	DSB_2114	<i>Haplonsiscus</i>	sp. # 2	H11	BOLD:ADL3124	51179 ZMH K-57716	Haplonscidae	W	A3	192	X
HapIP072	DSB_2115	<i>Mastigoniscus</i>	sp. # 8	H02	BOLD:ADL3126	51180 ZMH K-57717	Haplonscidae	W	A3	192	X
HapIP073	DSB_2116	<i>Mastigoniscus</i>	sp. # 5	H20	BOLD:ADL2987	51181 ZMH K-57718	Haplonscidae	W	A3	192	X
HapIP074	DSB_2117	<i>Mastigoniscus</i>	sp. # 3	H22	BOLD:ADL6395	51182 ZMH K-57719	Haplonscidae	W	IOM	81	X
MacrD104	DSB_1208	<i>Macrotylis</i>	sp. 03	M02	BOLD:ADL4636	50271 SMF 54160	Macrotylidae	BS	DISCOL	37	X
MacrD109	DSB_1251	<i>Macrotylis</i>	sp. 03	M02	BOLD:ADL3134	50356 SMF 54164	Macrotylidae	BS	DISCOL	117	X
MacrD106	DSB_1310	<i>Macrotylis</i>	sp. 04	M00	BOLD:ADL9487	50375 SMF 54161	Macrotylidae	BS	DISCOL	85	X
MacrD107	DSB_1311	<i>Macrotylis</i>	sp. 03	M02	BOLD:ADL4636	50376 SMF 54162	Macrotylidae	BS	DISCOL	85	X
MacrD108	DSB_1312	<i>Macrotylis</i>	sp. 03	M02	BOLD:ADL4636	50377 SMF 54163	Macrotylidae	BS	DISCOL	81	X
MacrIP001	DSB_1668	<i>Macrotylis</i>	sp. M cf. <i>metallica</i>	M05	BOLD:ADG1797	50733 SMF 54165	Macrotylidae	BS	GC	20	X
MacrIP002	DSB_1669	<i>Macrotylis</i>	sp. M cf. <i>metallica</i>	M05	BOLD:ADG1797	50734 SMF 54166	Macrotylidae	BS	GC	20	X
MacrIP003	DSB_1670	<i>Macrotylis</i>	sp. M cf. <i>metallica</i>	M05	BOLD:ADG1798	50735 SMF 54167	Macrotylidae	BS	GC	20	X
MacrIP004	DSB_1671	<i>Macrotylis</i>	sp. M cf. <i>metallica</i>	M05	BOLD:ADG1798	50736 SMF 54168	Macrotylidae	BS	GC	20	X
MacrIP005	DSB_1672	<i>Macrotylis</i>	sp. # 1	M01	BOLD:ADL4493	50737 SMF 54169	Macrotylidae	BS	GC	20	X
MacrIP006	DSB_1673	<i>Macrotylis</i>	sp. M cf. <i>metallica</i>	M05	BOLD:ADG1798	50738 SMF 54170	Macrotylidae	BS	GC	20	X
MacrIP007	DSB_1674	<i>Macrotylis</i>	sp. M cf. <i>metallica</i>	M05	BOLD:ADG1798	50739 SMF 54171	Macrotylidae	BS	GC	20	X
MacrIP008	DSB_1675	<i>Macrotylis</i>	sp. M cf. <i>metallica</i>	M05	BOLD:ADG1798	50740 SMF 54172	Macrotylidae	BS	GC	20	X
MacrIP009	DSB_1676	<i>Macrotylis</i>	sp. M cf. <i>metallica</i>	M05	BOLD:ADL3953	50741 SMF 54173	Macrotylidae	BS	GC	20	X
MacrIP010	DSB_1677	<i>Macrotylis</i>	sp. M cf. <i>metallica</i>	M01		SMF 54174	Macrotylidae	BS	GC	20	X
MacrIP011	DSB_1678	<i>Macrotylis</i>	sp. M cf. <i>metallica</i>	M05	BOLD:ADG1797	50743 SMF 54175	Macrotylidae	BS	GC	20	X
MacrIP012	DSB_1679	<i>Macrotylis</i>	sp. M cf. <i>metallica</i>	M05	BOLD:ADG1798	50744 SMF 54176	Macrotylidae	BS	GC	24	X
MacrIP013	DSB_1680	<i>Macrotylis</i>	sp. M cf. <i>metallica</i>	M05	BOLD:ADL2993	50745 SMF 54177	Macrotylidae	BS	GC	24	X
MacrIP014	DSB_1681	<i>Macrotylis</i>	sp. M cf. <i>metallica</i>	M05	BOLD:ADL4161	50746 SMF 54178	Macrotylidae	BS	GC	24	X
MacrIP015	DSB_1682	<i>Macrotylis</i>	sp. M cf. <i>metallica</i>	M05	BOLD:ADG1797	50747 SMF 54179	Macrotylidae	BS	GC	24	X
MacrIP016	DSB_1683	<i>Macrotylis</i>	cf. sp. # 1	M01	BOLD:ADL4493	50748 SMF 54180	Macrotylidae	BS	GC	24	X



MacrIP017	DSB_1684	Macrotylis	sp. # 1	M01	BOLD-ADL4493	50749 SMF 54181	Macrotylidae	BS	GC	24	X
MacrIP018	DSB_1685	Macrotylis	sp. M cf. metallica	M05	BOLD-ADG1798	50750 SMF 54182	Macrotylidae	BS	GC	24	X
MacrIP019	DSB_1686	Macrotylis	sp. M cf. metallica	M05	BOLD-ADG1797	50751 SMF 54183	Macrotylidae	BS	GC	24	X
MacrIP020	DSB_1687	Macrotylis	sp. M cf. metallica	M05	BOLD-ADL2993	50752 SMF 54184	Macrotylidae	BS	GC	59	X
MacrIP021	DSB_1688	Macrotylis	sp. M cf. metallica	M05	BOLD-ADL2993	50753 SMF 54185	Macrotylidae	BS	GC	59	X
MacrIP022	DSB_1689	Macrotylis	sp. M cf. metallica	M05	BOLD-ADL2993	50754 SMF 54186	Macrotylidae	BS	GC	59	X
MacrIP023	DSB_1690	Macrotylis	sp. M cf. metallica	M05	BOLD-ADL4161	50755 SMF 54187	Macrotylidae	BS	GC	59	X
MacrIP024	DSB_1691	Macrotylis	sp. M cf. metallica	M05	BOLD-ADL2993	50756 SMF 54188	Macrotylidae	BS	GC	59	X
MacrIP025	DSB_1692	Macrotylis	sp. M cf. metallica	M05	BOLD-ADL2993	50757 SMF 54189	Macrotylidae	BS	GC	59	X
MacrIP026	DSB_1693	Macrotylis	sp. M cf. metallica	M06	BOLD-ADL4496	50758 SMF 54190	Macrotylidae	BS	GC	50	X
MacrIP027	DSB_1694	Macrotylis	sp. M cf. metallica	M06	BOLD-ADL4496	50759 SMF 54191	Macrotylidae	BS	GC	50	X
MacrIP028	DSB_1695	Macrotylis	sp. M cf. metallica	M06	BOLD-ADL4496	50760 SMF 54192	Macrotylidae	BS	GC	50	X
MacrIP029	DSB_1696	Macrotylis	sp. M cf. metallica	M05	BOLD-ADL2993	50761 SMF 54193	Macrotylidae	BS	GC	50	X
MacrIP030	DSB_1697	Macrotylis	sp. M cf. metallica	M06	BOLD-ADL4496	50762 SMF 54194	Macrotylidae	BS	GC	50	X
MacrIP031	DSB_1698	Macrotylis	sp. M cf. metallica	M06	BOLD-ADL4496	50763 SMF 54195	Macrotylidae	BS	GC	50	X
MacrIP032	DSB_1699	Macrotylis	sp. M cf. metallica	M06	BOLD-ADL4496	50764 SMF 54196	Macrotylidae	BS	GC	50	X
MacrIP033	DSB_1700	Macrotylis	sp. M cf. metallica	M06	BOLD-ADL4496	50765 SMF 54197	Macrotylidae	BS	GC	50	X
MacrIP034	DSB_1701	Macrotylis	sp. M cf. metallica	M06	BOLD-ADL4496	50766 SMF 54198	Macrotylidae	BS	GC	50	X
MacrIP035	DSB_1702	Macrotylis	sp. M cf. metallica	M05	BOLD-ADL2993	50767 SMF 54199	Macrotylidae	BS	IOM	81	X
MacrIP036	DSB_1703	Macrotylis	sp. M cf. metallica	M05	BOLD-ADL4637	50768 SMF 54200	Macrotylidae	BS	IOM	81	X
MacrIP037	DSB_1704	Macrotylis	sp. M cf. metallica	M05	BOLD-ADL2993	50769 SMF 54201	Macrotylidae	BS	IOM	81	X
MacrIP038	DSB_1705	Macrotylis	cf. sp. # 1	M01	BOLD-ADL4493	50770 SMF 54202	Macrotylidae	BS	IOM	81	X
MacrIP039	DSB_1706	Macrotylis	sp. M cf. metallica	M05	BOLD-ADL4637	50771 SMF 54203	Macrotylidae	BS	IOM	99	X
MacrIP040	DSB_1707	Macrotylis	sp. M cf. metallica	M05	BOLD-ADL4637	50772 SMF 54204	Macrotylidae	BS	IOM	99	X
