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

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Abstract

~~Aim of our study is to gain a better knowledge about the isopod crustacean fauna of the abyssal Clarion Clipperton Fracture Zone (CCZ) located in the central Pacific Ocean. In total, we examined 22 EBS samples taken at 6 abyssal areas in the central pacific manganese nodule area (CCZ and DISCOL). The dataset comprised 619 specimens belonging to 187 species of four different isopod families: 91 species (48.6 % of total) belonging to Munnopsidae, 63 (33.6 %) to Desmosomatidae, 24 (12.8%) to Haploniscidae and 9 (4.8 %) to Macrostylidae. The total number of species found was relatively similar between sites ranging from 38 (German Contractor area) to 50 species (French contractor area). 68 species were represented by 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~~

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~~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.~~

With increasing pressures to extract minerals from the deep seabed, understanding the ecological and evolutionary processes that limit the spatial distribution of species is critical to assessing ecosystem resilience to mining impacts. The aim of our study is to gain a better knowledge about the abyssal isopod crustacean fauna of the central Pacific manganese nodule province (Clarion Clipperton Fracture Zone, CCZ). In total, we examined 22 epibenthic sledge (EBS) samples taken at five abyssal areas located in the central northern Pacific including four contracting areas and one Area of Particular Environmental Interest (APEI3). Additional samples come from the DISCOL Area situated in the Peru Basin, south-eastern Pacific. Using an integrative approach that combined morphological and genetic methods with species delimitation analyses (SD) we assessed patterns of species range size, diversity and community composition for four different isopod families (Munnopsidae Lilljeborg, 1864; Desmosomatidae Sars, 1897; Haploniscidae Hansen, 1916 and Macrostylidae Hansen, 1916) displaying different dispersal capacities as adults. Isopods are brooders, so their distribution and connectivity cannot be explained by larval dispersal, but rather by adult locomotion. In particular, our objectives were to 1) identify potential differences in the distributional ranges of isopod families relative to their locomotory potential, and to 2) evaluate the representativeness of the APEI for the preservation of regional biodiversity in the CCZ following mining disturbances. From 619 specimens, our SD analysis could distinguish 170 species, most of which were new to science (94.1%). We found that increased locomotory ability correlated with higher species diversity with nine species of Macrostylidae, 23 of Haploniscidae, 52 of Desmosomatidae and 86 of Munnopsidae. This is supported by family-level rarefaction analyses. As expected, we found the largest species ranges in the families with swimming abilities, with a maximum recorded species range of 5245 km and 4480 km in Munnopsidae and Desmosomatidae respectively. The less motile Haploniscidae and Macrostylidae had maximal species ranges of 1391 km and 1440 km respectively. Overall, rarefaction analyses indicated that species richness did not vary much between areas, but the real number of species was still not sufficiently sampled. This is also indicated by the large proportion of singletons (40.5%) found in this study. The contractor areas in the CCZ were more similar in species composition and had a higher proportion of shared species between each other than the closely located APEI3 and the distantly located DISCOL Area. In fact, the DISCOL Area, located in the Peru Basin had more species in common with the core CCZ areas than APEI3. In this regard, APEI3 does not appear to be representative to serve as a reservoir for the fauna of the investigated contractor areas, at least in isopods, as it has a different species composition. Certainly, more data from other APEIs, as well as preservation reference zones within contractor areas, are urgently needed in order to assess their potential as sources of re-colonization of impacted seabed.

1 Introduction

Spanning 60% of the Earth's surface, deep-sea areas (below 200 m water depth) ~~harbour~~harbor 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 the challenges to initial ~~endeavours~~endeavors 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~~a reality (Wedding et al. 2015~~; Jones et al. 2017~~).

The abyssal Clarion Clipperton Fracture Zone (CCZ, ~~Fig~~Figure. 1~~)~~), located in the tropical north-eastern Pacific is commercially the most important area ~~of proposed~~for prospecting 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).~~As part of their Environmental Management Plan (EMP), the International Seabed Authority (ISA) designated a network of nine of Areas of Particular Environmental Interest (APEIs) bordering the CCZ, where no mining takes place, to enable recovery of impacted populations and communities (Smith et al. 2008a; Wedding et al. 2013, 2015; Lodge et al. 2014). The prerequisite for these areas is that they are representative in terms of biodiversity and

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species composition and cover the entire spectrum of the habitat and community types available in the CCZ. However, data from APEIs, which have been very limited to date, bring into question their representativeness and suitability as a biodiversity reservoir (Vanreusel et al. 2016; Bonifacio et al. 2020; Christodoulou et al. 2020).

As mining will severely impact the communities along large swathes of the seafloor, recovery will only be possible through recolonization from surrounding areas. In order to make predictions on the recolonization potential of the deep-sea fauna, ~~an~~sound 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~~compared to species with ~~a limited dispersal capacity.~~narrower geographic ranges, which likely have an increased risk of local extinction following regional mining disturbance (Roberts & Hawkins 1999). In turn, this understanding ~~-~~would contribute to defining the ~~design~~extent and ~~establishment~~location 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~~

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~~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'~~adult lifestyle in determining the large-scale distribution of asellote isopods across the CCZ. ~~Asellote isopods~~Asellota of the superfamily Janiroidea are one of the most numerous and diverse crustacean taxon encountered within abyssal benthic samples (Brandt et al~~.,~~., 2007). With only 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).~~ 1992). For these reasons, they have been frequently used as model organisms to study patterns of species range size and diversity in the deep sea (Hessler and Wilson 1983; Rex et al. 1993; Brandt 1995; Wilson 1998; Stuart et al. 2003; Brandt et al. 2007, 2012; Kaiser et al. 2007; Janssen et al. 2015; Wilson et al. 2017; Brix et al. 2018, Jennings et al. 2019). Asellotes are principally detritivores and foraminiferivores, but different groups show different lifestyles.

In this study, we chose four families along a spectrum of adult locomotion abilities, the Munnopsidae Lilljeborg, 1864, the Desmosomatidae Sars, 1897, the Haploniscidae Hansen, 1916 and the Macrostylidae Hansen, 1916 (Figure 2).

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~~.~~ (Malyutina et al. 2020, Riehl et al. 2020). Some munnopsid species have moved towards a benthopelagic (e.g., in *Munnopsoides* Tattersall, 1905) or even holopelagic (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). In the Desmosomatidae~~ Sars 1897~~, usually referred to as an epifaunal family, swimming

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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~~are expected to have the least dispersal potential and thus the smallest distributional ranges ~~may be very limited. Their~~. However, their sexual dimorphism may allow males of some ~~species~~lineages to be more mobile on the suprabenthos compared to the females ~~however~~ (Harrison 1989; Hessler and Strömberg~~,~~ 1989; Riehl ~~&~~and 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 and faunistic dissimilarity 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~~may be ~~highly beneficial to~~useful in forecasting faunal recolonization potential following disturbance events and related environmental changes. ~~This information would be essential~~Such proxies become useful for defining operational units for conservation planning due to their high richness of, unfortunately, largely undescribed isopod species.

In the course of the *Joint Programming Initiative Healthy and Productive Seas and Oceans (JPI Oceans) pilot action "Ecological aspects of deep-sea mining"*, sampling was conducted during the SO239 and SO242 expeditions in 2015 to obtain samples from contractor areas in the CCZ andAPEI3as well as

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the DISCOL Area in the Peru basin. From these samples, the isopod fauna has been examined. The primary objective of this study is two-fold: first, to identify ~~the~~potential differences in distributional ranges of four different deep-sea janiroid families with varying lifestyles (Munnopsidae, Desmosomatidae, Haploniscidae, and Macrostylidae) ~~with varying lifestyles~~ and in order to determine if these can be used as a ~~proxy~~surrogates to estimate dispersal distances. Second, to gain knowledge of the diverse species composition and connectivity of the core CCZ contractor areas in contrast to a closely located APEI and a distantly located Mn-nodule area DISCOL.

2 Material and Methods

2.1 Sampling and sample preparation

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,~~ Area in the north-eastern and south-eastern Pacific respectively (Martinez Arbizu & Haeckel 2015; Figure 1). Within the CCZ, samples were collected from four different contacting areas~~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~~) and one APEI (APEI3 ~~(:~~ Area of Particular Environmental Interest number 3). Isopod specimens were collected with an epibenthic sledge (EBS) in the CCZ (SO239 cruise, 13 EBS deployments, Suppl. Table 1) and the Peru Basin (SO242-1 cruise, nine EBS deployments, Suppl. Table 1) from the RV *Sonne* in 2015. ~~) was sampled. The sediment samples~~

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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~~will be stored at the Center of Natural History, Hamburg (CeNak) or the crustacean collection Senckenberg, Frankfurt ~~(Table 1).~~after final species descriptions. Before being formally described, the isopod specimens are remaining in the DZMB storage. After DNA extraction, all isopod specimens were identified morphologically to species level using a LEICA MZ 12.5 stereomicroscope by SB, NB, and MM. All determinations were entered into the excel spreadsheet (~~table~~Suppl. Table 1) using this as baseline for creating maps in QGIS, as well as for statistical analysis.

2.2 Data storage and handling

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~~DISCOL - 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~~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.~~

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~~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.~~

2.3 Molecular Methods

We carried out a molecular analysis of two mitochondrial DNA markers (COI and 16S) backed up by morphological determinations, to delineate species in an integrative approach. Based on this species delimitation, we compared species richness and community composition of the different areas (APEI vs. contractor areas vs. DISCOL). 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~~single 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.

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*

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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.

2.4 Molecular species delimitation

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~~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~~same 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 the starting point. We ran ~~3~~three MCMC chains for each analysis and assessed chain convergence by checking average standard deviation of delimitation support values (ASDDSV) across the ~~3~~three 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 the number of supported clades being within

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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~~, thus singletons were removed from mPTP and retained for PTP and ABGD.

2.5 Isopod Communities and diversity analyses

Analysis of community similarity between areas and their diversity was performed in R using the 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~~two to ~~8~~eight deployments per sampling area, therefore the similarity between communities was done using relative abundance (Chord distance, see Legendre ~~&~~and Gallagher 2001) and ~~using~~ ‘presence-absence’ to explore faunistic differences. Ordination was done using nMDS. The community table (~~Appendix_supplement1~~Suppl. Table 2) 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 ~~&~~and 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~~based 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 ~~&~~and 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 ~~&~~and 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~~jackknife approach. Changes in turnover and

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nestedness are attributable to the area each time excluded from the analysis. UpSet Plots were done using R package UpSetR (Conway et al., 2017).

~~1.2~~3 Results

~~In total, we examined 22 EBS samples taken at six abyssal areas. The dataset comprised 619 specimens belonging to 168 putative species (~~

3.1 Species Delimitation

~~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~~Figures 3-6). As expected with fast evolving genes such as COI and 16S, good resolution ~~is~~was given at the tips of the tree and most recent relationships such as species and sometimes even generic level~~. However~~, 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.~~

It is notable that the percentage of species new to science was quite high, reaching 94.1% in our dataset. Of the ten described species, five were either described in the course of the JPIO sampling campaign or other CCZ and DISCOL collections (Malyutina & Wägele 2001; Malyutina 2011; Malyutina

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et al. 2020; Riehl & De Smet 2020). The remaining species, all belonging to the Munnopsidae, appear to have wide (pan-oceanic) distributions.

The congruent species delimitation resulted in 86 munnopsid species OTUs (Suppl. Table 1, Figure ~~2~~3). Putative species clade definition based on genetic data ~~suggests~~suggested there ~~is~~was 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.~~seven higher level clades. 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~~regions, 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~~52 desmosomatid species OTUs (Suppl. Table 1, Figure ~~3~~4). The genera *Chelator* Hessler, 1970 (6 spp.), ~~*Oecidibranchus*~~*Oecidiobranchus* Hessler, 1970 (1 sp.), *Mirabilicoxa* Hessler, 1970 (12 spp.), *Eugerdella* (~~kussakin~~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~~4).

