

DIFFERENCES OF COPEPODA COMPOSITION ANALYSIS IN MARICULTURE PONDS THROUGH MORPHOLOGICAL TAXONOMY AND DIFFERENT METAGENETIC APPROACHES

WU, S.¹ – ZHANG, X.² – DAI, L. L.³ – NI, J. J.^{4,5} – WANG, Y. Y.⁶ – LI, J. J.⁷ – DING, W. J.^{1*}

¹*School of Basic Medical Sciences, Chengdu University of Traditional Chinese Medicine, Chengdu 611137, China*

²*Zhejiang Mariculture Research Institute; Zhejiang Key Laboratory of Exploitation and Preservation of Coastal Bio-Resource; Wenzhou Key Laboratory of Marine Biological Genetics and Breeding, Wenzhou 325005, China*

³*Yangtze River Fisheries Research Institute, Chinese Academy of Fishery Sciences, Wuhan 430223, China*

⁴*Meilikang Research and Development Center, Guangdong Meilikang Bio-Science Ltd., Foshan 528315, China*

⁵*Dongguan Key Laboratory of Medical Bioactive Molecular Developmental and Translational Research, Guangdong Medical University, Dongguan 523808, China*

⁶*Fisheries College, Jimei University, Xiamen 36100, China*

⁷*School of Life Science, Qilu Normal University, Jinan 250200, China*

*Corresponding author

e-mail: Dingweijun@cdutcm.edu.cn; phone: +86-286-180-0104

(Received 12th Dec 2022; accepted 17th Mar 2023)

Abstract. Copepods play a fundamental role in aquatic ecosystems and are an important food source for fish at an early stage. However, little attention has been given to changes in copepod communities in aquaculture water. This is mainly limited by the copepod analysis method. In this study, we designed a pair of copepod primers, Cop18SF/Cop18SR, for the analysis of copepod communities to promote the investigation of copepods in aquaculture water. Our results showed that the common-used primer pair Uni18S/Uni18SR non-specifically amplified many DNA sequences from bacteria, whereas the primer pair LSUCop-D2F/LSUCop-D2R abnormally enriched OTU denovo438, which was an unidentified Eukaryota zooplankton. Although *Eurytemora pacifica* was classified into 26 OTUs with 97% sequence identity using our designed primer pair Cop18SF/Cop18SR, other results indicated that the primer pair Cop18SF/Cop18SR was superior to the other two primer pairs. Moreover, different primer pairs yielded different plankton community structures, which caused their correlations with environmental factors to be obviously different. These results imply that the primer pair Cop18SF/Cop18SR can be used to analyze the dynamic changes in the copepod community structure and the relationship between the community structure and abiotic and biological factors in aquaculture water.

Keywords: *taxon-specific primers, aquaculture, species identification, zooplankton ecology, barcode sequence*

Introduction

Copepods are the dominant mesozooplankton in marine environments (Takenaka et al., 2012), comprising as much as 80% of their total biomass (Kjørboe, 1998). Copepoda consist of 10 orders in total, among which harpacticoids, calanoids, and cyclopoids are

the three major copepods in aquaculture production (Nisar et al., 2022). There are approximately 12,000 identified copepod species with 2,500 species of marine origin, and new species are being regularly identified (Bron et al., 2011; Blanco-Bercial et al., 2014). They are important grazers of phytoplankton and microzooplankton (Atkinson, 1996) and form a major trophic link to many predatory invertebrates and fish (Hirst and Bunker, 2003; Kwok et al., 2015). Copepods also play a fundamental role in the upper ocean exporting, redistributing, and repackaging of carbon and nutrients (Banse, 1995; Frangoulis et al., 2005, 2011), and they support fisheries of important species such as cod, herring, and salmon (Beaugrand et al., 2003; Hansen, 2017). When copepods are added to the diet, shrimps show better growth and survival rates (Nisar et al., 2022). Therefore, ecological investigation of copepods is an important part of aquatic ecology (Brun et al., 2016). However, little attention has been given to the changes in copepod communities in aquaculture water.

Copepods may be free-living (pelagic or benthic) or parasitic. They are a very diverse group of crustaceans that exhibit a wide range of forms and sizes (Bron et al., 2011). Copepods have 13 distinct life stages (egg, six naupliar stages, five copepodite stages, and adult), and many species are sexually dimorphic (Kwok et al., 2015). Moreover, copepods can produce resting eggs that accumulate in the sediment, leading to the formation of an “egg bank” (Glippa et al., 2011; Baumgartner and Tarrant, 2017). These life history traits and their importance in the aquatic food web make copepods suitable candidates as reference organisms for ecotoxicology (Kwok et al., 2015). The complex life-history traits, high species diversity, and relatively small size have made morphological identification of copepods extremely difficult; nonetheless, morphological identification is the commonly used means in ecological research on copepods (Bron et al., 2011; Wu et al., 2022).

Molecular approaches to species identification have allowed the rapid detection, discrimination, and identification of species based on DNA sequencing of single specimens and environmental samples (Blanco-Bercial et al., 2014). With the development of high-throughput sequencing technology and bioinformatics, molecular approaches have been widely used to analyze the species composition of prokaryotic and eukaryotic microbial communities in various ecosystems (Ni et al., 2018; Wu et al., 2019; Chen et al., 2020; Liu et al., 2022). Molecular approaches have also been used to analyze zooplankton and copepod community diversity (Hirai et al., 2017; Gao et al., 2020). However, primer defects limit the accurate analysis of copepod community structure in aquatic environments by molecular approaches. To overcome these defects, we designed a pair of copepod-specific primers based on the 18S small ribosomal subunit (18S rRNA) gene and compared them with two pairs of commonly used primers used in zooplankton community studies, one pair of which are eukaryotic universal primers also based on the 18S rRNA gene, and the other pair are copepod-specific primers based on the ribosomal large subunit gene.

Materials and Methods

Primer design and verification

According to our previous research (Wu et al., 2015), we designed a pair of copepod-specific primers, Cop18SF (5'-TGCCAGTAGTCATATGCTCGTCTC-3') and Cop18SR (5'-CCACTGTGAGCGTCTATGCC-3'), using Primer Premier 5.0 to amplify the hypervariable V1-V2 region of 18S rRNA gene. To evaluate the specificity of the

primers and the ability to distinguish copepod species, we used the primers to carry out PCR amplification, agarose gel electrophoresis, and denaturing gradient gel electrophoresis (DGGE) analysis on nine copepod species (i.e., *Sinergasilus* sp. (Poecilostomatoida, Ergasilidae), *Mesocyclops leuckarti* (Cyclopoida, Cyclopidae), *Neutrodiaptomus incongruens* (Calanoida, Diaptomidae), *Sinodiaptomus* sp. (Calanoida, Diaptomidae), *Paracyclops fimbriatus* (Cyclopoida, Cyclopidae), *Eucyclops* sp. (Cyclopoida, Cyclopidae), *Cyclops vicinus vicinus* (Cyclopoida, Cyclopidae), *Thermocyclops taihokuensis* (Cyclopoida, Cyclopidae), and *Microcyclops* sp. (Cyclopoida, Cyclopidae)), and six non-copepod species representing different plankton taxa. Three of the non-copepods (i.e., a species of Nematoda, *Asplanchna* sp. (Rotifera), and *Moina micrura* (Branchiopoda, Cladocera)) were collected with nine copepods from East Lake (114.37 E, 30.55 N) and its surrounding ponds in Wuhan, China; the other three non-copepods were laboratory-pure cultured species (i.e., *Chlorella pyrenoidosa* (Chlorophyta), *Escherichia coli* (Proteobacteria), and *Tetrahymena pyriformis* GL (Ciliophora)). Species identification was mainly carried out with reference to the description in the book “Fauna Sinica: Arthropoda, Crustacea, Freshwater copepoda” (Crustacean Research Group, 1979) (See *Appendix 1* for morphological features). A planktonic assemblage from East Lake (114.37 E, 30.55 N) was collected by filtering 1 L of lake water through a 0.22 µm pore size cellulose acetate filter (Millipore). Genomic DNA was extracted from each sample by using the method described by Ni et al. (2010). PCR was conducted under the following thermal cycling conditions: an initial predenaturation step at 94 °C for 10 min, followed by 30 cycles at 94 °C for 30 s, 52 °C for 30 s, and 72 °C for 30 s, and a final extension at 72 °C for 10 min. PCR amplifications were performed in duplicate with 25 µL reaction mix containing 1 × PCR buffer, 0.25 U of Taq DNA polymerase (Transgen Biotech, China), 0.2 mM of each deoxynucleoside triphosphate, 1.0 µM of each primer, and 10 ng of microbial genomic DNA. After amplification, the PCR products were subjected to electrophoresis on 1.2% agarose gel to test the amplification effect. DGGE was conducted according to the method described by Ni et al. (2010) with a denaturing gradient ranging from 30% to 60%.

Moreover, the primer pairs of the large ribosomal subunit (LSU) D2 region (approximately 400 bp) LSUCop-D2F (5'-AGACCGATAGCAAACAAGTAC-3') and LSUCop-D2R (5'-GTCCGTGTTTCAAGACGG-3') (Hirai et al., 2015) and the 18S rRNA hypervariable V4 region Uni18S (5'-AGGGCAAKEYCTGGTGCCAGC-3') and Uni18SR (5'-GRCGGTATCTRATCGYCTT-3') (Zhan et al., 2013; Brown et al., 2016) were used to assess the performance of our designed primers in high-throughput sequencing analysis.