MacrIP041	DSB_1708	Macrotylis	sp. M cf. metallica	M05	BOLD-ADL4637	50773 SMF 54205	Macrotylidae	BS	IOM	99	X
MacrIP042	DSB_1709	Macrotylis	sp. M cf. metallica	M05	BOLD-ADL4637	50774 SMF 54206	Macrotylidae	BS	IOM	99	X
MacrIP043	DSB_1710	Macrotylis	sp. M cf. metallica	M05	BOLD-ADL4490	50775 SMF 54207	Macrotylidae	BS	BC	118	X
MacrIP044	DSB_1711	Macrotylis	sp. M cf. metallica	M05	BOLD-ADL4490	50776 SMF 54208	Macrotylidae	BS	BC	118	X
MacrIP045	DSB_1712	Macrotylis	sp. M cf. metallica	M05	BOLD-ADL4490	50777 SMF 54209	Macrotylidae	BS	BC	118	X
MacrIP046	DSB_1713	Macrotylis	sp. M cf. metallica	M07	BOLD-ADL3132	50778 SMF 54210	Macrotylidae	BS	BC	118	X
MacrIP047	DSB_1714	Macrotylis	sp. M cf. metallica	M07	BOLD-ADL3132	50779 SMF 54211	Macrotylidae	BS	BC	118	X
MacrIP048	DSB_1715	Macrotylis	sp. M cf. metallica	M05	BOLD-ADL4490	50780 SMF 54212	Macrotylidae	BS	BC	133	X
MacrIP049	DSB_1716	Macrotylis	sp. M cf. metallica	M05	BOLD-ADL4490	50781 SMF 54213	Macrotylidae	BS	BC	133	X
MacrIP050	DSB_1717	Macrotylis	sp. M cf. metallica	M03	BOLD-ADL3133	50782 SMF 54214	Macrotylidae	BS	BC	133	X
MacrIP052	DSB_1719	Macrotylis	sp. M cf. metallica	M05	BOLD-ADL4490	50784 SMF 54215	Macrotylidae	BS	BC	133	X
MacrIP053	DSB_1720	Macrotylis	sp. M cf. metallica	M03	BOLD-ADL3133	50785 SMF 54216	Macrotylidae	BS	BC	133	X
MacrIP054	DSB_1721	Macrotylis	sp. M cf. metallica	M03	BOLD-ADL3133	50786 SMF 54217	Macrotylidae	BS	BC	133	X
MacrIP055	DSB_1722	Macrotylis	sp. M cf. metallica	M03	BOLD-ADL9486	50787 SMF 54218	Macrotylidae	BS	FC	158	X
MacrIP057	DSB_1724	Macrotylis	sp. M cf. metallica	M03	BOLD-ADL9675	50789 SMF 54219	Macrotylidae	BS	FC	171	X
MacrIP058	DSB_1725	Macrotylis	sp. M cf. metallica	M05	BOLD-ADL4492	50790 SMF 54220	Macrotylidae	BS	FC	171	X
MacrIP059	DSB_1726	Macrotylis	sp. M cf. metallica	M05	BOLD-ADL3135	50791 SMF 54221	Macrotylidae	BS	FC	171	X
MacrIP060	DSB_1727	Macrotylis	sp. M cf. metallica	M03	BOLD-ADL9300	50792 SMF 54222	Macrotylidae	BS	FC	171	X
MacrIP061	DSB_1728	Macrotylis	sp. M cf. metallica	M03	BOLD-ADL9300	50793 SMF 54223	Macrotylidae	BS	FC	171	X
MacrIP062	DSB_1729	Macrotylis	sp. M cf. metallica	M03	BOLD-ADL9674	50794 SMF 54224	Macrotylidae	BS	FC	171	X
MacrIP063	DSB_1730	Macrotylis	sp. M cf. metallica	M05	BOLD-ADL3136	50795 SMF 54225	Macrotylidae	BS	FC	171	X
MacrIP064	DSB_1731	Macrotylis	sp. M cf. metallica	M05	BOLD-ADL4492	50796 SMF 54226	Macrotylidae	BS	FC	171	X
MacrIP065	DSB_1732	Macrotylis	sp. M cf. metallica	M05	BOLD-ADL4492	50797 SMF 54227	Macrotylidae	BS	FC	171	X
MacrIP066	DSB_1733	Macrotylis	sp. M cf. metallica	M05	BOLD-ADL4492	50798 SMF 54228	Macrotylidae	BS	FC	171	X
MacrIP067	DSB_1734	Macrotylis	sp. M cf. metallica	M03	BOLD-ADL9300	50799 SMF 54229	Macrotylidae	BS	FC	171	X
MacrIP068	DSB_1735	Macrotylis	sp. M cf. metallica	M05	BOLD-ADL3135	50800 SMF 54230	Macrotylidae	BS	FC	171	X
MacrIP069	DSB_1736	Macrotylis	sp. M cf. metallica	M05	BOLD-AAG9589	50801 SMF 54231	Macrotylidae	BS	FC	171	X
MacrIP070	DSB_1737	Macrotylis	sp. M cf. metallica	M05	BOLD-ADL3135	50802 SMF 54232	Macrotylidae	BS	FC	171	X
MacrIP071	DSB_1738	Macrotylis	sp. M cf. metallica	M05	BOLD-ADL4492	50803 SMF 54233	Macrotylidae	BS	FC	171	X
MacrIP072	DSB_1739	Macrotylis	sp. M cf. metallica	M03	BOLD-ADL9675	50804 SMF 54234	Macrotylidae	BS	FC	171	X
MacrIP073	DSB_1740	Macrotylis	sp. M cf. metallica	M05	BOLD-ADL4492	50805 SMF 54235	Macrotylidae	BS	A3	192	X
MacrIP074	DSB_1741	Macrotylis	sp. # 2	M08	BOLD-ADL4491	50806 SMF 54236	Macrotylidae	BS	A3	210	X
MacrIP075	DSB_1742	Macrotylis	sp. M cf. metallica	M04	BOLD-ADL4494	50807 SMF 54237	Macrotylidae	BS	A3	210	X
MacrIP076	DSB_1743	Macrotylis	sp. M cf. metallica	M04	BOLD-ADL4494	50808 SMF 54238	Macrotylidae	BS	A3	197	X
MacrIP077	DSB_1744	Macrotylis	sp. M cf. metallica	M04	BOLD-ADL4494	50809 SMF 54239	Macrotylidae	BS	A3	197	X
MacrIP078	DSB_1745	Macrotylis	sp. M cf. metallica	M04	BOLD-ADL4494	50810 SMF 54240	Macrotylidae	BS	A3	197	X
MacrIP079	DSB_1746	Macrotylis	sp. M cf. metallica	M04	BOLD-ADL4494	50811 SMF 54241	Macrotylidae	BS	A3	197	X
MacrIP080	DSB_1747	Macrotylis	sp. M cf. metallica	M04	BOLD-ADL4494	50812 SMF 54242	Macrotylidae	BS	A3	197	X
MacrIP081	DSB_1748	Macrotylis	sp. M cf. metallica	M04	BOLD-ADL4494	50813 SMF 54243	Macrotylidae	BS	A3	192	X
MacrIP082	DSB_1749	Macrotylis	sp. M cf. metallica	M04	BOLD-ADL4494	50814 SMF 54244	Macrotylidae	BS	A3	192	X



MacriP083	DSB_1750	Macrotylis	sp. # 2	M08	BOLD:ADL4497	50815 SMF 54245	Macrotylidae	BS	A3	192	X	X
MacriP084	DSB_1751	Macrotylis	sp. # 2	M08	BOLD:ADL4497	50816 SMF 54246	Macrotylidae	BS	A3	192	X	X
MacriP085	DSB_1752	Macrotylis	sp. # 2	M08	BOLD:ADL4491	50817 SMF 54247	Macrotylidae	BS	A3	192	X	X
MacriP086	DSB_1753	Macrotylis	sp. # 2	M08	BOLD:ADL4491	50818 SMF 54248	Macrotylidae	BS	A3	192	X	X
MacriP087	DSB_1754	Macrotylis	sp. # 2	M08	BOLD:ADL4491	50819 SMF 54249	Macrotylidae	BS	A3	192	X	X
MacriP088	DSB_1755	Macrotylis	sp. # 2	M08	BOLD:ADL4491	50820 SMF 54250	Macrotylidae	BS	A3	192	X	X
MacriP089	DSB_1756	Macrotylis	sp. M cf. metallica	M04	BOLD:ADL4494	50821 SMF 54251	Macrotylidae	BS	A3	192	X	X
MacriP090	DSB_1757	Macrotylis	sp. M cf. metallica	M04	BOLD:ADL4494	50822 SMF 54252	Macrotylidae	BS	A3	192	X	X
MacriP091	DSB_1758	Macrotylis	sp. # 2	M08	BOLD:ADL4495	50823 SMF 54253	Macrotylidae	BS	A3	192	X	X
MunpD02	DSB_1203	Eurycope	sp. 05	Mu28	BOLD:ADL4531	50266 SMF 54254	Munnopsidae	S	DISCOL	37	X	X
MunpD03	DSB_1204	Betamorpho	sp. 01	Mu20	BOLD:ADM1455	50267 SMF 54255	Munnopsidae	S	DISCOL	37	X	X