The congruent species delimitation resulted in 23 haploniscid species OTUs (Suppl. Table 1, ~~Fig. 4).~~Figure 5), which are all new to science. 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~~nine macrostylid species in this mongeneric family (Suppl. Table 1, ~~Fig. 5~~Figure 6). 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~~Figure 6). Only two of these putative species clades can be easily distinguished from

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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~~nine 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~~Figure 6, 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.

3.2 Diversity Comparison by Family

The dataset comprised 619 specimens belonging to 170 putative genetic species (=OTUs) (Suppl. Table 1). Munnopsidae was represented in the whole dataset by 294 specimens (199 in CCZ) belonging to 86 species (71 in CCZ, 20 in DISCOL). Desmosomatidae was represented by 143 specimens (103 in CCZ) belonging to 52 species (42 in CCZ, 11 in DISCOL). Haploniscidae was represented by 88 specimens (53 in CCZ) belonging to 23 species (18 in CCZ, five in DISCOL). Macrostylidae was represented by 94 specimens (70 in CCZ) belonging to only nine species (seven in CCZ, two in DISCOL) (Table 3).

The rarefaction curves of the Munnopsidae and Desmosomatidiae showed no signs of saturation (Figure 7). This is supported by the Chao1, which predicted the expected number of Munnopsidae and Desmosomatidae species as 110 and 98 respectively (Table 3). In contrast, the curves of Haploniscidae and Macrostylidae approached saturation, a state also indicated by the predicted number of species by Chao1, which suggested that no additional (unseen) species of Haploniscidae and Macrostylidae were expected in the present dataset (Figure 7, Table 3).

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Total beta diversity (βSOR) and species turnover (βSIM) increased 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, Table 3). This pattern was not evident when comparing sites within the CCZ (Table 3). Macrostylidae had 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).

3.3 Community and Diversity ~~*comparison*~~Comparison by ~~*area*~~Area

~~The community table (supplement 1) shows the counts of each species by area. The diversity values are summarized in Table 2. A~~In total~~ of~~, we examined 22 ~~sites (~~EBS deployments~~) were sampled at 6~~ taken from six abyssal areas. Sampling effort was uneven between sampling sites, with most samples taken in the DISCOL area ~~in~~of 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 170 species ~~was~~were recorded in all ~~6~~six areas~~, while the~~. The most common species was ~~Macrostylidae~~ *Macrostylis*_M05 with 46 specimens ~~(~~and was present in all areas besides DISCOL~~).~~. Other species (see Appendix supplement 1) with ~~10~~ten or more specimens were the munnopsids: *Disconectes*_Mu11 (22 specimens), *Eurycope*_Mu37, *Disconectes*_Mu08 (both with 18 specimens), and *Munneurycope*_Mu67, the haploniscids: *Haploniscus*_H10 (13 specimens each) *Mastigoniscus*_H22 (with 12 specimens~~) and with 10 specimens~~), the desmosomatid, *Eugerdella*_D39, and the macrostylids: *Macrostylis*_M03 and *Macrostylis*_M04~~. The reminding~~ (with 10 specimens each). The remaining 177 species had less than ~~10 records~~ten specimens, 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). ~~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~~Pearson correlation 0.34, p=0.49), nor with number of sampling sites per area (~~pearson~~Pearson correlation -0.02, p=0.95). IOM ~~presented~~supported 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~~ %)~~% unique) and FC (~~Ifremer~~IFREMER; 34 species 68% unique). All other areas had less unique species. ~~%).~~ ~~All other areas had less unique species.~~ The

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extrapolated number of species present per area ranged between 49 (GC: BGR) and 80 (BC: GSR) according to Chao1, and between 53 (GC: BGR) and 80 (FC: ~~Ifremer~~IFREMER) according to ACE~~.~~ ~~Between~~ , which Chao1 and ACE predicted between 50% and 12% of the species remained unrecorded ~~as predicted by Chao1 and ACE.~~. Diversity values (Shannon, Simpson and Jaccard) ~~are~~were similarly high ~~at~~in all areas~~. Nevertheless, lowest~~, with the exception of low diversity values ~~were recorded at~~from the 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~~two thirds of the specimens (425) and ~~2/3~~two thirds of the species (117) recorded, instead of the half that would be expected. A total of 99 species (84% of all species) were found exclusively in the CCZ area. ~~. 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. Rarefaction analysis (Figure 8) shows that all areas are similar in terms of species richness with the lowest curve at BGR (slightly lower diversity) and the highest at IOM. No curves show signs of having reached an asymptote (Figure 8).

~~*CCZ areas show highest number of shared species*~~

Table ~~3~~2 shows the faunistic similarity between areas. The greatest number of shared species ~~are~~were between CCZ areas. For instance, GSR shares 16 species with each of BGR and IOM areas, and 11 species with IFREMER~~. While GSR shares~~, yet only ~~4~~four species with DISCOL and ~~2~~only two with APEI3~~.~~ (Table 2).

The highest number of non-shared species is present in APEI3 (19 species) followed by DISCOL (17 species) and IFREMER (16 species) areas (Figure 10). 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~~)~~, Table 2), although the t-test shows no significant difference between them (p=0.58). The lower panel of the upset plot depicts the connectivity network. Few species are shared between areas, 11 species were shared between two areas, seven species between three areas, three species between four areas and just one species is present in five areas. The least connected site is APEI3, sharing only four species with other

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areas, followed by DISCOL sharing five species. BGR and GSR were better connected, sharing 13 and 14 species with other areas respectively.

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

The Upset Plots (Figure 12) summarizes number of shared species between areas considering all taxa together as well as by taxa. The highest number of non-shared species is present in APEI3 (19 species) followed by DISCOL (17 species) and IFREMER (16 species) areas. The other CCZ contractor areas were more similar to each other having just eight or less non-shared species. The lower panel of the upset plot depicts the connectivity network. Only few species are shared between areas, 11 species are shared between two areas, seven species between three areas, three species between four areas and just one species is present in five areas. The less connected site is APEI3, sharing only three species with other areas, followed by DISCOL sharing five species. BGR and GSR area better connected sharing up to 14 species with other areas. Considering the Upset Plots by isopod family it becomes evident that there are less connections (shared species) between areas the less motile the family is, Munnopsidae and Desmosomatidae showing a diverse set of connections and Haploniscidae and Macrostylidae showing less connections (see below).

Total multi-site beta diversity was high (total βSOR 0.885, Table ~~2~~1), meaning that the overall 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.

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~~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~~Figure 9), 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~~Figure 10) 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 (Figure 11) 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. Remarkably, core CCZ (IFREMER, IOM, GSR, and BGR) and APEI3/DISCOL areas were more similar within than between despite APEI3 and CCZ being much closer to CCZ than to DISCOL.

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

~~The species abundance diversity greatly differs~~

3.4 Range Size

Connectivity between areas differed 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.~~

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~~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.~~, Figure 12). 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.~~

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~~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~~species of any family was present in all six ~~studies~~study areas~~. While~~, and only one munnopsid and one macrostylid species ~~belonging to Munnopsidae was~~were 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.~~ Table 4). In total 77% of the species were recorded just in a single area, 13.9% in ~~2~~two areas, 5.3% in three areas, ~~5.3% in 3 areas,~~ 2.6% in ~~4~~four areas and 1% in ~~5 areas.~~five areas. A total of six (66.6%) out of nine species of Macrostylidae were recorded in a single area. The most widely distributed species of Desmosomatidae was present in all four CCZ areas. The proportion of species present in a single area varies between families and this proportion is the lowest within Munnopsidae, i.e. 75.8% occurred only in one area, and it is higher in Desmosomatidae (77.7%) and Haploniscidae (83%) this showing, that less motile families tend to have species with more restricted distributions

~~1.3 **Discussion**~~

The ~~most common biological unit is~~ Upset plots (Figure 12) illustrate the ~~"~~unique and shared diversity for the total dataset as well as for each family across sampling locations. The lower part of the plots represents the connectivity network for all species~~". A general public understanding of~~ and by family. Each vertical line represents a ~~healthy ecosystem is to have~~set of sites with shared species and the vertical bars represent how many species ~~living~~are shared in ~~it. The definition of "what is a species" is tricky, and often discussed, more than 20~~each combination. While Macrostylidae and Haploniscidae show only three and fourset of sites with shared species ~~definitions exist (summary~~, the connectivity network is more complex for Desmosomatidae and Munnopsidae with 11 and 17 sets respectively. The complexity of the connectivity network increases with increasing locomotory ability of the family.

Species ranges by family are summarized in Table 5. Ranges were calculated after excluding singletons. A total of 60 species of munnopsids, 29 desmosomatids, 19 haploniscids and eight of macrostylids were represented by more than one specimen in the dataset. The maximum distribution range was higher for the natatory families Munnopsidae and Desmosomatidae, 5245 km and 4480 km

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respectively. The less motile families Haploniscidae and Macrostylidae had maximun ranges of 1391 km and 1440 km respectively. The minimum ranges per family also correlated with locomotory ability being for Munnopsidae 253 km, for Desmosomatidae 40 km, for Haploniscidae 1 km and for Macrostylidae 130 m (Table 5).

4. Discussion

4.2 Lifestyle of adults determines species' distributional ranges

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, 2019). 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. ~~Fišer et al.~~2018; Brix et al.2018, Christodoulou et al. 2020). However, biological data on dispersal distances of deep-sea species are still fragmentary due to the low sampling effort compared to the sheer area of deep-sea floor, and the scant knowledge of species' taxonomy. The large proportion of new species commonly found in deep-sea environments (Brandt et al. 2007, Brix et al. 2018, Jennings et al. 2019, Kaiser et al. 2017~~).~~), also seen in our dataset (Figures 3-6), remains a major impediment to understanding large-scale distributional patterns. With our ~~SD~~species delimitation analysis accompanied by morphological assessment, however, we ~~provide~~provided a stable system ~~to define~~for defining a species in the deep sea as ~~baseline~~the basis for a more ~~closer~~detailed ecological ~~view on~~ examination of the samples.

Our results ~~indicate~~indicated, that life-style, and more precisely the ~~locomotion~~locomotory (dispersal) capabilities of adult deep-sea asellotes are structuring their biodiversity patterns at medium

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and large scales. ~~The~~ In-line with our hypothesis, we found species within the family Munnopsidae ~~is~~exhibited the ~~most mobile of~~widest geographic ranges among 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~~examined (Table 5). The second most mobile family ~~is~~was the Desmosomatidae~~. They~~, who live on the surface of the sediments, but have posterior appendages modified for swimming ~~(~~, though not as pronounced as in the Munnopsidae~~). On contrary~~. In contrast, there is no evidence that ~~Haplonoscidae~~ Haploniscidae can swim. These asellotes live on or in the sediments and have short walking legs that they use for crawling. ~~Macrostyllidae~~ Macrostylidae are assumed to likely live ~~most probably~~ in tubes ~~into~~in the sediment, although some males of this family are good swimmers~~.~~ (Riehl et al. 2020).

~~The diversity patterns seems to correspond with these differences in locomotory capabilities.~~Brandt et al. (2011) considered the influence of locomotion (mobility types) for the distribution of isopod families, but the study by Bober et al. (2018) is the only other known analysis to assess distributional ranges in abyssal isopods relative to locomotive capacity using molecular markers. Bober et al. (2018) compared differences in the dispersal capacity of species in four isopod families (Munnopsidae, Desmosomatidae, Nannoniscidae and Macrostylidae), which were collected along the Vema fracture zone and found on both sides of the MAR. Although their study was based on only a few model species, they could see patterns like those in our analysis. For example, Bober et al. (2018) were able to detect the same haplotypes across the MAR in the swimming munnopsid *Acanthocope galathea* Wolff, 1962. The molecular analysis of *A. galathea* samples from the Vema Facture Zone and CCZ confirmed a pan-oceanic distribution in this species (Bober, pers. Communication). By contrast, for the non-swimming Macrostylidae and weakly-swimming Desmosomatidae and Nannoniscidae, the MAR seemed to be a dispersal barrier (Bober et al. 2008). Notably, in their analysis two species of Macrostylidae and Desmosomatidae each crossed the MAR, but there was no evidence of genetic exchange. Using data from the same sampling campaign, Brix et al. (2018) showed that even robustly-sampled species within Nannoniscidae and Desmosomatidae exhibit "small" ranges of around 500 km, and only three species were distributed in the order of 1,000–2,500 km. But we need to take into account that species ranges are

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biased by the sampling design and that there is a higher probability of sampling an abundant species than a widely distributed but rare species.