Sample collection, morphological identification, and high-throughput sequencing of DNA barcoding sequences

Six ocean water samples were collected from 0.5 m below the surface of six mariculture ponds at a mariculture company on March 29, 2022 (*Appendix 2*). A total of 12 L of each water sample was filtered through a 64 µm mesh net, half of which was fixed with 4% formalin, and the other half was filtered using a GF/C glass fiber (Whatman, Metestone, UK) with a 0.22 µm aperture to collect the plankton. The filters were cut into small scraps and used to extract DNA using a PowerSoil DNA isolation kit (QIAGEN, Germany) as previously described (Li et al., 2022). Planktonic organisms were examined using an Axioplan 2 imaging microscope (Zeiss, Jena, Germany) according to a previous study (Ni et al., 2010).

Sample-specific barcode sequences of 12 nt length were added to the 5'-end of the forward primer in primer synthesis to allow for distinguishing samples (Ni et al., 2019). The sequences of the LSU D2 region and hypervariable V4 region were amplified using primer pairs as previously described (Zhan et al., 2013; Hirai et al., 2015). The hypervariable V1-V2 region was amplified using our designed primer pair, as described above. After amplification, the two PCR products were mixed and subjected to electrophoresis on a 1.2% agarose gel (Xiang et al., 2018) for purification using an AxyPrep DNA gel extraction kit (Axygen, China). All purified amplicons were pooled together with equal molar amounts from each sample and sequenced using an Illumina HiSeq 3000 system at Guangdong Meilikang Bio-Science, Ltd., China.

All DNA sequences were deposited into the NCBI Sequence Read Archive database with accession number PRJNA902127.

Determination of water physicochemical factors

Water temperature (WT), pH, salinity, and dissolved oxygen (DO) were measured using a Multi 3410 SET5 digital multiparameter analyser (WTW, Germany). The chemical oxygen demand (COD), nitrate (NO₃⁻-N), and nitrite (NO₂⁻-N) contents were measured using the K₂Cr₂O₇ standard method, zinc/chromium (II) reduction method, and n-(1-naphthyl)-ethylenediamine dihydrochloride spectrophotometric method, respectively (Ni et al., 2018). The ammonia nitrogen (NH₄⁺-N) content was measured using the indophenol blue spectrophotometry method (Wang et al., 2019). The available phosphorus content (PO₄³⁺-P) was determined using molybdenum blue spectrophotometry (Lin et al., 2021). Suspended particles (SS), inorganic nitrogen (IN), and chlorophyll-a (Chla) were measured according to the method described by Huang (2000).

Data analysis

The raw reads were merged using FLASH 1.2.8 (Magoc and Salzberg, 2011) to generate sequence tags, and the sequence tags were processed using QIIME 1.9.0 (Caporaso et al., 2010) as previously described (Xiang et al., 2018; Ni et al., 2021) with the exception that the reference dataset for taxonomic assignments was SILVA132 (<https://www.arb-silva.de/documentation/release-132/>). Singletons were removed to remove erroneous operational taxonomic units (OTUs) with low-abundance sequences in the sequencing analysis. The α -diversity indices (species richness, Shannon index, Simpson index, and Chao1 index) were calculated using the R vegan package (Dixon, 2003) in R 4.2.0 (R Core Team, 2013) based on the OTU table.

Results

Evaluation of the specificity of single copepod species fragments amplified by DGGE

Agarose gel electrophoresis results showed that all copepod species could amplify target bands of the expected size, whereas non-copepod species could not amplify the target bands (Fig. 1A). The DGGE results showed that except for the bands of *Cyclops vicinus vicinus* and *Thermocyclops taihokuensis*, which were too close to distinguish, the bands of other copepod species could be clearly distinguished, except for the PCR amplification product of *Sinodiaptomus* sp., which contained weak bands, while those of the other species contained a single band (Fig. 1B). These results suggest that the designed

primers can specifically amplify copepod species and obtain a single amplification sequence for each species. Based on the known sequences of copepods, it is estimated that the primer pair Cop18SF/Cop18SR can effectively amplify the 18S gene sequences of most copepods, except for the genus *Acartia*, which is highly divergent from other copepod species. Furthermore, 92% of the copepod sequences mismatched with the specific primer Cop18SR by no more than two bases and never mismatched with the last base of the 3' end of the primer. Even if the sequence of *Microcyclops* sp. (SP9) has three bases mismatched with Cop18SR, it can be amplified by the primer pair Cop18SF/Cop18SR (Fig. 1A).

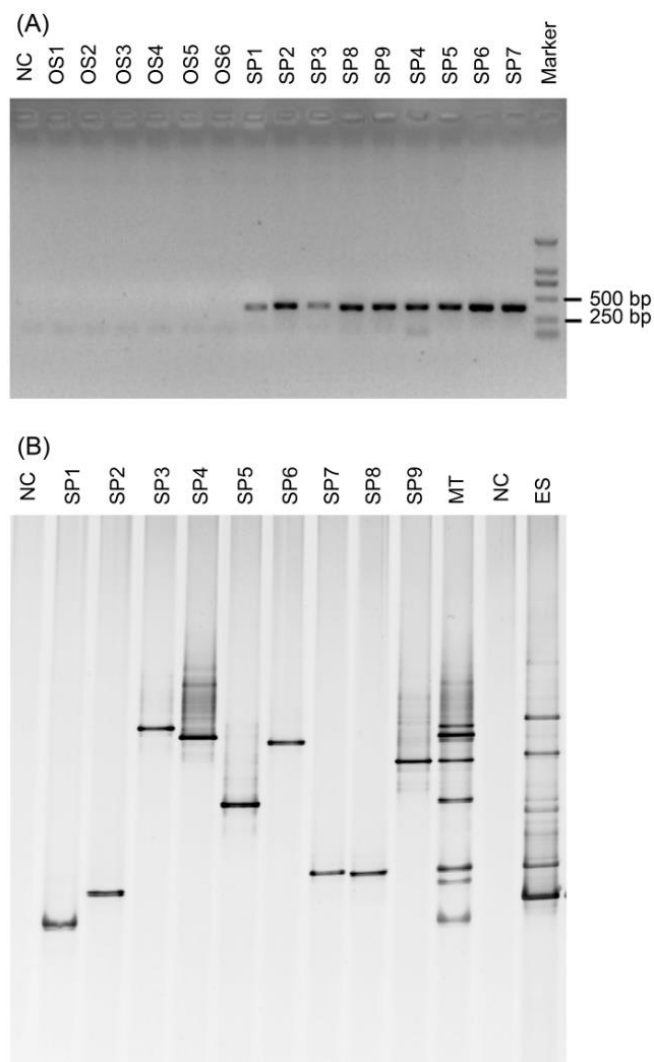


Figure 1. Agarose gel (1.2%; A) and DGGE fingerprints (B) show the detection of PCR products amplified from copepod species and out-group organisms. The concentration range of the denaturant was from 30% to 60%. NC, negative control; SP1, *Sinergasilus* sp.; SP2, *Mesocyclops leuckartii*; SP3, *Neutrodiaptomus incongruens*; SP4, *Sinodiaptomus* sp.; SP5, *Paracyclops fimbriatus*; SP6, *Eucyclops* sp.; SP7, *Cyclops vicinus vicinus*; SP8, *Thermocyclops taihokuensis*; SP9, *Microcyclops* sp.; OS1, A species of *Nematoda*; OS2, *Tetrahymena pyriformis* GL; OS3, *Escherichia coli*; OS4, *Asplanchna* sp.; OS5, *Chlorella pyrenoidosa*; OS6, *Moina micrura*; MT, a mixture of PCR products from the 9 copepod species; ES, a freshwater planktonic assemblage collected from East Lake (114.37 E, 30.55 N) in Wuhan, China

Copepod composition in mariculture pond water

Morphological taxonomy analysis showed that only two (*Sinocalanus tenellus* and *Oithona similis*), two (*O. similis* and *Pseudodiaptomus poplesia*), three (*O. similis*, *P. poplesia*, and *Schmackeria poplesia*), two (*O. similis* and *Eurytemora* sp.), two (*O. similis* and *P. poplesia*), and one (*O. similis*) copepod species and many larvae were detected in the P1, P2, P3, P4, P5, and P6 samples, respectively (Appendix 3). In addition, these samples contained some highly abundant non-copepod zooplankton, such as *Polydora latispinosa*, rotifers, and protozoa (Appendix 3).

