https://doi.org/10.5194/bg-2019-358
Preprint. Discussion started: 2 October 2019

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

Saskia Brix[1], Karen J. Osborn[2], Stefanie Kaiser[1,3], Sarit B. Truskey[2], Sarah M. Schnurr[1,4], Nils Brenke[1], Marina Malyutina[5] & Pedro M. Martinez[1,4]

[1] *Senckenberg am Meer, German Centre for Marine Biodiversity Research (DZMB) c/o Biocenter Grindel, Center of Natural History, Universität Hamburg, Martin-Luther-King-Platz 3, 20146 Hamburg, Germany*
[2] *Smithsonian National Museum of Natural History, 10th and Constitution Ave NW, Washington, DC, 20013 USA*
[3]*CeNak, Center of Natural History, Universität Hamburg, Martin-Luther-King-Platz 3, 20146 Hamburg, Germany*
[4] *University of Oldenburg, FK V, IBU, AG Marine Biodiversitätsforschung, Ammerländer Heerstraße 114-118, 26129 Oldenburg*
[5] *A.V. Zhirmunsky National Scientific Center of Marine Biology, Far Eastern Branch, Russian Academy of Sciences, Palchevsky St, 17, Vladivostok 690041, Russia*

Correspondence to: Saskia Brix (sbrix@senckenberg.de)

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 singeletons. 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 rarefraction 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.

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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 ferromangansese crusts, 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 there are a 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 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 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 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, 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 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 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

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to estimate dispersal distances. Samples were collected during two expeditions in the course of the JPI Oceans Pilot Action "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

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 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 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 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).

Outgroups for each family tree consisted of the following: Macrostylidae = *Thaumastosoma diva* KY951731, *Thaumastosoma platycarpus* IDesm10, *Ketosoma vemae* VTDes013 (16S only), KM14-Iso261 *Ketosoma* sp. 2, KY951731, and *Ketosoma hessleri* KY951729. Haploniscidae = *Ianiropsis epilittoralis* AF260835, AF260836, AF260858, and AF260859. Desmosomatids = *Betamorpha fusiformis* EF116524, EF116525, EF116527, EF116528, and *Betamorpha africana* EF682292. Munnopsidae = *Thaumastosoma platycarpus* IDesm10, *Ketosoma vemae* VTDes013, *Ketosoma werneri* D3D60 (COI only), 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 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 MAAFT 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 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 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 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 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 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 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, 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 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 contribution of every area to species turnover and nestedness, these values were calculated taking one area out each time in a jackkniffe 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, 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) 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

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 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 *Pirinectes* Malyutina & Brix gen. nov., Riehl & De Smet in press for *Macrostylis* cf. *metallicola*, Brix et al. 2018 for *Eugerdella* cf. *egoni*). Emphasis is put here on "may be", 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 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 different regions and was found to be within the same putative species clade as a specimen identified as *Munnopsis abyssalis*. Of the six putative *Betamorpha* 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, 1965) (18 spp.), *Disparella* Hessler, 1970 (5 spp.), *Prochelator* Hessler, 1970 (4 spp.) and *Eugerda* 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 *Mastigoniscus* (9 spp.), *Haploniscus* (9 spp.) and *Chauliodoniscus* (5 spp.). In Haploniscidae, 100 % of species collected are new to science.

The congruent species delimitation resulted in eight macrostylid species in this mongeneric family (Table 1, Fig. 5). Putative species "*Macrostylis* sp. 1", collected from both GC area and adjacent to IOM area, was strongly supported as sister to the rest of the available macrostylids. The remainder of the macrostylids 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 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 X1, 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.

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) whiles 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).

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

Total multi-site beta diversity was high (total βSOR 0.885, Table 2), meaning that the similarity between areas was low. The beta diversity between CCZ only areas was lower (total βSOR 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 (βSIM) with only a small proportion accounting for nestedness (βSNE), but the nestedness proportion is 3 times greater within CCZ areas (βSNE = 0.021) than when considering all areas together (βSNE = 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 (βSNE goes from 0.007 to 0.011), while the removal of any of the CCZ areas either does not change βSNE or it decreases up to βSNE = 0.004.

The known unknown: real number of species still not sampled

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 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.

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 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 dataset, while the expected number of Munnopsidae and Desmosomatidae is 110 and 98 respectively.

Total beta diversity (βSOR) and species turnover (βSIM) increases in this sequence Munnopsidae (βSOR = 0.873; βSIM = 0.860), Desmosomatidae (βSOR = 0.904; βSIM = 0.895) and Haploniscidae (βSOR = 0.916; βSIM = 0.898). This pattern is not evident when comparing within the CCZ (see Table 4). Macrostylidae has lower beta diversity and species turnover (βSOR = 0.809; βSIM = 0.777) mainly due to a single species that shows a large distribution range (see discussion).
The ranges of distribution differ between families (Table 5). No species of either family was present in all six studies areas. While only 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 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 SD analysis, we provide a stable system to define a species in the deep sea as baseline 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 (citation here). The second most mobile family is the Desmosomatidae. They live on the surface of the sediments, but have appendages modified for swimming (not as pronounced as Munnopsidae). On contrary there is no evidence that Haplonoscidae can swim. These asellotes live on or in the sediments and have short legs that they use for crawling. Macrostyllidae 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 nevertheless most of the time sitting on the sediments were they feed on foraminifera and only swim occasionally (citation). 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 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 unsusal 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 if 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 it the males would have showed a strong sexual dimorphism, but this was not the case in the individuals available in our dataset.

Haploniscidae 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).

Brandt et al. (2011) considered the distribution of isopod families sorted by mobility types: walking, swimming, burrowing, walking-swimming, walking-burrowing. There is a low 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.

Bober et al. (2018) used only one munnopsid species with a known pan-ocean distribution, *Acanthocope galatheae* 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, nannonicids 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 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 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 hetereogeneity 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 (2015) tested the distance of distribution during the PLD in the North Atlantic Ocean using physical particals 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 assellote families in the 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. However, four species of Macrostylidae and Desmosomatidae did cross the MAR, but evidence for regular unrestricted gene

https://doi.org/10.5194/bg-2019-358
Preprint. Discussion started: 2 October 2019

flow is lacking. Brix et al. (2018) observed from SD data for desomomatids 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 km^2.

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 endemicity 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* Haugsness

& 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 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 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 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

Cardaso 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 wehre over 87 % of the isopod species are new to science or described within the last two years, indicates the need for quick assessment tools like species delimitation 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 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 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.

Acknowledgements

We appreciate the teamwork for our paper, which was greatly supported by the working groups at the DZMB in Wilhelmshaven and Hamburg (Germany) as well as at the Smithsonian Institution, Washington D.C. (USA). Amy Driskell and the Smithsonian lab staff kindly supported us in the very beginning with access to the Smithsonian LAB for Sarah Schnurr, Saskia Brix and Karen Jeskulke. Amy continued helping with tricky BoLD uploads of sequence data. Magdalini Christoudolu is thanked for helping with the BoLD management of the whole pacific project from which we extracted our dataset. Nele Johanssen and Torben Riehl gave us a first impression on the morphological determination of JPIO haplonicids and macrostylids. Karen Jeskulke not only helped with the lab work at the Smithsonian and the DZMB in Hamburg, she contributed largely to the databank entries at DZMB HH. We thank Sven Petersen (GEOMAR) for enabling to Saskia the QGIS entries of the shape file for the contractor areas. The cruises SO239 and SO242 were financed by the German Ministry of Education and Science (BMBF) as a contribution to the European project JPI Oceans ‘‘Ecological Aspects of Deep-Sea Mining’’. The authors acknowledge funding from BMBF under Contract 03F0707E.

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Figures

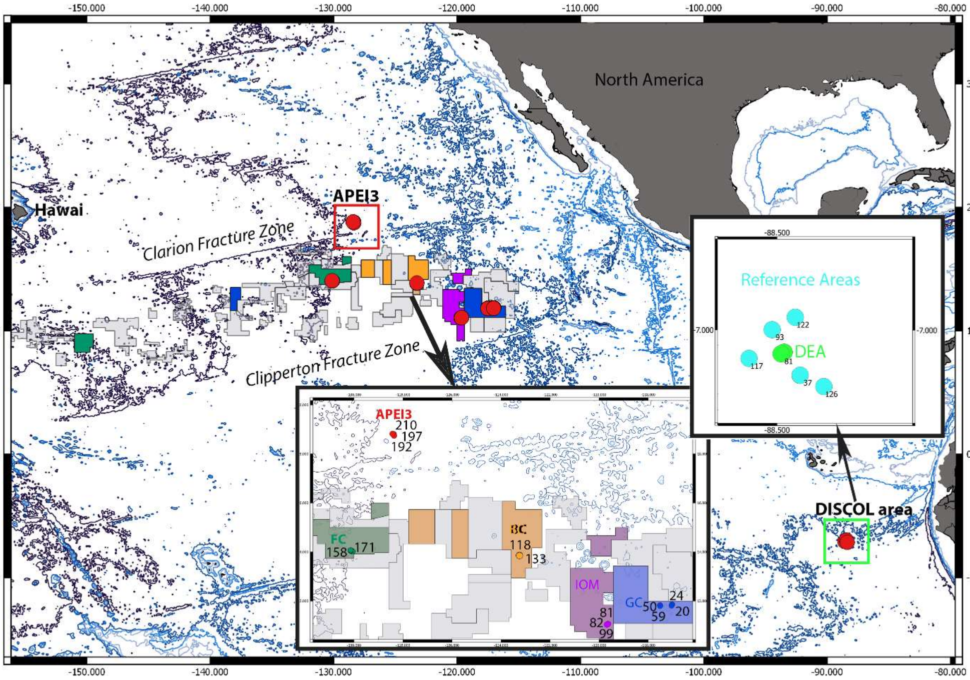


Fig. 1: Map of the locations of the EBS sampling sites (red dots) within the manganese nodule contractor and the DISCOL Experimental Area (DEA) areas in the north- and south-eastern Pacific. The colourcode in this map reflects the colourcode given in the circle trees (Fig.s 2 – 5), but is not reflected 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).

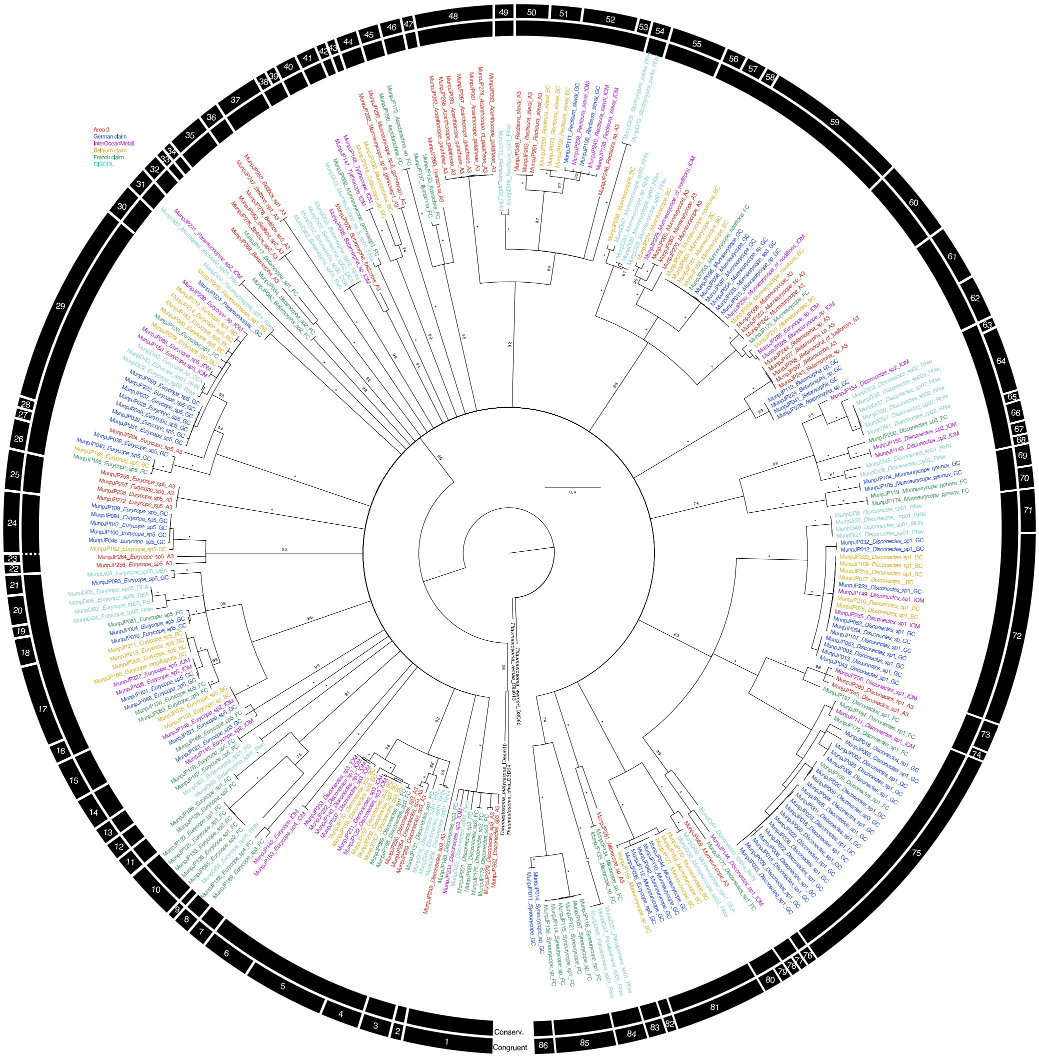


Figure 2. Phylogenetic tree of all munnopsid samples based on 16S and COI sequences for 294 specimens. Colours indicate collection location, with black indicating outgroups. All unsupported branches were collapsed and bootstrap support indicated with asterisks indicating 100 % bootstrap support. The 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.