MunpD05	DSB_1220	Eurycope	sp. 05	Mu28	BOLD:ADL4531	50283 SMF 54256	Munnopsidae	S	DISCOL	81	X	X
MunpD08	DSB_1223	Eurycope	sp. 05	Mu29	BOLD:ADL4916	50286 SMF 54259	Munnopsidae	S	DISCOL	85	X	X
MunpD09	DSB_1224	Munneurycope	sp. 01	Mu80	BOLD:ADL4913	50287 SMF 54260	Munnopsidae	S	DISCOL	85	X	X
MunpD06	DSB_1225	Eurycope	sp. 05	Mu28	BOLD:ADL4531	50288 SMF 54257	Munnopsidae	S	DISCOL	81	X	X
MunpD07	DSB_1229	Betamorpho	sp. 02	Mu45	BOLD:ADL3690	50294 SMF 54258	Munnopsidae	S	DISCOL	81	X	X
MunpD12	DSB_1230	Betamorpho	sp. 02	Mu45	BOLD:ADL3690	50295 SMF 54261	Munnopsidae	S	DISCOL	85	X	X
MunpD13	DSB_1231	Stortygura	parka	Mu62	BOLD:ADL3683	50296 SMF 54262	Munnopsidae	S	DISCOL	93	X	X
MunpD15	DSB_1233	Disconectes	sp. 01	Mu02	BOLD:ADL3686	50298 SMF 54263	Munnopsidae	S	DISCOL	93	X	X
MunpD16	DSB_1234	Rectisura	sp. 01	Mu57	BOLD:ADL3689	50299 SMF 54264	Munnopsidae	S	DISCOL	93	X	X
MunpD20	DSB_1238	Munneurycope	sp. 03	Mu63	BOLD:ADL5073	50303 SMF 54265	Munnopsidae	S	DISCOL	93	X	X
MunpD21	DSB_1239	Disconectes	sp. 01	Mu07	BOLD:ADL4533	50304 SMF 54266	Munnopsidae	S	DISCOL	93	X	X
MunpD22	DSB_1240	Eurycope	sp. 05	Mu37	BOLD:ADL5069	50305 SMF 54267	Munnopsidae	S	DISCOL	93	X	X
MunpD23	DSB_1241	Munneurycope sp 6	sp. 01	Mu48	BOLD:ADL4419	50306 SMF 54268	Munnopsidae	S	DISCOL	93	X	X
MunpD24	DSB_1242	Eurycope	sp. 05	Mu27	BOLD:ADL5075	50307 SMF 54269	Munnopsidae	S	DISCOL	93	X	X
MunpD26	DSB_1244	Disconectes	sp. 02	Mu76	BOLD:ADL5096	50309 SMF 54270	Munnopsidae	S	DISCOL	93	X	X
MunpD27	DSB_1245	Disconectes	sp. 02	Mu72	BOLD:ADL5096	50310 SMF 54271	Munnopsidae	S	DISCOL	93	X	X
MunpD28	DSB_1246	Munneurycope	sp. 01	Mu63	BOLD:ADL5073	50311 SMF 54272	Munnopsidae	S	DISCOL	93	X	X
MunpD29	DSB_1247	Stortygura	parka	Mu62	BOLD:ADL3683	50312 SMF 54273	Munnopsidae	S	DISCOL	93	X	X
MunpD30	DSB_1248	Disconectes	sp. 02	Mu72	BOLD:ADL5096	50313 SMF 54274	Munnopsidae	S	DISCOL	93	X	X
MunpD31	DSB_1249	Paralipomera	sp. 01	Mu84	BOLD:ADL9556	50314 SMF 54275	Munnopsidae	S	DISCOL	93	X	X
MunpD32	DSB_1250	Disconectes	sp. 02a	Mu72	BOLD:ADL5096	50315 SMF 54276	Munnopsidae	S	DISCOL	93	X	X
MunpD33	DSB_1253	Eurycope	sp.	Mu37	BOLD:ADL4914	50318 SMF 54277	Munnopsidae	S	DISCOL	85	X	X
MunpD36	DSB_1256	Disconectes	sp. 01	Mu07	BOLD:ADL9556	50321 SMF 54278	Munnopsidae	S	DISCOL	93	X	X
MunpD37	DSB_1257	Paralipomera	sp. 01	Mu84	BOLD:ADL9556	50322 SMF 54279	Munnopsidae	S	DISCOL	93	X	X
MunpD38	DSB_1258	Munneurycope	sp. 03	Mu80	BOLD:ADL4913	50323 SMF 54280	Munnopsidae	S	DISCOL	93	X	X
MunpD41	DSB_1259	Disconectes	sp. 02	Mu72	BOLD:ADL5096	50324 SMF 54281	Munnopsidae	S	DISCOL	117	X	X
MunpD43	DSB_1261	Eurycope	sp. 01	Mu37	BOLD:ADL4914	50326 SMF 54282	Munnopsidae	S	DISCOL	122	X	X
MunpD45	DSB_1263	Disconectes	sp. 01	Mu02	BOLD:ADL3686	50328 SMF 54283	Munnopsidae	S	DISCOL	122	X	X
MunpD46	DSB_1264	Disconectes	sp. 01	Mu07	BOLD:ADL4533	50329 SMF 54284	Munnopsidae	S	DISCOL	122	X	X
MunpD47	DSB_1265	Munneurycope	sp. 03	Mu63	BOLD:ADL3688	50330 SMF 54285	Munnopsidae	S	DISCOL	122	X	X
MunpD49	DSB_1267	Disconectes	sp. 01	Mu75	BOLD:ADL4918	50332 SMF 54286	Munnopsidae	S	DISCOL	122	X	X
MunpD50	DSB_1268	Disconectes	sp. 01	Mu07	BOLD:ADL4533	50333 SMF 54287	Munnopsidae	S	DISCOL	122	X	X
MunpD51	DSB_1269	Munneurycope	sp.	Mu63	BOLD:ADL5073	50334 SMF 54288	Munnopsidae	S	DISCOL	122	X	X
MunpD53	DSB_1271	Rectisura	sp. 02	Mu57	BOLD:ADL3687	50336 SMF 54289	Munnopsidae	S	DISCOL	122	X	X
MunpD54	DSB_1272	Disconectes	sp. 02	Mu72	BOLD:ADL3684	50337 SMF 54290	Munnopsidae	S	DISCOL	117	X	X
MunpD55	DSB_1273	Betamorpho	sp. 02	Mu45	BOLD:ADL3690	50338 SMF 54291	Munnopsidae	S	DISCOL	122	X	X
MunpD56	DSB_1274	Disconectes	sp. 01	Mu02	BOLD:ADL3686	50339 SMF 54292	Munnopsidae	S	DISCOL	122	X	X
MunpD57	DSB_1275	Disconectes	sp. 02	Mu72	BOLD:ADL5096	50340 SMF 54293	Munnopsidae	S	DISCOL	122	X	X
MunpD60	DSB_1278	Betamorpho	sp. 01	Mu20	BOLD:ADM1455	50343 SMF 54294	Munnopsidae	S	DISCOL	126	X	X
MunpD62	DSB_1280	Munnopsis	abyssalis /sp. 01	Mu39	BOLD:ADL3685	50345 SMF 54295	Munnopsidae	S	DISCOL	126	X	X
MunpD63	DSB_1281	Betamorpho	sp. 01	Mu45	BOLD:ADL3690	50346 SMF 54296	Munnopsidae	S	DISCOL	126	X	X
MunpD64	DSB_1282	Paramunnopsis	sp. 01	Mu38	BOLD:ADL3456	50347 SMF 54297	Munnopsidae	S	DISCOL	126	X	X
MunpD65	DSB_1283	Disconectes	sp. 03	Mu01	BOLD:ADL9556	50348 SMF 54298	Munnopsidae	S	DISCOL	126	X	X
MunpD66	DSB_1284	Paralipomera	sp. 01	Mu84	BOLD:ADL9556	50349 SMF 54299	Munnopsidae	S	DISCOL	126	X	X
MunpD001	DSB_1386		sp. 1	Mu11	BOLD:ADL4575	50451 SMF 54300	Munnopsidae	S	GC	50	X	X
MunpD002	DSB_1387		sp. 1	Mu11	BOLD:ADL4593	50452 SMF 54301	Munnopsidae	S	GC	50	X	X
MunpD003	DSB_1388	Disconectes	sp. 1	Mu08	BOLD:ADL3511	50453 SMF 54302	Munnopsidae	S	GC	50	X	X
MunpD004	DSB_1389	Eurycope	sp. 5	Mu26	BOLD:ADL4378	50454 SMF 54303	Munnopsidae	S	GC	50	X	X
MunpD005	DSB_1390	Disconectes	sp. 1	Mu11	BOLD:ADL4575	50455 SMF 54304	Munnopsidae	S	GC	50	X	X
MunpD006	DSB_1391	Disconectes	sp. 1	Mu11	BOLD:ADL4575	50456 SMF 54305	Munnopsidae	S	GC	50	X	X
MunpD008	DSB_1393	Disconectes	sp. 1	Mu11	BOLD:ADL4593	50458 SMF 54306	Munnopsidae	S	GC	50	X	X
MunpD009	DSB_1394	Disconectes	sp. 3	Mu11	BOLD:ADL4379	50459 SMF 54307	Munnopsidae	S	GC	50	X	X
MunpD010	DSB_1395	Eurycope	sp. 5	Mu26	BOLD:ADL4378	50460 SMF 54308	Munnopsidae	S	GC	50	X	X



MunpJP012	DSB_1397	Disconectes	sp. 1	Mu08	BOLD:ADL5266	50462 SMF 54309	Munnopsidae	S	GC	50	X	X
MunpJP013	DSB_1398	Disconectes	sp. 1	Mu08	BOLD:ADL3511	50463 SMF 54310	Munnopsidae	S	GC	50	X	X