A total of 327 *de novo* OTUs were obtained from plankton community samples from six mariculture ponds using three primer pairs in this study, of which 93 OTUs were assigned to Copepoda (Appendix 3) and 78 OTUs dominated the communities (Fig. 2). A heatmap combined with cluster analysis showed that the samples were clustered strictly according to the primer pairs (Fig. 2). The primer pair Uni18S/Uni18SR nonspecifically amplified many DNA sequences from bacteria (such as *Mycobacterium*, *Rhodococcus erythropolis*, *Microbacterium*, *Marivita*, and *Phaeodactylibacter xiamenensis*), whereas the primer pair LSUCop-D2F/LSUCop-D2R abnormally enriched OTU denovo438, which was an unidentified Eukaryota plankton, and the number of sequences it contained accounted for $78.12 \pm 5.45\%$ of the total number of analysis sequences (Fig. 2). Considering that the OTUs may not be phylogenetically annotated because of the selection of the reference dataset, we researched the DNA sequences corresponding to the OTUs in the GenBank database using Blastn and found that the sequences were most likely from *Eurytemora* (E-value = 0, query cover = 100%, and percent identity = 99.76%). Moreover, some non-copepod Eukaryota, such as Spionida (Polychaeta), Ploimida (Rotifera), Hypocreales (Fungi), *Zoothamnium* (Protozoa), *Myrionecta* (Protozoa), and *Eufolliculina* (Protozoa), were also detected using the primer pair Uni18S/Uni18SR; however, there were only three OTUs ($5.88 \pm 2.32\%$ analysed sequences) in Copepoda, which were *Eurytemora pacifica* (OTU denovo943), *Acartia pacifica* (OTU denovo1562), and Calanoida (OTU denovo18) (Appendix 4). Planktons with the highest abundances that were detected using the primer pair Cop18SF/Cop18SR were *Eurytemora pacifica* (denovo454) and two unidentified copepod OTUs (denovo1258 and denovo1578; Fig. 2). These results suggest that the OTU denovo438 detected using the primer pair LSUCop-D2F/LSUCop-D2R was devised into multiple OTUs using the primer pair Cop18SF/Cop18SR. Notably, 26 OTUs were classified as *E. pacifica* (Calanoida, Temoridae) at 97% sequence identity using the primer pair Cop18SF/Cop18SR (Appendix 4); thus, *E. pacifica* probably had high intraspecific genetic diversity. Another possibility is that multiple or one cryptic species are closely related (probably of the same genus or family) to *E. pacifica* in these cultured ponds. Based on morphological identification, an adult copepod belonging to the genus *Eurytemora* was found in only one of the sampled ponds (Appendix 3). However, the OTU of *E. pacifica* was detected in all ponds using the Cop18SF/Cop18SR primer pair. This indicated that these OTUs were probably from copepod larvae (copepodites and nauplii), which had not been morphologically identified. Other copepods, such as *Bradya* sp. (Harpacticoida; OTU denovo555), *Paracyclops nana* (Cyclopoida; OTU denovo456), *Parvocalanus crassirostris* (Calanoida; OTU denovo1296), *Nitokra spinipes* (Harpacticoida; OTU denovo1476), *Sinocalanus sinensis* (Calanoida; OTU denovo1595), and *Ameira scotti* (Harpacticoida; OTU denovo471) were also detected and dominated the plankton communities revealed using the Cop18SF/Cop18SR primer pair.

correlation analysis, $P < 0.05$), whereas salinity exhibited significant negative correlations with the OTUs that were significantly correlated with that factor (Pearson correlation analysis, $P < 0.05$; Fig. 4). Although there was a more complex correlation pattern between these environmental factors and the plankton communities analysed by the primer pair Uni18S/Uni18SR, NO_3^- -N and NH_4^+ -N exhibited significant positive correlations with the OTUs that were significantly correlated with these factors (Pearson correlation analysis, $P < 0.05$; Fig. 4).

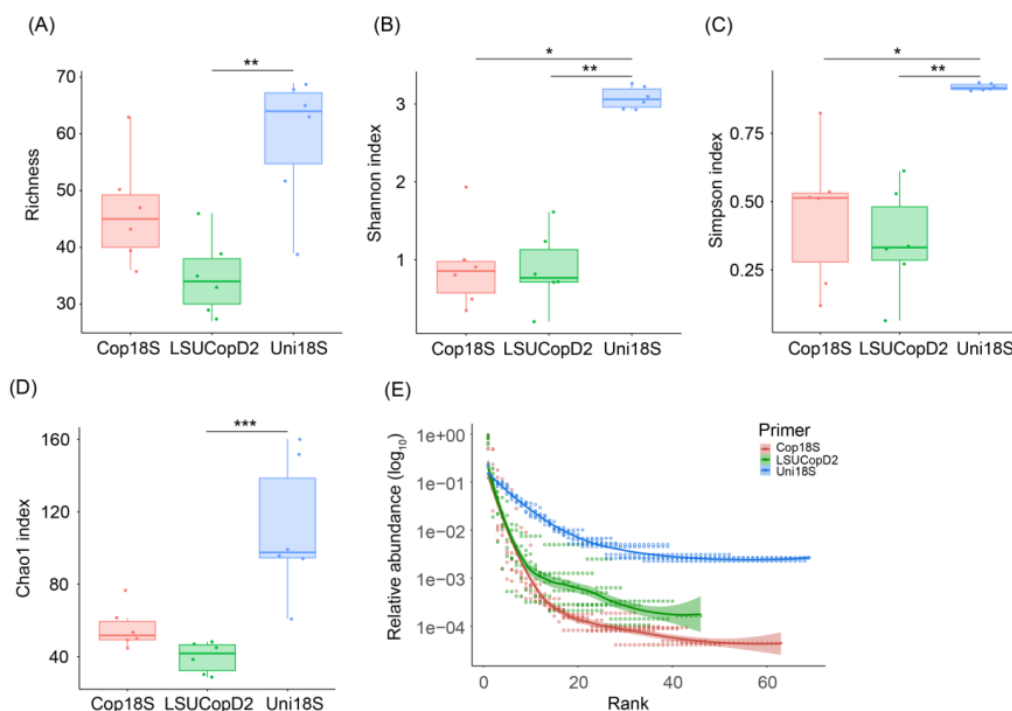


Figure 3. α -Diversity indices and rank-abundance curve of copepod and other plankton communities in the mariculture pond water. (A) Species richness; (B) Shannon index; (C) Simpson index; (D) Chao1 index; (E) rank-abundance curve

Plankton communities revealed by the primer pair Cop18SF/Cop18SR were composed of various copepod OTUs, among which *E. pacifica* (OTU denovo517), a species of Harpacticoida (OTU denovo1058), and an unidentified copepod OTU (OTU denovo1372) were significantly positively correlated with PO_4^{3+} -P, NO_2^- -N, NH_4^+ -N, and IN (Fig. 4A and Appendix 4). Many copepod OTUs were significantly positively correlated with SS and NO_3^- -N, including *Parvocalanus crassirostris* (OTU denovo1296), *Sinocalanus sinensis* (OTU denovo1595), *Nitokra spinipes* (OTU denovo1476), *Bradya* sp. (OTUs denovo555, denovo1455, and denovo42), a species of Calanoida (OTU denovo85), a species of Harpacticoida (OTUs denovo800 and denovo748), a species of Siphonostomatoida (OTU denovo609), and an unidentified copepod OTU (OTU denovo1573) (Fig. 4A and Appendix 4). *Tachidius triangularis* (OTUs denovo891 and denovo1498), a species of Siphonostomatoida (OTU denovo522), and several unidentified copepod OTUs (OTUs denovo326, denovo1344, denovo702, denovo1228, and denovo1545) were significantly negatively correlated with salinity (Fig. 4A and Appendix 4), suggesting that these OTUs are freshwater or brackish water copepods.

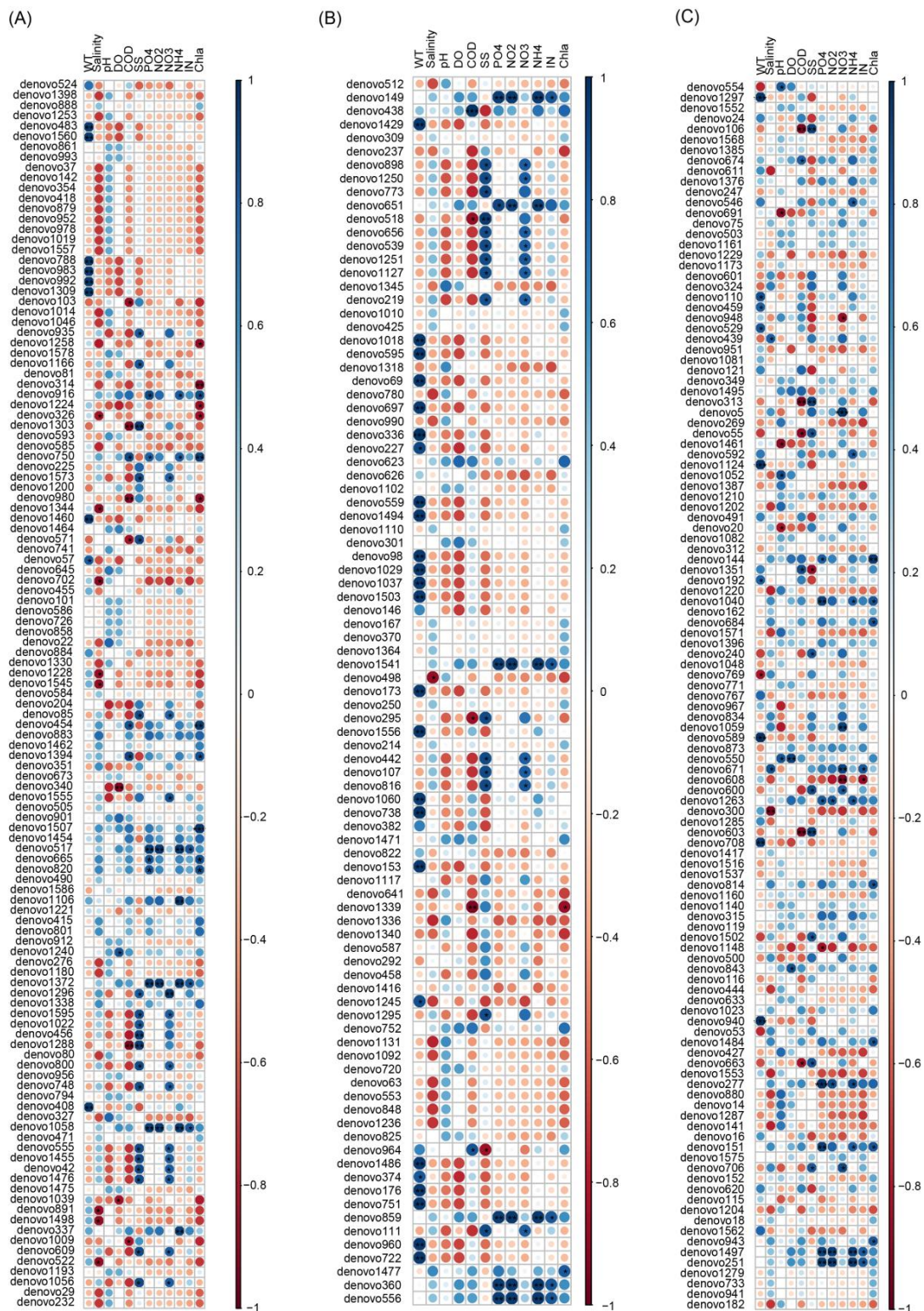


Figure 4. Correlations between environmental factors and plankton community composition in mariculture ponds detected using different primer pairs