Although larval dispersal does not apply to isopods, since they brood their young, we would like to point out, that most of the isopod species reported here are very small, in the range of few millimeters as adult. In this size range it is clear that also adult isopods will be transported by bottom currents, once they swim just a few centimeters above the bottom. Etter and Bower (2015) tested the distribution distance of planktonic larvae in the North Atlantic Ocean using physical particles as models. Their experiment showed that dispersal over hundreds of kilometers and even through current systems with a strong temperature gradient is possible. Pelagic species and pelagic life stages of many benthic species can drift and swim across and/or between oceans during their lifetime. Fully benthic species, on the other hand, spend most of their life on or in the seabed, and thus may be dispersing over much shorter distances (Costello et al. 2017). Actively swimming taxa, such as the 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~~ that can swim 10s to 1000s of meters above the bottom, sometimes show a broad distribution that is 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%).~~ influenced by local water masses (Schnurr et al. 2014, 2018). For other asellote families in the present dataset, local and regional bottom currents are likely to play a major role in shaping their distribution patterns (Riehl et al. 2018; S. Kaiser pers. communication).

Macrostylidae deserves ~~as~~a special mention. ~~This sediment dwelling~~Species within this 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~~narrow distribution range, as ~~6~~six out of ~~9~~nine species were found in a single area and two species in two contiguous areas~~.~~ (Table 4). This pattern

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would have reinforced our hypothesis~~. But~~, except that 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.~~ Suppl. Table 1, Figure 6) is present in five areas. In our study, low morphological variation is contrasted by genetic differentiation in *Macrostylis* sp. M (cf. *metallicola*), which belongs to at ~~minimum~~least three different species according to our SD~~.~~ (Figure 6). If a real ~~affiliation to~~ identification as *M. 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~~ 2020). These authors ~~state~~stated that ~~also in their distribution data,~~ they ~~find~~found molecular hints of *M. metallicola* being a complex of more (cryptic) species and thus, the ~~morphological~~ morphologically uniform appearance leads to underestimating biodiversity or ~~we may observe ongoing~~possibly the population is in the early stages of a radiation ~~processes. However, as a result any~~. Either way, mining ~~impact on the populations of this species would disturb~~would disrupt this evolutionary process ~~or~~and limit the genetic potential of the population and thus, cause changes in the radiation and distribution pattern of this species complex. The wide distribution of species M05 would have been easily explained if the males had shown a strong sexual dimorphism, but this was not the case in the individuals collected here.

~~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~~A change to a more epifaunal or even swimming lifestyle ~~with~~in sexually mature males ~~reproducing~~that mate with ~~probably~~likely stationary

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females was discussed in species descriptions of strongly sexual dimorphic species such as those belonging to the Macrostylidae (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,~~ there are no documented dispersal~~ -~~-effecting sexual dimorphisms~~ are apparent.~~. In ~~desmosomatids~~desmosomatid and ~~nannoniscids~~haploniscids, sexual dimorphism is more pronounced than in munnopsids, ~~for example,~~in that males show more adaptations to swimming than females in various species. ~~The~~ For example, the species delimitation done on the ~~KuramBIO~~KuramBio II dataset for desmosomatids and nannoniscids (Jennings et al. ~~in press~~2020) revealed that a strong sexual dimorphism, especially in the genus *Mirabilicoxa*, limits morphological species determination and only the integrated approach combining genetics and morphology 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.~~

We found both wide-ranging species and many singletons or species that occurred in a single area, especially within the Munnopsidae (Figure 3). Rarity like this, is a widespread phenomenon in deep-sea ecosystems (Brandt et al. 2007; Connolly et al. 2014). The high number of singletons in our dataset (Supplementary Table 1) may reflect the always insufficient sampling effort of deep-sea studies (Kaiser et al. 2007; Janssen et al. 2015). This interpretation is further supported by the rarefaction curves that show no asymptote, suggesting incomplete sampling of the isopod biodiversity in the region (Figure 8). Kaiser et al. (unpublished data) examined the phylogeographic structure in a genus of poorly dispersing nannoniscid isopods from the CCZ and found similarly contrasting distribution patterns. Some species show a wide geographic distribution (>1400 km), while other species show evidence of restricted distributions or limited species ranges. These authors found that isolation by distance seemed to explain the distribution patterns to some extent, but the degree of habitat heterogeneity and oceanographic currents were equally important.

4.4 APEIs are similar in diversity but not in species composition compared to contractor areas

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Mining will fundamentally change the structure and function of resident communities and ecosystems. Thus, the implementation of set-aside areas, which remain untouched, can facilitate recolonization of impacted seafloor from external source populations (Cuvelier et al. 2018). ~~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~~

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~~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 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,~~

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~~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.~~

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~~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~~Initially, a network of APEIs were defined on the basis of large-scale hydrographic and bathymetric features, incl. nodule densities, carbon flux and seamount distribution (Wedding et al. 2013). Furthermore, assumed dispersal distances of species were considered to promote population persistence. Until 2015, however, no biological sample was taken from any APEI in order to assess its suitability as a biodiversity reservoir. Only in the course of JPI Oceans and Abyssline projects, were the first samples collected from APEIs No. 3 and 6 (Amon et al. 2016, Martinez & Häckel 2015). Published data on a number of fauna groups based on these samples indicate little resemblance between APEI communities and the contractor areas studied (Vanreusel et al. 2016; Jakiel et al. 2019; Bonifacio et al. 2020, Christodoulou et al. 2020). Bonifacio et al. (2020), for instance, investigated polychaete communities from the same sampling campaign as ours, and found considerably lower densities, diversity and similarity in species composition of APEI3 relative to contractor areas. Data on tanaidaceans from APEI3 also showed relatively low densities and species richness (Jakiel et al. 2019; Blazewicz et al. 2019). Further, Jakiel et al. (2019) found that only one-third of CCZ pseudotanaid richness was present in the APEI. Christodoulou et al. (2020) studied the brittle stars in the CCZ, APEI3 and DISCOL and similar to the present study, they showed a greater faunistic similarity between core CCZ contractor areas than to other areas. In addition, the similarity of the core CCZ area was greater to the most distant DISCOL area that to the relatively close APEI3. For isopods in our study, diversity levels perceived from APEI3 were similar to the contractor areas (Table 1), but species composition was different with only a few shared species (Table 2). This supports the idea, that distance is not the only factor determining community similarity between areas. Christodoulou et al. (2020) suggest marked differences in POC-flux as a possible structuring factor. The APEI3 is located in an area with very low surface productivity compared to the core CCZ areas and the DISCOL region. Environmental conditions have been shown to differ significantly in the APEI compared to areas in the CCZ, notably lower POC fluxes to the seafloor, lower total organic carbon (TOC) content, as well as lower clay content (Volz et al. 2018). These differences likely explain the observed community differences (Blazewicz et al. 2019; Bonifacio et al. 2020, Christodoulou et al. 2020). In a study of Icelandic isopods, Brix et al. (2018), TOC and mud content were shown to be the main explanatory variables for variation in distribution of families, with different lifestyles (e.g., in-, vs. epi., vs. suprafauna) and thus likely differential use of food resources and substrate associations.

The CCZ is delimited to the north by the Clarion Fracture Zone (Hall and Gurnis, 2005). Bonifacio et al. (2020) argue that the latter limits dispersal between peripheral APEIs and CCZ contractor areas, at least for some taxa, similar to what was seen for the MAR (Bober et al. 2018; Guggolz et al. 2018; Riehl et al. 2018). As previously discussed, Bober et al. (2018) found highly mobile munnopsids were able to cross the MAR, while the distribution of species in more poorly dispersing taxa, such as the Desmosomatidae, Nannoniscidaea and Macrostylidae, was restricted. Similarly, our study showed the swimming families Munnopsidae and Desmosomatidae have little similarity between APEI3 and contractor areas. Therefore, we believe that other factors like contrasting food supply rather than physical barriers, shape the standing stocks of these species.

Taboada et al. (2018) investigated microsatellite data of a common demosponge species (*Plenaster craigi* Lim & Wiklund, 2017) with a limited dispersal capacity from three contractor areas (UK-1A, UK-1B and OMS) of the CCZ and one APEI (No. 6). Their data revealed higher connectivity of distant populations (~800 km apart) compared to those only 10s of km apart. This unexpected pattern was attributed to hydrodynamic conditions on a small and larger scale, which on the one hand facilitates species dispersal over large distances, but locally may interrupt gene flow between populations (Taboada et al. 2018). Although they found evidence of genetic connectivity between UK-1A and APEI No. 6

(which is located closely, to the UK-1A area) in *P. craigi*, they concluded that APEI alone does not appear to adequately preserve the genetic diversity of *P. craigi* in the region. At this stage more data from the remaining APEIs, particularly those situated to the south, are required to further assess the appropriateness of APEIs for conservation purposes, particularly in terms of representative environmental conditions, fauna, and overall size of these reserves. Together, these studies suggest that APEIs are inappropriate or insufficient to capture the biodiversity of the CCZThe aim should therefore be to re-evaluate the suitability of the APEIs for the re-colonization of the proposed mining areas (Vanreusel et al. 2016; Blazewicz et al. 2019; Jakiel et al. 2019; Taboada et al. 2018, this study).

4.5 Implications for Conservation

Small-sized meio- and macrofaunal invertebrates, such as isopods make up a large proportion of CCZ diversity. Thus, especially for these small-sized faunal elements, studies on species richness and distribution patterns are needed for the development of management strategies for the preservation of abyssal biodiversity (Blazewicz et al. 2019). The widespread distribution of many munnopsid species suggests that at least some species may be able to recolonize affected areas, provided that the integrity of the habitat is restored. However, some species, like the Macrostylidae and some Haploniscidae are limited in their distribution, having been found in just one of the contractor areas. Therefore, their local loss may thus become a global loss. But even for widely distributed species, extinction of connecting population may result in loss of genetic diversity and recovery potential (Riehl and De Smet 2020). Janssen et al. (2019) 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~~(2019) suggested a similar pattern in isopods, they showed spatial genetic structuring of isopod populations ~~do~~did imply weak barriers to gene flow. They ~~conclude~~concluded that mining-related habitat destruction will most likely impact the continuity of isopod populations~~. This is based on the assumption~~ more severely than for other groups such as polychaetes. As a result of this study we can add that not all isopod families will be equally affected. Less motile families will be more severely affected. This assumes that ecosystem recovery after major impacts is predicted to occur slowly at evolutionary time scales. ~~As~~

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~~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.~~Haffert et al. (2020) calculated that the recovery of the biochemical fluxes in the upper centimeters of abyssal sediments after mining will take over 200 years.

Most species in our study are new to science or undescribed, and with increasing species accumulation curves, we are far from knowing how many isopod species live in the CCZ and how widespread they are. Our study of a community where over 94% of the isopod species are new to science or described within the last two years, indicates the need for quick assessment tools like molecular 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 single species (Brix et al. 2018). In addition, the exchange of images and sample sketches of species provided by taxonomist would contribute to taxonomic standardization between contractor areas and thus improve and refine biodiversity and biogeographic patterns.

We have been able to show, that less motile families of Isopoda, have more restricted distribution ranges. This has direct implications for recovery after mining operations. For these families, recolonization will need to start from nearby non-impacted areas. It is unlikely that pristine areas located far away from the mining operations will act as source-populations because they will most probably harbor a different set of species. The considerable differences we found between isopod communities of APEI3 and contractor areas cause doubts of the representativity of APEIs for conserving biodiversity in the CCZ as a whole. However, our study has the obvious limitation that we have sampled only contractor areas located in the eastern CCZ and we have sampled only one APEI. Therefore, more data from other APEIs are urgently needed to assess the diversity and composition of their communities and the degree of faunal connectivity, which must lead to a new assessment and revision of protected areas for the CCZ. We strongly suggest a declaration of APEIs within the core CCZ region as clear strategy to protect a more similar fauna to the areas that will be affected by mining.