MunpJP014	DSB_1399	Syneurycope	sp.	Mu86	BOLD:ADM2063	50464 SMF 54311	Munnopsidae	S	GC	50	X	X
MunpJP016	DSB_1400	Disconectes	sp. 1	Mu11	BOLD:ADL4575	50465 SMF 54312	Munnopsidae	S	GC	50	X	X
MunpJP015	DSB_1401	Munneurycope	sp.	Mu67	BOLD:ADL2777	50466 SMF 54313	Munnopsidae	S	GC	50	X	X
MunpJP018	DSB_1402	Disconectes	sp. 1	Mu11	BOLD:ADL5267	50467 SMF 54314	Munnopsidae	S	GC	50	X	X
MunpJP019	DSB_1403	Disconectes	sp. 1	Mu11	BOLD:ADL4575	50468 SMF 54315	Munnopsidae	S	GC	50	X	X
MunpJP020	DSB_1404	Disconectes	sp. 1	Mu11	BOLD:ADL4379	50469 SMF 54316	Munnopsidae	S	GC	50	X	X
MunpJP021	DSB_1405	Eurycope	sp. 3	Mu22	BOLD:ADL2909	50470 SMF 54317	Munnopsidae	S	GC	50	X	X
MunpJP022	DSB_1406	Disconectes	sp. 1	Mu11	BOLD:ADL4575	50471 SMF 54318	Munnopsidae	S	GC	50	X	X
MunpJP023	DSB_1407	Disconectes	sp. 1	Mu11	BOLD:ADL4575	50472 SMF 54319	Munnopsidae	S	GC	50	X	X
MunpJP024	DSB_1408	Paramunnopsis	indet	Mu38	BOLD:ADL3456	50473 SMF 54320	Munnopsidae	S	GC	50	X	X
MunpJP025	DSB_1409	Disconectes	sp. 1	Mu11	BOLD:ADL4593	50474 SMF 54321	Munnopsidae	S	GC	50	X	X
MunpJP026	DSB_1410	Disconectes	sp. 1	Mu11	BOLD:ADL4575	50475 SMF 54322	Munnopsidae	S	GC	50	X	X
MunpJP027	DSB_1411	Disconectes	sp. 2a	Mu37	BOLD:ADL5268	50476 SMF 54323	Munnopsidae	S	GC	50	X	X
MunpJP028	DSB_1412	Eurycope	sp. 5	Mu37	BOLD:ADL3657	50477 SMF 54324	Munnopsidae	S	GC	50	X	X
MunpJP029	DSB_1413	Disconectes	sp. 1	Mu11	BOLD:ADL4575	50478 SMF 54325	Munnopsidae	S	GC	50	X	X
MunpJP032	DSB_1416	Disconectes	sp. 1	Mu08	BOLD:ADL5266	50481 SMF 54326	Munnopsidae	S	GC	50	X	X
MunpJP033	DSB_1417	Disconectes	sp. 1	Mu11	BOLD:ADL4575	50482 SMF 54327	Munnopsidae	S	GC	50	X	X
MunpJP034	DSB_1418	Munneurycope	sp.	Mu67	BOLD:ADL2777	50483 SMF 54328	Munnopsidae	S	GC	20	X	X
MunpJP035	DSB_1419	Munneurycope	sp. 3	Mu67	BOLD:ADL2777	50484 SMF 54329	Munnopsidae	S	GC	20	X	X
MunpJP036	DSB_1420	Munneurycope	indet	Mu81	BOLD:ADL4576	50485 SMF 54330	Munnopsidae	S	GC	20	X	X
MunpJP038	DSB_1422	Eurycope	sp. 5	Mu35	BOLD:ADL4447	50487 SMF 54331	Munnopsidae	S	GC	20	X	X
MunpJP039	DSB_1423	Eurycope	sp. 5	Mu37	BOLD:ADL3657	50488 SMF 54332	Munnopsidae	S	GC	20	X	X
MunpJP041	DSB_1425	Betamorphia	indet	Mu70	BOLD:ADL4078	50490 SMF 54333	Munnopsidae	S	GC	20	X	X
MunpJP042	DSB_1426	Munneurycope	indet	Mu81	BOLD:ADL4576	50491 SMF 54334	Munnopsidae	S	GC	20	X	X
MunpJP043	DSB_1427	Disconectes	sp. 1	Mu08	BOLD:ADL3511	50492 SMF 54335	Munnopsidae	S	GC	20	X	X
MunpJP044	DSB_1428	Munneurycope	indet	Mu81	BOLD:ADL4576	50493 SMF 54336	Munnopsidae	S	GC	20	X	X
MunpJP046	DSB_1430	Eurycope	sp. 5	Mu32	BOLD:ADL4077	50495 SMF 54337	Munnopsidae	S	GC	20	X	X
MunpJP047	DSB_1431	Eurycope	sp. 5	Mu32	BOLD:ADL4077	50496 SMF 54338	Munnopsidae	S	GC	20	X	X
MunpJP049	DSB_1433	Eurycope	sp. 5	Mu37	BOLD:ADL3657	50498 SMF 54339	Munnopsidae	S	GC	20	X	X
MunpJP051	DSB_1435	Eurycope	sp. 5	Mu37	BOLD:ADL3657	50500 SMF 54340	Munnopsidae	S	GC	20	X	X
MunpJP052	DSB_1436	Disconectes	sp. 1	Mu08	BOLD:ADL3511	50501 SMF 54341	Munnopsidae	S	GC	20	X	X
MunpJP053	DSB_1437	Disconectes	sp. 1	Mu08	BOLD:ADL3511	50502 SMF 54342	Munnopsidae	S	GC	20	X	X
MunpJP054	DSB_1438	Disconectes	sp.	Mu08	BOLD:ADL5271	50503 SMF 54343	Munnopsidae	S	GC	20	X	X
MunpJP055	DSB_1439	Munneurycope	indet	Mu67	BOLD:ADL2777	50504 SMF 54344	Munnopsidae	S	BC	133	X	X
MunpJP056	DSB_1440	Munneurycope	indet	Mu63	BOLD:ADL3656	50505 SMF 54345	Munnopsidae	S	BC	133	X	X
MunpJP057	DSB_1441	Syneurycope	sp.	Mu85	BOLD:ADM2098	50506 SMF 54346	Munnopsidae	S	FC	171	X	X
MunpJP058	DSB_1442	Eurycope	sp. 5	Mu22	BOLD:ADL4573	50507 SMF 54347	Munnopsidae	S	FC	171	X	X
MunpJP060	DSB_1444	Bellibos	sp. 2	Mu43	BOLD:ADL3457	50509 SMF 54348	Munnopsidae	S	A3	192	X	X
MunpJP061	DSB_1445	Acanthocope	cf. galathea	Mu56	BOLD:ADL4687	50510 SMF 54349	Munnopsidae	S	A3	192	X	X
MunpJP062	DSB_1446	Acanthocope	cf. galathea	Mu56	BOLD:ADL4977	50511 SMF 54350	Munnopsidae	S	A3	192	X	X
MunpJP063	DSB_1447	Acanthocope	cf. galathea	Mu56	BOLD:ADL4687	50512 SMF 54351	Munnopsidae	S	A3	192	X	X
MunpJP064	DSB_1448	Disconectes	sp. 1	Mu11	BOLD:ADL4379	50513 SMF 54352	Munnopsidae	S	GC	59	X	X
MunpJP065	DSB_1449	Disconectes	sp. 1	Mu11	BOLD:ADL5272	50514 SMF 54353	Munnopsidae	S	GC	59	X	X
MunpJP066	DSB_1450	Disconectes	sp. 1	Mu11	BOLD:ADL4575	50515 SMF 54354	Munnopsidae	S	GC	59	X	X
MunpJP067	DSB_1451	Betamorphia	indet	Mu69	BOLD:ADL4076	50516 SMF 54355	Munnopsidae	S	A3	197	X	X
MunpJP068	DSB_1452	Munneurycope	indet	Mu68	BOLD:ADL4075	50517 SMF 54356	Munnopsidae	S	A3	197	X	X
MunpJP069	DSB_1453	Munneurycope	indet	Mu79	BOLD:ADL4074	50518 SMF 54357	Munnopsidae	S	A3	197	X	X
MunpJP070	DSB_1454	Betamorphia	fusiformis	Mu47	BOLD:ADL4073	50519 SMF 54358	Munnopsidae	S	A3	197	X	X
MunpJP071	DSB_1455	Syneurycope	indet	Mu86	BOLD:ADM2063	50520 SMF 54359	Munnopsidae	S	GC	59	X	X
MunpJP072	DSB_1456	Disconectes	sp. 1	Mu11	BOLD:ADL4575	50521 SMF 54360	Munnopsidae	S	GC	59	X	X
MunpJP073	DSB_1457	Rectisura	slavai	Mu59	BOLD:ADL5293	50522 SMF 54361	Munnopsidae	S	BC	118	X	X
MunpJP074	DSB_1458	Munneurycope	indet	Mu64	BOLD:ADL3754	50523 SMF 54362	Munnopsidae	S	BC	118	X	X
MunpJP075	DSB_1459	Disconectes	sp. 1	Mu08	BOLD:ADL5271	50524 SMF 54363	Munnopsidae	S	BC	118	X	X
MunpJP076	DSB_1460	Eurycope	sp. 5	Mu23	BOLD:ADL2919	50525 SMF 54364	Munnopsidae	S	BC	118	X	X
MunpJP077	DSB_1461	Disconectes	indet	Mu08	BOLD:ADL5271	50526 SMF 54365	Munnopsidae	S	BC	118	X	X
MunpJP078	DSB_1462	Munneurycope	nodifrons	Mu67	BOLD:ADL2777	50527 SMF 54366	Munnopsidae	S	BC	118	X	X
MunpJP079	DSB_1463	Eurycope	sp. 5	Mu37	BOLD:ADL2918	50528 SMF 54367	Munnopsidae	S	BC	118	X	X