Discussion

The copepod community has attracted the attention of ecologists and environmentalists as an important part of aquatic ecosystems (Chew and Chong, 2011; Hirai et al., 2015; Dahms et al., 2016; McGinty et al., 2021). Owing to their high nutritional content, some copepod species have also been studied in depth as feed for cultured fish (Payne and Rippingale, 2000; Blanda et al., 2017; Hansen, 2017; Altaff and Vijayaraj, 2021). For instance, the provision of copepod nauplii in the early larval diet often increases survival in some fish, such as red snappers, groupers, and seabass (Payne and Rippingale, 2000; Rajkumar and Kumaraguru vasagam, 2006). The provision of copepods in the early larval diet decreases malpigmentation in halibut (*Hippoglossus hippoglossus*) and increases stress resistance in mahi-mahi (*Coryphaena hippurus*) (Kraul et al., 1993; McEvoy et al., 1998). Therefore, copepods are considered to be an ideal feed for fish at an early stage. However, little attention has been given to changes in copepod communities in aquaculture water, and this is mainly limited by the copepod analysis method. In this study, we designed a pair of primers for the analysis of copepod communities to promote the investigation of copepods in aquaculture water.

Morphological identification is a commonly used method in ecological research on copepods (Beltrão et al., 2011; García-Comas et al., 2016; Blanda et al., 2017; Hure et al., 2020; McGinty et al., 2021). However, the complex life-history traits, high species diversity, and relatively small size have made the morphological identification of copepods extremely difficult. Nonetheless, because taxonomic identification of copepod nauplii is even more difficult, molecular taxonomic identification methods have been introduced for the study of copepods (Brown et al., 2016; Hirai et al., 2017; Xue et al., 2018). The primer pair Uni18S/Uni18SR is commonly used to analyse zooplankton communities because of its ability to recover a wide range of zooplankton groups (Zhan et al., 2014; Gao et al., 2020). However, our results indicate that the primer pair nonspecifically amplified the bacterial genomic sequences, thus interfering with the results, and significantly underestimated the abundance and α -diversity of copepods. Other primer pairs have also been used to analyse zooplankton communities. Using universal primers of the zooplankton community to analyse copepod communities inevitably reduces the efficiency of the analysis. Therefore, researchers have designed copepod-specific primers to analyse copepod community structures in aquatic environments (Hirai et al., 2017). The primer pair for the LSU D2 region, LSUCop-D2F/LSUCop-D2R, was designed and assessed to analyse copepod communities (Hirai et al., 2015; Hirai et al., 2017). However, because of the relative shortage of LSU datasets and the relatively limited resolution of the primer pair LSUCop-D2F/LSUCop-D2R for copepods, our results showed that most of the sequences obtained based on the primer pair LSUCop-D2F/LSUCop-D2R were not well distinguished and phylogenetically annotated. Therefore, we were unable to assess the specificity of this primer pair for copepods. We designed a pair of copepod-specific primers Cop18SF/Cop18SR to be used to preferentially amplify copepod plankton except in the genus *Acartia*. Using the primer pair Cop18SF/Cop18SR, four orders of copepods (Cyclopoida, Calanoida, Harpacticoida, and Siphonostomatoida) were detected in plankton samples from mariculture ponds in this study. Although *E. pacifica* was classified into 26 OTUs with 97% sequence identity using the primer pair Cop18SF/Cop18SR, other results indicated that the primer pair Cop18SF/Cop18SR was superior to the other two primer pairs. Of course, we do not deny the value of the primer pair LSUCop-D2F/LSUCop-D2R designed by Hirai et al. (2015, 2017) for studying copepod communities. This is because different gene markers and

primers designed based on these gene sequences have their own advantages and disadvantages, which involve taxonomic resolution, specificity, universality, and other aspects that are difficult to balance. In addition to the large and small subunit genes of ribosomes compared in this study, there are also other genetic markers commonly used in biodiversity research, such as mitochondrial cytochrome c oxidase subunit I (COI) gene. The COI gene is indeed a useful diagnostic character for species-level identification of zooplankton including copepods (Laakmann et al., 2013; Prosser et al., 2013; Blanco-Bercial et al., 2014). Due to the high degree of variation of the COI gene, it also has advantages in discovering cryptic species (Baek et al., 2016). However, the relatively conserved 18S gene has an advantage over the highly variable COI gene in designing taxa-specific primers that are universal within the target taxa at a high taxonomic level. The purpose of this study is to design specific primers for the copepods, to ensure the specificity of the taxon and to ensure the generality in the copepoda as much as possible. Therefore, we designed copepod-specific primers based on the 18S gene. We suggest that appropriate primers or combinations of multiple primers should be used according to the specific research needs to obtain better results. For example, when the selected marker genes have high sequence specificity, it is necessary to combine multiple primers to analyse biodiversity with specific functions (Chi et al., 2018). In order to obtain higher taxonomic resolution, it is also recommended to use multiple genetic markers (Loos and Nijland, 2020). Multiple primer sets are conducive to a more comprehensive understanding of the community structure (Bradley et al., 2016; Sawaya et al., 2018). In terms of improving the detection rates of species, especially for rare target taxa, multiple primer sets have significant advantages over single primer pair (Govender et al., 2022). Compared with universal primer set, the use of taxa-specific primers can also improve the detection rates of target taxa (Govender et al., 2022).

The greatest challenge faced by fish farmers is to control the many complex abiotic and biotic factors that influence the success of fish rearing. An example of the complexity involved in managing aquatic systems is the need to control copepod communities by manipulating the pond environment (Piasecki et al., 2004). In this study, we designed a new primer pair, Cop18SF/Cop18SR, to analyse copepod communities in aquaculture environments through high-throughput sequencing technology, which provided an important method for the subsequent analysis of the impact of abiotic and biological factors on copepod communities and the establishment of a technology to control copepod communities.

The phylogenetic system of zooplankton does not strictly describe species phylogeny according to the order of phylum, class, order, family, genus, and species, which greatly hinders the phylogenetic analysis of sequences through database searches. Therefore, we suggest building a reference database of genetic information and phylogeny of species unique to zooplankton, which will help conduct a more in-depth and large-scale investigation of zooplankton and copepod communities. Our results also indicated that the primers had a significant impact on the analysis of copepod community structure. Therefore, it is important to select appropriate primers for the analysis of copepod community structure. Although the primer Cop18SF/Cop18SR has only been verified in the copepod community in mariculture ponds, we believe that this primer pair can also be used for the study of the copepod community structure in marine and freshwater environments.

Conclusions

We designed a copepod-specific primer pair, Cop18SF and Cop18SR, and used it to analyse the copepod community structure in six mariculture pond waters. Although *E. pacifica* was classified into 26 OTUs with 97% sequence identity using our designed primer pair Cop18SF/Cop18SR, other results indicated the superiority of the designed primer pair to the other two primer pairs. This primer pair can be used to analyse the dynamic changes in the copepod community structure and the relationship between the community structure and abiotic and biological factors in aquaculture water.

Acknowledgments. This research was funded by the Sichuan Science and Technology Program (Grant No. 2023NSFSC1701), and Project of Science and Technology Department of Sichuan Province (2021YJ0112). Thanks to Dr. Yuhe Yu from the Institute of Hydrobiology, Chinese Academy of Sciences for his inspiration and help in this research.