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Author contributions

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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: manuscript writing, 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,~~

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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 Arbizu: Paper idea and statistical analyses, manuscript writing and statistical figures.

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Sample availability

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

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Competing interests

The authors declare that they have no conflict of interest.

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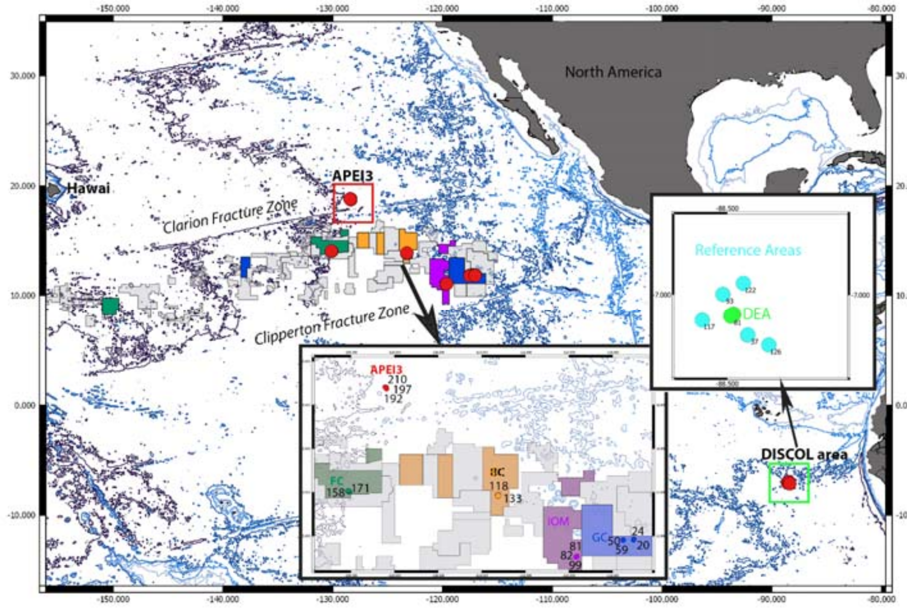

~~Fig. 1: Map of the locations of the EBS sampling sites (red dots) within the manganese nodule contractor and the DISCOL Experimental Area (DEA) areas in the north- and south-eastern Pacific. The colourcode in this map reflects the colourcode given in the circle trees (Fig.s 2 – 5), but is not reflected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

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~~In addition, the APEI3 (red - Area of Particular Environmental Interest number 3) and DISCOL Experimental Area (light green/blue – DEA and Reference Areas).~~

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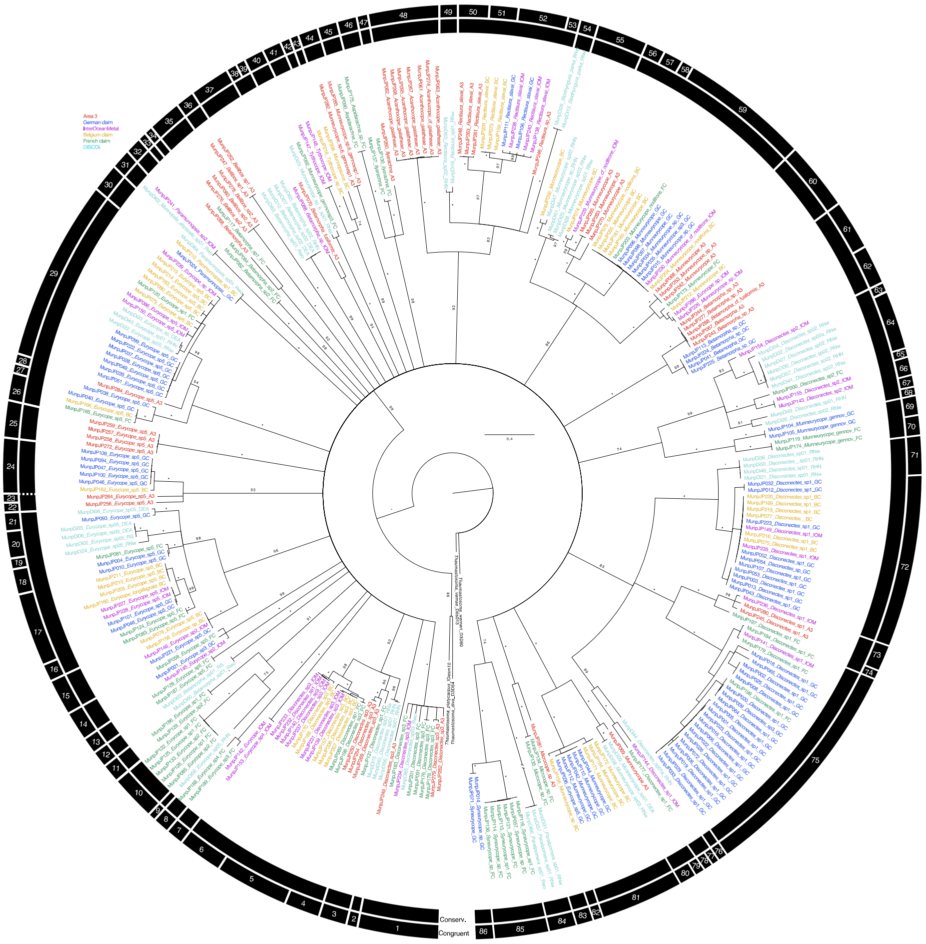

~~*Figure 2.* Phylogenetic tree of all munnopsid samples based on 16S and COI sequences for 294 specimens. Colours indicate collection location, with black indicating outgroups. All unsupported~~

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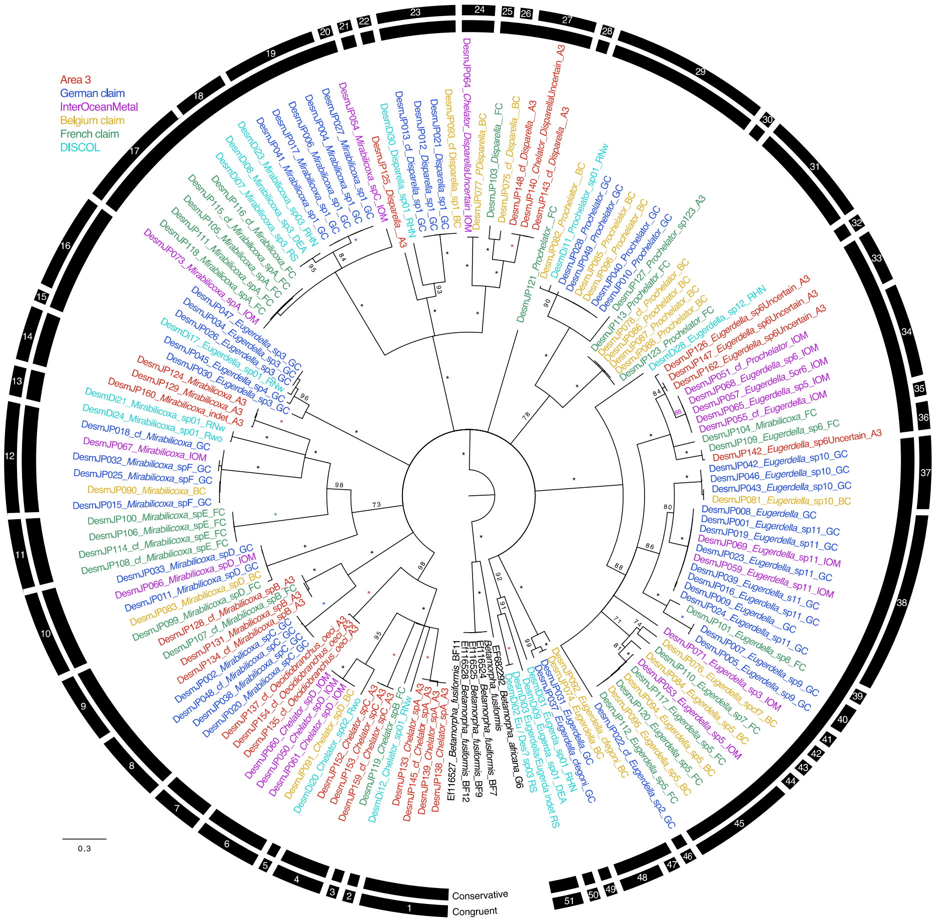
~~branches were collapsed and bootstrap support indicated with asterisks indicating 100 % bootstrap support. The outer two bars summarize the results of the species delimitation analyses which included morphological determination, Vsearch for individual genes, ABGD for individual genes, PTP and mPTP 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~~

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~~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.~~

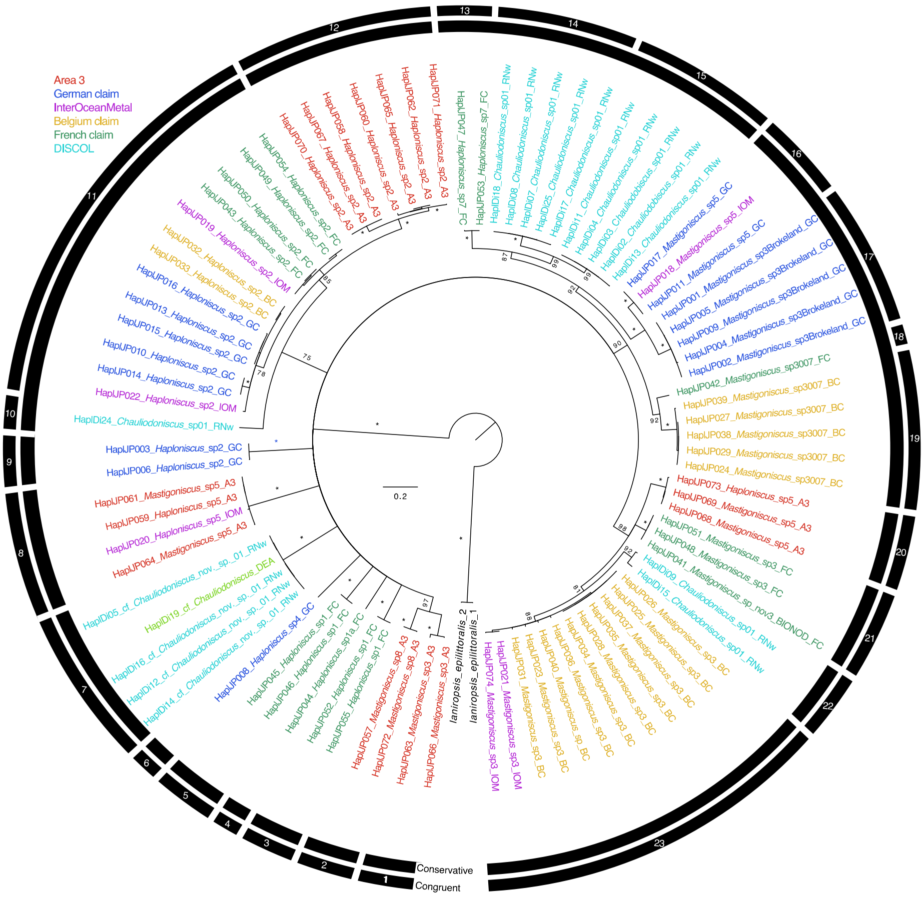

Figure 4: ~~Phylogenetic tree of all haploniscid samples based on 16S and COI sequences for 88 specimens. Colors indicate collection location, with black indicating outgroups. All unsupported branches were collapsed and bootstrap support indicated with asterisks indicating 100 % bootstrap support. The outer~~