MunpJP080	DSB_1464	Eurycope	sp. 5	Mu37	BOLD:ADL2918	50529 SMF 54368	Munnopsidae	S	BC	118	X	X
MunpJP081	DSB_1465	Eurycope	sp. 5	Mu26	BOLD:ADL3755	50530 SMF 54369	Munnopsidae	S	FC	171	X	X
MunpJP082	DSB_1466	Betamorphia	sp. 2	Mu40	BOLD:ADL4072	50531 SMF 54370	Munnopsidae	S	FC	171	X	X
MunpJP083	DSB_1467	Eurycope	sp. 5	Mu24	BOLD:ADL3752	50532 SMF 54371	Munnopsidae	S	FC	171	X	X
MunpJP084	DSB_1468	Betamorphia	sp. 2	Mu40	BOLD:ADL4072	50533 SMF 54372	Munnopsidae	S	FC	171	X	X



MunpJP085	DSB_1469	<i>Eurycope</i>	sp. 2	Mu18	BOLD:ADL4333	50534 SMF 54373	Munnopsidae	S	FC	171	X	X
MunpJP086	DSB_1470	<i>Eurycope</i>	sp. 5	Mu37	BOLD:ADL3753	50535 SMF 54374	Munnopsidae	S	IOM	99	X	X
MunpJP088	DSB_1472	<i>Betamorphia</i>	sp.	Mu46	BOLD:ADL4080	50537 SMF 54375	Munnopsidae	S	IOM	99	X	X
MunpJP089	DSB_1473	<i>Disconectes</i>	sp. 1	Mu04	BOLD:ADL4015	50538 SMF 54376	Munnopsidae	S	FC	158	X	X
MunpJP090	DSB_1474	<i>Aspidarachna</i>	indet	Mu53	BOLD:ADL5239	50539 SMF 54377	Munnopsidae	S	FC	158	X	X
MunpJP091	DSB_1475	<i>Disconectes</i>	sp. 3	Mu01	BOLD:ADL4465	50540 SMF 54378	Munnopsidae	S	FC	158	X	X
MunpJP092	DSB_1476	<i>Munneurycope</i>	gen. nov. sp. 3	Mu48	BOLD:ADL4079	50541 SMF 54379	Munnopsidae	S	FC	158	X	X
MunpJP093	DSB_1477	<i>Eurycope</i>	sp. 5	Mu29	BOLD:ADL3751	50542 SMF 54380	Munnopsidae	S	GC	20	X	X
MunpJP094	DSB_1478	<i>Eurycope</i>	sp. 5	Mu32	BOLD:ADL4077	50543 SMF 54381	Munnopsidae	S	GC	20	X	X
MunpJP095	DSB_1479	<i>Acanthoscope</i>	cf. <i>galathea</i>	Mu56	BOLD:ADL4687	50544 SMF 54382	Munnopsidae	S	A3	197	X	X
MunpJP096	DSB_1480	<i>Munneurycope</i>	indet	Mu67	BOLD:ADL2777	50545 SMF 54383	Munnopsidae	S	GC	24	X	X
MunpJP097	DSB_1481	<i>Munneurycope</i>	indet	Mu67	BOLD:ADL2777	50546 SMF 54384	Munnopsidae	S	GC	24	X	X
MunpJP098	DSB_1482	<i>Munneurycope</i>	indet	Mu67	BOLD:ADL2777	50547 SMF 54385	Munnopsidae	S	GC	24	X	X
MunpJP099	DSB_1483	<i>Eurycope</i>	sp. 5	Mu37	BOLD:ADL3657	50548 SMF 54386	Munnopsidae	S	GC	24	X	X
MunpJP100	DSB_1484	<i>Eurycope</i>	sp. 5	Mu32	BOLD:ADL4077	50549 SMF 54387	Munnopsidae	S	GC	24	X	X
MunpJP101	DSB_1485	<i>Eurycope</i>	sp. 5	Mu25	BOLD:ADL1444	50550 SMF 54388	Munnopsidae	S	GC	24	X	X
MunpJP104	DSB_1488	<i>Prinectes</i>	gen. nov.	Mu77	BOLD:ADL5270	50553 SMF 54389	Munnopsidae	S	GC	24	X	X
MunpJP105	DSB_1489	<i>Prinectes</i>	gen. nov.	Mu77	BOLD:ADL5270	50554 SMF 54390	Munnopsidae	S	GC	24	X	X
MunpJP106	DSB_1490	<i>Rectisura</i>	<i>slavai</i>	Mu60		50555 SMF 54391	Munnopsidae	S	GC	24	X	X
MunpJP107	DSB_1491	<i>Disconectes</i>	sp. 1	Mu08		50556 SMF 54392	Munnopsidae	S	GC	24	X	X
MunpJP109	DSB_1493	<i>Eurycope</i>	sp. 5	Mu32	BOLD:ADL4077	50558 SMF 54393	Munnopsidae	S	GC	24	X	X
MunpJP110	DSB_1494	<i>Munneurycope</i>	indet	Mu81	BOLD:ADL4576	50559 SMF 54394	Munnopsidae	S	GC	24	X	X
MunpJP111	DSB_1495	<i>Rectisura</i>	<i>slavai</i>	Mu60	BOLD:ADL4976	50560 SMF 54395	Munnopsidae	S	GC	24	X	X
MunpJP112	DSB_1496	<i>Munneurycope</i>	indet	Mu81	BOLD:ADL4576	50561 SMF 54396	Munnopsidae	S	GC	24	X	X
MunpJP113	DSB_1497	<i>Betamorphia</i>	sp.	Mu70	BOLD:ADL4078	50562 SMF 54397	Munnopsidae	S	GC	24	X	X
MunpJP114	DSB_1498	<i>Syneurycope</i>	sp.	Mu85		50563 SMF 54398	Munnopsidae	S	FC	171	X	X
MunpJP115	DSB_1499	<i>Syneurycope</i>	sp. 1	Mu85		50564 SMF 54399	Munnopsidae	S	FC	171	X	X
MunpJP116	DSB_1500	<i>Syneurycope</i>	sp. 1	Mu85		50565 SMF 54400	Munnopsidae	S	FC	171	X	X
MunpJP117	DSB_1501	<i>Betamorphia</i>	sp. 1	Mu42	BOLD:ADL3458	50566 SMF 54401	Munnopsidae	S	FC	171	X	X
MunpJP119	DSB_1503	<i>Prinectes</i>	gen. nov.	Mu78	BOLD:ADL5438	50568 SMF 54402	Munnopsidae	S	FC	171	X	X
MunpJP120	DSB_1504	<i>Eurycope</i>	sp. 1	Mu37	BOLD:ADL2918	50569 SMF 54403	Munnopsidae	S	FC	171	X	X
MunpJP121	DSB_1505	<i>Syneurycope</i>	indet	Mu85		50570 SMF 54404	Munnopsidae	S	FC	171	X	X
MunpJP122	DSB_1506	<i>Eurycope</i>	sp. 1	Mu18	BOLD:ADL4333	50571 SMF 54405	Munnopsidae	S	FC	171	X	X
MunpJP124	DSB_1508	<i>Eurycope</i>	sp. 5	Mu24	BOLD:ADL3752	50573 SMF 54406	Munnopsidae	S	FC	171	X	X
MunpJP125	DSB_1509	<i>Eurycope</i>	sp. 1	Mu18	BOLD:ADL4333	50574 SMF 54407	Munnopsidae	S	FC	171	X	X
MunpJP126	DSB_1510	<i>Eurycope</i>	sp. 1	Mu18	BOLD:ADL4333	50575 SMF 54408	Munnopsidae	S	FC	171	X	X
MunpJP128	DSB_1512	<i>Eurycope</i>	sp. 5	Mu21	BOLD:ADL2775	50577 SMF 54409	Munnopsidae	S	FC	171	X	X
MunpJP129	DSB_1513	<i>Eurycope</i>	sp. 2	Mu19	BOLD:ADL4334	50578 SMF 54410	Munnopsidae	S	FC	171	X	X
MunpJP130	DSB_1514	<i>Ilyarachna</i>	indet	Mu54	BOLD:ADL5631	50579 SMF 54411	Munnopsidae	S	FC	171	X	X
MunpJP131	DSB_1515	<i>Disconectes</i>	sp. 1	Mu03	BOLD:ADL5437	50580 SMF 54412	Munnopsidae	S	FC	171	X	X
MunpJP133	DSB_1517	<i>Eurycope</i>	sp. 2	Mu18	BOLD:ADL4333	50582 SMF 54413	Munnopsidae	S	FC	171	X	X
MunpJP134	DSB_1518	<i>Microcope</i>	sp.	Mu83	BOLD:ADL5442	50583 SMF 54414	Munnopsidae	S	FC	171	X	X
MunpJP135	DSB_1519	<i>Microcope</i>	sp.	Mu83	BOLD:ADL5442	50584 SMF 54415	Munnopsidae	S	FC	171	X	X
MunpJP136	DSB_1520	<i>Syneurycope</i>	sp.	Mu85	BOLD:ADM0298	50585 SMF 54416	Munnopsidae	S	FC	171	X	X
MunpJP137	DSB_1521	<i>Ilyarachna</i>	indet	Mu54	BOLD:ADL5631	50586 SMF 54417	Munnopsidae	S	FC	171	X	X
MunpJP138	DSB_1522	<i>Rectisura</i>	<i>slavai</i>	Mu60		50587 SMF 54418	Munnopsidae	S	IOM	81	X	X
MunpJP139	DSB_1523	<i>Disconectes</i>	sp. 3	Mu04	BOLD:ADL5441	50588 SMF 54419	Munnopsidae	S	IOM	81	X	X
MunpJP140	DSB_1524	<i>Disconectes</i>	sp. 3	Mu05	BOLD:ADL5440	50589 SMF 54420	Munnopsidae	S	IOM	81	X	X