REFERENCES

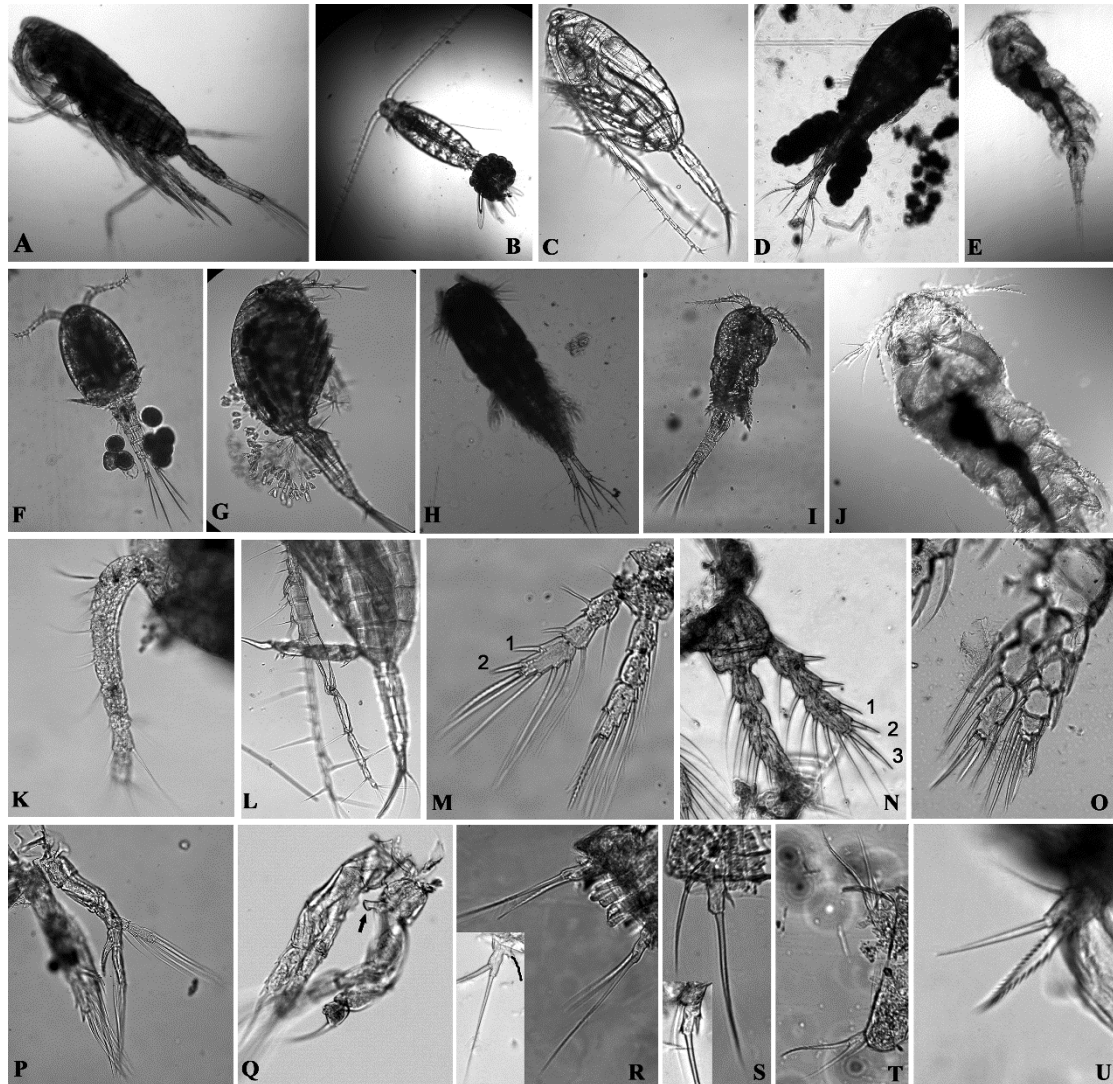
- [1] Altaff, K., Vijayaraj, R. (2021): Micro-algal diet for copepod culture with reference to their nutritive value - a review. – *Journal of Current Research and Review* 13(7): 86-96.
- [2] Atkinson, A. (1996): Subantarctic copepods in an oceanic, low chlorophyll environment: Ciliate predation, food selectivity and impact on prey populations. – *Marine Ecology Progress Series* 130: 85-96.
- [3] Baek, S. Y., Jang, K. H., Choi, E. H., Ryu, S. H., Kim, S. K., Lee, J. H., Lim, Y. J., Lee, J., Jun, J., Kwak, M., Lee, Y. S., Hwang, J. S., Venmathi Maran, B. A., Chang, C. Y., Kim, I. H., Hwang, U. W. (2016): DNA Barcoding of Metazoan Zooplankton Copepods from South Korea. – *PLoS One* 11(7): e0157307.
- [4] Banse, K. (1995): Zooplankton: Pivotal role in the control of ocean production. – *ICES Journal of Marine Science* 52(3-4): 265-277.
- [5] Baumgartner, M. F., Tarrant, A. M. (2017): The Physiology and Ecology of Diapause in Marine Copepods. – *Annual review of marine science* 9: 387-411.
- [6] Beaugrand, G., Brander, K. M., Alistair Lindley, J., Souissi, S., Reid, P. C. (2003): Plankton effect on cod recruitment in the North Sea. – *Nature* 426(6967): 661-664.
- [7] Beltrão, R., Monde, M., Ueda, H. (2011): Characteristics and regional classification of the copepod community in Ariake Bay with note on comparison with 3 decades ago. – *Journal of Oceanography* 67(1): 47-58.
- [8] Blanco-Bercial, L., Cornils, A., Copley, N., Bucklin, A. (2014): DNA barcoding of marine copepods: assessment of analytical approaches to species identification. – *PLoS currents* 6.
- [9] Blanda, E., Drillet, G., Huang, C. C., Hwang, J. S., Hojgaard, J. K., Jakobsen, H. H., Rayner, T. A., Su, H. M., Hansen, B. W. (2017): An analysis of how to improve production of copepods as live feed from tropical Taiwanese outdoor aquaculture ponds. – *Aquaculture* 479: 432-441.
- [10] Bradley, I. M., Pinto, A. J., Guest, J. S. (2016): Design and Evaluation of Illumina MiSeq-Compatible, 18S rRNA Gene-Specific Primers for Improved Characterization of Mixed Phototrophic Communities. – *Applied and Environmental Microbiology* 82(19): 5878-5891.
- [11] Bron, J. E., Frisch, D., Goetze, E., Johnson, S. C., Lee, C. E., Wyngaard, G. A. (2011): Observing copepods through a genomic lens. – *Frontiers in Zoology* 8(1): 22.
- [12] Brown, E. A., Chain, F. J. J., Zhan, A. B., MacIsaac, H. J., Cristescu, M. E. (2016): Early detection of aquatic invaders using metabarcoding reveals a high number of non-indigenous species in Canadian ports. – *Diversity and Distributions* 22(10): 1045-1059.

- [13] Brun, P., Payne, M. R., Kiorboe, T. (2016): Trait biogeography of marine copepods - an analysis across scales. – *Ecology letters* 19(12): 1403-1413.
- [14] Caporaso, J. G., Kuczynski, J., Stombaugh, J., Bittinger, K., Bushman, F. D., Costello, E. K., Fierer, N., Pena, A. G., Goodrich, J. K., Gordon, J. I., Huttley, G. A., Kelley, S. T., Knights, D., Koenig, J. E., Ley, R. E., Lozupone, C. A., McDonald, D., Muegge, B. D., Pirrung, M., Reeder, J., Sevinsky, J. R., Turnbaugh, P. J., Walters, W. A., Widmann, J., Yatsunencko, T., Zaneveld, J., Knight, R. (2010): QIIME allows analysis of high-throughput community sequencing data. – *Nat Methods* 7(5): 335-336.
- [15] Chen, X., He, D., Zhou, L., Cao, Y., Li, Z. (2020): Influence of hydropower stations on the water microbiota in the downstream of Jinsha River, China. – *PeerJ* 8: e9500.
- [16] Chew, L. L., Chong, V. C. (2011): Copepod community structure and abundance in a tropical mangrove estuary, with comparisons to coastal waters. – *Hydrobiologia* 666(1): 127-143.
- [17] Chi, X. Q., Wang, L., Guo, R., Zhao, D., Li, J., Zhang, Y., Jiao, N. (2018): RuBisCO large subunit gene primers for assessing the CO₂-assimilating planktonic community structure in Jiaozhou Bay, China. – *FEMS microbiology letters* 365(14).
- [18] Crustacean Research Group (1979): *Fauna Sinica: Arthropoda, Crustacea, Freshwater copepoda*. – Institute of Zoology, Chinese Academy of Sciences. Science Press, Beijing.
- [19] Dahms, H. U., Won, E. J., Kim, H. S., Han, J., Park, H. G., Souissi, S., Raisuddin, S., Lee, J. S. (2016): Potential of the small cyclopoid copepod *Paracyclopina nana* as an invertebrate model for ecotoxicity testing. – *Aquatic toxicology* 180: 282-294.
- [20] Dixon, P. (2003): VEGAN, a package of R functions for community ecology. – *Journal of Vegetation Science* 14(16): 927-930.
- [21] Frangoulis, C., Christou, E. D., Hecq, J. H. (2005): Comparison of marine copepod outfluxes: nature, rate, fate and role in the carbon and nitrogen cycles. – *Advances in marine biology* 47: 253-309.
- [22] Frangoulis, C., Skliris, N., Lepoint, G., Elkalay, K., Goffart, A., Pinnegar, J. K., Hecq, J. H. (2011): Importance of copepod carcasses versus faecal pellets in the upper water column of an oligotrophic area. – *Estuarine Coastal and Shelf Science* 92(3): 456-463.
- [23] Gao, Y. C., Li, H. T., Wang, X. C., Sun, Y., Zhan, A. B., Aileen, T. S. H., Li, H. J. (2020): Research on zooplankton diversity using DNA-based metabarcoding technique: a case study in the Yalvjian Estuary. – *Acta Ecologica Sinica* 40(11): 3822-3832.
- [24] García-Comas, C., Lee, Y.-C., Chang, C.-Y., Gong, G.-C., Hsieh, C.-H. (2016): Comparison of copepod species-based and individual-size-based community structuring. – *Journal of Plankton Research* 38(4): 1006-1020.
- [25] Glippa, O., Souissi, S., Denis, L., Lesourd, S. (2011): Calanoid copepod resting egg abundance and hatching success in the sediment of the Seine estuary (France). – *Estuarine Coastal and Shelf Science* 92(2): 255-262.
- [26] Govender, A., Singh, S., Groeneveld, J., Pillay, S., Willows-Munro, S. (2022): Experimental validation of taxon-specific mini-barcode primers for metabarcoding of zooplankton. – *Ecological applications : a publication of the Ecological Society of America* 32(1): e02469.
- [27] Hansen, B. W. (2017): Advances using Copepods in Aquaculture. – *Journal of Plankton Research* 39(6): 972-974.
- [28] Hirai, J., Kuriyama, M., Ichikawa, T., Hidaka, K., Tsuda, A. (2015): A metagenetic approach for revealing community structure of marine planktonic copepods. – *Molecular Ecology Resources* 15(1): 68-80.
- [29] Hirai, J., Nagai, S., Hidaka, K. (2017): Evaluation of metagenetic community analysis of planktonic copepods using Illumina MiSeq: Comparisons with morphological classification and metagenetic analysis using Roche 454. – *PLoS One* 12(7): e0181452.
- [30] Hirst, A. G., Bunker, A. J. (2003): Growth of marine planktonic copepods: Global rates and patterns in relation to chlorophyll a, temperature, and body weight. – *Limnology and Oceanography* 48(5): 1988-2010.