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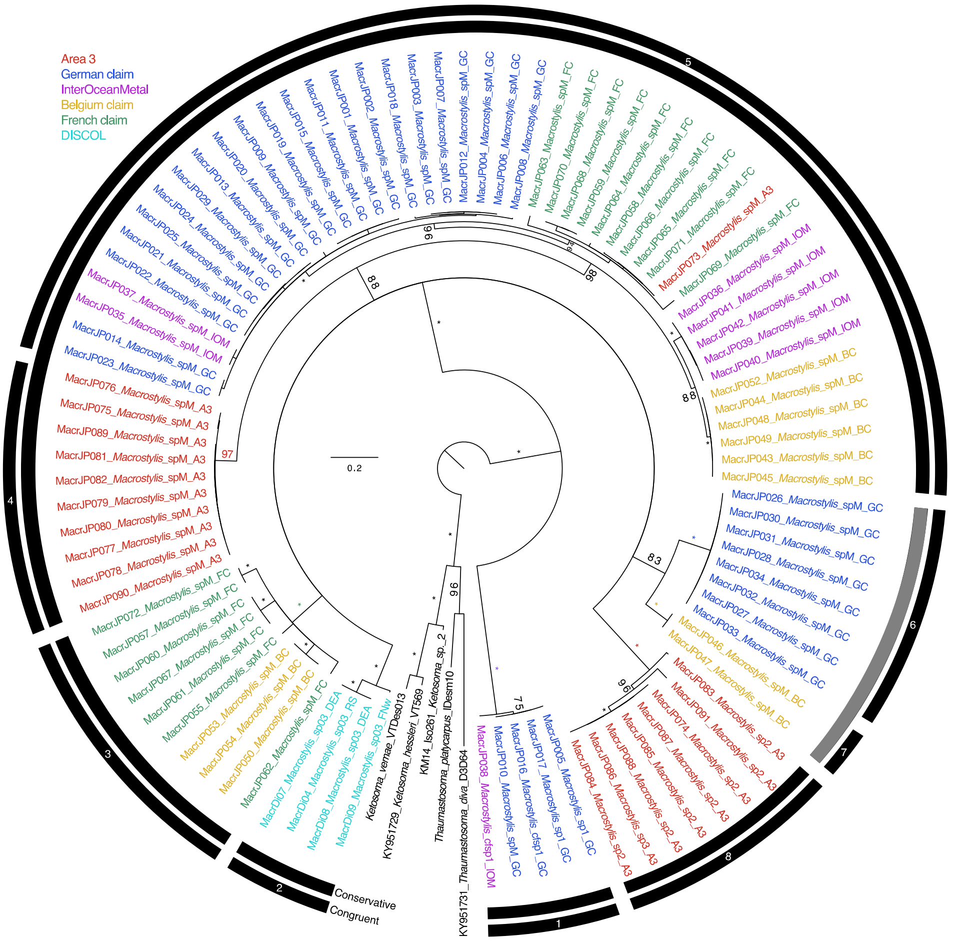
~~two bars summarize the results of the species delimitation analyses which included morphological determination, Vsearch for individual genes, ABGD for individual genes, PTP and mPTP for both individual genes and the concatenated datasets. The conservative bar indicates that all SD analyses supported 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 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~~

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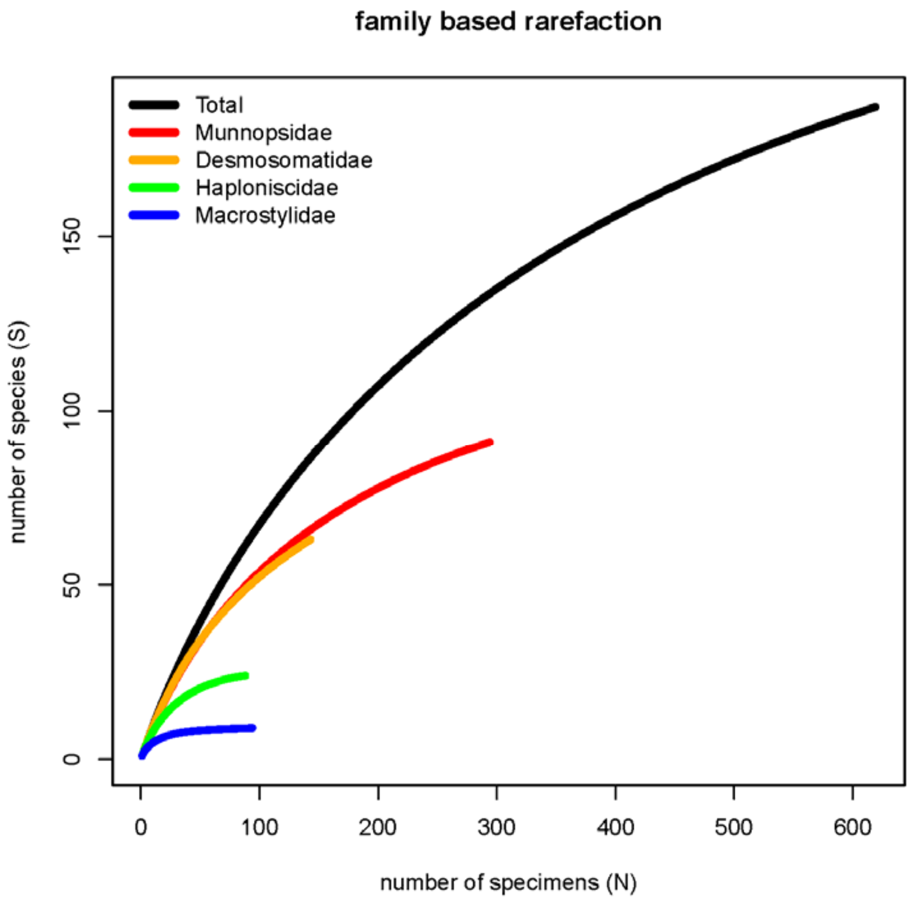
~~collapsed and bootstrap support indicated with asterisks indicating 100 % bootstrap support. The outer two bars summarize the results of the species delimitation analyses which included morphological determination, Vsearch for individual genes, ABGD for individual genes, PTP and mPTP for both individual genes and the concatenated datasets. The conservative bar indicates that all SD analyses supported that split, while the congruent bar indicates that the majority of SD analyses indicated that split. Numbers on congruent bars are arbitrary and provided to allow a way to refer to specific supported clades.~~



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

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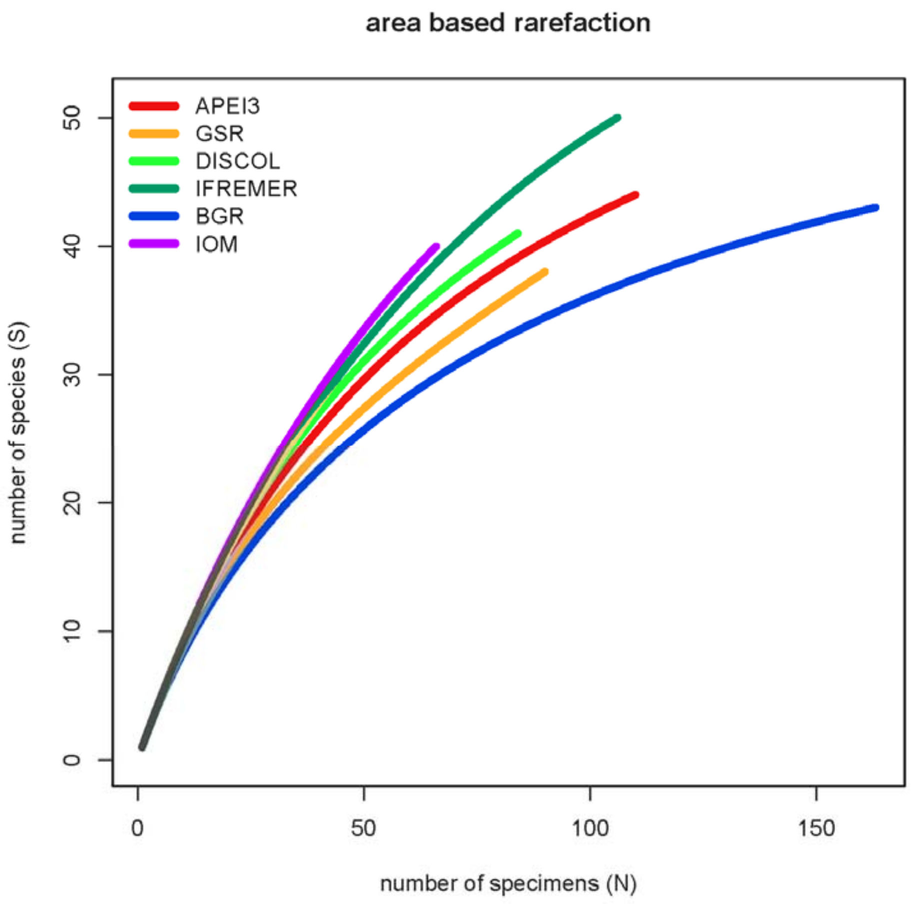

~~*Fig. 7:*~~ ~~Rarefaction analysis by area, considering all families together.~~

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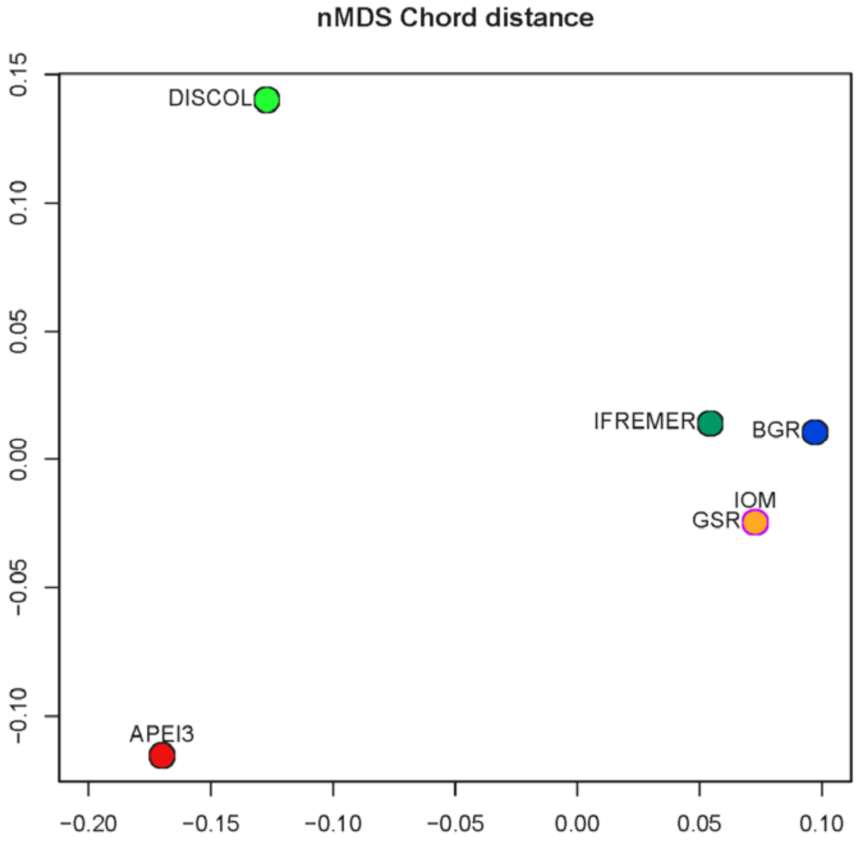