MunpJP141	DSB_1525	<i>Disconectes</i>	sp. 1	Mu11	BOLD:ADL5439	50590 SMF 54421	Munnopsidae	S	IOM	81	X	X
MunpJP142	DSB_1526	<i>Eurycope</i>	indet	Mu15	BOLD:ADL2778	50591 SMF 54422	Munnopsidae	S	IOM	81	X	X
MunpJP143	DSB_1527	<i>Disconectes</i>	sp. 2	Mu74	BOLD:ADL5444	50592 SMF 54423	Munnopsidae	S	IOM	99	X	X
MunpJP144	DSB_1528	<i>Disconectes</i>	sp. 1	Mu12	BOLD:ADL5443	50593 SMF 54424	Munnopsidae	S	IOM	99	X	X
MunpJP145	DSB_1529	<i>Eurycope</i>	sp. 2	Mu22	BOLD:ADL9336	50594 SMF 54425	Munnopsidae	S	IOM	99	X	X
MunpJP146	DSB_1530	<i>Eurycope</i>	sp. 2	Mu23		50595 SMF 54426	Munnopsidae	S	IOM	99	X	X
MunpJP147	DSB_1531	<i>Tythocope</i>	indet	Mu49	BOLD:ADL2887	50596 SMF 54427	Munnopsidae	S	IOM	99	X	X
MunpJP148	DSB_1532	<i>Tythocope</i>	indet	Mu49	BOLD:ADL2887	50597 SMF 54428	Munnopsidae	S	IOM	99	X	X
MunpJP149	DSB_1533	<i>Disconectes</i>	sp. 1	Mu08	BOLD:ADL5271	50598 SMF 54429	Munnopsidae	S	IOM	99	X	X
MunpJP150	DSB_1534	<i>Eurycope</i>	sp. 5	Mu37		50599 SMF 54430	Munnopsidae	S	IOM	99	X	X
MunpJP153	DSB_1537	<i>Eurycope</i>	sp. 4	Mu15	BOLD:ADL2778	50602 SMF 54431	Munnopsidae	S	IOM	99	X	X
MunpJP154	DSB_1538	<i>Disconectes</i>	sp. 2	Mu71	BOLD:ADL5605	50603 SMF 54432	Munnopsidae	S	IOM	99	X	X
MunpJP155	DSB_1539	<i>Disconectes</i>	sp. 2	Mu74	BOLD:ADL5444	50604 SMF 54433	Munnopsidae	S	IOM	99	X	X
MunpJP156	DSB_1540	<i>Munneurycope</i>	sp.	Mu81	BOLD:ADL3749	50605 SMF 54434	Munnopsidae	S	BC	133	X	X
MunpJP157	DSB_1541	<i>Disconectes</i>	sp. 3	Mu04	BOLD:ADL5441	50606 SMF 54435	Munnopsidae	S	BC	133	X	X
MunpJP158	DSB_1542	<i>Eurycope</i>	sp.	Mu23		50607 SMF 54436	Munnopsidae	S	BC	133	X	X



MunpJP159	DSB_1543	<i>Rectisura</i>	<i>slavai</i>	Mu59	BOLD:ADL5293	50608 SMF 54437	Munnopsidae	S	BC	133	X	X
MunpJP160	DSB_1544	<i>Eurycope</i>	<i>longiflagrata</i>	Mu25	BOLD:ADL2917	50609 SMF 54438	Munnopsidae	S	BC	133	X	X
MunpJP161	DSB_1545	<i>Munneurycope</i>	indet	Mu67	BOLD:ADL2777	50610 SMF 54439	Munnopsidae	S	BC	133	X	X
MunpJP162	DSB_1546	<i>Eurycope</i>	sp. 5	Mu32	BOLD:ADM2325	50611 SMF 54440	Munnopsidae	S	BC	133	X	X
MunpJP163	DSB_1547	<i>Eurycope</i>	sp. 5	Mu37	BOLD:ADL2918	50612 SMF 54441	Munnopsidae	S	BC	133	X	X
MunpJP164	DSB_1548	<i>Munneurycope</i>	indet	Mu81	BOLD:ADL3750	50613 SMF 54442	Munnopsidae	S	BC	133	X	X
MunpJP165	DSB_1549	<i>Munneurycope</i>	indet	Mu67	BOLD:ADL2777	50614 SMF 54443	Munnopsidae	S	BC	133	X	X
MunpJP166	DSB_1550	<i>Eurycope</i>	sp. 5	Mu34	BOLD:ADL4574	50615 SMF 54444	Munnopsidae	S	BC	133	X	X
MunpJP168	DSB_1552	<i>Disconectes</i>	sp. 3	Mu04	BOLD:ADL5606	50617 SMF 54445	Munnopsidae	S	BC	133	X	X
MunpJP169	DSB_1553	<i>Disconectes</i>	sp. 1	Mu08		50618 SMF 54446	Munnopsidae	S	BC	133	X	X
MunpJP170	DSB_1554	<i>Disconectes</i>	sp. 3	Mu05	BOLD:ADL5440	50619 SMF 54447	Munnopsidae	S	BC	133	X	X
MunpJP171	DSB_1555	<i>Munneurycope</i>	indet	Mu81	BOLD:ADL3750	50620 SMF 54448	Munnopsidae	S	BC	133	X	X
MunpJP172	DSB_1556	<i>Munneurycope</i>	indet	Mu81	BOLD:ADL3750	50621 SMF 54449	Munnopsidae	S	BC	133	X	X
MunpJP173	DSB_1557	<i>Munneurycope</i>	indet	Mu68	BOLD:ADL5567	50622 SMF 54450	Munnopsidae	S	FC	158	X	X
MunpJP174	DSB_1558	<i>Prinnectes</i>	gen. nov.	Mu78	BOLD:ADL5438	50623 SMF 54451	Munnopsidae	S	FC	158	X	X
MunpJP177	DSB_1559	<i>Disconectes</i>	sp. 1	Mu13	BOLD:ADL5603	50624 SMF 54452	Munnopsidae	S	FC	158	X	X
MunpJP175	DSB_1560	<i>Aspidarachna</i>	sp.	Mu53	BOLD:ADL5239	50625 SMF 54453	Munnopsidae	S	FC	158	X	X
MunpJP176	DSB_1561	<i>Disconectes</i>	sp. 3	Mu01		50626 SMF 54454	Munnopsidae	S	FC	158	X	X
MunpJP178	DSB_1562	<i>Disconectes</i>	sp. 3	Mu01	BOLD:ADL5604	50627 SMF 54455	Munnopsidae	S	FC	158	X	X
MunpJP179	DSB_1563	<i>Disconectes</i>	sp. 1	Mu11	BOLD:ADL5439	50628 SMF 54456	Munnopsidae	S	FC	158	X	X
MunpJP183	DSB_1567	<i>Disconectes</i>	sp. 3	Mu01		50632 SMF 54457	Munnopsidae	S	FC	158	X	X
MunpJP184	DSB_1568	<i>Disconectes</i>	sp. 1	Mu11	BOLD:ADL5439	50633 SMF 54458	Munnopsidae	S	FC	158	X	X
MunpJP185	DSB_1569	<i>Eurycope</i>	sp. 5	Mu34	BOLD:ADL4574	50634 SMF 54459	Munnopsidae	S	FC	158	X	X
MunpJP186	DSB_1570	<i>Eurycope</i>	sp. 1	Mu19	BOLD:ADL4334	50635 SMF 54460	Munnopsidae	S	FC	158	X	X
MunpJP187	DSB_1571	<i>Eurycope</i>	sp. 5	Mu21	BOLD:ADL2775	50636 SMF 54461	Munnopsidae	S	FC	158	X	X
MunpJP188	DSB_1572	<i>Eurycope</i>	sp. 4	Mu16	BOLD:ADL4755	50637 SMF 54462	Munnopsidae	S	FC	158	X	X
MunpJP189	DSB_1573	<i>Eurycope</i>	sp. 3	Mu16		50638 SMF 54463	Munnopsidae	S	FC	158	X	X
MunpJP197	DSB_1580	<i>Disconectes</i>	sp. 1	Mu10	BOLD:ADL5601	50645 SMF 54464	Munnopsidae	S	FC	158	X	X
MunpJP198	DSB_1581	<i>Disconectes</i>	sp. 3	Mu04	BOLD:ADL4015	50646 SMF 54465	Munnopsidae	S	FC	158	X	X
MunpJP199	DSB_1582	<i>Disconectes</i>	sp. 1	Mu11	BOLD:ADL4379	50647 SMF 54466	Munnopsidae	S	FC	158	X	X
MunpJP200	DSB_1583	<i>Disconectes</i>	sp. 2	Mu73	BOLD:ADM0870	50648 SMF 54467	Munnopsidae	S	FC	158	X	X
MunpJP201	DSB_1584	<i>Disconectes</i>	sp. 3	Mu01	BOLD:ADL5602	50649 SMF 54468	Munnopsidae	S	FC	158	X	X
MunpJP203	DSB_1586	<i>Munneurycope</i>	<i>nodifrons</i>	Mu67	BOLD:ADL2777	50651 SMF 54469	Munnopsidae	S	FC	158	X	X
MunpJP204	DSB_1587	<i>Munneurycope</i>	<i>nodifrons</i>	Mu67	BOLD:ADL2777	50652 SMF 54470	Munnopsidae	S	BC	118	X	X
MunpJP205	DSB_1588	<i>Eurycope</i>	sp. 5	Mu25	BOLD:ADL2917	50653 SMF 54471	Munnopsidae	S	BC	118	X	X
MunpJP206	DSB_1589	<i>Munnopsurus</i>	indet	Mu51	BOLD:ADL3118	50654 SMF 54472	Munnopsidae	S	BC	118	X	X
MunpJP207	DSB_1590	<i>Disconectes</i>	sp. 3	Mu04	BOLD:ADL5441	50655 SMF 54473	Munnopsidae	S	BC	118	X	X
MunpJP208	DSB_1591	<i>Disconectes</i>	sp. 3	Mu04	BOLD:ADL5441	50656 SMF 54474	Munnopsidae	S	BC	118	X	X