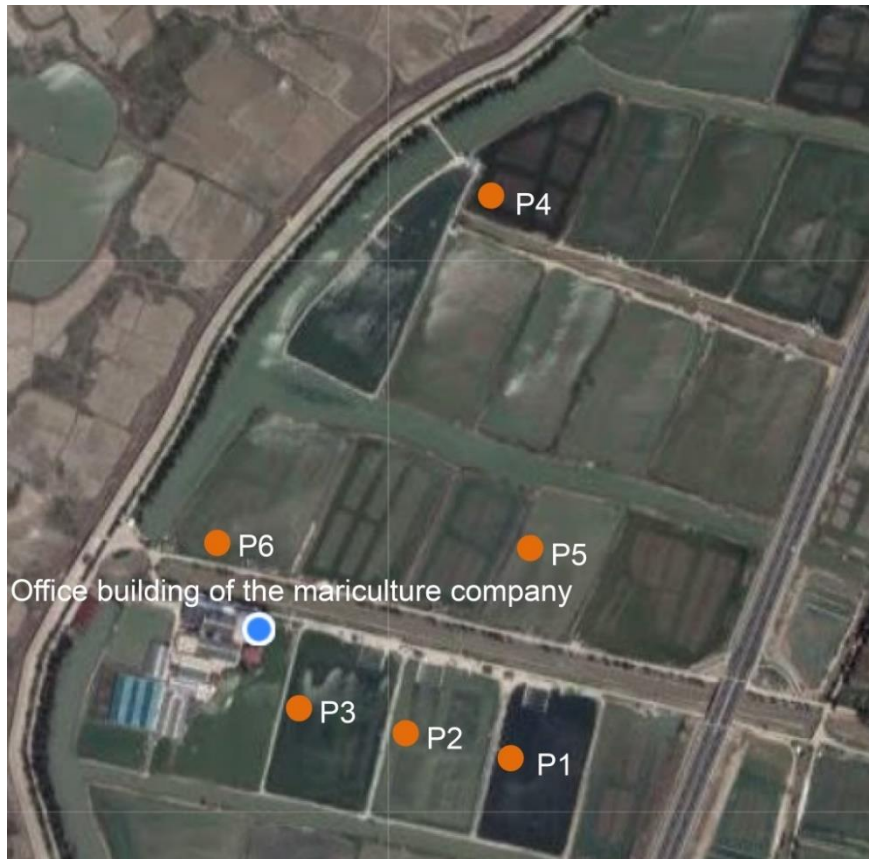
- [31] Huang, X. F. (2000): observation and analysis of lake ecology. – China Standard Press, Beijing.
- [32] Hure, M., Batistic, M., Kovacevic, V., Bensi, M., Garic, R. (2020): Copepod Community Structure in Pre- and Post-Winter Conditions in the Southern Adriatic Sea (NE Mediterranean). – Journal of Marine Science and Engineering 8(8).
- [33] Kiørboe, T. (1998): Population regulation and role of mesozooplankton in shaping marine pelagic food webs. – Hydrobiologia 363: 13-27.
- [34] Kraul, S., Brittain, K., Cantrell, R., Nagao, T., Ako, H., Ogasawara, A., Kitagawa, H. (1993): Nutritional factors affecting stress resistance in the larval mahimahi *Coryphaena hippurus*. – Journal of the World Aquaculture Society 24(2): 186-193.
- [35] Kwok, K. W. H., Souissi, S., Dur, G., Won, E. J., Lee, J. S. (2015): Copepods as reference species in estuarine and marine waters. – In: Aquatic Ecotoxicology: Advancing Tools for Dealing with Emerging Risks. Academic Press, Pittsburgh, USA.
- [36] Laakmann, S., Gerdts, G., Erler, R., Knebelsberger, T., Martinez Arbizu, P., Raupach, M. J. (2013): Comparison of molecular species identification for North Sea calanoid copepods (Crustacea) using proteome fingerprints and DNA sequences. – Molecular Ecology Resources 13(5): 862-876.
- [37] Li, J. J., Li, J. L., Ni, J. J., Zhang, C. B., Jia, J. L., Wu, G. Y., Sun, H. Z., Wang, S. Z. (2022): Berberine Relieves Metabolic Syndrome in Mice by Inhibiting Liver Inflammation Caused by a High-Fat Diet and Potential Association With Gut Microbiota. – Frontiers in Microbiology 12.
- [38] Lin, X., Zhang, J., Chen, H., Han, L. (2021): Determination of available phosphorus in alkaline soil by molybdenum blue spectrophotometry. – IOP Conf. Series: Earth and Environmental Science 781: 052003.
- [39] Liu, Q., Lai, Z., Wang, C., Ni, J., Gao, Y. (2022): Seasonal variation significantly affected bacterioplankton and eukaryoplankton community composition in Xijiang River, China. – Environmental monitoring and assessment 194(2): 55.
- [40] Magoc, T., Salzberg, S. L. (2011): FLASH: fast length adjustment of short reads to improve genome assemblies. – Bioinformatics 27(21): 2957-2963.
- [41] McEvoy, L. A., Naess, T., Lie, O. (1998): Lipid and fatty acid composition of normal and malpigmented atlantic halibut (*Hippoglossus hippoglossus*) fed enriched *Artemia*: a comparison with fry fed wild copepods. – Aquaculture 163: 237-250.
- [42] McGinty, N., Barton, A. D., Record, N. R., Finkel, Z. V., Johns, D. G., Stock, C. A., Irwin, A. J. (2021): Anthropogenic climate change impacts on copepod trait biogeography. – Global change biology 27(7): 1431-1442.
- [43] Ni, J., Yu, Y., Feng, W., Yan, Q., Pan, G., Yang, B., Zhang, X., Li, X. (2010): Impacts of algal blooms removal by chitosan-modified soils on zooplankton community in Taihu Lake, China. – Journal of Environmental Sciences 22(10): 1500-1507.
- [44] Ni, J. J., Li, X. J., Chen, F., Wu, H. H., Xu, M. Y. (2018): Community Structure and Potential Nitrogen Metabolisms of Subtropical Aquaculture Pond Microbiota. – Applied Ecology and Environmental Research 16(6): 7687-7697.
- [45] Ni, J. J., Huang, R., Zhou, H. F., Xu, X. P., Li, Y., Cao, P. H., Zhong, K. B., Ge, M., Chen, X. X., Hou, B. H., Yu, M., Peng, B. G., Li, Q., Zhang, P., Gao, Y. (2019): Analysis of the Relationship Between the Degree of Dysbiosis in Gut Microbiota and Prognosis at Different Stages of Primary Hepatocellular Carcinoma. – Frontiers in Microbiology 10.
- [46] Ni, J., Fu, C., Huang, R., Li, Z., Li, S., Cao, P., Zhong, K., Ge, M., Gao, Y. (2021): Metabolic syndrome cannot mask the changes of faecal microbiota compositions caused by primary hepatocellular carcinoma. – Letters in Applied Microbiology 73(1): 73-80.
- [47] Nisar, U., Peng, D., Mu, Y., Sun, Y. (2022): A Solution for Sustainable Utilization of Aquaculture Waste: A Comprehensive Review of Biofloc Technology and Aquamimicry. – Frontiers in Nutrition 8: 791738.
- [48] Payne, M. F., Rippingale, R. J. (2000): Evaluation of diets for culture of the calanoid copepod *Gladioferens imparipes*. – Aquaculture 187: 85-96.