~~Fig. 8: nMDS ordination plot of Chord distance between areas.~~

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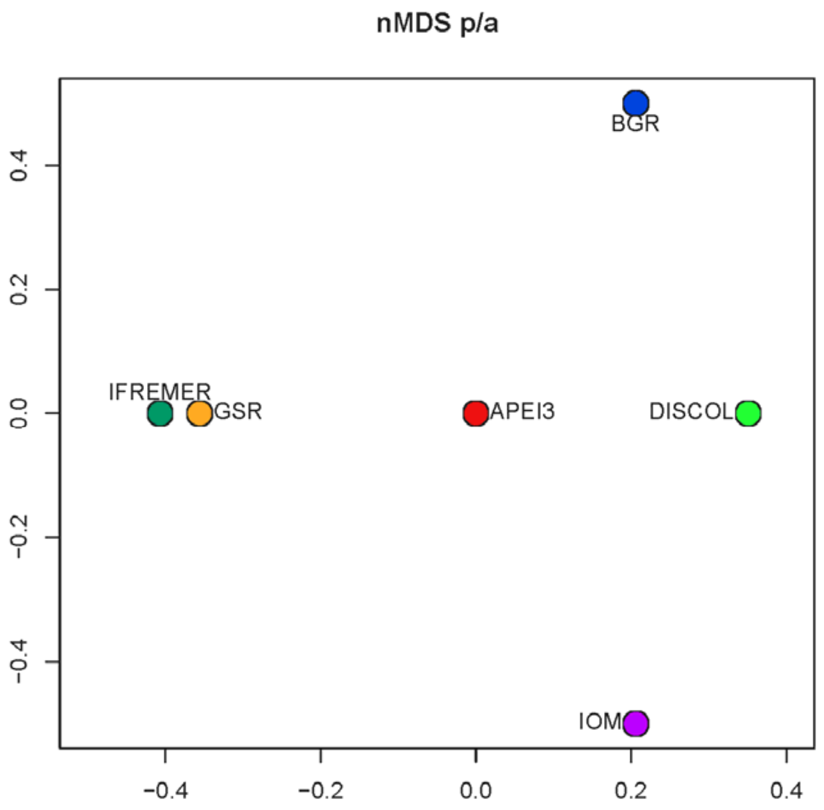

~~Fig. 9: nMDS ordination plot of Euclidean-distance between areas of presence-absence transformed data.~~

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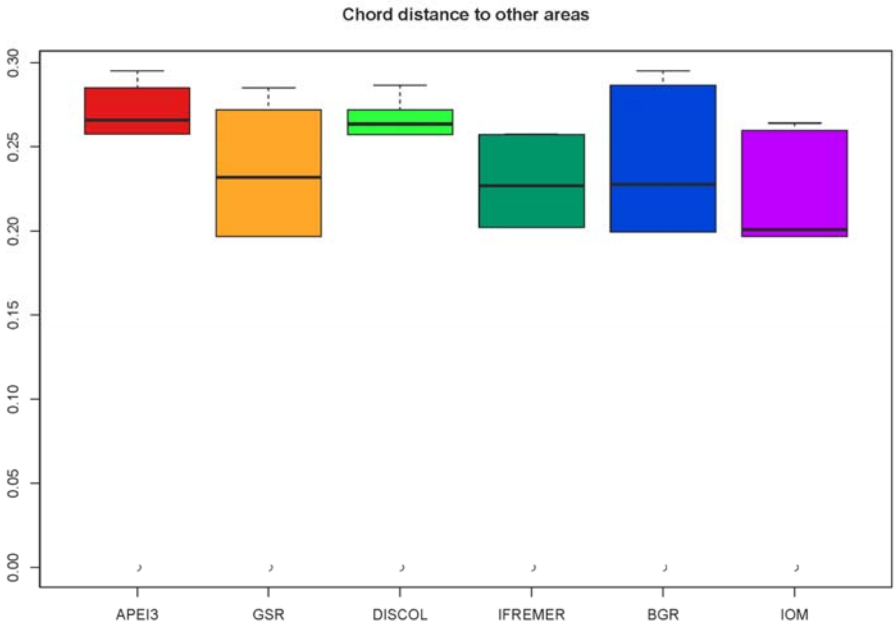

Fig. 10: ~~Box and whiskers plot showing the median and range of the Chord distance of every area to other areas.~~

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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.*~~

~~*Table 2*~~**Table 1.** 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, [illegible] 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. βSOR, βSIM and βSNE 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**	**βSOR**	**βSIM**	**βSNE**
BGR	**4**	**163**	**43**	**11 (25%)**	**49.5±4.8**	**56.2±3.2**	**3.84**	**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
GSR	2	90	38	18 (47%)	80±25.9	69.2±5	3.34	0.95	0.91	0.900	0.894	0.005
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
CCZ only	11	425	117	99 (84%)	146	137	4.21	0.97	0.80	0.767	0.746	0.021
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
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
Total	22	619	187	-	235.46	252.15	4.76	0.98	0.91	0.885	0.878	0.007

Table ~~3~~2. Faunistic similarity between areas. ~~*Upper diagonal = number*~~Number of shared species~~, *lower diagonal* =~~ upper quadrant, number of ~~*not*~~ non-shared species~~.~~ lower quadrant. Total number of species per site, bold in diagonal.

~~Not shared\shared~~	~~APEI3~~BGR	~~GSR~~IOM	~~DISCOL~~GSR		~~BGR~~APEI3	~~IOM~~DISCOL

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	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

~~APEI3~~BGR	~~0\44~~43	~~2~~15	~~1~~16	~~6~~8	1	5
~~GSR~~IOM	~~78~~53	~~0\38~~40	416	~~11~~12	~~16~~5	~~16~~2
~~DISCOL~~GSR	~~83~~49	~~71~~46	~~0\41~~38	~~2~~11	~~5~~2	~~2~~4
	~~82~~77	66	~~87~~66	~~0\~~**50**	~~8~~6	~~12~~2
~~BGR~~APEI3	85	~~49~~74	~~74~~78	~~77~~82	~~0\43~~44	~~15~~1
~~IOM~~DISCOL	74	~~46~~77	~~77~~71	~~66~~87	~~53~~83	~~0\40~~41

Table ~~4~~**3.** 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~~)~~).

Table ~~5~~**4.** 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

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Table 5. Species distribution range by family. Data show the maximum distribution range of the species of each family excluding singletons.

Family	**N**	**absolute max range**	**mean max range**	**mean min range**
Munnopsidae	60	5245 km	800 km	253 km
Desmosomatidae	29	4480 km	628 km	40 km
Haploniscidae	19	1391 km	183 km	1 km
Macrostylidae	8	1440 km	315 km	0.13 km

Supplementary Table 1. 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.

PLEASE SEE SEPARATE FILE because this is a 16 page table.

Figure 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).

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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. Illustration of the locomotion of the four isopod families. From right to left: Munnopsidae – swimming, Desmosomatidae – walking/swimming, Haploniscidae – walking, Macrostylidae – burrowing.

Figure 3. Phylogenetic tree of all munnopsid samples based on 16S and COI sequences for 294 specimens. Colours indicate collection location, with black indicating outgroups. All unsupported branches were collapsed and bootstrap support indicated with asterisks indicating 100 % bootstrap support. The outer two bars summarize the results of the species delimitation analyses which included morphological determination, Vsearch for individual genes, ABGD for individual genes, PTP and mPTP for both individual genes and the concatenated datasets. The conservative bar indicates that all SD analyses supported that split, while the congruent bar indicates that the majority of SD analyses indicated that split. Numbers on congruent bars are arbitrary and provided to allow a way to refer to specific supported clades.

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Figure 4. Phylogenetic tree of all desmosomatid samples based on 16S and COI sequences for 143 specimens. Colors indicate collection location, with black indicating outgroups. All unsupported branches were collapsed and bootstrap support indicated with asterisks indicating 100 % bootstrap support. The outer two bars summarize the results of the species delimitation analyses which included morphological determination, Vsearch for individual genes, ABGD for individual genes, PTP and mPTP for both individual genes and the concatenated datasets. The conservative bar indicates that all SD analyses supported that split, while the congruent bar indicates that the majority of SD analyses indicated that split. Numbers on congruent bars are arbitrary and provided to allow a way to refer to specific supported clades.

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Figure 5. Phylogenetic tree of all 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.

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Figure 6. 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.

Figure 7. Rarefaction analysis by isopod family, considering all areas together.

Figure 8. Rarefaction analysis by area, considering all families together.

Figure 9. nMDS ordination plot of Chord-distance between areas.

Figure 10. nMDS ordination plot of Euclidean-distance between areas of presence-absence transformed data.

Figure 11. Box and whiskers plot showing the median and range of the Chord distance of every area to other areas.

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Figure 12. Upset plot showing the number of species shared between sampling sites. The lower panel shows the sets of combination of sites. Sites sharing species are indicated by dots joined by a vertical line. The corresponding bar in the upper panel shows the number species co-occurring in this particular set of stations.

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Kommentarzeichen

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Correspondence Char: (Keine Überprüfung)

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Seite 16: [53] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: 12 Pt.

Seite 16: [54] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: 12 Pt.

Seite 16: [55] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: 12 Pt.

Seite 16: [56] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: 12 Pt.

Seite 16: [57] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: 12 Pt.

Seite 16: [58] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: 12 Pt.

Seite 16: [59] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: 12 Pt.

Seite 16: [60] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: 12 Pt.

Seite 16: [61] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: 12 Pt.

Seite 16: [62] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: 12 Pt.

Seite 16: [63] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: 12 Pt.

Seite 16: [64] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: 12 Pt.

Seite 16: [65] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: 12 Pt.

Seite 16: [66] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: 12 Pt.

Seite 16: [67] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: 12 Pt.

Seite 16: [68] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: 12 Pt.

Seite 16: [69] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: 12 Pt.

Seite 16: [70] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: 12 Pt.

Seite 16: [71] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: 12 Pt.

Seite 16: [72] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: 12 Pt.

Seite 16: [73] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: 12 Pt.

Seite 16: [74] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: 12 Pt.

Seite 16: [75] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: 12 Pt.

Seite 16: [76] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: 12 Pt.

Seite 16: [77] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: 12 Pt.

Seite 16: [78] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: 12 Pt.

Seite 16: [79] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: 12 Pt.

Seite 16: [80] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: 12 Pt.

Seite 16: [81] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: 12 Pt.

Seite 16: [82] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: 12 Pt.

Seite 16: [83] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: 12 Pt.

Seite 16: [84] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: 12 Pt.

Seite 16: [85] hat formatiert **Osborn** **31.07.2020 15:28:00**
Schriftart: 12 Pt.

Seite 24: [86] hat formatiert **Osborn** **31.07.2020 15:28:00**
Schriftart: 12 Pt., Englisch (Vereinigte Staaten)

Seite 24: [87] hat formatiert **Osborn** **31.07.2020 15:28:00**
Schriftart: 12 Pt., Englisch (Vereinigte Staaten)

Seite 24: [88] hat formatiert **Osborn** **31.07.2020 15:28:00**
Schriftart: 12 Pt., Englisch (Vereinigte Staaten)

Seite 24: [89] hat formatiert **Osborn** **31.07.2020 15:28:00**
Schriftart: 12 Pt., Englisch (Vereinigte Staaten)

Seite 24: [90] hat formatiert **Osborn** **31.07.2020 15:28:00**
Schriftart: 12 Pt., Englisch (Vereinigte Staaten)

Seite 24: [91] hat formatiert **Osborn** **31.07.2020 15:28:00**
Schriftart: 12 Pt., Englisch (Vereinigte Staaten)

Seite 24: [92] hat formatiert **Osborn** **31.07.2020 15:28:00**
Schriftart: 12 Pt., Englisch (Vereinigte Staaten)

Seite 24: [93] hat formatiert **Osborn** **31.07.2020 15:28:00**
Schriftart: 12 Pt., Englisch (Vereinigte Staaten)

Seite 24: [94] hat formatiert **Osborn** **31.07.2020 15:28:00**
Schriftart: 12 Pt., Englisch (Vereinigte Staaten)

Seite 24: [95] hat formatiert **Osborn** **31.07.2020 15:28:00**
Schriftart: 12 Pt., Englisch (Vereinigte Staaten)

Seite 24: [96] hat formatiert **Osborn** **31.07.2020 15:28:00**
Schriftart: 12 Pt., Englisch (Vereinigte Staaten)

Seite 24: [97] hat formatiert **Osborn** **31.07.2020 15:28:00**
Schriftart: 12 Pt., Englisch (Vereinigte Staaten)