MunpJP209	DSB_1592	<i>Rectisura</i>	<i>slavai</i>	Mu59	BOLD:ADL5293	50657 SMF 54475	Munnopsidae	S	BC	118	X	X
MunpJP210	DSB_1593	<i>Paramunnopsis</i>	sp. 1	Mu38	BOLD:ADL3456	50658 SMF 54476	Munnopsidae	S	BC	118	X	X
MunpJP211	DSB_1594	<i>Eurycope</i>	sp. 5	Mu25		50659 SMF 54477	Munnopsidae	S	BC	118	X	X
MunpJP212	DSB_1595	<i>Munneurycope</i>	indet	Mu68	BOLD:ADL3937	50660 SMF 54478	Munnopsidae	S	BC	118	X	X
MunpJP213	DSB_1596	<i>Eurycope</i>	sp. 5	Mu25	BOLD:ADL2917	50661 SMF 54479	Munnopsidae	S	BC	118	X	X
MunpJP214	DSB_1597	<i>Eurycope</i>	sp. 5	Mu37	BOLD:ADL2918	50662 SMF 54480	Munnopsidae	S	BC	118	X	X
MunpJP215	DSB_1598	<i>Disconectes</i>	sp. 1	Mu08	BOLD:ADL5271	50663 SMF 54481	Munnopsidae	S	BC	118	X	X
MunpJP216	DSB_1599	<i>Disconectes</i>	sp. 1	Mu08	BOLD:ADL5271	50664 SMF 54482	Munnopsidae	S	BC	118	X	X
MunpJP218	DSB_1601	<i>Tythocope</i>	sp.	Mu50	BOLD:ADL4751	50666 SMF 54483	Munnopsidae	S	BC	118	X	X
MunpJP219	DSB_1602	<i>Eurycope</i>	sp. 5	Mu37	BOLD:ADL2918	50667 SMF 54484	Munnopsidae	S	BC	118	X	X
MunpJP220	DSB_1603	<i>Disconectes</i>	sp. 1	Mu08	BOLD:ADL5271	50668 SMF 54485	Munnopsidae	S	BC	118	X	X
MunpJP221	DSB_1604	<i>Eurycope</i>	sp. 5	Mu23	BOLD:ADL2919	50669 SMF 54486	Munnopsidae	S	GC	20	X	X
MunpJP222	DSB_1605	<i>Eurycope</i>	sp. 5	Mu37	BOLD:ADL3657	50670 SMF 54487	Munnopsidae	S	GC	20	X	X
MunpJP223	DSB_1606	<i>Disconectes</i>	sp. 1	Mu08	BOLD:ADL5271	50671 SMF 54488	Munnopsidae	S	GC	20	X	X
MunpJP224	DSB_1607	<i>Betamorpho</i>	sp.	Mu70	BOLD:ADL4078	50672 SMF 54489	Munnopsidae	S	GC	20	X	X
MunpJP225	DSB_1608	<i>Betamorpho</i>	sp.	Mu70	BOLD:ADL4078	50673 SMF 54490	Munnopsidae	S	GC	20	X	X
MunpJP226	DSB_1609	<i>Munneurycope</i>	sp.	Mu68	BOLD:ADL2922	50674 SMF 54491	Munnopsidae	S	IOM	81	X	X
MunpJP227	DSB_1610	<i>Eurycope</i>	sp. 5	Mu25	BOLD:ADG1444	50675 SMF 54492	Munnopsidae	S	IOM	81	X	X
MunpJP228	DSB_1611	<i>Eurycope</i>	sp. 5	Mu25	BOLD:ADG1444	50676 SMF 54493	Munnopsidae	S	IOM	81	X	X
MunpJP229	DSB_1612	<i>Munneurycope</i>	<i>cf. nodifrons</i>	Mu64	BOLD:ADL2920	50677 SMF 54494	Munnopsidae	S	IOM	81	X	X
MunpJP230	DSB_1613	<i>Munneurycope</i>	<i>cf. nodifrons</i>	Mu67	BOLD:ADL2777	50678 SMF 54495	Munnopsidae	S	IOM	81	X	X
MunpJP231	DSB_1614	<i>Disconectes</i>	sp. 3	Mu04	BOLD:ADL5441	50679 SMF 54496	Munnopsidae	S	IOM	81	X	X
MunpJP232	DSB_1615	<i>Disconectes</i>	sp. 1	Mu05	BOLD:ADL5440	50680 SMF 54497	Munnopsidae	S	IOM	81	X	X
MunpJP233	DSB_1616	<i>Disconectes</i>	sp. 3	Mu05	BOLD:ADL5440	50681 SMF 54498	Munnopsidae	S	IOM	81	X	X
MunpJP234	DSB_1617	<i>Disconectes</i>	sp. 3	Mu01	BOLD:ADL2645	50682 SMF 54499	Munnopsidae	S	IOM	81	X	X
MunpJP235	DSB_1618	<i>Disconectes</i>	sp. 1	Mu08	BOLD:ADL5271	50683 SMF 54500	Munnopsidae	S	IOM	81	X	X



MunpJP236	DSB_1619	<i>Disconectes</i>	sp. 1	Mu09	BOLD:ADL5599	50684 SMF 54501	Munnopsidae	S	IOM	81	X	X
MunpJP237	DSB_1620	<i>Disconectes</i>	sp. 3	Mu05	BOLD:ADL5440	50685 SMF 54502	Munnopsidae	S	IOM	81	X	X
MunpJP238	DSB_1621	<i>Rectisura</i>	slavai	Mu60	BOLD:ADL4976	50686 SMF 54503	Munnopsidae	S	IOM	81	X	X
MunpJP239	DSB_1622	<i>Eurycope</i>	sp.	Mu37	BOLD:ADL2921	50687 SMF 54504	Munnopsidae	S	IOM	81	X	X
MunpJP240	DSB_1623	<i>Rectisura</i>	slavai	Mu60	BOLD:ADL4976	50688 SMF 54505	Munnopsidae	S	IOM	81	X	X
MunpJP241	DSB_1624	<i>Paramunopsis</i>	sp. 2	Mu39	BOLD:ADL3685	50689 SMF 54506	Munnopsidae	S	IOM	81	X	X
MunpJP242	DSB_1625	<i>Munneurycope</i>	indet	Mu68	BOLD:ADL4075	50690 SMF 54507	Munnopsidae	S	A3	210	X	X
MunpJP243	DSB_1626	<i>Betamorpha</i>	sp.	Mu69	BOLD:ADL4076	50691 SMF 54508	Munnopsidae	S	A3	210	X	X
MunpJP244	DSB_1627	<i>Betamorpha</i>	sp.	Mu69	BOLD:ADL4076	50692 SMF 54509	Munnopsidae	S	A3	210	X	X
MunpJP245	DSB_1628	<i>Disconectes</i>	sp. 1	Mu09	BOLD:ADL5600	50693 SMF 54510	Munnopsidae	S	A3	210	X	X
MunpJP246	DSB_1629	<i>Rectisura</i>	sp.	Mu61	BOLD:ADL3110	50694 SMF 54511	Munnopsidae	S	A3	210	X	X
MunpJP247	DSB_1630	<i>Bellibos</i>	sp. 1	Mu44	BOLD:ADL4771	50695 SMF 54512	Munnopsidae	S	A3	210	X	X
MunpJP248	DSB_1631	<i>Rectisura</i>	slavai	Mu58	BOLD:ADL4772	50696 SMF 54513	Munnopsidae	S	A3	210	X	X
MunpJP249	DSB_1632	<i>Disconectes</i>	sp. 3	Mu06	BOLD:ADL5597	50697 SMF 54514	Munnopsidae	S	A3	210	X	X
MunpJP250	DSB_1633	<i>Disconectes</i>	sp. 3	Mu03	BOLD:ADL5598	50698 SMF 54515	Munnopsidae	S	A3	210	X	X
MunpJP252	DSB_1635	<i>Bellibos</i>	sp. 1	Mu44	BOLD:ADL4771	50700 SMF 54516	Munnopsidae	S	A3	210	X	X
MunpJP253	DSB_1636	<i>Munneurycope</i>	sp.	Mu68	BOLD:ADL4075	50701 SMF 54517	Munnopsidae	S	A3	210	X	X
MunpJP254	DSB_1637	<i>Disconectes</i>	sp. 3	Mu03	BOLD:ADL5598	50702 SMF 54518	Munnopsidae	S	A3	210	X	X
MunpJP256	DSB_1639	<i>Eurycope</i>	sp. 5	Mu30	BOLD:ADL4756	50704 SMF 54519	Munnopsidae	S	A3	210	X	X
MunpJP257	DSB_1640	<i>Eurycope</i>	sp. 5	Mu33	BOLD:ADL2967	50705 SMF 54520	Munnopsidae	S	A3	210	X	X
MunpJP258	DSB_1641	<i>Eurycope</i>	sp. 5	Mu33	BOLD:ADL2967	50706 SMF 54521	Munnopsidae	S	A3	210	X	X
MunpJP259	DSB_1642	<i>Eurycope</i>	sp. 5	Mu33	BOLD:ADL2967	50707 SMF 54522	Munnopsidae	S	A3	210	X	X
MunpJP260	DSB_1643	<i>Ilyarachna</i>	indet	Mu55	BOLD:ADL2886	50708 SMF 54523	Munnopsidae	S	A3	197	X	X
MunpJP261	DSB_1644	<i>Rectisura</i>	slavai	Mu58	BOLD:ADL4772	50709 SMF 54524	Munnopsidae	S	A3	197	X	X
MunpJP262	DSB_1645	<i>Disconectes</i>	sp. 3	Mu01		50710 SMF 54525	Munnopsidae	S	A3	197	X	X
MunpJP263	DSB_1646	<i>Rectisura</i>	slavai	Mu58	BOLD:ADL4772	50711 SMF 54526	Munnopsidae	S	A3	197	X	X