- [49] Piasecki, W., Goodwin, A. E., Eiras, J. C., Nowak, B. F. (2004): Importance of Copepoda in freshwater aquaculture. – *Zoological Studies* 43(2): 193-205.
- [50] Prosser, S., Martinez-Arce, A., Elias-Gutierrez, M. (2013): A new set of primers for COI amplification from freshwater microcrustaceans. – *Molecular Ecology Resources* 13(6): 1151-1155.
- [51] Rajkumar, M., Kumaraguru vasagam, K. P. (2006): Suitability of the copepod, *Acartia clausi* as a live feed for Seabass larvae (*Lates calcarifer* Bloch): Compared to traditional live-food organisms with special emphasis on the nutritional value. – *Aquaculture Research* 261: 649-658.
- [52] Sawaya, N. A., Djurhuus, A., Closek, C. J., Hepner, M., Olesin, E., Visser, L., Kelble, C., Hubbard, K., Breitbart, M. (2019): Assessing eukaryotic biodiversity in the Florida Keys National Marine Sanctuary through environmental DNA metabarcoding. – *Ecology and Evolution* 9(3): 1029-1040.
- [53] Takenaka, Y., Yamaguchi, A., Tsuruoka, N., Torimura, M., Gojobori, T., Shigeri, Y. (2012): Molecular Biology and Evolution. – *Molecular biology and evolution* 29(6): 1669-1681.
- [54] Team, R. C. (2013): R Foundation for Statistical Computing. – Vienna.
- [55] van der Loos, L. M., Nijland, R. (2021): Biases in bulk: DNA metabarcoding of marine communities and the methodology involved. – *Molecular Ecology* 30(13): 3270-3288.
- [56] Wang, J., Li, H., Zhang, W., Liu, C., Liu, B., Sun, H., Zhang, Q. (2019): Comparison of two colorimetric methods for the determination of trace ammonia in water. – *Univ. Chem.* 34(3): 36-41.
- [57] Wu, S., Xiong, J., Yu, Y. (2015): Taxonomic resolutions based on 18S rRNA genes: a case study of subclass copepoda. – *PLoS One* 10(6): e0131498.
- [58] Wu, L., Shu, F., Ou, Z., Chen, Q., Wang, L., Wang, H., Xu, Z. (2019): Compositions of Prokaryote Communities and Their Relationship to Physiochemical Factors in December in Chaohu Lake and Three Urban Rivers in China. – *Applied Ecology and Environmental Research* 17(4): 7265-7281.
- [59] Wu, L., Ji, L., Chen, X. J., Ni, J. J., Zhang, Y., Geng, M. (2022): Distribution of Zooplankton Functional Groups in the Chaohu Lake Basin, China. – *Water* 14(13).
- [60] Xiang, J. G., He, T. Y., Wang, P. P., Xie, M., Xiang, J., Ni, J. J. (2018): Opportunistic pathogens are abundant in the gut of cultured giant spiny frog (*Paa spinosa*). – *Aquaculture Research* 49(5): 2033-2041.
- [61] Xue, Y., Chen, H., Yang, J. R., Liu, M., Huang, B., Yang, J. (2018): Distinct patterns and processes of abundant and rare eukaryotic plankton communities following a reservoir cyanobacterial bloom. – *The ISME journal* 12(9): 2263-2277.
- [62] Zhan, A. B., Hulak, M., Sylvester, F., Huang, X., Adebayo, A. A., Abbott, C. L., Adamowicz, S. J., Heath, D. D., Cristescu, M. E., MacIsaac, H. J. (2013): High sensitivity of 454 pyrosequencing for detection of rare species in aquatic communities. – *Methods in Ecology and Evolution* 4(6): 558-565.
- [63] Zhan, A. B., Bailey, S. A., Heath, D. D., MacIsaac, H. J. (2014): Performance comparison of genetic markers for high-throughput sequencing-based biodiversity assessment in complex communities. – *Molecular Ecology Resources* 14(5): 1049-1059.

APPENDIX



Appendix 1. Images of the copepods applied for primer verification. A) *Sinodiaptomus* sp. (male); B) *Neurodiaptomus incongruens* (female); C) *Neurodiaptomus incongruens* (male); D) *Thermocyclops taihokuensis* (female); E) *Sinergasilus* sp.; F) *Microcyclops* sp. (female); G) *Mesocyclops leuckarti* (female); H) *Cyclops vicinus vicinus* (male); I) *Paracyclops fimbriatus* (female); J) The head of *Sinergasilus* sp.; K) The first antenna of *Microcyclops* sp.; L) The right first antenna of the male *Neurodiaptomus incongruens*; M and N) The first (M) and the second (N) thoracic legs of *Cyclops vicinus vicinus*, and the limbs of the third section of exopodites were numbered; O) The fourth thoracic leg of *Eucyclops* sp.; P-U) The fifth thoracic legs of the female (P) and the male (Q) *Sinodiaptomus* sp. (arrow indicates the special spoon shaped projection of this species), *Mesocyclops leuckarti* (R) (the artificially drawn black line represents a bristle that was broken during dissection), *Cyclops vicinus vicinus* (S), *Thermocyclops taihokuensis* (T), and *Eucyclops* sp. (U)



Appendix 2. Geographic distributions of six sampling mariculture ponds. P1 (121.242415E, 28.283977N), P2 (121.241426E, 28.284048N), P3 (121.240472E, 28.284140N), P4 (121.242444E, 28.289016N), P5 (121.242693E, 28.285520N), and P6 (121.239553E, 28.286024N) are the sampling ponds located in Wenzhou City, China

Appendix 3. Composition of copepod and non-copepod zooplankton in mariculture ponds based on morphological taxonomy analysis

Taxa	P1	P2	P3	P4	P5	P6
<i>Sinocalanus tenellus</i> (Copepoda, Calanoida)	2	0	0	0	0	0
<i>Oithona similis</i> (Copepoda, Cyclopoida)	3	8	2	10	1	27
<i>Pseudodiaptomus poplesia</i> (Copepoda, Calanoida)	0	5	1	0	3	0
<i>Schmackeria poplesia</i> Shen (Copepoda, Calanoida)	0	0	3	0	0	0
<i>Eurytemora</i> sp. (Copepoda, Calanoida)	0	0	0	2	0	0
copepodites (Copepoda)	7	15	1	2	8	50
nauplii (Copepoda)	7	9	16	2	38	243
Brachyura zoea (Decapoda, Pleocyemata)	0	1	0	0	0	0
<i>Polydora latispinosa</i> (Polychaeta, Spionidae)	5981	194	460	12	56	37
Nematoda	3	4	12	4	10	0
Rotifera	0	0	68	0	0	19000
Protozoa	0	0	0	2446	3562	0

Appendix 4. OTU table shows the composition of plankton communities in mariculture ponds detected based on barcoding high-throughput sequencing

OTUID	Taxonomy	CopP1	CopP2	CopP3	CopP4	CopP5	CopP6
denovo454	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria; D6_Arthropoda; D7_Crustacea; D8_Maxillopoda; D9_Copepoda; D10_Calanoida; D11_Eurytemora pacifica	0.125156	0.177511	0.476209	0.488779	0.891005	0.938427
denovo1258	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria; D6_Arthropoda; D7_Crustacea; D8_Maxillopoda; D9_Copepoda	0.660966	0.250445	0.011033	0.495818	0.009923	0.01229
denovo1578	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria; D6_Arthropoda; D7_Crustacea; D8_Maxillopoda; D9_Copepoda	0.188828	0.116281	0.487341	0.006086	0.007843	0.01192
denovo555	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria; D6_Arthropoda; D7_Crustacea; D8_Maxillopoda; D9_Copepoda; D10_Harpacticoida; D11_Bradya sp. Greenland-RJH-2004	0.001473	0.234622	0.003202	0.001532	0.003201	0.003699
denovo1296	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria; D6_Arthropoda; D7_Crustacea; D8_Maxillopoda; D9_Copepoda; D10_Calanoida; D11_Parvocalanus crassirostris	0.000447	0.069095	0.000985	0.000373	0.00136	0.025114
denovo456	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria; D6_Arthropoda; D7_Crustacea; D8_Maxillopoda; D9_Copepoda; D10_Cyclopoida; D11_Paracyclopina nana	0.012368	0.090722	0.000739	0.000869	0.005602	0.001315
denovo584	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria; D6_Arthropoda; D7_Crustacea; D8_Maxillopoda; D9_Copepoda; D10_Calanoida	0.002143	0.000281	0.001034	0.000952	0.072583	0.001521
denovo1166	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria; D6_Arthropoda; D7_Crustacea; D8_Maxillopoda; D9_Copepoda	0.000491	0.028087	0.009851	0.000414	0.0004	0.001192
denovo1476	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria; D6_Arthropoda; D7_Crustacea; D8_Maxillopoda; D9_Copepoda; D10_Harpacticoida; D11_Nitokra spinipes	0	0.011329	0	8.28E-05	8.00E-05	0.000288

OTUID	Taxonomy	CopP1	CopP2	CopP3	CopP4	CopP5	CopP6
denovo1595	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria; D6_Arthropoda; D7_Crustacea; D8_Maxillopoda; D9_Copepoda; D10_Calanoida; D11_Sinocalanus sinensis	0	0.008988	9.85E-05	0.000166	0.00016	4.11E-05
denovo81	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria; D6_Arthropoda; D7_Crustacea; D8_Maxillopoda; D9_Copepoda	0.001429	0.000749	0.002414	4.14E-05	0	0
denovo800	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria; D6_Arthropoda; D7_Crustacea; D8_Maxillopoda; D9_Copepoda; D10_Harpacticoida	4.47E-05	0.004868	0	0	0.00016	4.11E-05
denovo956	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria; D6_Arthropoda; D7_Crustacea; D8_Maxillopoda; D9_Copepoda; D10_Harpacticoida	0	0.000374	0.002217	0	0	8.22E-05
denovo471	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria; D6_Arthropoda; D7_Crustacea; D8_Maxillopoda; D9_Copepoda; D10_Harpacticoida; D11_Ameira scotti	0	0	0	0	0.003361	8.22E-05
denovo883	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria; D6_Arthropoda; D7_Crustacea; D8_Maxillopoda; D9_Copepoda; D10_Calanoida; D11_Eurytemora pacifica	0	0.000281	9.85E-05	0.000331	0.00064	0.000699
denovo314	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria; D6_Arthropoda; D7_Crustacea; D8_Maxillopoda; D9_Copepoda	0.000848	0.000468	0	0.000538	0	0
denovo337	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria; D6_Arthropoda; D7_Crustacea; D8_Maxillopoda; D9_Copepoda; D10_Siphonostomatoida	0.000223	0.000187	0.000246	0.000373	0.00016	0.000534
denovo916	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria; D6_Arthropoda; D7_Crustacea; D8_Maxillopoda; D9_Copepoda	8.93E-05	0	0.000246	8.28E-05	0.0004	0.000781
denovo1394	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria; D6_Arthropoda;	0	0	0.000148	0.000207	0.00032	0.000329