Seite 24: [98] hat formatiert **Osborn** **31.07.2020 15:28:00**
Schriftart: 12 Pt., Englisch (Vereinigte Staaten)

Seite 24: [99] hat formatiert **Osborn** **31.07.2020 15:28:00**
Schriftart: 12 Pt., Englisch (Vereinigte Staaten)

Seite 24: [100] hat formatiert **Osborn** **31.07.2020 15:28:00**
Schriftart: 12 Pt., Englisch (Vereinigte Staaten)

Seite 24: [101] hat formatiert **Osborn** **31.07.2020 15:28:00**
Schriftart: 12 Pt., Englisch (Vereinigte Staaten)

Seite 24: [102] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: 12 Pt., Englisch (Vereinigte Staaten)

Seite 24: [103] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: 12 Pt., Englisch (Vereinigte Staaten)

Seite 24: [104] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: 12 Pt., Englisch (Vereinigte Staaten)

Seite 62: [105] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Nicht Kursiv

Seite 62: [106] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

Seite 62: [106] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

Seite 62: [107] Formatiert **Unknown** **31.07.2020 15:28:00**

Zentriert

Seite 62: [108] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

Seite 62: [108] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

Seite 62: [109] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

Seite 62: [109] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

Seite 62: [110] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

Seite 62: [110] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

Seite 62: [111] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

Seite 62: [111] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

Seite 62: [112] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

Seite 62: [112] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

Seite 62: [113] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

Seite 62: [113] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

Seite 62: [114] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

Seite 62: [114] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

Seite 62: [115] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

Seite 62: [115] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

Seite 62: [116] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

Seite 62: [116] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

Seite 62: [117] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

Seite 62: [117] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

Seite 62: [118] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

Seite 62: [118] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

Seite 62: [119] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

Seite 62: [119] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

Seite 62: [120] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

Seite 62: [120] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

Seite 62: [121] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

Seite 62: [122] Formatiert **Unknown** **31.07.2020 15:28:00**

Zentriert

Seite 62: [123] hat formatiert **Osborn** **31.07.2020 15:28:00**
Schriftart: Times New Roman, 11 Pt.

Seite 62: [124] hat formatiert **Osborn** **31.07.2020 15:28:00**
Schriftart: Times New Roman, 10 Pt.

Seite 62: [124] hat formatiert **Osborn** **31.07.2020 15:28:00**
Schriftart: Times New Roman, 10 Pt.

Seite 62: [125] hat formatiert **Osborn** **31.07.2020 15:28:00**
Schriftart: Times New Roman, 10 Pt.

Seite 62: [125] hat formatiert **Osborn** **31.07.2020 15:28:00**
Schriftart: Times New Roman, 10 Pt.

Seite 62: [126] hat formatiert **Osborn** **31.07.2020 15:28:00**
Schriftart: Times New Roman, 10 Pt.

Seite 62: [126] hat formatiert **Osborn** **31.07.2020 15:28:00**
Schriftart: Times New Roman, 10 Pt.

Seite 62: [127] hat formatiert **Osborn** **31.07.2020 15:28:00**
Schriftart: Times New Roman, 10 Pt.

Seite 62: [127] hat formatiert **Osborn** **31.07.2020 15:28:00**
Schriftart: Times New Roman, 10 Pt.

Seite 62: [128] hat formatiert **Osborn** **31.07.2020 15:28:00**
Schriftart: Times New Roman, 10 Pt.

Seite 62: [128] hat formatiert **Osborn** **31.07.2020 15:28:00**
Schriftart: Times New Roman, 10 Pt.

Seite 62: [129] hat formatiert **Osborn** **31.07.2020 15:28:00**
Schriftart: Times New Roman, 10 Pt.

Seite 62: [129] hat formatiert **Osborn** **31.07.2020 15:28:00**
Schriftart: Times New Roman, 10 Pt.

Seite 62: [130] hat formatiert **Osborn** **31.07.2020 15:28:00**
Schriftart: Times New Roman, 10 Pt.

Seite 62: [130] hat formatiert **Osborn** **31.07.2020 15:28:00**
Schriftart: Times New Roman, 10 Pt.

Seite 62: [131] hat formatiert **Osborn** **31.07.2020 15:28:00**
Schriftart: Times New Roman, 10 Pt.

Seite 62: [131] hat formatiert **Osborn** **31.07.2020 15:28:00**
Schriftart: Times New Roman, 10 Pt.

Seite 62: [132] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

Seite 62: [132] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

Seite 62: [133] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

Seite 62: [133] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

Seite 62: [134] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

Seite 62: [134] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

Seite 62: [135] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

Seite 62: [135] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

Seite 62: [136] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

Seite 62: [137] Formatiert **Unknown** **31.07.2020 15:28:00**

Zentriert

Seite 62: [138] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 11 Pt.

Seite 62: [139] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

Seite 62: [139] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

Seite 62: [140] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

Seite 62: [140] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

Seite 62: [141] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

Seite 62: [141] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

Seite 62: [142] hat formatiert	Osborn	31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 62: [142] hat formatiert	Osborn	31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 62: [143] hat formatiert	Osborn	31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 62: [143] hat formatiert	Osborn	31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 62: [144] hat formatiert	Osborn	31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 62: [144] hat formatiert	Osborn	31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 62: [145] hat formatiert	Osborn	31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 62: [145] hat formatiert	Osborn	31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 62: [146] hat formatiert	Osborn	31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 62: [146] hat formatiert	Osborn	31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 62: [147] hat formatiert	Osborn	31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 62: [147] hat formatiert	Osborn	31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 62: [148] hat formatiert	Osborn	31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 62: [148] hat formatiert	Osborn	31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 62: [149] hat formatiert	Osborn	31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 62: [149] hat formatiert	Osborn	31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 62: [150] hat formatiert	Osborn	31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 62: [150] hat formatiert	Osborn	31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 62: [151] hat formatiert **Osborn** **31.07.2020 15:28:00**
Schriftart: Times New Roman, 10 Pt.

Seite 62: [152] Formatiert **Unknown** **31.07.2020 15:28:00**
Zentriert

Seite 62: [153] hat formatiert **Osborn** **31.07.2020 15:28:00**
Schriftart: Times New Roman, 11 Pt.

Seite 62: [154] hat formatiert **Osborn** **31.07.2020 15:28:00**
Schriftart: Times New Roman, 10 Pt.

Seite 62: [154] hat formatiert **Osborn** **31.07.2020 15:28:00**
Schriftart: Times New Roman, 10 Pt.

Seite 62: [155] hat formatiert **Osborn** **31.07.2020 15:28:00**
Schriftart: Times New Roman, 10 Pt.

Seite 62: [155] hat formatiert **Osborn** **31.07.2020 15:28:00**
Schriftart: Times New Roman, 10 Pt.

Seite 62: [156] hat formatiert **Osborn** **31.07.2020 15:28:00**
Schriftart: Times New Roman, 10 Pt.

Seite 62: [156] hat formatiert **Osborn** **31.07.2020 15:28:00**
Schriftart: Times New Roman, 10 Pt.

Seite 62: [157] hat formatiert **Osborn** **31.07.2020 15:28:00**
Schriftart: Times New Roman, 10 Pt.

Seite 62: [157] hat formatiert **Osborn** **31.07.2020 15:28:00**
Schriftart: Times New Roman, 10 Pt.

Seite 62: [158] hat formatiert **Osborn** **31.07.2020 15:28:00**
Schriftart: Times New Roman, 10 Pt.

Seite 62: [158] hat formatiert **Osborn** **31.07.2020 15:28:00**
Schriftart: Times New Roman, 10 Pt.

Seite 62: [159] hat formatiert **Osborn** **31.07.2020 15:28:00**
Schriftart: Times New Roman, 10 Pt.

Seite 62: [159] hat formatiert **Osborn** **31.07.2020 15:28:00**
Schriftart: Times New Roman, 10 Pt.

Seite 62: [160] hat formatiert **Osborn** **31.07.2020 15:28:00**
Schriftart: Times New Roman, 10 Pt.

Seite 62: [160] hat formatiert **Osborn** **31.07.2020 15:28:00**
Schriftart: Times New Roman, 10 Pt.

Seite 62: [161] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 62: [161] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 62: [162] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 62: [162] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 62: [163] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 62: [163] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 62: [164] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 62: [164] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 62: [165] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 62: [165] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 62: [166] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 62: [167] Formatiert Unknown 31.07.2020 15:28:00

Zentriert

Seite 62: [168] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 11 Pt.

Seite 62: [169] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 62: [169] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 62: [170] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 62: [170] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 62: [171] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

Seite 62: [171] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

Seite 62: [172] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

Seite 62: [172] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

Seite 62: [173] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

Seite 62: [173] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

Seite 62: [174] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

Seite 62: [174] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

Seite 62: [175] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

Seite 62: [175] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

Seite 62: [176] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

Seite 62: [176] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

Seite 62: [177] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

Seite 62: [177] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

Seite 62: [178] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

Seite 62: [178] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

Seite 62: [179] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

Seite 62: [179] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

Seite 62: [180] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 12 Pt., Fett

Seite 62: [181] Formatiert **Osborn** **31.07.2020 15:28:00**

Beschriftung, Abstand Nach: 0 Pt., Zeilenabstand: einfach

Seite 62: [182] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Fett, Nicht Kursiv

Seite 62: [182] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Fett, Nicht Kursiv

Seite 62: [182] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Fett, Nicht Kursiv

Seite 62: [182] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Fett, Nicht Kursiv

Seite 62: [182] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Fett, Nicht Kursiv

Seite 62: [183] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 12 Pt., Schriftfarbe: Text 1

Seite 62: [184] Formatiert **Unknown** **31.07.2020 15:28:00**

Zentriert

Seite 62: [185] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 12 Pt., Schriftfarbe: Text 1

Seite 62: [186] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 12 Pt., Schriftfarbe: Text 1

Seite 62: [187] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 12 Pt., Schriftfarbe: Text 1

Seite 62: [188] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 12 Pt., Schriftfarbe: Text 1

Seite 62: [189] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 12 Pt., Schriftfarbe: Text 1

Seite 63: [190] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 12 Pt., Nicht Fett, Schriftfarbe: Text 1

Seite 63: [191] Formatiert **Unknown** **31.07.2020 15:28:00**

Zentriert

Seite 63: [192] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 12 Pt., Schriftfarbe: Text 1

Seite 63: [193] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 12 Pt., Schriftfarbe: Text 1

Seite 63: [194] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 12 Pt., Schriftfarbe: Text 1

Seite 63: [195] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 12 Pt., Schriftfarbe: Text 1

Seite 63: [196] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 12 Pt., Nicht Fett, Schriftfarbe: Text 1

Seite 63: [197] Formatiert Unknown 31.07.2020 15:28:00

Zentriert

Seite 63: [198] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 12 Pt., Schriftfarbe: Text 1

Seite 63: [199] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 12 Pt., Schriftfarbe: Text 1

Seite 63: [200] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 12 Pt., Schriftfarbe: Text 1

Seite 63: [201] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 12 Pt., Schriftfarbe: Text 1

Seite 63: [202] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 12 Pt., Schriftfarbe: Text 1

Seite 63: [203] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 12 Pt., Schriftfarbe: Text 1

Seite 63: [204] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 12 Pt., Nicht Fett, Schriftfarbe: Text 1

Seite 63: [205] Formatiert Unknown 31.07.2020 15:28:00

Zentriert

Seite 63: [206] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 12 Pt., Fett, Schriftfarbe: Text 1

Seite 63: [207] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 12 Pt., Fett, Schriftfarbe: Text 1

Seite 63: [208] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 12 Pt., Schriftfarbe: Text 1

Seite 63: [209] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 12 Pt., Schriftfarbe: Text 1

Seite 63: [210] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 12 Pt., Schriftfarbe: Text 1

Seite 63: [211] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 12 Pt., Schriftfarbe: Text 1

Seite 63: [212] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 12 Pt., Schriftfarbe: Text 1