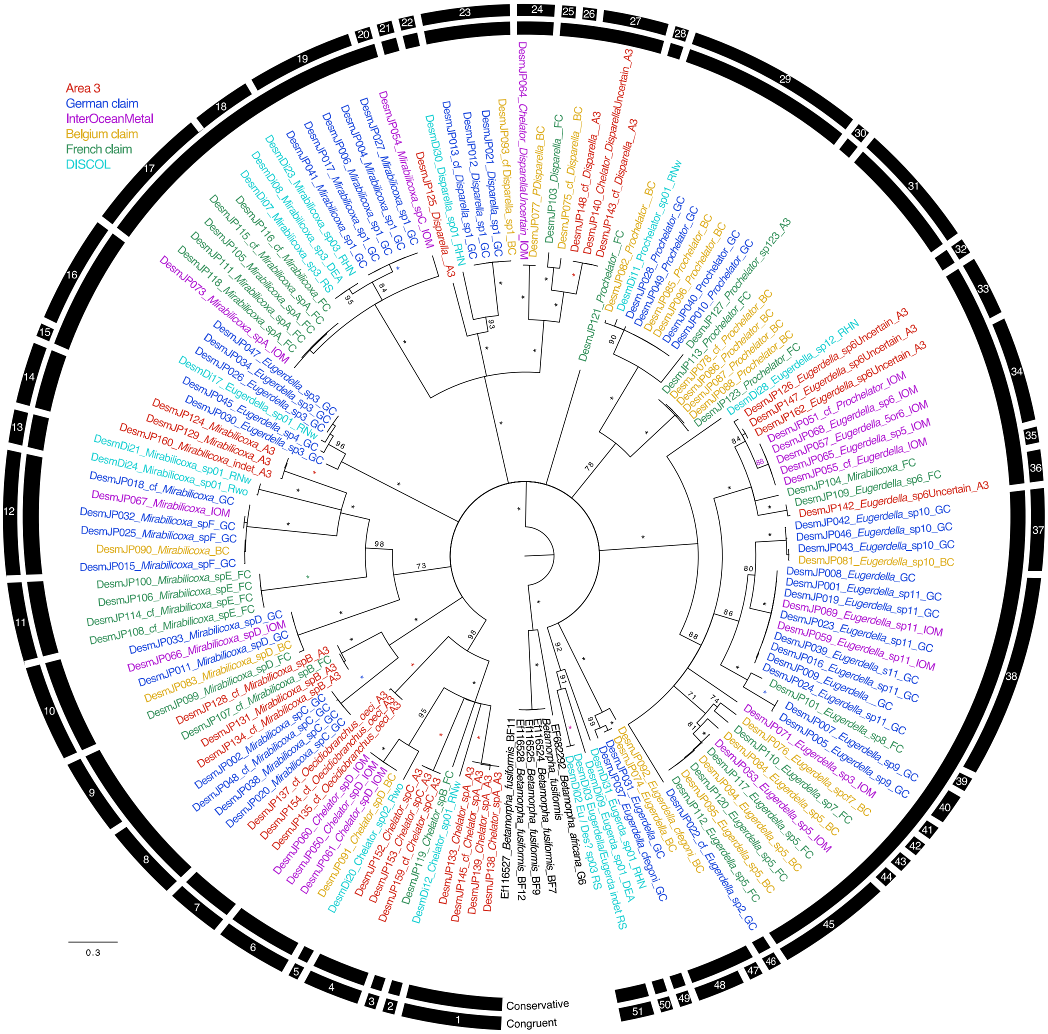
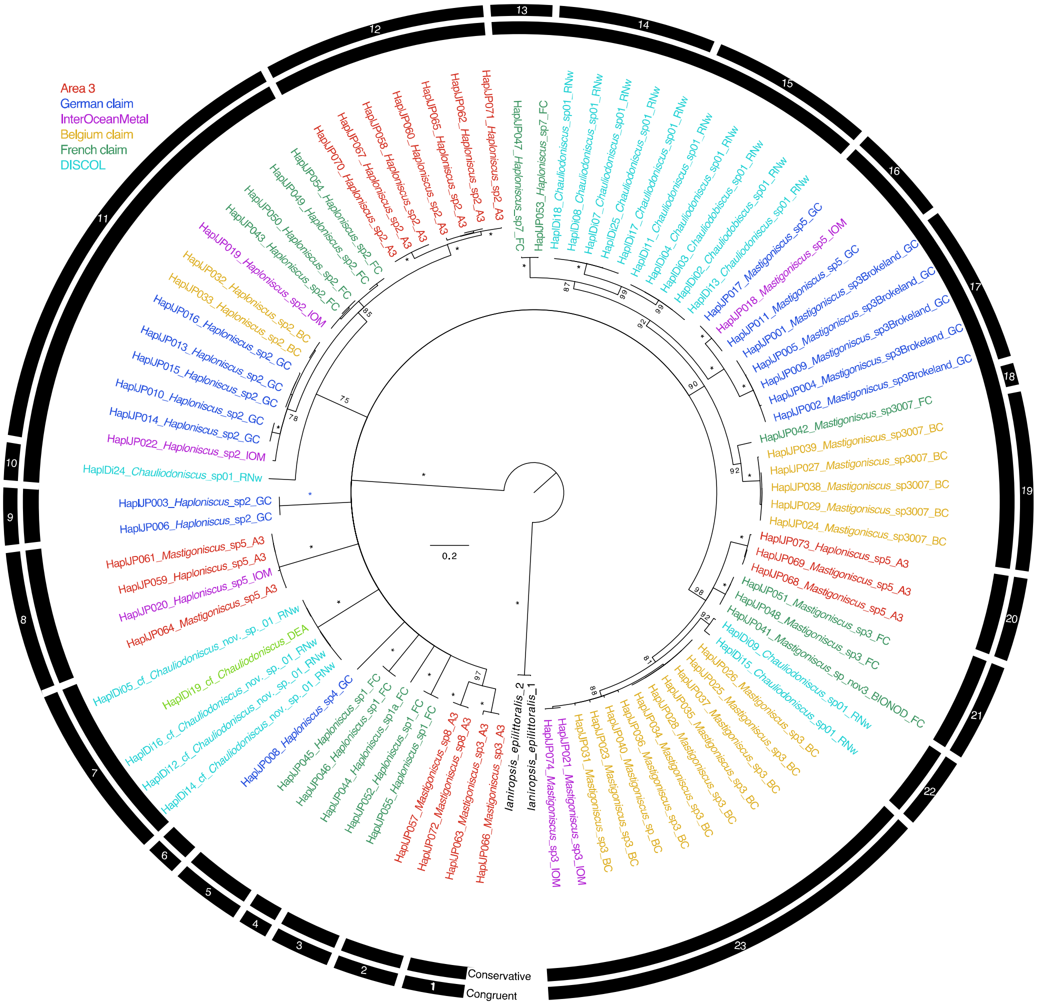


Figure 3: Phylogenetic tree of all desmosomatid samples based on 16S and COI sequences for 143 specimens. Colors indicate collection location, with black indicating outgroups. All unsupported branches were collapsed and bootstrap support indicated with asterisks indicating 100 % bootstrap support. The 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.

https://doi.org/10.5194/bg-2019-358
Preprint. Discussion started: 2 October 2019



725 **Figure 4: Phylogenetic tree of all haploniscid samples based on 16S and COI sequences for 88 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.**

https://doi.org/10.5194/bg-2019-358
Preprint. Discussion started: 2 October 2019

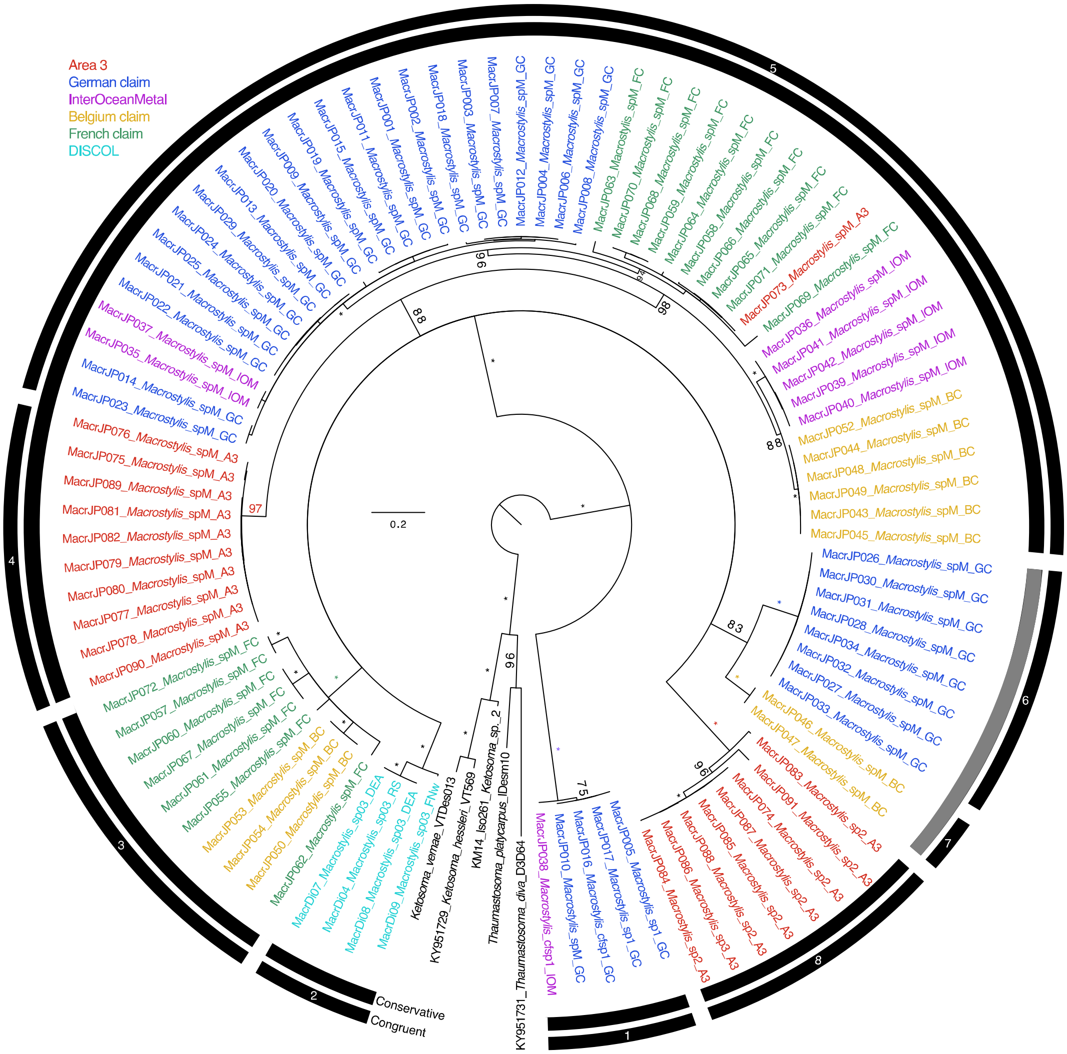


Figure 5: Phylogenetic tree of all macrostylid samples based on 16S and COI sequences for 94 specimens. Colors indicate collection location, with black indicating outgroups. All unsupported branches were collapsed and bootstrap support indicated with asterisks indicating 100 % bootstrap support. The 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.

https://doi.org/10.5194/bg-2019-358
Preprint. Discussion started: 2 October 2019

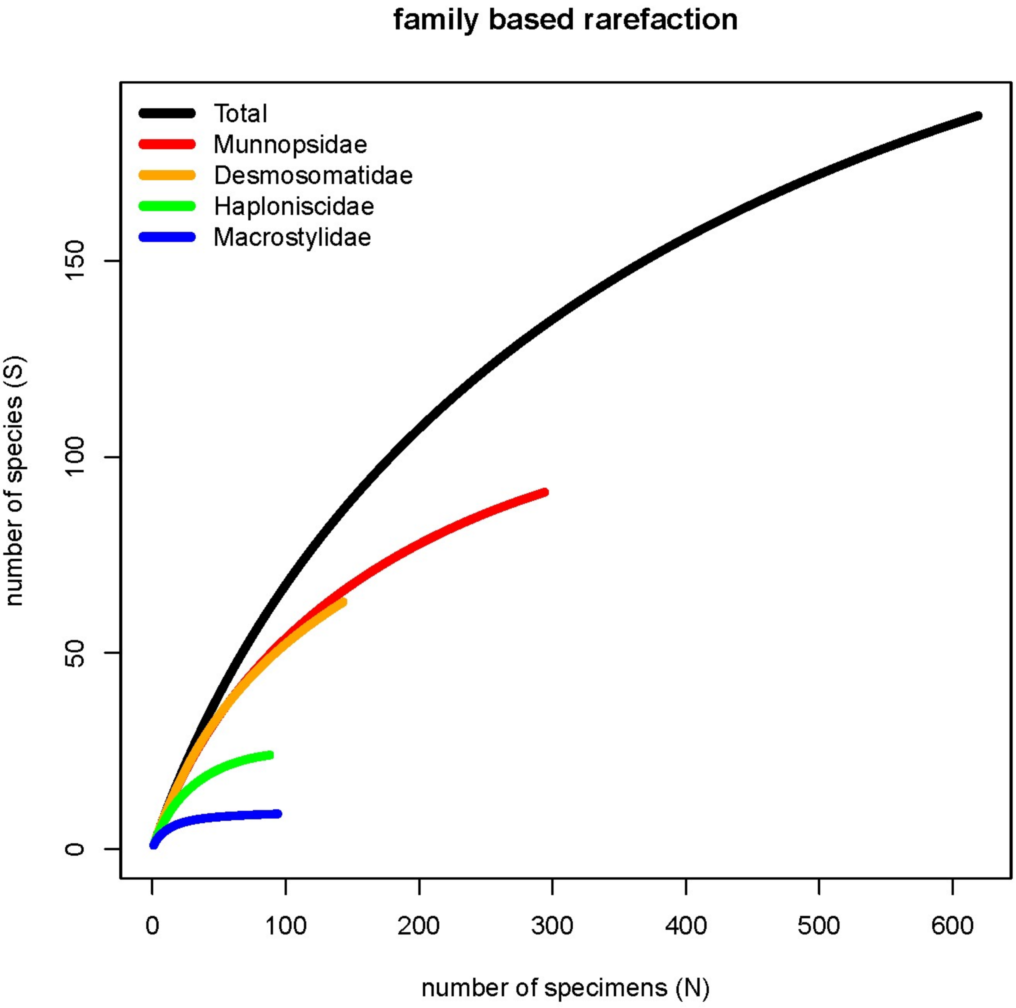
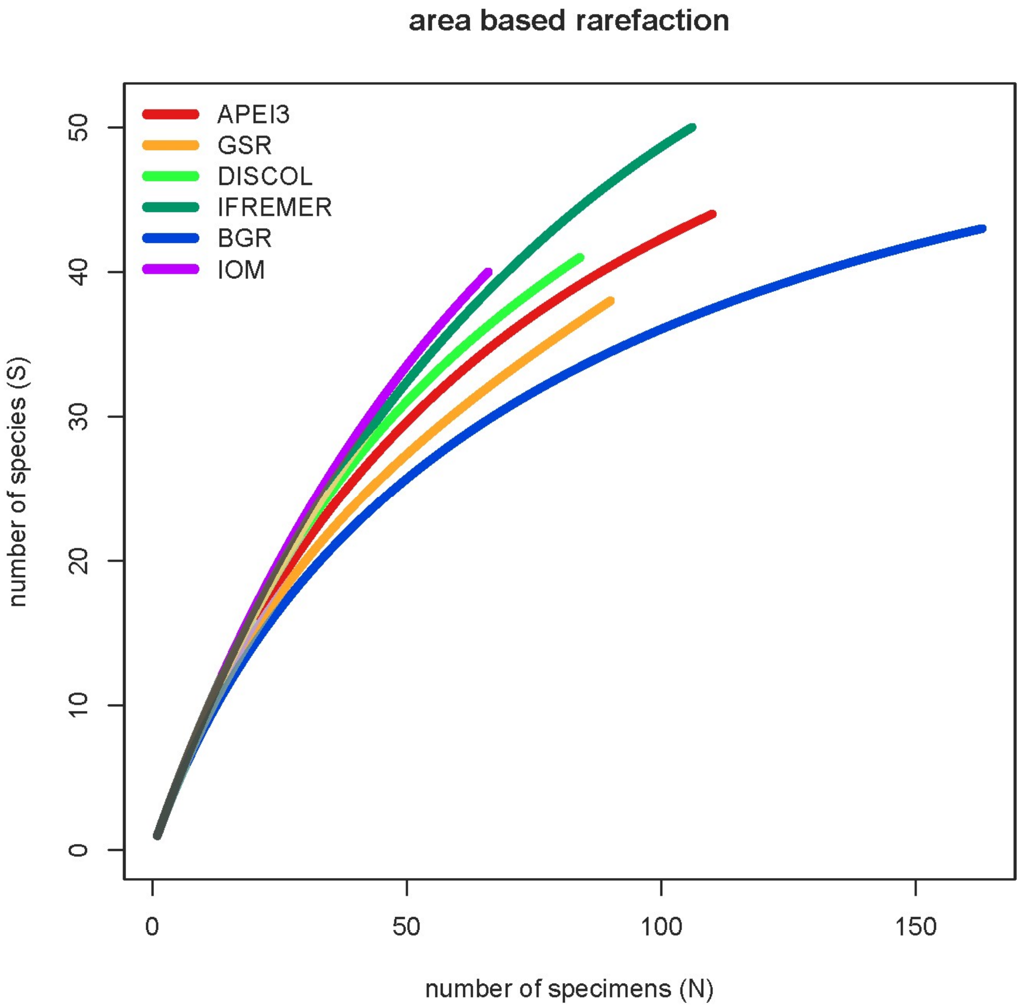


Fig. 6: Rarefaction analysis by isopod family, considering all areas together.