MunpJP264	DSB_1647	<i>Eurycope</i>	sp. 5	Mu31	BOLD:ADL2968	50712 SMF 54527	Munnopsidae	S	A3	197	X	X
MunpJP265	DSB_1648	<i>Munneurycope</i>	indet	Mu65	BOLD:ADL4773	50713 SMF 54528	Munnopsidae	S	A3	197	X	X
MunpJP266	DSB_1649	<i>Acanthocope</i>	cf. <i>galathea</i>	Mu56	BOLD:ADL4687	50714 SMF 54529	Munnopsidae	S	A3	197	X	X
MunpJP267	DSB_1650	<i>Acanthocope</i>	cf. <i>galathea</i>	Mu56	BOLD:ADL4687	50715 SMF 54530	Munnopsidae	S	A3	197	X	X
MunpJP268	DSB_1651	<i>Betamorpha</i>	indet	Mu41	BOLD:ADL5566	50716 SMF 54531	Munnopsidae	S	A3	197	X	X
MunpJP269	DSB_1652	<i>Disconectes</i>	sp. 3	Mu03	BOLD:ADL2644	50717 SMF 54532	Munnopsidae	S	A3	197	X	X
MunpJP270	DSB_1653	<i>Munneurycope</i>	indet	Mu66	BOLD:ADL4774	50718 SMF 54533	Munnopsidae	S	A3	197	X	X
MunpJP272	DSB_1655	<i>Eurycope</i>	sp. 5	Mu33	BOLD:ADL2967	50720 SMF 54534	Munnopsidae	S	A3	197	X	X
MunpJP274	DSB_1657	<i>Acanthocope</i>	cf. <i>galathea</i>	Mu56	BOLD:ADL4687	50722 SMF 54535	Munnopsidae	S	A3	197	X	X
MunpJP276	DSB_1659	<i>Bellibos</i>	sp. 2	Mu43	BOLD:ADL3457	50724 SMF 54536	Munnopsidae	S	A3	192	X	X
MunpJP277	DSB_1660	<i>Betamorpha</i>	sp.	Mu69		50725 SMF 54537	Munnopsidae	S	A3	192	X	X
MunpJP278	DSB_1661	<i>Bellibos</i>	sp. 2	Mu43	BOLD:ADL3457	50726 SMF 54538	Munnopsidae	S	A3	192	X	X
MunpJP279	DSB_1662	<i>Disconectes</i>	sp. 3	Mu01	BOLD:ADL9613	50727 SMF 54539	Munnopsidae	S	A3	192	X	X
MunpJP280	DSB_1663	<i>Disconectes</i>	sp. 1	Mu09	BOLD:ADL2643	50728 SMF 54540	Munnopsidae	S	A3	192	X	X
MunpJP281	DSB_1664	<i>Microcope</i>	sp.	Mu82	BOLD:ADM0130	50729 SMF 54541	Munnopsidae	S	A3	192	X	X
MunpJP282	DSB_1665	<i>Munneurycope</i>	gen. nov sp. 1	Mu52	BOLD:ADL4064	50730 SMF 54542	Munnopsidae	S	A3	192	X	X
MunpJP283	DSB_1666	<i>Munneurycope</i>	indet	Mu65	BOLD:ADL4773	50731 SMF 54543	Munnopsidae	S	A3	192	X	X
MunpJP284	DSB_1667	<i>Eurycope</i>	sp. 5	Mu36	BOLD:ADL2969	50732 SMF 54544	Munnopsidae	S	A3	192	X	X
MunpJP285	DSB_1761	<i>Munneurycope</i>	sp. 6	Mu52	BOLD:ADL4064	50826 SMF 54545	Munnopsidae	S	A3	192	X	X
MunpJP286	DSB_2011	<i>Eurycope</i>	gen. nov sp. 1	Mu68	BOLD:ADL2922	51076 SMF 54546	Munnopsidae	S	IOM	82	X	X
MunpJP288	DSB_2013	<i>Betamorpha</i>	cf. <i>fusiformis</i>	Mu69	BOLD:ADL4076	51078 SMF 54547	Munnopsidae	S	A3	210	X	X



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Table 2 Summary of diversity parameters per sampled area. Sites = number of Epibenthic Sledge deployments, N = number of specimens, S = number of Species, Usp = number of unique species, Chao±SE = Chao estimated number of species with standard error, ACE±SE = ACE estimated number of species with standard error, H' = Shannon Diversity, 1-D = Simpson Diversity and J = Jaccard's Evenness. β_{SOR} , β_{SIM} and β_{SNE} express multiple-site total beta diversity, multiple-site species turnover and multiple-site nestedness respectively. Note that in the rows of each area the beta-diversity values are the result of excluding this area, except for the row Total (which includes all areas) and CCZ only (which includes all but APEI3 and DISCOL).

AREA	Sites	N	S	Usp (%)	Chao±SE	ACE±SE	H'	1-D	J	β_{SOR}	β_{SIM}	β_{SNE}
APEI3	3	110	44	14 (32%)	59.3±9.5	63.7±4.4	3.52	0.96	0.93	0.845	0.833	0.011
GSR	2	90	38	18 (47%)	80±25.9	69.2±5	3.34	0.95	0.91	0.900	0.894	0.005
DISCOL	8	84	41	31 (76%)	62.1±12.6	59.5±3.8	3.53	0.96	0.95	0.845	0.833	0.011
IFREMER	2	106	50	34 (68%)	64±7.7	80.3±5.9	3.66	0.96	0.93	0.873	0.868	0.004
BGR	4	163	43	11 (25%)	49.5±4.8	53.2±3.2	3.34	0.94	0.88	0.892	0.884	0.007
IOM	3	66	40	36 (90%)	63±12.4	77±5.4	3.51	0.96	0.95	0.897	0.890	0.002
CCZ only	11	425	117	99 (84%)	146	137	4.21	0.97	0.80	0.767	0.746	0.021
Total	22	619	187	-	235.46	252.15	4.76	0.98	0.91	0.885	0.878	0.007

Table 3 Faunistic similarity between areas. Upper diagonal = number of shared species, lower diagonal = number of not shared species.

Not shared\shared	APEI3	GSR	DISCOL	IFREMER	BGR	IOM
APEI3	0\44	2	1	6	1	5
GSR	78	0\38	4	11	16	16
DISCOL	83	71	0\41	2	5	2
IFREMER	82	66	87	0\50	8	12
BGR	85	49	74	77	0\43	15
IOM	74	46	77	66	53	0\40

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Table 4 Beta-diversity decomposition of Isopod Families. N = number of specimens, S = number of Species. β_{SOR} , β_{SIM} and β_{SNE} express multiple-site total beta diversity, multiple-site species turnover and multiple-site nestedness respectively. Columns ccz N, ccz S, ccz β_{SOR} , ccz β_{SIM} and ccz β_{SNE} consider only samples taken within the CCZ (excluding APEI3 and DISCOL)

	N	S	Chao±SE	β_{SOR}	β_{SIM}	β_{SNE}	ccz N	ccz S	ccz β_{SOR}	ccz β_{SIM}	ccz β_{SNE}
Munnopsidae	294	91	110±8.9	0.873	0.860	0.013	199	55	0.743	0.704	0.039
Desmosomatidae	143	63	98.7±17	0.904	0.895	0.009	103	43	0.817	0.802	0.014
Haploniscidae	88	24	24.6±1.1	0.916	0.898	0.0183	53	14	0.803	0.739	0.067
Macrostylidae	94	9	9.0±0.2	0.809	0.777	0.031	70	5	0.583	0.500	0.083
Total	619	187	235.46	0.885	0.878	0.007	425	117	0.767	0.746	0.021

Table 5 Number and percentage of species of the studied families present in only 1 to 6 areas. Total considers all areas together.

	1 area	2 areas	3 areas	4 areas	5 areas	6 areas	Total
Munnopsidae	69 (75.8%)	11 (12%)	7 (7.6%)	3 (3.2%)	1 (1%)	0 (0%)	91 (48.6%)
Desmosomatidae	49 (77.7%)	10 (15.8%)	3 (4.7%)	1 (1.5%)	0 (0%)	0 (0%)	63 (33.6%)
Haploniscidae	20 (83 %)	3 (12.5%)	0 (0%)	1 (4.1%)	0 (0%)	0 (0%)	24 (12.8%)
Macrostylidae	6 (66.6%)	2 (22.2%)	0 (0%)	0 (0%)	1 (11.1%)	0 (0%)	9 (4.8%)
Total	144 (77%)	26 (13.9%)	10 (5.3%)	5 (2.6%)	2 (1%)	0 (0%)	187