Seite 63: [212] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 12 Pt., Schriftfarbe: Text 1

Seite 63: [213] Formatiert Unknown 31.07.2020 15:28:00

Zentriert

Seite 63: [214] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 12 Pt., Schriftfarbe: Text 1

Seite 63: [215] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 12 Pt., Schriftfarbe: Text 1

Seite 63: [216] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 12 Pt., Fett, Schriftfarbe: Text 1

Seite 63: [216] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 12 Pt., Fett, Schriftfarbe: Text 1

Seite 63: [217] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 12 Pt., Schriftfarbe: Text 1

Seite 63: [218] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 12 Pt., Schriftfarbe: Text 1

Seite 63: [219] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 12 Pt., Nicht Fett, Schriftfarbe: Text 1

Seite 63: [220] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 12 Pt., Schriftfarbe: Text 1

Seite 63: [221] Formatiert Unknown 31.07.2020 15:28:00

Zentriert

Seite 63: [222] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 12 Pt., Schriftfarbe: Text 1

Seite 63: [223] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 12 Pt., Schriftfarbe: Text 1

Seite 63: [224] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 12 Pt., Schriftfarbe: Text 1

Seite 63: [225] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 12 Pt., Fett, Schriftfarbe: Text 1

Seite 63: [226] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 12 Pt., Schriftfarbe: Text 1

Seite 63: [227] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 12 Pt., Nicht Fett, Schriftfarbe: Text 1

Seite 63: [228] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 12 Pt., Schriftfarbe: Text 1

Seite 63: [229] Formatiert Unknown 31.07.2020 15:28:00

Zentriert

Seite 63: [230] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 12 Pt., Schriftfarbe: Text 1

Seite 63: [231] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 12 Pt., Schriftfarbe: Text 1

Seite 63: [232] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 12 Pt., Schriftfarbe: Text 1

Seite 63: [233] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 12 Pt., Schriftfarbe: Text 1

Seite 63: [234] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 12 Pt., Schriftfarbe: Text 1

Seite 63: [235] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Fett, Nicht Kursiv

Seite 63: [236] Formatiert Osborn 31.07.2020 15:28:00

Abstand Vor: 0 Pt.

Seite 63: [237] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Nicht Kursiv

Seite 63: [237] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Nicht Kursiv

Seite 63: [238] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman

Seite 63: [239] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt., Nicht Fett

Seite 63: [240] Formatiert Unknown 31.07.2020 15:28:00

Zentriert, Position: Horizontal: Links, Gemessen von: Seitenrand, Vertikal: 3,9 cm, Gemessen von: Seite, Horizontal: 0,32 cm, Umschließen

Seite 63: [241] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 11 Pt.

Seite 63: [242] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt., Nicht Fett

Seite 63: [242] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt., Nicht Fett

Seite 63: [243] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt., Nicht Fett

Seite 63: [243] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt., Nicht Fett

Seite 63: [244] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt., Nicht Fett

Seite 63: [244] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt., Nicht Fett

Seite 63: [245] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt., Nicht Fett

Seite 63: [245] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt., Nicht Fett

Seite 63: [246] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt., Nicht Fett

Seite 63: [246] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt., Nicht Fett

Seite 63: [247] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt., Nicht Fett

Seite 63: [247] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt., Nicht Fett

Seite 63: [248] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt., Nicht Fett

Seite 63: [248] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt., Nicht Fett

Seite 63: [249] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt., Nicht Fett

Seite 63: [249] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt., Nicht Fett

Seite 63: [250] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt., Nicht Fett

Seite 63: [250] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt., Nicht Fett

Seite 63: [251] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt., Nicht Fett

Seite 63: [251] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt., Nicht Fett

Seite 63: [252] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 63: [252] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 63: [253] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 63: [254] Formatiert Unknown 31.07.2020 15:28:00

Zentriert, Position: Horizontal: Links, Gemessen von: Seitenrand, Vertikal: 3,9 cm, Gemessen von: Seite, Horizontal: 0,32 cm, Umschließen

Seite 63: [255] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 11 Pt.

Seite 63: [256] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 63: [256] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 63: [257] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 63: [257] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 63: [258] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 63: [258] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 63: [259] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 63: [259] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 63: [260] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 63: [260] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 63: [261] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 63: [261] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 63: [262] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 63: [262] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 63: [263] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 63: [263] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 63: [264] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 63: [264] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 63: [265] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 63: [265] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 63: [266] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 63: [266] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 63: [267] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 63: [268] Formatiert Unknown 31.07.2020 15:28:00

Zentriert, Position: Horizontal: Links, Gemessen von: Seitenrand, Vertikal: 3,9 cm, Gemessen von: Seite, Horizontal: 0,32 cm, Umschließen

Seite 63: [269] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 11 Pt.

Seite 63: [270] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 63: [270] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

Seite 63: [271] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

Seite 63: [271] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

Seite 63: [272] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

Seite 63: [272] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

Seite 63: [273] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

Seite 63: [273] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

Seite 63: [274] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

Seite 63: [274] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

Seite 63: [275] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

Seite 63: [275] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

Seite 63: [276] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

Seite 63: [276] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

Seite 63: [277] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

Seite 63: [277] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

Seite 63: [278] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

Seite 63: [278] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

Seite 63: [279] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

Seite 63: [279] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

Seite 63: [280] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

Seite 63: [280] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

Seite 63: [281] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

Seite 63: [282] Formatiert **Unknown** **31.07.2020 15:28:00**

Zentriert, Position: Horizontal: Links, Gemessen von: Seitenrand, Vertikal: 3,9 cm, Gemessen von: Seite, Horizontal: 0,32 cm, Umschließen

Seite 63: [283] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 11 Pt.

Seite 63: [284] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

Seite 63: [284] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

Seite 63: [285] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

Seite 63: [285] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

Seite 63: [286] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

Seite 63: [286] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

Seite 63: [287] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

Seite 63: [287] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

Seite 63: [288] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

Seite 63: [288] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

Seite 63: [289] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 63: [289] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 63: [290] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 63: [290] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 63: [291] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 63: [291] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 63: [292] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 63: [292] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 63: [293] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 63: [293] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 63: [294] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 63: [294] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 63: [295] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 63: [296] Formatiert Unknown 31.07.2020 15:28:00

Zentriert, Position: Horizontal: Links, Gemessen von: Seitenrand, Vertikal: 3,9 cm, Gemessen von: Seite, Horizontal: 0,32 cm, Umschließen

Seite 63: [297] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 11 Pt.

Seite 63: [298] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 63: [298] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 63: [299] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 63: [299] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 63: [300] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 63: [300] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 63: [301] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 63: [301] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 63: [302] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 63: [302] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 63: [303] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 63: [303] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 63: [304] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 63: [304] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 63: [305] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 63: [305] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 63: [306] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 63: [306] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 63: [307] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 63: [307] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 63: [308] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 63: [308] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 63: [309] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 63: [310] Formatiert Unknown 31.07.2020 15:28:00

Zentriert, Position: Horizontal: Links, Gemessen von: Seitenrand, Vertikal: 3,9 cm, Gemessen von: Seite, Horizontal: 0,32 cm, Umschließen

Seite 63: [311] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 11 Pt.

Seite 63: [312] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 63: [312] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 63: [313] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 63: [313] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 63: [314] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 63: [314] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 63: [315] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 63: [315] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 63: [316] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 63: [316] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 63: [317] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 63: [317] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 63: [318] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

Seite 63: [318] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

Seite 63: [319] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

Seite 63: [319] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

Seite 63: [320] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

Seite 63: [320] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

Seite 63: [321] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

Seite 63: [321] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

Seite 63: [322] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Fett, Nicht Kursiv

Seite 63: [323] Formatiert **Osborn** **31.07.2020 15:28:00**

Abstand Vor: 0 Pt.

Seite 63: [324] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Nicht Kursiv

Seite 63: [325] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: 12 Pt.

Seite 63: [326] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 11 Pt.

Seite 63: [327] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

Seite 63: [328] Formatiert **Unknown** **31.07.2020 15:28:00**

Zentriert

Seite 63: [329] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 11 Pt.

Seite 63: [330] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

Seite 63: [330] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 63: [331] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

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Schriftart: Times New Roman, 10 Pt.

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Schriftart: Times New Roman, 10 Pt.

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Schriftart: Times New Roman, 10 Pt.

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Schriftart: Times New Roman, 10 Pt.

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Schriftart: Times New Roman, 10 Pt.

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Schriftart: Times New Roman, 10 Pt.

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Schriftart: Times New Roman, 10 Pt.

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Schriftart: Times New Roman, 10 Pt.

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Schriftart: Times New Roman, 10 Pt.

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Schriftart: Times New Roman, 10 Pt.

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Schriftart: Times New Roman, 10 Pt.

Seite 63: [338] Formatiert Unknown 31.07.2020 15:28:00

Zentriert

Seite 63: [339] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 11 Pt.

Seite 63: [340] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 63: [340] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

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Schriftart: Times New Roman, 10 Pt.

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Schriftart: Times New Roman, 10 Pt.

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Schriftart: Times New Roman, 10 Pt.

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Schriftart: Times New Roman, 10 Pt.

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Schriftart: Times New Roman, 10 Pt.

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Schriftart: Times New Roman, 10 Pt.

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Schriftart: Times New Roman, 10 Pt.

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Schriftart: Times New Roman, 10 Pt.

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Schriftart: Times New Roman, 10 Pt.

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Schriftart: Times New Roman, 10 Pt.

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Schriftart: Times New Roman, 10 Pt.

Seite 63: [346] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

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Schriftart: Times New Roman, 10 Pt.

Seite 63: [348] Formatiert **Unknown** **31.07.2020 15:28:00**

Zentriert

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Schriftart: Times New Roman, 11 Pt.

Seite 63: [350] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

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Schriftart: Times New Roman, 10 Pt.

Seite 63: [351] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

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Schriftart: Times New Roman, 10 Pt.

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Schriftart: Times New Roman, 10 Pt.

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Schriftart: Times New Roman, 10 Pt.

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Schriftart: Times New Roman, 10 Pt.

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Schriftart: Times New Roman, 10 Pt.

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Schriftart: Times New Roman, 10 Pt.

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Schriftart: Times New Roman, 10 Pt.

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Schriftart: Times New Roman, 10 Pt.

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Schriftart: Times New Roman, 10 Pt.

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Schriftart: Times New Roman, 10 Pt.

Seite 63: [358] Formatiert Unknown 31.07.2020 15:28:00

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Schriftart: Times New Roman, 11 Pt.

Seite 63: [360] hat formatiert Osborn 31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

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Schriftart: Times New Roman, 10 Pt.

Seite 63: [361] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

Seite 63: [361] hat formatiert **Osborn** **31.07.2020 15:28:00**

Schriftart: Times New Roman, 10 Pt.

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Schriftart: Times New Roman, 10 Pt.

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Schriftart: Times New Roman, 10 Pt.

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Schriftart: Times New Roman, 10 Pt.

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Schriftart: Times New Roman, 10 Pt.

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Schriftart: Times New Roman, 10 Pt.

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Schriftart: Times New Roman, 10 Pt.

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Seite 63: [368] Formatiert **Unknown** **31.07.2020 15:28:00**

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Schriftart: Times New Roman, 11 Pt.

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Schriftart: Times New Roman, 10 Pt.

Seite 63: [371] hat formatiert	Osborn	31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 63: [371] hat formatiert	Osborn	31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 63: [372] hat formatiert	Osborn	31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

Seite 63: [372] hat formatiert	Osborn	31.07.2020 15:28:00

Schriftart: Times New Roman, 10 Pt.

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Seite 63: [378] Formatiert	Unknown	31.07.2020 15:28:00

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Seite 63: [379] hat formatiert	Osborn	31.07.2020 15:28:00

Schriftart: Times New Roman, 11 Pt.

Seite 63: [380] hat formatiert	Osborn	31.07.2020 15:28:00

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Schriftart: Times New Roman, 10 Pt.

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