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

https://doi.org/10.5194/bg-2019-358
Preprint. Discussion started: 2 October 2019

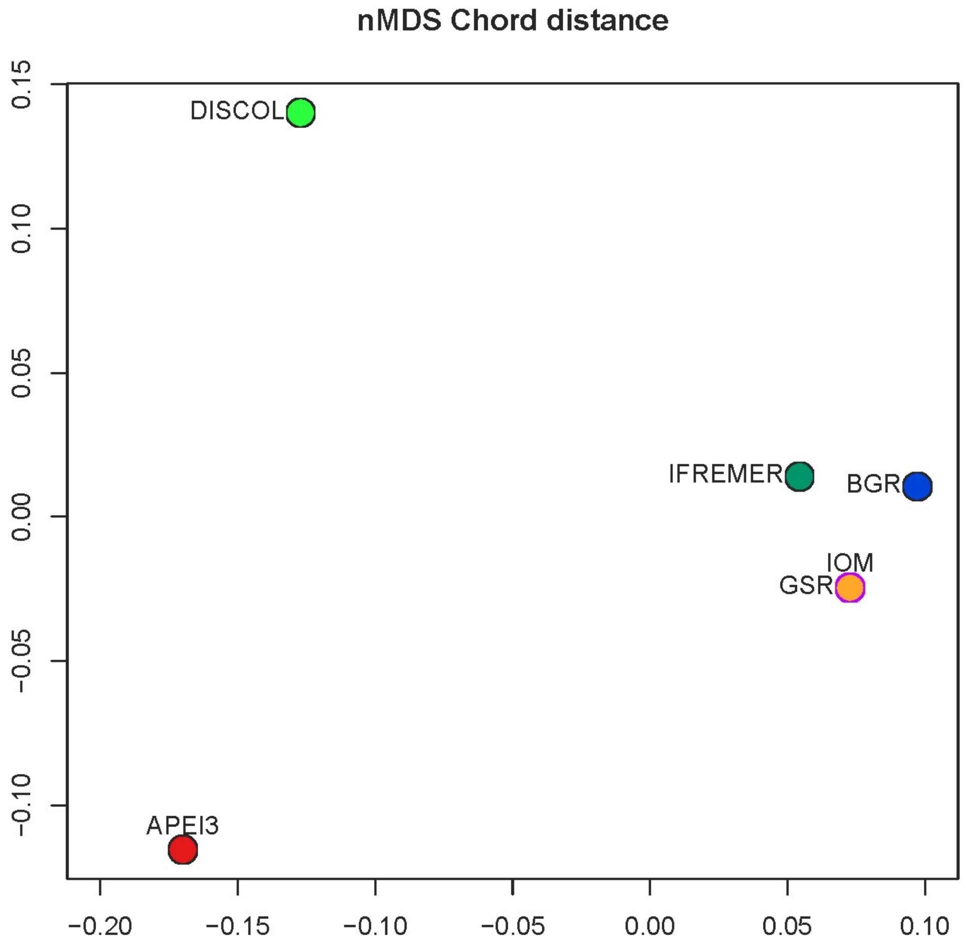


Fig. 8: nMDS ordination plot of Chord-distance between areas.

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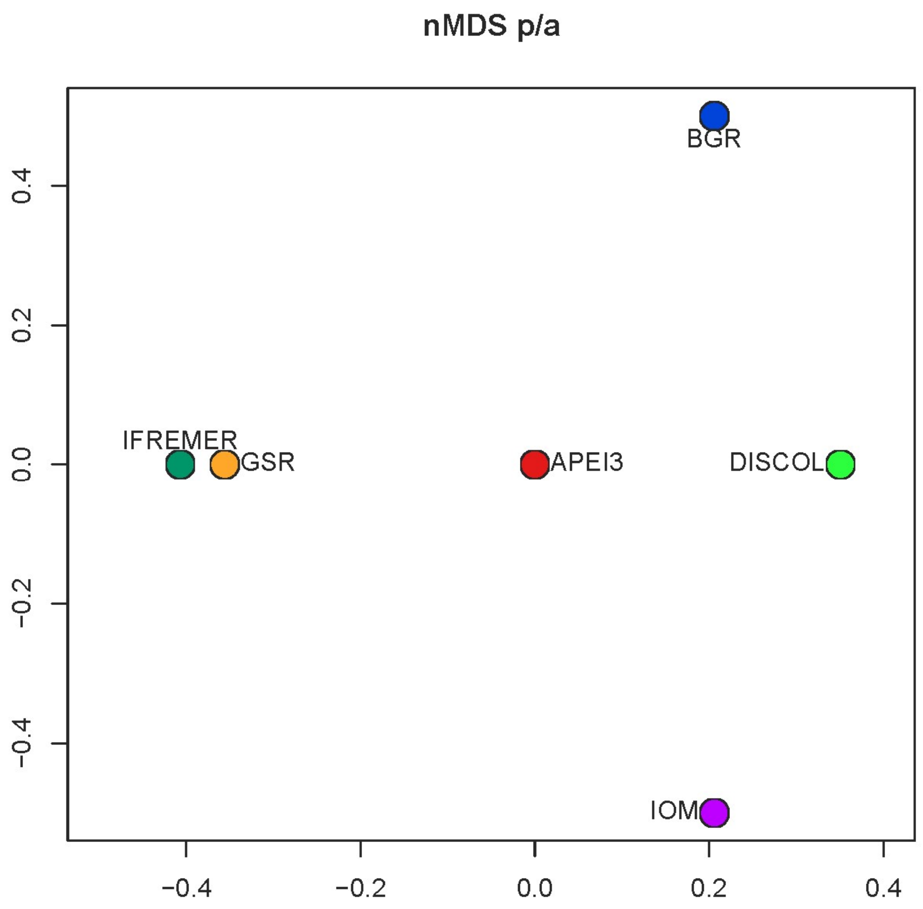

745 **Fig. 9: nMDS ordination plot of Euclidean-distance between areas of presence-absence transformed data.**

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Preprint. Discussion started: 2 October 2019

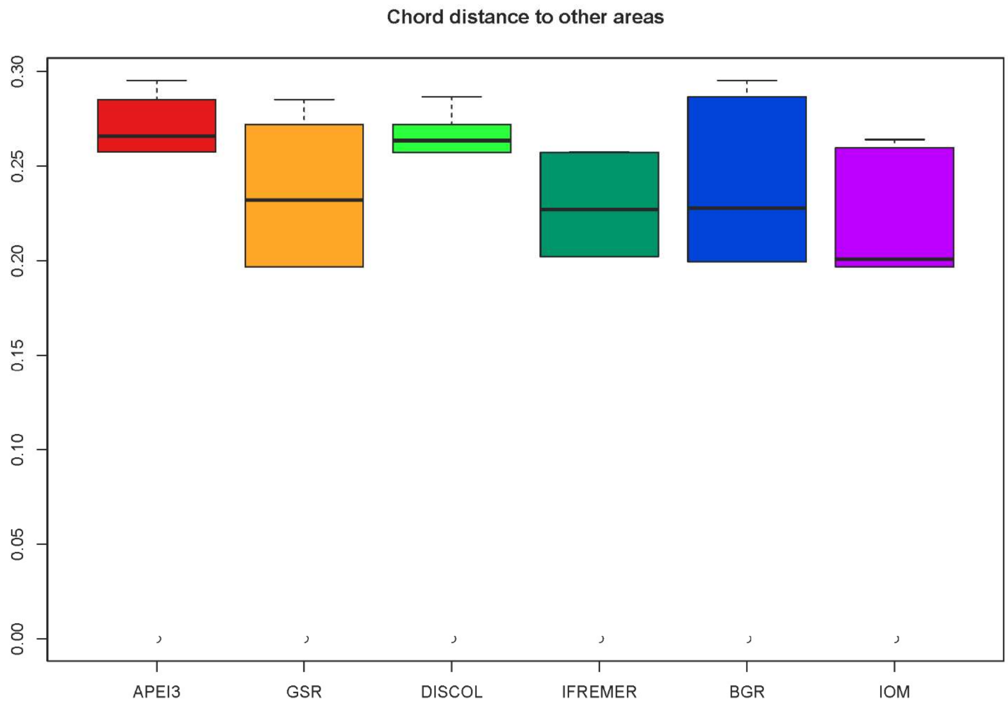

Fig. 10: Box and whiskers plot showing the median and range of the Chord distance of every area to other areas.

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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.

original Field_ID (used in circle trees)	BoLD sample ID	genus	morphospecies	OTU (congruent)	BIN (BoLD)	database_ID DZMB HH	museum catalogue number	family	loco type	RegionCode	station	GenBank no COI	GenBank no 16S
DesmDi02	DSB_1214	cf. *Eugerda*	sp. 03	D52	BOLD:ADL4889	50277	ZMH K-56556	Desmosomatidae	WS	DISCOL	37	X	
DesmDi03	DSB_1215	cf. *Eugerda*	indet	D52	BOLD:ADL4889	50278	ZMH K-57490	Desmosomatidae	WS	DISCOL	45	X	
DesmDi07	DSB_1219	*Mirabilicoxa*	sp. 3	D19	BOLD:ADL2574	50282	ZMH K-57491	Desmosomatidae	WS	DISCOL	37	X	X
DesmDi08	DSB_1292	*Mirabilicoxa*	sp. 3	D19	BOLD:ADL2574	50357	ZMH K-57492	Desmosomatidae	WS	DISCOL	81	X	X
DesmDi09	DSB_1293	*Eugerda*	sp. 01	D51	BOLD:ADL2893	50358	ZMH K-57493	Desmosomatidae	WS	DISCOL	85	X	X
DesmDi11	DSB_1295	*Prochelator*	sp. 01	D30	BOLD:ADL2576	50360	ZMH K-57494	Desmosomatidae	WS	DISCOL	93	X	
DesmDi12	DSB_1296	*Chelator*	sp. 01	D03	BOLD:ADM1410	50361	ZMH K-57495	Desmosomatidae	WS	DISCOL	93	X	X
DesmDi17	DSB_1301	*Eugerdella*	sp. 01	D17	BOLD:ADL5038	50366	ZMH K-57496	Desmosomatidae	WS	DISCOL	93	X	
DesmDi20	DSB_1345	*Chelator*	sp. 02	D06	BOLD:ADL9249	50410	ZMH K-57497	Desmosomatidae	WS	DISCOL	126	X	X
DesmDi21	DSB_1346	*Mirabilicoxa*	sp. 01	D15	BOLD:ADL5368	50411	ZMH K-57498	Desmosomatidae	WS	DISCOL	117	X	X
DesmDi23	DSB_1348	*Mirabilicoxa*	sp. 03	D19	BOLD:ADL2574	50413	ZMH K-57499	Desmosomatidae	WS	DISCOL	122	X	X
DesmDi24	DSB_1349	*Mirabilicoxa*	sp. 01	D15	BOLD:ADL5368	50414	ZMH K-57500	Desmosomatidae	WS	DISCOL	126	X	X
DesmDi28	DSB_1353	*Eugerdella*	sp. 12	D33	BOLD:ADL4885	50418	ZMH K-57501	Desmosomatidae	WS	DISCOL	122	X	X
DesmDi30	DSB_1355	*Disparella*	sp. 01	D23	BOLD:ADL5538	50420	ZMH K-57502	Desmosomatidae	WS	DISCOL	122	X	X
DesmDi31	DSB_1356	*Eugerda*	sp. 01	D50		50421	ZMH K-57503	Desmosomatidae	WS	DISCOL	122		X
DesmJP001	DSB_1762	*Eugerdella*	sp.11	D39	BOLD:ADW6372	50827	ZMH K-57504	Desmosomatidae	WS	GC	20	X	X
DesmJP002	DSB_1763	*Mirabilicoxa*	sp.C	D09	BOLD:ADL5035	50828	ZMH K-57505	Desmosomatidae	WS	GC	20	X	X
DesmJP004	DSB_1765	*Mirabilicoxa*	sp.1	D20	BOLD:ADL5037	50830	ZMH K-57506	Desmosomatidae	WS	GC	20	X	X
DesmJP005	DSB_1766	*Eugerdella*	sp.9	D41	BOLD:ADG0134	50831	ZMH K-57507	Desmosomatidae	WS	GC	20	X	
DesmJP006	DSB_1767	*Mirabilicoxa*	sp.1	D20	BOLD:ADL5037	50832	ZMH K-57508	Desmosomatidae	WS	GC	20	X	X
DesmJP007	DSB_1768	*Eugerdella*	sp.9	D41	BOLD:ADG0134	50833	ZMH K-57509	Desmosomatidae	WS	GC	20	X	
DesmJP008	DSB_1769	*Eugerdella*	indet	D39		50834	ZMH K-57510	Desmosomatidae	WS	GC	20		X
DesmJP009	DSB_1770	*Eugerdella*	indet	D39	BOLD:ADW6372	50835	ZMH K-57511	Desmosomatidae	WS	GC	20	X	X
DesmJP010	DSB_1771	*Prochelator*	indet	D30	BOLD:ADF9936	50836	ZMH K-57512	Desmosomatidae	WS	GC	20	X	
DesmJP011	DSB_1772	*Mirabilicoxa*	sp.D	D11	BOLD:ADL5366	50837	ZMH K-57513	Desmosomatidae	WS	GC	20	X	
DesmJP012	DSB_1773	*Disparella*	sp.1	D24	BOLD:ADL4887	50838	ZMH K-57514	Desmosomatidae	WS	GC	20	X	X
DesmJP013	DSB_1774	cf. *Disparella*	sp.1	D24	BOLD:ADL4887	50839	ZMH K-57515	Desmosomatidae	WS	GC	20	X	X
DesmJP015	DSB_1776	*Mirabilicoxa*	sp.F	D13	BOLD:ACY9838	50841	ZMH K-57516	Desmosomatidae	WS	GC	24	X	X
DesmJP016	DSB_1777	*Eugerdella*	sp.11	D39	BOLD:ADW6372	50842	ZMH K-57517	Desmosomatidae	WS	GC	24	X	X
DesmJP017	DSB_1778	*Mirabilicoxa*	sp.1	D20	BOLD:ADL5037	50843	ZMH K-57518	Desmosomatidae	WS	GC	24	X	X
DesmJP018	DSB_1779	cf. *Mirabilicoxa*	indet	D13	BOLD:ACY9838	50844	ZMH K-57519	Desmosomatidae	WS	GC	24	X	
DesmJP019	DSB_1780	*Eugerdella*	sp.11	D39	BOLD:ADW6372	50845	ZMH K-57520	Desmosomatidae	WS	GC	24	X	X
DesmJP020	DSB_1781	*Mirabilicoxa*	sp.C	D09	BOLD:ADL5035	50846	ZMH K-57521	Desmosomatidae	WS	GC	24	X	X
DesmJP021	DSB_1782	*Disparella*	sp.1	D24	BOLD:ADL4887	50847	ZMH K-57522	Desmosomatidae	WS	GC	24	X	X
DesmJP022	DSB_1783	cf. *Eugerdella*	sp.2	D47	BOLD:ADL4886	50848	ZMH K-57523	Desmosomatidae	WS	GC	24	X	
DesmJP023	DSB_1784	*Eugerdella*	sp.11	D39	BOLD:ADW6372	50849	ZMH K-57524	Desmosomatidae	WS	GC	24	X	X
DesmJP024	DSB_1785	*Eugerdella*	sp.11	D39	BOLD:ADW6372	50850	ZMH K-57525	Desmosomatidae	WS	GC	24	X	X
DesmJP025	DSB_1786	*Mirabilicoxa*	sp.F	D13	BOLD:ACY9838	50851	ZMH K-57526	Desmosomatidae	WS	GC	24	X	X
DesmJP026	DSB_1787	*Eugerdella*	sp. 3	D17	BOLD:ADL5370	50852	ZMH K-57527	Desmosomatidae	WS	GC	50	X	
DesmJP027	DSB_1788	*Mirabilicoxa*	sp.1	D20	BOLD:ADL5037	50853	ZMH K-57528	Desmosomatidae	WS	GC	50	X	X
DesmJP028	DSB_1789	*Prochelator*	indet	D30	BOLD:ADF9936	50854	ZMH K-57529	Desmosomatidae	WS	GC	50	X	
DesmJP030	DSB_1791	*Eugerdella*	sp. 3	D16	BOLD:ADM0377	50856	ZMH K-57530	Desmosomatidae	WS	GC	50	X	
DesmJP031	DSB_1792	*Eugerdella*	indet	D49	BOLD:ADL2572	50857	ZMH K-57531	Desmosomatidae	WS	GC	50	X	
DesmJP032	DSB_1793	*Mirabilicoxa*	sp.F	D13	BOLD:ACY9838	50858	ZMH K-57532	Desmosomatidae	WS	GC	50	X	X
DesmJP033	DSB_1794	*Mirabilicoxa*	sp.D	D11	BOLD:ADL5366	50859	ZMH K-57533	Desmosomatidae	WS	GC	50	X	X
DesmJP034	DSB_1795	*Eugerdella*	sp. 3	D17	BOLD:ADL5370	50860	ZMH K-57534	Desmosomatidae	WS	GC	50	X	
DesmJP037	DSB_1798	*Eugerdella*	cf. *egoni*	D49	BOLD:ADL5536	50863	ZMH K-57535	Desmosomatidae	WS	GC	50	X	
DesmJP038	DSB_1799	*Mirabilicoxa*	sp.C	D09	BOLD:ADL5035	50864	ZMH K-57536	Desmosomatidae	WS	GC	59	X	X
DesmJP039	DSB_1800	*Eugerdella*	sp.11	D39	BOLD:ADW6372	50865	ZMH K-57537	Desmosomatidae	WS	GC	59	X	X
DesmJP040	DSB_1801	*Prochelator*	indet	D30	BOLD:ADF9936	50866	ZMH K-57538	Desmosomatidae	WS	GC	59	X	
DesmJP041	DSB_1802	*Mirabilicoxa*	sp.1	D20	BOLD:ADL5037	50867	ZMH K-57539	Desmosomatidae	WS	GC	59	X	X
DesmJP042	DSB_1803	*Eugerdella*	sp.10	D38	BOLD:ADL5031	50868	ZMH K-57540	Desmosomatidae	WS	GC	59	X	X
DesmJP043	DSB_1804	*Eugerdella*	sp.10	D38	BOLD:ADL5031	50869	ZMH K-57541	Desmosomatidae	WS	GC	59	X	X
DesmJP045	DSB_1806	*Eugerdella*	sp. 4	D17	BOLD:ACY6387	50871	ZMH K-57542	Desmosomatidae	WS	GC	59	X	
DesmJP046	DSB_1807	*Eugerdella*	sp.10	D38	BOLD:ADL5031	50872	ZMH K-57543	Desmosomatidae	WS	GC	59	X	X
DesmJP047	DSB_1808	*Eugerdella*	sp. 3	D17	BOLD:ADL5370	50873	ZMH K-57544	Desmosomatidae	WS	GC	59	X	
DesmJP048	DSB_1809	cf. *Mirabilicoxa*	sp.C	D09	BOLD:ADL5035	50874	ZMH K-57545	Desmosomatidae	WS	GC	59	X	X
DesmJP049	DSB_1810	*Prochelator*	indet	D30	BOLD:ADF9936	50875	ZMH K-57546	Desmosomatidae	WS	GC	59	X	
DesmJP050	DSB_1811	*Chelator*	sp.D	D07	BOLD:ADL5034	50876	ZMH K-57547	Desmosomatidae	WS	IOM	81	X	X
DesmJP051	DSB_1812	cf. *Eugerdella*	indet	D36	BOLD:ADG1796	50877	ZMH K-57548	Desmosomatidae	WS	IOM	81	X	

https://doi.org/10.5194/bg-2019-358
Preprint. Discussion started: 2 October 2019

DesmJP053	DSB_1814	*Eugerdella*	sp.5	D44	BOLD:ADL5216	50879	ZMH K-57549	Desmosomatidae	WS	IOM	81	X	X
DesmJP054	DSB_1815	*Mirabilicoxa*	sp.C	D21	BOLD:ADL2890	50880	ZMH K-57550	Desmosomatidae	WS	IOM	81	X	X
DesmJP055	DSB_1816	cf. *Eugerdella*	indet	D36	BOLD:ADG1796	50881	ZMH K-57551	Desmosomatidae	WS	IOM	81	X	
DesmJP057	DSB_1818	*Eugerdella*	5 or 6	D36	BOLD:ADG1796	50883	ZMH K-57552	Desmosomatidae	WS	IOM	81	X	
DesmJP059	DSB_1820	*Eugerdella*	sp.11	D39	BOLD:ADW6372	50885	ZMH K-57553	Desmosomatidae	WS	IOM	81	X	X
DesmJP060	DSB_1821	*Chelator*	sp.D	D07	BOLD:ADL5034	50886	ZMH K-57554	Desmosomatidae	WS	IOM	81	X	X
DesmJP061	DSB_1822	*Chelator*	sp.D	D07	BOLD:ADL5034	50887	ZMH K-57555	Desmosomatidae	WS	IOM	81	X	X
DesmJP064	DSB_1825	cf. *Disparella*	indet	D25	BOLD:ADL5032	50890	ZMH K-57556	Desmosomatidae	WS	IOM	99	X	X
DesmJP065	DSB_1826	*Eugerdella*	sp. 5	D36	BOLD:ADG1796	50891	ZMH K-57557	Desmosomatidae	WS	IOM	99	X	
DesmJP066	DSB_1827	*Mirabilicoxa*	sp.D	D11	BOLD:ADL5366	50892	ZMH K-57558	Desmosomatidae	WS	IOM	99	X	X
DesmJP067	DSB_1828	*Mirabilicoxa*	indet	D13	BOLD:ACY9838	50893	ZMH K-57559	Desmosomatidae	WS	IOM	99	X	
DesmJP068	DSB_1829	*Eugerdella*	sp. 6	D36	BOLD:ADG1796	50894	ZMH K-57560	Desmosomatidae	WS	IOM	99	X	
DesmJP069	DSB_1830	*Eugerdella*	sp.11	D39	BOLD:ADW6372	50895	ZMH K-57561	Desmosomatidae	WS	IOM	99	X	X
DesmJP071	DSB_1832	*Eugerdella*	sp. 3	D42	BOLD:ADM1411	50897	ZMH K-57562	Desmosomatidae	WS	IOM	99	X	
DesmJP073	DSB_1834	*Mirabilicoxa*	sp.A	D18	BOLD:ACY5985	50899	ZMH K-57563	Desmosomatidae	WS	IOM	99	X	X
DesmJP074	DSB_1835	*Eugerdella*	indet	D49	BOLD:ADL2572	50900	ZMH K-57564	Desmosomatidae	WS	BC	118	X	
DesmJP075	DSB_1836	cf. *Disparella*	indet	D27	BOLD:ADL5535	50901	ZMH K-57565	Desmosomatidae	WS	BC	118	X	X
DesmJP076	DSB_1837	*Eugerdella*	sp. cf.7	D45	BOLD:ADL2895	50902	ZMH K-57566	Desmosomatidae	WS	BC	118	X	X
DesmJP077	DSB_1838	*Disparella*	indet	D25	BOLD:ADL5032	50903	ZMH K-57567	Desmosomatidae	WS	BC	118	X	X
DesmJP078	DSB_1839	cf. *Prochelator*	sp.1	D32	BOLD:ADL3300	50904	ZMH K-57568	Desmosomatidae	WS	BC	118	X	
DesmJP081	DSB_1842	*Eugerdella*	sp.10	D38	BOLD:ADL5031	50907	ZMH K-57569	Desmosomatidae	WS	BC	118	X	X
DesmJP082	DSB_1843	*Prochelator*	indet	D30	BOLD:ADF9936	50908	ZMH K-57570	Desmosomatidae	WS	BC	118	X	
DesmJP083	DSB_1844	*Mirabilicoxa*	sp.D	D11	BOLD:ADL5366	50909	ZMH K-57571	Desmosomatidae	WS	BC	118	X	
DesmJP084	DSB_1845	*Eugerdella*	sp. 5	D43	BOLD:ADL5372	50910	ZMH K-57572	Desmosomatidae	WS	BC	118	X	X
DesmJP085	DSB_1846	*Prochelator*	indet	D30	BOLD:ADF9936	50911	ZMH K-57573	Desmosomatidae	WS	BC	118	X	
DesmJP086	DSB_1847	*Prochelator*	sp.1	D32	BOLD:ADL3300	50912	ZMH K-57574	Desmosomatidae	WS	BC	118	X	
DesmJP087	DSB_1848	*Prochelator*	sp.1	D32	BOLD:ADL3300	50913	ZMH K-57575	Desmosomatidae	WS	BC	133	X	
DesmJP088	DSB_1849	*Prochelator*	sp.1	D32	BOLD:ADL3300	50914	ZMH K-57576	Desmosomatidae	WS	BC	133	X	
DesmJP090	DSB_1851	*Mirabilicoxa*	indet	D13	BOLD:ACY9838	50916	ZMH K-57577	Desmosomatidae	WS	BC	133	X	
DesmJP091	DSB_1852	*Chelator*	sp.D	D07	BOLD:ADL5034	50917	ZMH K-57578	Desmosomatidae	WS	BC	133	X	X
DesmJP092	DSB_1853	*Eugerdella*	cf. *egoni*	D48	BOLD:ADL5371	50918	ZMH K-57579	Desmosomatidae	WS	BC	133	X	
DesmJP093	DSB_1854	cf. *Disparella*	sp.1	D24	BOLD:ADL4887	50919	ZMH K-57580	Desmosomatidae	WS	BC	133	X	X
DesmJP094	DSB_1855	*Eugerdella*	sp. 5	D44	BOLD:ADL5216	50920	ZMH K-57581	Desmosomatidae	WS	BC	133	X	X
DesmJP095	DSB_1856	*Eugerdella*	sp.5	D44	BOLD:ADL5216	50921	ZMH K-57582	Desmosomatidae	WS	BC	133	X	X
DesmJP096	DSB_1857	*Prochelator*	indet	D30	BOLD:ADF9936	50922	ZMH K-57583	Desmosomatidae	WS	BC	133	X	
DesmJP099	DSB_1860	*Mirabilicoxa*	sp.D	D11	BOLD:ADL5215	50925	ZMH K-57584	Desmosomatidae	WS	FC	158	X	X
DesmJP100	DSB_1861	*Mirabilicoxa*	sp.E	D12	BOLD:ADL5213	50926	ZMH K-57585	Desmosomatidae	WS	FC	158	X	X
DesmJP101	DSB_1862	*Eugerdella*	sp. 8	D40	BOLD:ADL2751	50927	ZMH K-57586	Desmosomatidae	WS	FC	158	X	X
DesmJP103	DSB_1864	*Disparella*	indet	D26	BOLD:ADL2577	50929	ZMH K-57587	Desmosomatidae	WS	FC	158	X	X
DesmJP104	DSB_1865	*Mirabilicoxa*	indet	D37	BOLD:ADL5211	50930	ZMH K-57588	Desmosomatidae	WS	FC	158	X	
DesmJP105	DSB_1866	*Mirabilicoxa*	sp.A	D18	BOLD:ACY5985	50931	ZMH K-57589	Desmosomatidae	WS	FC	158	X	X
DesmJP106	DSB_1867	*Mirabilicoxa*	sp.E	D12	BOLD:ADL5213	50932	ZMH K-57590	Desmosomatidae	WS	FC	158	X	X
DesmJP107	DSB_1868	cf. *Mirabilicoxa*	sp.B	D10	BOLD:ADL4888	50933	ZMH K-57591	Desmosomatidae	WS	FC	158	X	X
DesmJP108	DSB_1869	cf. *Mirabilicoxa*	sp.E	D12	BOLD:ADL5213	50934	ZMH K-57592	Desmosomatidae	WS	FC	158	X	X
DesmJP109	DSB_1870	*Eugerdella*	sp. 6	D34	BOLD:ADL5033	50935	ZMH K-57593	Desmosomatidae	WS	FC	158	X	
DesmJP110	DSB_1871	*Eugerdella*	sp. 7	D46	BOLD:ADL2578	50936	ZMH K-57594	Desmosomatidae	WS	FC	158	X	X
DesmJP111	DSB_1872	*Mirabilicoxa*	sp.A	D18	BOLD:ACY5985	50937	ZMH K-57595	Desmosomatidae	WS	FC	171	X	X
DesmJP112	DSB_1873	*Eugerdella*	sp.5	D44	BOLD:ADL5216	50938	ZMH K-57596	Desmosomatidae	WS	FC	171	X	X
DesmJP113	DSB_1874	*Prochelator*	indet	D32	BOLD:ADL3300	50939	ZMH K-57597	Desmosomatidae	WS	FC	171	X	
DesmJP114	DSB_1875	cf. *Mirabilicoxa*	sp.E	D12	BOLD:ADL5213	50940	ZMH K-57598	Desmosomatidae	WS	FC	171	X	X
DesmJP115	DSB_1876	cf. *Mirabilicoxa*	sp.A	D18	BOLD:ACY5985	50941	ZMH K-57599	Desmosomatidae	WS	FC	171	X	X
DesmJP116	DSB_1877	cf. *Mirabilicoxa*	indet	D18	BOLD:ACY5985	50942	ZMH K-57600	Desmosomatidae	WS	FC	171	X	
DesmJP117	DSB_1878	*Eugerdella*	sp.5	D44	BOLD:ADL5216	50943	ZMH K-57601	Desmosomatidae	WS	FC	171	X	X
DesmJP118	DSB_1879	*Mirabilicoxa*	sp.A	D18	BOLD:ACY5985	50944	ZMH K-57602	Desmosomatidae	WS	FC	171	X	X
DesmJP119	DSB_1880	*Chelator*	sp.B	D04	BOLD:ADL5212	50945	ZMH K-57603	Desmosomatidae	WS	FC	171	X	X
DesmJP120	DSB_1881	*Eugerdella*	sp.5	D44	BOLD:ADL5216	50946	ZMH K-57604	Desmosomatidae	WS	FC	171	X	X
DesmJP121	DSB_1882	*Prochelator*	indet	D29	BOLD:ADL2573	50947	ZMH K-57605	Desmosomatidae	WS	FC	171	X	
DesmJP123	DSB_1884	*Prochelator*	sp.1	D32	BOLD:ADL3300	50949	ZMH K-57606	Desmosomatidae	WS	FC	171	X	
DesmJP124	DSB_1885	*Mirabilicoxa*	indet	D14	BOLD:ADL5365	50950	ZMH K-57607	Desmosomatidae	WS	A3	192	X	
DesmJP125	DSB_1886	*Disparella*	indet	D22	BOLD:ADL2753	50951	ZMH K-57608	Desmosomatidae	WS	A3	192	X	X
DesmJP126	DSB_1887	*Eugerdella*	sp. 6 ?	D35	BOLD:ADL5217	50952	ZMH K-57609	Desmosomatidae	WS	A3	192	X	
DesmJP127	DSB_1888	*Prochelator*	sp. 123	D31	BOLD:ADL2579	50953	ZMH K-57610	Desmosomatidae	WS	A3	192	X	
DesmJP128	DSB_1889	cf. *Mirabilicoxa*	sp.B	D10	BOLD:ADL4888	50954	ZMH K-57611	Desmosomatidae	WS	A3	192	X	X
DesmJP129	DSB_1890	*Mirabilicoxa*	indet	D14	BOLD:ADL5365	50955	ZMH K-57612	Desmosomatidae	WS	A3	192	X	

DesmJP131	DSB_1892	*Mirabilicoxa*	sp.B	D10	BOLD:ADL4888	50957	ZMH K-57613	Desmosomatidae	WS	A3	192	X	X
DesmJP133	DSB_1894	*Chelator*	sp.A	D01	BOLD:ADL5030	50959	ZMH K-57614	Desmosomatidae	WS	A3	192	X	X
DesmJP134	DSB_1895	cf. *Mirabilicoxa*	sp.B	D10	BOLD:ADL4888	50960	ZMH K-57615	Desmosomatidae	WS	A3	192	X	X
DesmJP135	DSB_1896	*Oecidiobranchus*	oeci	D08	BOLD:ADL5367	50961	ZMH K-57616	Desmosomatidae	WS	A3	192	X	X
DesmJP137	DSB_1898	*Oecidiobranchus*	oeci	D08	BOLD:ADL5367	50963	ZMH K-57617	Desmosomatidae	WS	A3	197	X	X
DesmJP138	DSB_1899	*Chelator*	sp.A	D01	BOLD:ADL5030	50964	ZMH K-57618	Desmosomatidae	WS	A3	197	X	X
DesmJP139	DSB_1900	*Chelator*	sp.A	D01		50965	ZMH K-57619	Desmosomatidae	WS	A3	197		X
DesmJP140	DSB_1901	cf. *Disparella*	indet	D28	BOLD:ADL3347	50966	ZMH K-57620	Desmosomatidae	WS	A3	197	X	X
DesmJP142	DSB_1903	*Eugerdella*	sp. 6 ?	D34	BOLD:ADL5033	50968	ZMH K-57621	Desmosomatidae	WS	A3	197	X	
DesmJP143	DSB_1904	cf. *Disparella*	indet	D28	BOLD:ADL3347	50969	ZMH K-57622	Desmosomatidae	WS	A3	197	X	X
DesmJP145	DSB_1906	cf. *Chelator*	sp.A	D01	BOLD:ADL5030	50971	ZMH K-57623	Desmosomatidae	WS	A3	197	X	X
DesmJP147	DSB_1908	*Eugerdella*	sp. 6 ?	D35	BOLD:ADL5217	50973	ZMH K-57624	Desmosomatidae	WS	A3	197	X	
DesmJP148	DSB_1909	cf. *Disparella*	indet	D28	BOLD:ADL3347	50974	ZMH K-57625	Desmosomatidae	WS	A3	210	X	X
DesmJP152	DSB_1913	*Chelator*	sp.C	D05	BOLD:ADL2581	50978	ZMH K-57626	Desmosomatidae	WS	A3	210	X	X
DesmJP153	DSB_1914	*Chelator*	sp.C	D05	BOLD:ADL2581	50979	ZMH K-57627	Desmosomatidae	WS	A3	210	X	X
DesmJP154	DSB_1915	*Oecidiobranchus*	oeci	D08	BOLD:ADL5367	50980	ZMH K-57628	Desmosomatidae	WS	A3	210	X	X
DesmJP159	DSB_1920	cf. *Chelator*	sp.C	D05	BOLD:ADL2581	50985	ZMH K-57629	Desmosomatidae	WS	A3	210	X	X
DesmJP160	DSB_1921	*Mirabilicoxa*	indet	D14	BOLD:ADL5365	50986	ZMH K-57630	Desmosomatidae	WS	A3	210	X	X
DesmJP162	DSB_1949	*Eugerdella*	sp. 6 ?	D35	BOLD:ADL5217	51014	ZMH K-57631	Desmosomatidae	WS	A3	197	X	
HaplDi02	DSB_1320	*Chauliodobiscus*	sp. 01	H15	BOLD:ADL2819	50385	ZMH K-57632	Haploniscidae	W	DISCOL	93	X	X
HaplDi03	DSB_1321	*Chauliodobiscus*	sp. 01	H15	BOLD:ADL2819	50386	ZMH K-57633	Haploniscidae	W	DISCOL	93	X	X
HaplDi04	DSB_1322	*Chauliodoniscus*	sp. 01	H15	BOLD:ADL2819	50387	ZMH K-57634	Haploniscidae	W	DISCOL	93	X	X
HaplDi05	DSB_1323	cf. *Chauliodoniscus*	indet	H07	BOLD:ADL3283	50388	ZMH K-57635	Haploniscidae	W	DISCOL	93	X	
HaplDi07	DSB_1325	*Chauliodoniscus*	sp. 01	H14	BOLD:ADL2983	50390	ZMH K-57636	Haploniscidae	W	DISCOL	93	X	X
HaplDi08	DSB_1326	*Chauliodoniscus*	sp. 01	H14	BOLD:ADL2983	50391	ZMH K-57637	Haploniscidae	W	DISCOL	93	X	X
HaplDi09	DSB_1327	*Chauliodoniscus*	sp. 01	H23	BOLD:ADL3281	50392	ZMH K-57638	Haploniscidae	W	DISCOL	93	X	
HaplDi11	DSB_1329	*Chauliodoniscus*	sp. 01	H15	BOLD:ADL2819	50394	ZMH K-57639	Haploniscidae	W	DISCOL	93	X	X
HaplDi12	DSB_1330	cf. *Chauliodoniscus*	indet	H07	BOLD:ADL3283	50395	ZMH K-57640	Haploniscidae	W	DISCOL	93	X	
HaplDi13	DSB_1331	*Chauliodoniscus*	sp. 01	H15	BOLD:ADL2819	50396	ZMH K-57641	Haploniscidae	W	DISCOL	93	X	X
HaplDi14	DSB_1332	cf. *Chauliodoniscus*	indet	H07	BOLD:ADL3283	50397	ZMH K-57642	Haploniscidae	W	DISCOL	93	X	
HaplDi15	DSB_1333	*Chauliodoniscus*	sp. 01	H23	BOLD:ADL2981	50398	ZMH K-57643	Haploniscidae	W	DISCOL	93	X	
HaplDi16	DSB_1334	cf. *Chauliodoniscus*	indet	H07	BOLD:ADL3283	50399	ZMH K-57644	Haploniscidae	W	DISCOL	93	X	
HaplDi17	DSB_1335	*Chauliodoniscus*	sp. 01	H14	BOLD:ADL2983	50400	ZMH K-57645	Haploniscidae	W	DISCOL	93	X	X
HaplDi18	DSB_1336	*Chauliodoniscus*	sp. 01	H14	BOLD:ADL2983	50401	ZMH K-57646	Haploniscidae	W	DISCOL	93	X	X
HaplDi19	DSB_1337	cf. *Chauliodoniscus*	indet	H07	BOLD:ADL3283	50402	ZMH K-57647	Haploniscidae	W	DISCOL	85	X	
HaplDi24	DSB_1342	*Chauliodoniscus*	sp. 01	H09	BOLD:ADL6396	50407	ZMH K-57648	Haploniscidae	W	DISCOL	117	X	
HaplDi25	DSB_1343	*Chauliodoniscus*	sp. 01	H14	BOLD:ADL2983	50408	ZMH K-57649	Haploniscidae	W	DISCOL	117	X	X
HaplJP001	DSB_2044	*Mastigoniscus*	sp. # 3	H17	BOLD:ADL3127	51109	ZMH K-57650	Haploniscidae	W	GC	20	X	X
HaplJP002	DSB_2045	*Mastigoniscus*	sp. # 3	H17	BOLD:ADL3127	51110	ZMH K-57651	Haploniscidae	W	GC	20	X	X
HaplJP003	DSB_2046	*Haploniscus*	sp. # 2	H12	BOLD:ADL3122	51111	ZMH K-57652	Haploniscidae	W	GC	20	X	X
HaplJP004	DSB_2047	*Mastigoniscus*	sp. # 3	H17	BOLD:ADL3127	51112	ZMH K-57653	Haploniscidae	W	GC	20	X	X
HaplJP005	DSB_2048	*Mastigoniscus*	sp. # 3	H17	BOLD:ADL3127	51113	ZMH K-57654	Haploniscidae	W	GC	20	X	X
HaplJP006	DSB_2049	*Haploniscus*	sp. # 2	H12	BOLD:ADL3122	51114	ZMH K-57655	Haploniscidae	W	GC	24	X	
HaplJP008	DSB_2051	*Haploniscus*	sp. # 4	H06	BOLD:ADL6761	51116	ZMH K-57656	Haploniscidae	W	GC	24	X	
HaplJP009	DSB_2052	*Mastigoniscus*	sp. # 3	H17	BOLD:ADL3127	51117	ZMH K-57657	Haploniscidae	W	GC	24	X	X
HaplJP010	DSB_2053	*Haploniscus*	sp. # 2	H10	BOLD:ADL3282	51118	ZMH K-57658	Haploniscidae	W	GC	50	X	
HaplJP011	DSB_2054	*Mastigoniscus*	sp. # 5	H16	BOLD:ADL2988	51119	ZMH K-57659	Haploniscidae	W	GC	50	X	X
HaplJP013	DSB_2056	*Haploniscus*	sp. # 2	H10	BOLD:ADL4714	51121	ZMH K-57660	Haploniscidae	W	GC	50	X	
HaplJP014	DSB_2057	*Haploniscus*	sp. # 2	H10	BOLD:ADL3282	51122	ZMH K-57661	Haploniscidae	W	GC	50	X	
HaplJP015	DSB_2058	*Haploniscus*	sp. # 2	H10	BOLD:ADL4714	51123	ZMH K-57662	Haploniscidae	W	GC	50	X	X
HaplJP016	DSB_2059	*Haploniscus*	sp. # 2	H10	BOLD:ADL4714	51124	ZMH K-57663	Haploniscidae	W	GC	50	X	X
HaplJP017	DSB_2060	*Mastigoniscus*	sp. # 5	H16	BOLD:ADL2988	51125	ZMH K-57664	Haploniscidae	W	GC	59	X	X
HaplJP018	DSB_2061	*Mastigoniscus*	sp. # 5	H16	BOLD:ADL2988	51126	ZMH K-57665	Haploniscidae	W	IOM	81	X	X
HaplJP019	DSB_2062	*Haploniscus*	sp. # 2	H10	BOLD:ADL3123	51127	ZMH K-57666	Haploniscidae	W	IOM	81	X	
HaplJP020	DSB_2063	*Mastigoniscus*	sp. # 5	H08	BOLD:ADL2984	51128	ZMH K-57667	Haploniscidae	W	IOM	81	X	
HaplJP021	DSB_2064	*Mastigoniscus*	sp. # 3	H22	BOLD:ADL6395	51129	ZMH K-57668	Haploniscidae	W	IOM	81	X	
HaplJP022	DSB_2065	*Haploniscus*	sp. # 2	H10	BOLD:ADL4710	51130	ZMH K-57669	Haploniscidae	W	IOM	99	X	X
HaplJP023	DSB_2066	*Mastigoniscus*	sp. # 3	H22	BOLD:ADL2982	51131	ZMH K-57670	Haploniscidae	W	BC	118	X	
HaplJP024	DSB_2067	*Mastigoniscus*	sp. # 3007	H19	BOLD:ADL2985	51132	ZMH K-57671	Haploniscidae	W	BC	118		X
HaplJP025	DSB_2068	*Mastigoniscus*	sp. # 3	H22	BOLD:ADL2982	51133	ZMH K-57672	Haploniscidae	W	BC	118	X	
HaplJP026	DSB_2069	*Mastigoniscus*	sp. # 3	H22	BOLD:ADL2982	51134	ZMH K-57673	Haploniscidae	W	BC	118	X	
HaplJP027	DSB_2070	*Mastigoniscus*	sp. # 3007	H19	BOLD:ADL2985	51135	ZMH K-57674	Haploniscidae	W	BC	118	X	X
HaplJP028	DSB_2071	*Mastigoniscus*	sp. # 3	H22	BOLD:ADL2982	51136	ZMH K-57675	Haploniscidae	W	BC	118	X	
HaplJP029	DSB_2072	*Mastigoniscus*	sp. # 3007	H19	BOLD:ADL2985	51137	ZMH K-57676	Haploniscidae	W	BC	118	X	X

https://doi.org/10.5194/bg-2019-358
Preprint. Discussion started: 2 October 2019

HaplJP031	DSB_2074	*Mastigoniscus*	sp. # 3	H22	BOLD:ADL2982	51139	ZMH K-57677	Haploniscidae	W	BC	118	X	
HaplJP032	DSB_2075	*Haploniscus*	sp. # 2	H10	BOLD:ADL3968	51140	ZMH K-57678	Haploniscidae	W	BC	118	X	
HaplJP033	DSB_2076	*Haploniscus*	sp. # 2	H10	BOLD:ADL3968	51141	ZMH K-57679	Haploniscidae	W	BC	118	X	X
HaplJP034	DSB_2077	*Mastigoniscus*	sp. # 3	H22	BOLD:ADL2982	51142	ZMH K-57680	Haploniscidae	W	BC	118	X	
HaplJP035	DSB_2078	*Mastigoniscus*	sp. # 3	H22	BOLD:ADL2982	51143	ZMH K-57681	Haploniscidae	W	BC	133	X	
HaplJP036	DSB_2079	*Mastigoniscus*	sp. # 3	H22	BOLD:ADL2982	51144	ZMH K-57682	Haploniscidae	W	BC	133	X	
HaplJP037	DSB_2080	*Mastigoniscus*	sp. # 3	H22	BOLD:ADL2982	51145	ZMH K-57683	Haploniscidae	W	BC	133	X	
HaplJP038	DSB_2081	*Mastigoniscus*	sp. # 3007	H19	BOLD:ADL2985	51146	ZMH K-57684	Haploniscidae	W	BC	133	X	X
HaplJP039	DSB_2082	*Mastigoniscus*	sp. # 3007	H19	BOLD:ADL2985	51147	ZMH K-57685	Haploniscidae	W	BC	133	X	X
HaplJP040	DSB_2083	*Mastigoniscus*	sp.	H22	BOLD:ADL2982	51148	ZMH K-57686	Haploniscidae	W	BC	133	X	X
HaplJP041	DSB_2084	*Mastigoniscus*	sp. # 3	H21	BOLD:ADL3128	51149	ZMH K-57687	Haploniscidae	W	FC	158	X	X
HaplJP042	DSB_2085	*Mastigoniscus*	sp. # 3007	H18	BOLD:ADL6560	51150	ZMH K-57688	Haploniscidae	W	FC	158	X	X
HaplJP043	DSB_2086	*Haploniscus*	sp. # 2	H10	BOLD:ADL3123	51151	ZMH K-57689	Haploniscidae	W	FC	158	X	
HaplJP044	DSB_2087	*Haploniscus*	sp. # 1a	H05	BOLD:ADL6397	51152	ZMH K-57690	Haploniscidae	W	FC	158	X	X
HaplJP045	DSB_2088	*Haploniscus*	sp. # 1	H04	BOLD:ADL3129	51153	ZMH K-57691	Haploniscidae	W	FC	158	X	
HaplJP046	DSB_2089	*Haploniscus*	sp. # 1	H04	BOLD:ADL3129	51154	ZMH K-57692	Haploniscidae	W	FC	158	X	
HaplJP047	DSB_2090	*Mastigoniscus*	sp. # 7	H13	BOLD:ADL3125	51155	ZMH K-57693	Haploniscidae	W	FC	171	X	X
HaplJP048	DSB_2091	*Mastigoniscus*	sp. # 3	H21	BOLD:ADL3128	51156	ZMH K-57694	Haploniscidae	W	FC	171	X	
HaplJP049	DSB_2092	*Haploniscus*	sp. # 2	H10	BOLD:ADL2986	51157	ZMH K-57695	Haploniscidae	W	FC	171	X	X
HaplJP050	DSB_2093	*Haploniscus*	sp. # 2	H10	BOLD:ADL3123	51158	ZMH K-57696	Haploniscidae	W	FC	171	X	X
HaplJP051	DSB_2094	*Mastigoniscus*	sp. # 3	H21	BOLD:ADL3128	51159	ZMH K-57697	Haploniscidae	W	FC	171	X	
HaplJP052	DSB_2095	*Haploniscus*	sp. # 1	H03	BOLD:ADL2989	51160	ZMH K-57698	Haploniscidae	W	FC	171	X	X
HaplJP053	DSB_2096	*Mastigoniscus*	sp. # 7	H13	BOLD:ADL3125	51161	ZMH K-57699	Haploniscidae	W	FC	171	X	X
HaplJP054	DSB_2097	*Haploniscus*	sp. # 2	H10	BOLD:ADL2986	51162	ZMH K-57700	Haploniscidae	W	FC	171	X	
HaplJP055	DSB_2098	*Haploniscus*	sp. # 1	H03	BOLD:ADL2989	51163	ZMH K-57701	Haploniscidae	W	FC	171	X	X
HaplJP057	DSB_2100	*Mastigoniscus*	sp. # 8	H02	BOLD:ADL3126	51165	ZMH K-57702	Haploniscidae	W	A3	210	X	X
HaplJP058	DSB_2101	*Haploniscus*	sp. # 2	H11	BOLD:ADL2820	51166	ZMH K-57703	Haploniscidae	W	A3	210	X	X
HaplJP059	DSB_2102	*Mastigoniscus*	sp. # 5	H08	BOLD:ADL2984	51167	ZMH K-57704	Haploniscidae	W	A3	210	X	
HaplJP060	DSB_2103	*Haploniscus*	sp. # 2	H11	BOLD:ADL3124	51168	ZMH K-57705	Haploniscidae	W	A3	210	X	
HaplJP061	DSB_2104	*Mastigoniscus*	sp. # 5	H08	BOLD:ADL2984	51169	ZMH K-57706	Haploniscidae	W	A3	210	X	
HaplJP062	DSB_2105	*Haploniscus*	sp. # 2	H11	BOLD:ADL3124	51170	ZMH K-57707	Haploniscidae	W	A3	210	X	
HaplJP063	DSB_2106	*Mastigoniscus*	sp. # 3	H01	BOLD:ADL3280	51171	ZMH K-57708	Haploniscidae	W	A3	210	X	X
HaplJP064	DSB_2107	*Mastigoniscus*	sp. # 5	H08	BOLD:ADL2984	51172	ZMH K-57709	Haploniscidae	W	A3	210	X	
HaplJP065	DSB_2108	*Haploniscus*	sp. # 2	H11	BOLD:ADL3124	51173	ZMH K-57710	Haploniscidae	W	A3	197	X	X
HaplJP066	DSB_2109	*Mastigoniscus*	sp. # 3	H01	BOLD:ADL3130	51174	ZMH K-57711	Haploniscidae	W	A3	197		X
HaplJP067	DSB_2110	*Haploniscus*	sp. # 2	H11	BOLD:ADL2820	51175	ZMH K-57712	Haploniscidae	W	A3	192	X	
HaplJP068	DSB_2111	*Mastigoniscus*	sp. # 5	H20	BOLD:ADL2987	51176	ZMH K-57713	Haploniscidae	W	A3	192	X	
HaplJP069	DSB_2112	*Mastigoniscus*	sp. # 5	H20	BOLD:ADL2987	51177	ZMH K-57714	Haploniscidae	W	A3	192	X	
HaplJP070	DSB_2113	*Haploniscus*	sp. # 2	H11	BOLD:ADL2820	51178	ZMH K-57715	Haploniscidae	W	A3	192	X	
HaplJP071	DSB_2114	*Haploniscus*	sp. # 2	H11	BOLD:ADL3124	51179	ZMH K-57716	Haploniscidae	W	A3	192	X	
HaplJP072	DSB_2115	*Mastigoniscus*	sp. # 8	H02	BOLD:ADL3126	51180	ZMH K-57717	Haploniscidae	W	A3	192	X	
HaplJP073	DSB_2116	*Mastigoniscus*	sp. # 5	H20	BOLD:ADL2987	51181	ZMH K-57718	Haploniscidae	W	A3	192	X	
HaplJP074	DSB_2117	*Mastigoniscus*	sp. # 3	H22	BOLD:ADL6395	51182	ZMH K-57719	Haploniscidae	W	IOM	81	X	
MacrDi04	DSB_1208	*Macrostylis*	sp. 03	M02	BOLD:ADL4636	50271	SMF 54160	Macrostylidae	BS	DISCOL	37	X	
MacrDi09	DSB_1291	*Macrostylis*	sp. 03	M02	BOLD:ADL3134	50356	SMF 54164	Macrostylidae	BS	DISCOL	117	X	
MacrDi06	DSB_1310	*Macrostylis*	sp. 04	M00	BOLD:ADL9487	50375	SMF 54161	Macrostylidae	BS	DISCOL	85	X	
MacrDi07	DSB_1311	*Macrostylis*	sp. 03	M02	BOLD:ADL4636	50376	SMF 54162	Macrostylidae	BS	DISCOL	85	X	
MacrDi08	DSB_1312	*Macrostylis*	sp. 03	M02	BOLD:ADL4636	50377	SMF 54163	Macrostylidae	BS	DISCOL	81	X	
MacrJP001	DSB_1668	*Macrostylis*	sp. M cf. *metallicola*	M05	BOLD:ADG1797	50733	SMF 54165	Macrostylidae	BS	GC	20	X	X
MacrJP002	DSB_1669	*Macrostylis*	sp. M cf. *metallicola*	M05	BOLD:ADG1797	50734	SMF 54166	Macrostylidae	BS	GC	20	X	X
MacrJP003	DSB_1670	*Macrostylis*	sp. M cf. *metallicola*	M05	BOLD:ADG1798	50735	SMF 54167	Macrostylidae	BS	GC	20	X	X
MacrJP004	DSB_1671	*Macrostylis*	sp. M cf. *metallicola*	M05	BOLD:ADG1798	50736	SMF 54168	Macrostylidae	BS	GC	20	X	X
MacrJP005	DSB_1672	*Macrostylis*	sp. # 1	M01	BOLD:ADL4493	50737	SMF 54169	Macrostylidae	BS	GC	20	X	
MacrJP006	DSB_1673	*Macrostylis*	sp. M cf. *metallicola*	M05	BOLD:ADG1798	50738	SMF 54170	Macrostylidae	BS	GC	20	X	X
MacrJP007	DSB_1674	*Macrostylis*	sp. M cf. *metallicola*	M05	BOLD:ADG1798	50739	SMF 54171	Macrostylidae	BS	GC	20	X	X
MacrJP008	DSB_1675	*Macrostylis*	sp. M cf. *metallicola*	M05	BOLD:ADG1798	50740	SMF 54172	Macrostylidae	BS	GC	20	X	X
MacrJP009	DSB_1676	*Macrostylis*	sp. M cf. *metallicola*	M05	BOLD:ADL3953	50741	SMF 54173	Macrostylidae	BS	GC	20	X	X
MacrJP010	DSB_1677	*Macrostylis*	sp. M cf. *metallicola*	M01			SMF 54174	Macrostylidae	BS	GC	20		X
MacrJP011	DSB_1678	*Macrostylis*	sp. M cf. *metallicola*	M05	BOLD:ADG1797	50743	SMF 54175	Macrostylidae	BS	GC	20	X	X
MacrJP012	DSB_1679	*Macrostylis*	sp. M cf. *metallicola*	M05	BOLD:ADG1798	50744	SMF 54176	Macrostylidae	BS	GC	24	X	X
MacrJP013	DSB_1680	*Macrostylis*	sp. M cf. *metallicola*	M05	BOLD:ADL2993	50745	SMF 54177	Macrostylidae	BS	GC	24	X	X
MacrJP014	DSB_1681	*Macrostylis*	sp. M cf. *metallicola*	M05	BOLD:ADL4161	50746	SMF 54178	Macrostylidae	BS	GC	24	X	X
MacrJP015	DSB_1682	*Macrostylis*	sp. M cf. *metallicola*	M05	BOLD:ADG1797	50747	SMF 54179	Macrostylidae	BS	GC	24	X	X
MacrJP016	DSB_1683	*Macrostylis*	cf. sp. # 1	M01	BOLD:ADL4493	50748	SMF 54180	Macrostylidae	BS	GC	24	X	

MacrJP017	DSB_1684	*Macrostylis*	sp. # 1	M01	BOLD:ADL4493	50749	SMF 54181	Macrostylidae	BS	GC	24	X	
MacrJP018	DSB_1685	*Macrostylis*	sp. M cf. *metallicola*	M05	BOLD:ADG1798	50750	SMF 54182	Macrostylidae	BS	GC	24	X	X
MacrJP019	DSB_1686	*Macrostylis*	sp. M cf. *metallicola*	M05	BOLD:ADG1797	50751	SMF 54183	Macrostylidae	BS	GC	24	X	X
MacrJP020	DSB_1687	*Macrostylis*	sp. M cf. *metallicola*	M05	BOLD:ADL2993	50752	SMF 54184	Macrostylidae	BS	GC	59	X	X
MacrJP021	DSB_1688	*Macrostylis*	sp. M cf. *metallicola*	M05	BOLD:ADL2993	50753	SMF 54185	Macrostylidae	BS	GC	59	X	X
MacrJP022	DSB_1689	*Macrostylis*	sp. M cf. *metallicola*	M05	BOLD:ADL2993	50754	SMF 54186	Macrostylidae	BS	GC	59	X	X
MacrJP023	DSB_1690	*Macrostylis*	sp. M cf. *metallicola*	M05	BOLD:ADL4161	50755	SMF 54187	Macrostylidae	BS	GC	59	X	X
MacrJP024	DSB_1691	*Macrostylis*	sp. M cf. *metallicola*	M05	BOLD:ADL2993	50756	SMF 54188	Macrostylidae	BS	GC	59	X	X
MacrJP025	DSB_1692	*Macrostylis*	sp. M cf. *metallicola*	M05	BOLD:ADL2993	50757	SMF 54189	Macrostylidae	BS	GC	59	X	X
MacrJP026	DSB_1693	*Macrostylis*	sp. M cf. *metallicola*	M06	BOLD:ADL4496	50758	SMF 54190	Macrostylidae	BS	GC	50	X	X
MacrJP027	DSB_1694	*Macrostylis*	sp. M cf. *metallicola*	M06	BOLD:ADL4496	50759	SMF 54191	Macrostylidae	BS	GC	50	X	X
MacrJP028	DSB_1695	*Macrostylis*	sp. M cf. *metallicola*	M06	BOLD:ADL4496	50760	SMF 54192	Macrostylidae	BS	GC	50	X	X
MacrJP029	DSB_1696	*Macrostylis*	sp. M cf. *metallicola*	M05	BOLD:ADL2993	50761	SMF 54193	Macrostylidae	BS	GC	50	X	X
MacrJP030	DSB_1697	*Macrostylis*	sp. M cf. *metallicola*	M06	BOLD:ADL4496	50762	SMF 54194	Macrostylidae	BS	GC	50	X	X
MacrJP031	DSB_1698	*Macrostylis*	sp. M cf. *metallicola*	M06	BOLD:ADL4496	50763	SMF 54195	Macrostylidae	BS	GC	50	X	X
MacrJP032	DSB_1699	*Macrostylis*	sp. M cf. *metallicola*	M06	BOLD:ADL4496	50764	SMF 54196	Macrostylidae	BS	GC	50	X	X
MacrJP033	DSB_1700	*Macrostylis*	sp. M cf. *metallicola*	M06	BOLD:ADL4496	50765	SMF 54197	Macrostylidae	BS	GC	50	X	X
MacrJP034	DSB_1701	*Macrostylis*	sp. M cf. *metallicola*	M06	BOLD:ADL4496	50766	SMF 54198	Macrostylidae	BS	GC	50	X	X
MacrJP035	DSB_1702	*Macrostylis*	sp. M cf. *metallicola*	M05	BOLD:ADL2993	50767	SMF 54199	Macrostylidae	BS	IOM	81	X	X
MacrJP036	DSB_1703	*Macrostylis*	sp. M cf. *metallicola*	M05	BOLD:ADL4637	50768	SMF 54200	Macrostylidae	BS	IOM	81	X	X
MacrJP037	DSB_1704	*Macrostylis*	sp. M cf. *metallicola*	M05	BOLD:ADL2993	50769	SMF 54201	Macrostylidae	BS	IOM	81	X	X
MacrJP038	DSB_1705	*Macrostylis*	cf. sp. # 1	M01	BOLD:ADL4493	50770	SMF 54202	Macrostylidae	BS	IOM	81	X	
MacrJP039	DSB_1706	*Macrostylis*	sp. M cf. *metallicola*	M05	BOLD:ADL4637	50771	SMF 54203	Macrostylidae	BS	IOM	99	X	X
MacrJP040	DSB_1707	*Macrostylis*	sp. M cf. *metallicola*	M05	BOLD:ADL4637	50772	SMF 54204	Macrostylidae	BS	IOM	99	X	X
MacrJP041	DSB_1708	*Macrostylis*	sp. M cf. *metallicola*	M05		50773	SMF 54205	Macrostylidae	BS	IOM	99	X	X
MacrJP042	DSB_1709	*Macrostylis*	sp. M cf. *metallicola*	M05	BOLD:ADL4637	50774	SMF 54206	Macrostylidae	BS	IOM	99	X	X
MacrJP043	DSB_1710	*Macrostylis*	sp. M cf. *metallicola*	M05	BOLD:ADL4490	50775	SMF 54207	Macrostylidae	BS	BC	118	X	X
MacrJP044	DSB_1711	*Macrostylis*	sp. M cf. *metallicola*	M05	BOLD:ADL4490	50776	SMF 54208	Macrostylidae	BS	BC	118	X	X
MacrJP045	DSB_1712	*Macrostylis*	sp. M cf. *metallicola*	M05	BOLD:ADL4490	50777	SMF 54209	Macrostylidae	BS	BC	118	X	X
MacrJP046	DSB_1713	*Macrostylis*	sp. M cf. *metallicola*	M07	BOLD:ADL3132	50778	SMF 54210	Macrostylidae	BS	BC	118	X	X
MacrJP047	DSB_1714	*Macrostylis*	sp. M cf. *metallicola*	M07	BOLD:ADL3132	50779	SMF 54211	Macrostylidae	BS	BC	118	X	X
MacrJP048	DSB_1715	*Macrostylis*	sp. M cf. *metallicola*	M05	BOLD:ADL4490	50780	SMF 54212	Macrostylidae	BS	BC	133	X	X
MacrJP049	DSB_1716	*Macrostylis*	sp. M cf. *metallicola*	M05	BOLD:ADL4490	50781	SMF 54213	Macrostylidae	BS	BC	133	X	X
MacrJP050	DSB_1717	*Macrostylis*	sp. M cf. *metallicola*	M03	BOLD:ADL3133	50782	SMF 54214	Macrostylidae	BS	BC	133	X	
MacrJP052	DSB_1719	*Macrostylis*	sp. M cf. *metallicola*	M05	BOLD:ADL4490	50784	SMF 54215	Macrostylidae	BS	BC	133	X	X
MacrJP053	DSB_1720	*Macrostylis*	sp. M cf. *metallicola*	M03	BOLD:ADL3133	50785	SMF 54216	Macrostylidae	BS	BC	133	X	
MacrJP054	DSB_1721	*Macrostylis*	sp. M cf. *metallicola*	M03	BOLD:ADL3133	50786	SMF 54217	Macrostylidae	BS	BC	133	X	
MacrJP055	DSB_1722	*Macrostylis*	sp. M cf. *metallicola*	M03	BOLD:ADL9486	50787	SMF 54218	Macrostylidae	BS	FC	158	X	X
MacrJP057	DSB_1724	*Macrostylis*	sp. M cf. *metallicola*	M03	BOLD:ADL9675	50789	SMF 54219	Macrostylidae	BS	FC	171	X	X
MacrJP058	DSB_1725	*Macrostylis*	sp. M cf. *metallicola*	M05	BOLD:ADL4492	50790	SMF 54220	Macrostylidae	BS	FC	171	X	X
MacrJP059	DSB_1726	*Macrostylis*	sp. M cf. *metallicola*	M05	BOLD:ADL3135	50791	SMF 54221	Macrostylidae	BS	FC	171	X	X
MacrJP060	DSB_1727	*Macrostylis*	sp. M cf. *metallicola*	M03	BOLD:ADL9300	50792	SMF 54222	Macrostylidae	BS	FC	171	X	
MacrJP061	DSB_1728	*Macrostylis*	sp. M cf. *metallicola*	M03	BOLD:ADL9300	50793	SMF 54223	Macrostylidae	BS	FC	171	X	
MacrJP062	DSB_1729	*Macrostylis*	sp. M cf. *metallicola*	M03	BOLD:ADL9674	50794	SMF 54224	Macrostylidae	BS	FC	171	X	
MacrJP063	DSB_1730	*Macrostylis*	sp. M cf. *metallicola*	M05	BOLD:ADL3136	50795	SMF 54225	Macrostylidae	BS	FC	171	X	X
MacrJP064	DSB_1731	*Macrostylis*	sp. M cf. *metallicola*	M05	BOLD:ADL4492	50796	SMF 54226	Macrostylidae	BS	FC	171	X	X
MacrJP065	DSB_1732	*Macrostylis*	sp. M cf. *metallicola*	M05	BOLD:ADL4492	50797	SMF 54227	Macrostylidae	BS	FC	171	X	X
MacrJP066	DSB_1733	*Macrostylis*	sp. M cf. *metallicola*	M05	BOLD:ADL4492	50798	SMF 54228	Macrostylidae	BS	FC	171	X	X
MacrJP067	DSB_1734	*Macrostylis*	sp. M cf. *metallicola*	M03	BOLD:ADL9300	50799	SMF 54229	Macrostylidae	BS	FC	171	X	X
MacrJP068	DSB_1735	*Macrostylis*	sp. M cf. *metallicola*	M05	BOLD:ADL3135	50800	SMF 54230	Macrostylidae	BS	FC	171	X	X
MacrJP069	DSB_1736	*Macrostylis*	sp. M cf. *metallicola*	M05	BOLD:AAG9589	50801	SMF 54231	Macrostylidae	BS	FC	171	X	X
MacrJP070	DSB_1737	*Macrostylis*	sp. M cf. *metallicola*	M05	BOLD:ADL3135	50802	SMF 54232	Macrostylidae	BS	FC	171	X	X
MacrJP071	DSB_1738	*Macrostylis*	sp. M cf. *metallicola*	M05	BOLD:ADL4492	50803	SMF 54233	Macrostylidae	BS	FC	171	X	X
MacrJP072	DSB_1739	*Macrostylis*	sp. M cf. *metallicola*	M03	BOLD:ADL9675	50804	SMF 54234	Macrostylidae	BS	FC	171	X	
MacrJP073	DSB_1740	*Macrostylis*	sp. M cf. *metallicola*	M05	BOLD:ADL4492	50805	SMF 54235	Macrostylidae	BS	A3	192	X	X
MacrJP074	DSB_1741	*Macrostylis*	sp. # 2	M08	BOLD:ADL4491	50806	SMF 54236	Macrostylidae	BS	A3	210	X	X
MacrJP075	DSB_1742	*Macrostylis*	sp. M cf. *metallicola*	M04	BOLD:ADL4494	50807	SMF 54237	Macrostylidae	BS	A3	210	X	X
MacrJP076	DSB_1743	*Macrostylis*	sp. M cf. *metallicola*	M04	BOLD:ADL4494	50808	SMF 54238	Macrostylidae	BS	A3	197	X	X
MacrJP077	DSB_1744	*Macrostylis*	sp. M cf. *metallicola*	M04	BOLD:ADL4494	50809	SMF 54239	Macrostylidae	BS	A3	197	X	X
MacrJP078	DSB_1745	*Macrostylis*	sp. M cf. *metallicola*	M04	BOLD:ADL4494	50810	SMF 54240	Macrostylidae	BS	A3	197	X	X
MacrJP079	DSB_1746	*Macrostylis*	sp. M cf. *metallicola*	M04	BOLD:ADL4494	50811	SMF 54241	Macrostylidae	BS	A3	197	X	X
MacrJP080	DSB_1747	*Macrostylis*	sp. M cf. *metallicola*	M04	BOLD:ADL4494	50812	SMF 54242	Macrostylidae	BS	A3	197	X	X
MacrJP081	DSB_1748	*Macrostylis*	sp. M cf. *metallicola*	M04	BOLD:ADL4494	50813	SMF 54243	Macrostylidae	BS	A3	192	X	X
MacrJP082	DSB_1749	*Macrostylis*	sp. M cf. *metallicola*	M04	BOLD:ADL4494	50814	SMF 54244	Macrostylidae	BS	A3	192	X	X

https://doi.org/10.5194/bg-2019-358
Preprint. Discussion started: 2 October 2019

MacrJP083	DSB_1750	*Macrostylis*	sp. # 2	M08	BOLD:ADL4497	50815	SMF 54245	Macrostylidae	BS	A3	192	X	X
MacrJP084	DSB_1751	*Macrostylis*	sp. # 2	M08	BOLD:ADL4497	50816	SMF 54246	Macrostylidae	BS	A3	192		X
MacrJP085	DSB_1752	*Macrostylis*	sp. # 2	M08	BOLD:ADL4491	50817	SMF 54247	Macrostylidae	BS	A3	192	X	X
MacrJP086	DSB_1753	*Macrostylis*	sp. # 2	M08	BOLD:ADL4491	50818	SMF 54248	Macrostylidae	BS	A3	192	X	
MacrJP087	DSB_1754	*Macrostylis*	sp. # 2	M08	BOLD:ADL4491	50819	SMF 54249	Macrostylidae	BS	A3	192	X	X
MacrJP088	DSB_1755	*Macrostylis*	sp. # 2	M08	BOLD:ADL4491	50820	SMF 54250	Macrostylidae	BS	A3	192	X	X
MacrJP089	DSB_1756	*Macrostylis*	sp. M cf. *metallicola*	M04	BOLD:ADL4494	50821	SMF 54251	Macrostylidae	BS	A3	192	X	X
MacrJP090	DSB_1757	*Macrostylis*	sp. M cf. *metallicola*	M04	BOLD:ADL4494	50822	SMF 54252	Macrostylidae	BS	A3	192	X	
MacrJP091	DSB_1758	*Macrostylis*	sp. # 2	M08	BOLD:ADL4495	50823	SMF 54253	Macrostylidae	BS	A3	192	X	X
MunpDi02	DSB_1203	*Eurycope*	sp. 05	Mu28	BOLD:ADL4531	50266	SMF 54254	Munnopsidae	S	DISCOL	37	X	X
MunpDi03	DSB_1204	*Betamorpha*	sp. 01	Mu20	BOLD:ADM1455	50267	SMF 54255	Munnopsidae	S	DISCOL	37	X	X
MunpDi05	DSB_1220	*Eurycope*	sp. 05	Mu28	BOLD:ADL4531	50283	SMF 54256	Munnopsidae	S	DISCOL	81	X	X
MunpDi08	DSB_1223	*Eurycope*	sp. 05	Mu29	BOLD:ADL4916	50286	SMF 54259	Munnopsidae	S	DISCOL	85	X	X
MunpDi09	DSB_1224	*Munneurycope*	sp. 01	Mu80	BOLD:ADL4913	50287	SMF 54260	Munnopsidae	S	DISCOL	85	X	X
MunpDi06	DSB_1225	*Eurycope*	sp. 05	Mu28	BOLD:ADL4531	50288	SMF 54257	Munnopsidae	S	DISCOL	81	X	X
MunpDi07	DSB_1229	*Betamorpha*	sp. 02	Mu45	BOLD:ADL3690	50294	SMF 54258	Munnopsidae	S	DISCOL	81	X	
MunpDi12	DSB_1230	*Betamorpha*	sp. 02	Mu45	BOLD:ADL3690	50295	SMF 54261	Munnopsidae	S	DISCOL	85	X	
MunpDi13	DSB_1231	*Stortyngura*	*parka*	Mu62	BOLD:ADL3683	50296	SMF 54262	Munnopsidae	S	DISCOL	93	X	
MunpDi15	DSB_1233	*Disconectes*	sp. 01	Mu02	BOLD:ADL3686	50298	SMF 54263	Munnopsidae	S	DISCOL	93	X	
MunpDi16	DSB_1234	*Rectisura*	sp. 01	Mu57	BOLD:ADL3689	50299	SMF 54264	Munnopsidae	S	DISCOL	93	X	
MunpDi20	DSB_1238	*Munneurycope*	sp. 03	Mu63	BOLD:ADL5073	50303	SMF 54265	Munnopsidae	S	DISCOL	93	X	X
MunpDi21	DSB_1239	*Disconectes*	sp. 01	Mu07	BOLD:ADL4533	50304	SMF 54266	Munnopsidae	S	DISCOL	93	X	X
MunpDi22	DSB_1240	*Eurycope*	sp. 05	Mu37	BOLD:ADL5069	50305	SMF 54267	Munnopsidae	S	DISCOL	93	X	X
MunpDi23	DSB_1241	*Munneurycope sp 6*	sp. 01	Mu48	BOLD:ADL4419	50306	SMF 54268	Munnopsidae	S	DISCOL	93	X	X
MunpDi24	DSB_1242	*Eurycope*	sp. 05	Mu27	BOLD:ADL5075	50307	SMF 54269	Munnopsidae	S	DISCOL	93	X	X
MunpDi26	DSB_1244	*Disconectes*	sp. 02	Mu76		50309	SMF 54270	Munnopsidae	S	DISCOL	93		X
MunpDi27	DSB_1245	*Disconectes*	sp. 02	Mu72	BOLD:ADL5096	50310	SMF 54271	Munnopsidae	S	DISCOL	93	X	X
MunpDi28	DSB_1246	*Munneurycope*	sp. 01	Mu63	BOLD:ADL5073	50311	SMF 54272	Munnopsidae	S	DISCOL	93	X	X
MunpDi29	DSB_1247	*Stortyngura*	*parka*	Mu62	BOLD:ADL3683	50312	SMF 54273	Munnopsidae	S	DISCOL	93	X	
MunpDi30	DSB_1248	*Disconectes*	sp. 02	Mu72	BOLD:ADL5096	50313	SMF 54274	Munnopsidae	S	DISCOL	93	X	X
MunpDi31	DSB_1249	*Paralipomera*	sp. 01	Mu84	BOLD:ADL9556	50314	SMF 54275	Munnopsidae	S	DISCOL	93	X	X
MunpDi32	DSB_1250	*Disconectes*	sp. 02a	Mu72	BOLD:ADL5096	50315	SMF 54276	Munnopsidae	S	DISCOL	93	X	X
MunpDi33	DSB_1253	*Eurycope*	sp.	Mu37	BOLD:ADL4914	50318	SMF 54277	Munnopsidae	S	DISCOL	85	X	X
MunpDi36	DSB_1256	*Disconectes*	sp. 01	Mu07		50321	SMF 54278	Munnopsidae	S	DISCOL	93		X
MunpDi37	DSB_1257	*Paralipomera*	sp. 01	Mu84	BOLD:ADL9556	50322	SMF 54279	Munnopsidae	S	DISCOL	93	X	X
MunpDi38	DSB_1258	*Munneurycope*	sp. 03	Mu80	BOLD:ADL4913	50323	SMF 54280	Munnopsidae	S	DISCOL	93	X	X
MunpDi41	DSB_1259	*Disconectes*	sp. 02	Mu72	BOLD:ADL5096	50324	SMF 54281	Munnopsidae	S	DISCOL	117	X	X
MunpDi43	DSB_1261	*Eurycope*	sp. 01	Mu37	BOLD:ADL4914	50326	SMF 54282	Munnopsidae	S	DISCOL	122	X	X
MunpDi45	DSB_1263	*Disconectes*	sp. 01	Mu02	BOLD:ADL3686	50328	SMF 54283	Munnopsidae	S	DISCOL	122	X	
MunpDi46	DSB_1264	*Disconectes*	sp. 01	Mu07	BOLD:ADL4533	50329	SMF 54284	Munnopsidae	S	DISCOL	122	X	X
MunpDi47	DSB_1265	*Munneurycope*	sp. 03	Mu63	BOLD:ADL3688	50330	SMF 54285	Munnopsidae	S	DISCOL	122	X	X
MunpDi49	DSB_1267	*Disconectes*	sp. 01	Mu75	BOLD:ADL4918	50332	SMF 54286	Munnopsidae	S	DISCOL	122	X	X
MunpDi50	DSB_1268	*Disconectes*	sp. 01	Mu07	BOLD:ADL4533	50333	SMF 54287	Munnopsidae	S	DISCOL	122	X	X
MunpDi51	DSB_1269	*Munneurycope*	sp.	Mu63	BOLD:ADL5073	50334	SMF 54288	Munnopsidae	S	DISCOL	122	X	X
MunpDi53	DSB_1271	*Rectisura*	sp. 02	Mu57	BOLD:ADL3687	50336	SMF 54289	Munnopsidae	S	DISCOL	122	X	
MunpDi54	DSB_1272	*Disconectes*	sp. 02	Mu72	BOLD:ADL3684	50337	SMF 54290	Munnopsidae	S	DISCOL	117	X	X
MunpDi55	DSB_1273	*Betamorpha*	sp. 02	Mu45	BOLD:ADL3690	50338	SMF 54291	Munnopsidae	S	DISCOL	122	X	
MunpDi56	DSB_1274	*Disconectes*	sp. 01	Mu02	BOLD:ADL3686	50339	SMF 54292	Munnopsidae	S	DISCOL	122	X	
MunpDi57	DSB_1275	*Disconectes*	sp. 02	Mu72	BOLD:ADL5096	50340	SMF 54293	Munnopsidae	S	DISCOL	122	X	X
MunpDi60	DSB_1278	*Betamorpha*	sp. 01	Mu20	BOLD:ADM1455	50343	SMF 54294	Munnopsidae	S	DISCOL	126	X	
MunpDi62	DSB_1280	*Munnopsis*	*abyssalis* /sp. 01	Mu39	BOLD:ADL3685	50345	SMF 54295	Munnopsidae	S	DISCOL	126	X	X
MunpDi63	DSB_1281	*Betamorpha*	sp. 01	Mu45	BOLD:ADL3690	50346	SMF 54296	Munnopsidae	S	DISCOL	126	X	
MunpDi64	DSB_1282	*Paramunnopsis*	sp. 01	Mu38	BOLD:ADL3456	50347	SMF 54297	Munnopsidae	S	DISCOL	126	X	X
MunpDi65	DSB_1283	*Disconectes*	sp. 03	Mu01		50348	SMF 54298	Munnopsidae	S	DISCOL	126		X
MunpDi66	DSB_1284	*Paralipomera*	sp. 01	Mu84	BOLD:ADL9556	50349	SMF 54299	Munnopsidae	S	DISCOL	126	X	X
MunpJP001	DSB_1386		sp. 1	Mu11	BOLD:ADL4575	50451	SMF 54300	Munnopsidae	S	GC	50	X	
MunpJP002	DSB_1387		sp. 1	Mu11	BOLD:ADL4593	50452	SMF 54301	Munnopsidae	S	GC	50	X	
MunpJP003	DSB_1388	*Disconectes*	sp. 1	Mu08	BOLD:ADL3511	50453	SMF 54302	Munnopsidae	S	GC	50	X	X
MunpJP004	DSB_1389	*Eurycope*	sp. 5	Mu26	BOLD:ADL4378	50454	SMF 54303	Munnopsidae	S	GC	50	X	X
MunpJP005	DSB_1390	*Disconectes*	sp. 1	Mu11	BOLD:ADL4575	50455	SMF 54304	Munnopsidae	S	GC	50	X	X
MunpJP006	DSB_1391	*Disconectes*	sp. 1	Mu11	BOLD:ADL4575	50456	SMF 54305	Munnopsidae	S	GC	50	X	X
MunpJP008	DSB_1393	*Disconectes*	sp. 1	Mu11	BOLD:ADL4593	50458	SMF 54306	Munnopsidae	S	GC	50	X	
MunpJP009	DSB_1394	*Disconectes*	sp. 3	Mu11	BOLD:ADL4379	50459	SMF 54307	Munnopsidae	S	GC	50	X	X
MunpJP010	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
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	
MunpJP039	DSB_1423	*Eurycope*	sp. 5	Mu37	BOLD:ADL3657	50488	SMF 54332	Munnopsidae	S	GC	20	X	X
MunpJP041	DSB_1425	*Betamorpha*	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	
MunpJP044	DSB_1428	*Munneurycope*	indet	Mu81	BOLD:ADL4576	50493	SMF 54336	Munnopsidae	S	GC	20	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	
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		50501	SMF 54341	Munnopsidae	S	GC	20		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:ADM0298	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. *galatheae*	Mu56	BOLD:ADL4687	50510	SMF 54349	Munnopsidae	S	A3	192	X	X
MunpJP062	DSB_1446	*Acanthocope*	cf. *galatheae*	Mu56	BOLD:ADL4977	50511	SMF 54350	Munnopsidae	S	A3	192	X	X
MunpJP063	DSB_1447	*Acanthocope*	cf. *galatheae*	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	
MunpJP067	DSB_1451	*Betamorpha*	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	*Betamorpha*	*fusiformis*	Mu47	BOLD:ADL4073	50519	SMF 54358	Munnopsidae	S	A3	197	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	*Betamorpha*	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	*Betamorpha*	sp. 2	Mu40	BOLD:ADL4072	50533	SMF 54372	Munnopsidae	S	FC	171	X	

MunpJP085	DSB_1469	*Eurycope*	sp. 2	Mu18	BOLD:ADL4333	50534	SMF 54373	Munnopsidae	S	FC	171	X	X
MunpJP086	DSB_1470	*Eurycope*	sp. 5	Mu37	BOLD:ADL3753	50535	SMF 54374	Munnopsidae	S	IOM	99	X	X
MunpJP088	DSB_1472	*Betamorpha*	sp.	Mu46	BOLD:ADL4080	50537	SMF 54375	Munnopsidae	S	IOM	99	X	
MunpJP089	DSB_1473	*Disconectes*	sp. 1	Mu04	BOLD:ADL4015	50538	SMF 54376	Munnopsidae	S	FC	158	X	X
MunpJP090	DSB_1474	*Aspidarachna*	indet	Mu53	BOLD:ADL5239	50539	SMF 54377	Munnopsidae	S	FC	158	X	X
MunpJP091	DSB_1475	*Disconectes*	sp. 3	Mu01	BOLD:ADL4465	50540	SMF 54378	Munnopsidae	S	FC	158	X	X
MunpJP092	DSB_1476	*Munneurycope*	gen. nov sp. 3	Mu48	BOLD:ADL4079	50541	SMF 54379	Munnopsidae	S	FC	158	X	X
MunpJP093	DSB_1477	*Eurycope*	sp. 5	Mu29	BOLD:ADL3751	50542	SMF 54380	Munnopsidae	S	GC	20	X	X
MunpJP094	DSB_1478	*Eurycope*	sp. 5	Mu32	BOLD:ADL4077	50543	SMF 54381	Munnopsidae	S	GC	20	X	
MunpJP095	DSB_1479	*Acanthocope*	cf. *galatheae*	Mu56	BOLD:ADL4687	50544	SMF 54382	Munnopsidae	S	A3	197	X	X
MunpJP096	DSB_1480	*Munneurycope*	indet	Mu67	BOLD:ADL2777	50545	SMF 54383	Munnopsidae	S	GC	24	X	X
MunpJP097	DSB_1481	*Munneurycope*	indet	Mu67	BOLD:ADL2777	50546	SMF 54384	Munnopsidae	S	GC	24	X	X
MunpJP098	DSB_1482	*Munneurycope*	indet	Mu67	BOLD:ADL2777	50547	SMF 54385	Munnopsidae	S	GC	24	X	X
MunpJP099	DSB_1483	*Eurycope*	sp. 5	Mu37	BOLD:ADL3657	50548	SMF 54386	Munnopsidae	S	GC	24	X	X
MunpJP100	DSB_1484	*Eurycope*	sp. 5	Mu32	BOLD:ADL4077	50549	SMF 54387	Munnopsidae	S	GC	24	X	X
MunpJP101	DSB_1485	*Eurycope*	sp. 5	Mu25	BOLD:ADG1444	50550	SMF 54388	Munnopsidae	S	GC	24	X	X
MunpJP104	DSB_1488	*Pirinectes*	gen. nov	Mu77	BOLD:ADL5270	50553	SMF 54389	Munnopsidae	S	GC	24	X	X
MunpJP105	DSB_1489	*Pirinectes*	gen. nov	Mu77	BOLD:ADL5270	50554	SMF 54390	Munnopsidae	S	GC	24	X	X
MunpJP106	DSB_1490	*Rectisura*	*slavai*	Mu60		50555	SMF 54391	Munnopsidae	S	GC	24		X
MunpJP107	DSB_1491	*Disconectes*	sp. 1	Mu08		50556	SMF 54392	Munnopsidae	S	GC	24		X
MunpJP109	DSB_1493	*Eurycope*	sp. 5	Mu32	BOLD:ADL4077	50558	SMF 54393	Munnopsidae	S	GC	24	X	X
MunpJP110	DSB_1494	*Munneurycope*	indet	Mu81	BOLD:ADL4576	50559	SMF 54394	Munnopsidae	S	GC	24	X	
MunpJP111	DSB_1495	*Rectisura*	*slavai*	Mu60	BOLD:ADL4976	50560	SMF 54395	Munnopsidae	S	GC	24	X	X
MunpJP112	DSB_1496	*Munneurycope*	indet	Mu81	BOLD:ADL4576	50561	SMF 54396	Munnopsidae	S	GC	24	X	X
MunpJP113	DSB_1497	*Betamorpha*	sp.	Mu70	BOLD:ADL4078	50562	SMF 54397	Munnopsidae	S	GC	24	X	X
MunpJP114	DSB_1498	*Syneurycope*	sp.	Mu85		50563	SMF 54398	Munnopsidae	S	FC	171	X	X
MunpJP115	DSB_1499	*Syneurycope*	sp. 1	Mu85		50564	SMF 54399	Munnopsidae	S	FC	171	X	X
MunpJP116	DSB_1500	*Syneurycope*	sp. 1	Mu85		50565	SMF 54400	Munnopsidae	S	FC	171	X	X
MunpJP117	DSB_1501	*Betamorpha*	sp. 1	Mu42	BOLD:ADL3458	50566	SMF 54401	Munnopsidae	S	FC	171	X	
MunpJP119	DSB_1503	*Pirinectes*	gen. nov	Mu78	BOLD:ADL5438	50568	SMF 54402	Munnopsidae	S	FC	171	X	X
MunpJP120	DSB_1504	*Eurycope*	sp. 1	Mu37	BOLD:ADL2918	50569	SMF 54403	Munnopsidae	S	FC	171	X	X
MunpJP121	DSB_1505	*Syneurycope*	indet	Mu85		50570	SMF 54404	Munnopsidae	S	FC	171	X	X
MunpJP122	DSB_1506	*Eurycope*	sp. 1	Mu18	BOLD:ADL4333	50571	SMF 54405	Munnopsidae	S	FC	171	X	X
MunpJP124	DSB_1508	*Eurycope*	sp. 5	Mu24	BOLD:ADL3752	50573	SMF 54406	Munnopsidae	S	FC	171	X	X
MunpJP125	DSB_1509	*Eurycope*	sp. 1	Mu18	BOLD:ADL4333	50574	SMF 54407	Munnopsidae	S	FC	171	X	X
MunpJP126	DSB_1510	*Eurycope*	sp. 1	Mu18	BOLD:ADL4333	50575	SMF 54408	Munnopsidae	S	FC	171	X	X
MunpJP128	DSB_1512	*Eurycope*	sp. 5	Mu21	BOLD:ADL2775	50577	SMF 54409	Munnopsidae	S	FC	171	X	X
MunpJP129	DSB_1513	*Eurycope*	sp. 2	Mu19	BOLD:ADL4334	50578	SMF 54410	Munnopsidae	S	FC	171	X	X
MunpJP130	DSB_1514	*Ilyarachna*	indet	Mu54	BOLD:ADL5631	50579	SMF 54411	Munnopsidae	S	FC	171	X	X
MunpJP131	DSB_1515	*Disconectes*	sp. 1	Mu03	BOLD:ADL5437	50580	SMF 54412	Munnopsidae	S	FC	171	X	X
MunpJP133	DSB_1517	*Eurycope*	sp. 2	Mu18	BOLD:ADL4333	50582	SMF 54413	Munnopsidae	S	FC	171	X	X
MunpJP134	DSB_1518	*Microcope*	sp.	Mu83	BOLD:ADL5442	50583	SMF 54414	Munnopsidae	S	FC	171	X	X
MunpJP135	DSB_1519	*Microcope*	sp.	Mu83	BOLD:ADL5442	50584	SMF 54415	Munnopsidae	S	FC	171	X	X
MunpJP136	DSB_1520	*Syneurycope*	sp.	Mu85	BOLD:ADM0298	50585	SMF 54416	Munnopsidae	S	FC	171	X	X
MunpJP137	DSB_1521	*Ilyarachna*	indet	Mu54	BOLD:ADL5631	50586	SMF 54417	Munnopsidae	S	FC	171	X	X
MunpJP138	DSB_1522	*Rectisura*	slavai	Mu60		50587	SMF 54418	Munnopsidae	S	IOM	81		X
MunpJP139	DSB_1523	*Disconectes*	sp. 3	Mu04	BOLD:ADL5441	50588	SMF 54419	Munnopsidae	S	IOM	81	X	
MunpJP140	DSB_1524	*Disconectes*	sp. 3	Mu05	BOLD:ADL5440	50589	SMF 54420	Munnopsidae	S	IOM	81	X	
MunpJP141	DSB_1525	*Disconectes*	sp. 1	Mu11	BOLD:ADL5439	50590	SMF 54421	Munnopsidae	S	IOM	81	X	X
MunpJP142	DSB_1526	*Eurycope*	indet	Mu15	BOLD:ADL2778	50591	SMF 54422	Munnopsidae	S	IOM	81	X	X
MunpJP143	DSB_1527	*Disconectes*	sp. 2	Mu74	BOLD:ADL5444	50592	SMF 54423	Munnopsidae	S	IOM	99	X	X
MunpJP144	DSB_1528	*Disconectes*	sp. 1	Mu12	BOLD:ADL5443	50593	SMF 54424	Munnopsidae	S	IOM	99	X	X
MunpJP145	DSB_1529	*Eurycope*	sp. 2	Mu22	BOLD:ADL9336	50594	SMF 54425	Munnopsidae	S	IOM	99	X	X
MunpJP146	DSB_1530	*Eurycope*	sp. 2	Mu23		50595	SMF 54426	Munnopsidae	S	IOM	99		X
MunpJP147	DSB_1531	*Tytthocope*	indet	Mu49	BOLD:ADL2887	50596	SMF 54427	Munnopsidae	S	IOM	99	X	
MunpJP148	DSB_1532	*Tytthocope*	indet	Mu49	BOLD:ADL2887	50597	SMF 54428	Munnopsidae	S	IOM	99	X	
MunpJP149	DSB_1533	*Disconectes*	sp. 1	Mu08	BOLD:ADL5271	50598	SMF 54429	Munnopsidae	S	IOM	99	X	X
MunpJP150	DSB_1534	*Eurycope*	sp. 5	Mu37		50599	SMF 54430	Munnopsidae	S	IOM	99		X
MunpJP153	DSB_1537	*Eurycope*	sp. 4	Mu15	BOLD:ADL2778	50602	SMF 54431	Munnopsidae	S	IOM	99	X	X
MunpJP154	DSB_1538	*Disconectes*	sp. 2	Mu71	BOLD:ADL5605	50603	SMF 54432	Munnopsidae	S	IOM	99		X
MunpJP155	DSB_1539	*Disconectes*	sp. 2	Mu74	BOLD:ADL5444	50604	SMF 54433	Munnopsidae	S	IOM	99	X	X
MunpJP156	DSB_1540	*Munneurycope*	sp.	Mu81	BOLD:ADL3749	50605	SMF 54434	Munnopsidae	S	BC	133	X	X
MunpJP157	DSB_1541	*Disconectes*	sp. 3	Mu04	BOLD:ADL5441	50606	SMF 54435	Munnopsidae	S	BC	133	X	X
MunpJP158	DSB_1542	*Eurycope*	sp.	Mu23		50607	SMF 54436	Munnopsidae	S	BC	133		X

https://doi.org/10.5194/bg-2019-358
Preprint. Discussion started: 2 October 2019

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

MunpJP236	DSB_1619	*Disconectes*	sp. 1	Mu09	BOLD:ADL5599	50684	SMF 54501	Munnopsidae	S	IOM	81	X	X
MunpJP237	DSB_1620	*Disconectes*	sp. 3	Mu05	BOLD:ADL5440	50685	SMF 54502	Munnopsidae	S	IOM	81	X	X
MunpJP238	DSB_1621	*Rectisura*	*slavai*	Mu60	BOLD:ADL4976	50686	SMF 54503	Munnopsidae	S	IOM	81	X	X
MunpJP239	DSB_1622	*Eurycope*	sp	Mu37	BOLD:ADL2921	50687	SMF 54504	Munnopsidae	S	IOM	81	X	X
MunpJP240	DSB_1623	*Rectisura*	*slavai*	Mu60	BOLD:ADL4976	50688	SMF 54505	Munnopsidae	S	IOM	81	X	X
MunpJP241	DSB_1624	*Paramunnopsis*	sp. 2	Mu39	BOLD:ADL3685	50689	SMF 54506	Munnopsidae	S	IOM	81	X	X
MunpJP242	DSB_1625	*Munneurycope*	indet	Mu68	BOLD:ADL4075	50690	SMF 54507	Munnopsidae	S	A3	210	X	X
MunpJP243	DSB_1626	*Betamorpha*	sp.	Mu69	BOLD:ADL4076	50691	SMF 54508	Munnopsidae	S	A3	210		X
MunpJP244	DSB_1627	*Betamorpha*	sp.	Mu69	BOLD:ADL4076	50692	SMF 54509	Munnopsidae	S	A3	210		X
MunpJP245	DSB_1628	*Disconectes*	sp. 1	Mu09	BOLD:ADL5600	50693	SMF 54510	Munnopsidae	S	A3	210	X	X
MunpJP246	DSB_1629	*Rectisura*	sp.	Mu61	BOLD:ADL3110	50694	SMF 54511	Munnopsidae	S	A3	210	X	X
MunpJP247	DSB_1630	*Bellibos*	sp. 1	Mu44	BOLD:ADL4771	50695	SMF 54512	Munnopsidae	S	A3	210	X	
MunpJP248	DSB_1631	*Rectisura*	*slavai*	Mu58	BOLD:ADL4772	50696	SMF 54513	Munnopsidae	S	A3	210	X	X
MunpJP249	DSB_1632	*Disconectes*	sp. 3	Mu06	BOLD:ADL5597	50697	SMF 54514	Munnopsidae	S	A3	210	X	X
MunpJP250	DSB_1633	*Disconectes*	sp. 3	Mu03	BOLD:ADL5598	50698	SMF 54515	Munnopsidae	S	A3	210	X	
MunpJP252	DSB_1635	*Bellibos*	sp. 1	Mu44	BOLD:ADL4771	50700	SMF 54516	Munnopsidae	S	A3	210	X	
MunpJP253	DSB_1636	*Munneurycope*	sp.	Mu68	BOLD:ADL4075	50701	SMF 54517	Munnopsidae	S	A3	210	X	X
MunpJP254	DSB_1637	*Disconectes*	sp. 3	Mu03	BOLD:ADL5598	50702	SMF 54518	Munnopsidae	S	A3	210	X	X
MunpJP256	DSB_1639	*Eurycope*	sp. 5	Mu30	BOLD:ADL4756	50704	SMF 54519	Munnopsidae	S	A3	210	X	
MunpJP257	DSB_1640	*Eurycope*	sp. 5	Mu33	BOLD:ADL2967	50705	SMF 54520	Munnopsidae	S	A3	210	X	
MunpJP258	DSB_1641	*Eurycope*	sp. 5	Mu33	BOLD:ADL2967	50706	SMF 54521	Munnopsidae	S	A3	210	X	X
MunpJP259	DSB_1642	*Eurycope*	sp. 5	Mu33	BOLD:ADL2967	50707	SMF 54522	Munnopsidae	S	A3	210	X	X
MunpJP260	DSB_1643	*Ilyarachna*	indet	Mu55	BOLD:ADL2886	50708	SMF 54523	Munnopsidae	S	A3	197	X	X
MunpJP261	DSB_1644	*Rectisura*	*slavai*	Mu58	BOLD:ADL4772	50709	SMF 54524	Munnopsidae	S	A3	197	X	X
MunpJP262	DSB_1645	*Disconectes*	sp. 3	Mu01		50710	SMF 54525	Munnopsidae	S	A3	197		X
MunpJP263	DSB_1646	*Rectisura*	*slavai*	Mu58	BOLD:ADL4772	50711	SMF 54526	Munnopsidae	S	A3	197	X	X
MunpJP264	DSB_1647	*Eurycope*	sp. 5	Mu31	BOLD:ADL2968	50712	SMF 54527	Munnopsidae	S	A3	197	X	X
MunpJP265	DSB_1648	*Munneurycope*	indet	Mu65	BOLD:ADL4773	50713	SMF 54528	Munnopsidae	S	A3	197	X	X
MunpJP266	DSB_1649	*Acanthocope*	cf. *galatheae*	Mu56	BOLD:ADL4687	50714	SMF 54529	Munnopsidae	S	A3	197	X	X
MunpJP267	DSB_1650	*Acanthocope*	cf. *galatheae*	Mu56	BOLD:ADL4687	50715	SMF 54530	Munnopsidae	S	A3	197	X	X
MunpJP268	DSB_1651	*Betamorpha*	indet	Mu41	BOLD:ADL5566	50716	SMF 54531	Munnopsidae	S	A3	197	X	X
MunpJP269	DSB_1652	*Disconectes*	sp. 3	Mu03	BOLD:ADL2644	50717	SMF 54532	Munnopsidae	S	A3	197	X	
MunpJP270	DSB_1653	*Munneurycope*	indet	Mu66	BOLD:ADL4774	50718	SMF 54533	Munnopsidae	S	A3	197	X	X
MunpJP272	DSB_1655	*Eurycope*	sp. 5	Mu33	BOLD:ADL2967	50720	SMF 54534	Munnopsidae	S	A3	197	X	X
MunpJP274	DSB_1657	*Acanthocope*	cf. *galatheae*	Mu56	BOLD:ADL4687	50722	SMF 54S35	Munnopsidae	S	A3	197	X	X
MunpJP276	DSB_1659	*Bellibos*	sp. 2	Mu43	BOLD:ADL3457	50724	SMF 54536	Munnopsidae	S	A3	192	X	X
MunpJP277	DSB_1660	*Betamorpha*	sp.	Mu69		50725	SMF 54537	Munnopsidae	S	A3	192		X
MunpJP278	DSB_1661	*Bellibos*	sp. 2	Mu43	BOLD:ADL3457	50726	SMF 54538	Munnopsidae	S	A3	192	X	X
MunpJP279	DSB_1662	*Disconectes*	sp. 3	Mu01	BOLD:ADL9613	50727	SMF 54539	Munnopsidae	S	A3	192	X	X
MunpJP280	DSB_1663	*Disconectes*	sp. 1	Mu09	BOLD:ADL2643	50728	SMF 54540	Munnopsidae	S	A3	192	X	X
MunpJP281	DSB_1664	*Microcope*	sp.	Mu82	BOLD:ADM0130	50729	SMF 54541	Munnopsidae	S	A3	192	X	X
MunpJP282	DSB_1665	*Munneurycope sp.6*	gen. nov sp. 1	Mu52	BOLD:ADL4064	50730	SMF 54542	Munnopsidae	S	A3	192	X	
MunpJP283	DSB_1666	*Munneurycope*	indet	Mu65	BOLD:ADL4773	50731	SMF 54543	Munnopsidae	S	A3	192	X	X
MunpJP284	DSB_1667	*Eurycope*	sp. 5	Mu36	BOLD:ADL2969	50732	SMF 54544	Munnopsidae	S	A3	192	X	X
MunpJP285	DSB_1761	*Munneurycope sp.6*	gen. nov sp. 1	Mu52	BOLD:ADL4064	50826	SMF 54545	Munnopsidae	S	A3	192	X	
MunpJP286	DSB_2011	*Eurycope*	sp	Mu68	BOLD:ADL2922	51076	SMF 54546	Munnopsidae	S	IOM	82	X	X
MunpJP288	DSB_2013	*Betamorpha*	cf. *fusiformis*	Mu69	BOLD:ADL4076	51078	SMF 54547	Munnopsidae	S	A3	210	X	X

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	0.007
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

Table 4 Beta-diversity decomposition of Isopod Families. N = number of specimens, S = number of Species. βSOR, βSIM and βSNE express multiple-site total beta diversity, multiple-site species turnover and multiple-site nestedness respectively. Columns ccz N, ccz S, ccz βSOR, ccz βSIM and ccz βSNE 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