OTUID	Taxonomy	CopP1	CopP2	CopP3	CopP4	CopP5	CopP6
denovo1462	D7_Crustacea; D8_Maxillopoda; D9_Copepoda; D10_Calanoida; D11_Eurytemora pacifica D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria; D6_Arthropoda; D7_Crustacea; D8_Maxillopoda; D9_Copepoda; D10_Calanoida; D11_Eurytemora pacifica	4.47E-05	9.36E-05	0.000148	8.28E-05	0.00064	0.000206
denovo524	D0_Eukaryota D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria; D6_Arthropoda; D7_Crustacea; D8_Maxillopoda; D9_Copepoda; D10_Harpacticoida; D11_Tachidius triangularis	4.47E-05	0	0.000296	0.000331	0	4.11E-05
denovo1039	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria; D6_Arthropoda; D7_Crustacea; D8_Maxillopoda; D9_Copepoda; D10_Harpacticoida; D11_Tachidius triangularis	0.000223	0.000187	0	0.00029	8.00E-05	4.11E-05
denovo1224	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria; D6_Arthropoda; D7_Crustacea; D8_Maxillopoda; D9_Copepoda	0.000223	0.000281	0	0.000331	0	0
denovo1475	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria; D6_Arthropoda; D7_Crustacea; D8_Maxillopoda; D9_Copepoda; D10_Harpacticoida; D11_Paralaophonte congenera	0	0	0.000739	0	8.00E-05	0
denovo326	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria; D6_Arthropoda; D7_Crustacea; D8_Maxillopoda; D9_Copepoda	0.000357	9.36E-05	0	0.000248	0	0
denovo1014	D0_Eukaryota; D1_Excavata; D2_Discoba; D3_Discicristata; D4_Euglenozoa	0.00058	0	9.85E-05	0	0	0
denovo593	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria; D6_Arthropoda; D7_Crustacea; D8_Maxillopoda; D9_Copepoda	0.000179	9.36E-05	0.000296	0	0	0
denovo1303	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria; D6_Arthropoda; D7_Crustacea; D8_Maxillopoda; D9_Copepoda	0.000179	0.000374	9.85E-05	0	0	0
denovo1455	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria; D6_Arthropoda; D7_Crustacea; D8_Maxillopoda; D9_Copepoda; D10_Harpacticoida; D11_Bradya sp. Greenland-RJH-2004	0	0.000936	0	0	0	0

OTUID	Taxonomy	CopP1	CopP2	CopP3	CopP4	CopP5	CopP6
denovo585	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria; D6_Arthropoda; D7_Crustacea; D8_Maxillopoda; D9_Copepoda	0.000179	0	0	0.000124	8.00E-05	0
denovo673	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria; D6_Arthropoda; D7_Crustacea; D8_Maxillopoda; D9_Copepoda; D10_Calanoida; D11_Eurytemora pacifica	4.47E-05	9.36E-05	0.000296	0	0	0
denovo351	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria; D6_Arthropoda; D7_Crustacea; D8_Maxillopoda; D9_Copepoda; D10_Calanoida; D11_Eurytemora pacifica	0	0.000281	0	4.14E-05	0.00024	0
denovo750	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria; D6_Arthropoda; D7_Crustacea; D8_Maxillopoda; D9_Copepoda	0	0	4.93E-05	4.14E-05	8.00E-05	0.000123
denovo1398	D0_Eukaryota	0.000268	0	0	0	0	0
denovo103	D0_Eukaryota; D1_Excavata	0.000134	9.36E-05	4.93E-05	0	0	0
denovo204	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria; D6_Arthropoda; D7_Crustacea; D8_Maxillopoda; D9_Copepoda; D10_Calanoida	4.47E-05	0.000187	0	8.28E-05	0	0
denovo340	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria; D6_Arthropoda; D7_Crustacea; D8_Maxillopoda; D9_Copepoda; D10_Calanoida; D11_Eurytemora pacifica	4.47E-05	9.36E-05	0	8.28E-05	8.00E-05	0
denovo901	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria; D6_Arthropoda; D7_Crustacea; D8_Maxillopoda; D9_Copepoda; D10_Calanoida; D11_Eurytemora pacifica	0	0	0.000148	0	0	8.22E-05
denovo935	D0_Eukaryota; D1_Opisthokonta	0	0.000374	0	4.14E-05	0	0
denovo1009	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria; D6_Arthropoda; D7_Crustacea; D8_Maxillopoda; D9_Copepoda; D10_Siphonostomatoida	0.000179	9.36E-05	0	0	0	0

OTUID	Taxonomy	CopP1	CopP2	CopP3	CopP4	CopP5	CopP6
denovo1022	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria; D6_Arthropoda; D7_Crustacea; D8_Maxillopoda; D9_Copepoda; D10_Cyclopoida; D11_Oithona davisae	0	0.000281	9.85E-05	0	0	0
denovo1200	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria; D6_Arthropoda; D7_Crustacea; D8_Maxillopoda; D9_Copepoda	4.47E-05	9.36E-05	9.85E-05	0	0	4.11E-05
denovo1344	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria; D6_Arthropoda; D7_Crustacea; D8_Maxillopoda; D9_Copepoda	0.000134	0	0	8.28E-05	0	0
denovo1460	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria; D6_Arthropoda; D7_Crustacea; D8_Maxillopoda; D9_Copepoda	0	0	0	0.000207	0	0
denovo29	Unclassified	0.000179	0	0	0	0	0
denovo57	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria; D6_Arthropoda; D7_Crustacea; D8_Maxillopoda; D9_Copepoda	4.47E-05	0	0	0.000124	0	0
denovo225	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria; D6_Arthropoda; D7_Crustacea; D8_Maxillopoda; D9_Copepoda	0	0.000187	9.85E-05	0	0	0
denovo483	D0_Eukaryota	0	0	0	0.000166	0	0
denovo517	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria; D6_Arthropoda; D7_Crustacea; D8_Maxillopoda; D9_Copepoda; D10_Calanoida; D11_Eurytemora pacifica	0	0	0	0	0	0.000164
denovo980	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria; D6_Arthropoda; D7_Crustacea; D8_Maxillopoda; D9_Copepoda	8.93E-05	9.36E-05	0	4.14E-05	0	0
denovo1046	D0_Eukaryota; D1_Excavata; D2_Discoba; D3_Discicristata; D4_Euglenozoa; D5_Euglenida; D6_Euglenophyceae; D7_Euglenea	0.000179	0	0	0	0	0
denovo1338	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria; D6_Arthropoda; D7_Crustacea; D8_Maxillopoda; D9_Copepoda; D10_Calanoida; D11_Parvocalanus crassirostris	0	0	0	0	0.00016	8.22E-05

OTUID	Taxonomy	CopP1	CopP2	CopP3	CopP4	CopP5	CopP6
denovo1454	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria; D6_Arthropoda; D7_Crustacea; D8_Maxillopoda; D9_Copepoda; D10_Calanoida; D11_Eurytemora pacifica	0	0	0	4.14E-05	8.00E-05	8.22E-05
denovo1464	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria; D6_Arthropoda; D7_Crustacea; D8_Maxillopoda; D9_Copepoda	0	0	0.000148	0	0	4.11E-05
denovo1507	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria; D6_Arthropoda; D7_Crustacea; D8_Maxillopoda; D9_Copepoda; D10_Calanoida; D11_Eurytemora pacifica	0	0	4.93E-05	0	8.00E-05	8.22E-05
denovo1555	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria; D6_Arthropoda; D7_Crustacea; D8_Maxillopoda; D9_Copepoda; D10_Calanoida; D11_Eurytemora pacifica	0	0.000187	0	4.14E-05	0	4.11E-05
denovo42	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria; D6_Arthropoda; D7_Crustacea; D8_Maxillopoda; D9_Copepoda; D10_Harpacticoida; D11_Bradya sp. Greenland-RJH-2004	0	0.000281	0	0	0	0
denovo408	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria; D6_Arthropoda; D7_Crustacea; D8_Maxillopoda; D9_Copepoda; D10_Harpacticoida	0	0	0	8.28E-05	0	4.11E-05
denovo455	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria; D6_Arthropoda; D7_Crustacea; D8_Maxillopoda; D9_Copepoda	4.47E-05	0	0	4.14E-05	0	4.11E-05
denovo505	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria; D6_Arthropoda; D7_Crustacea; D8_Maxillopoda; D9_Copepoda; D10_Calanoida; D11_Eurytemora pacifica	0	0	0	0	0.00024	0
denovo571	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria; D6_Arthropoda; D7_Crustacea; D8_Maxillopoda; D9_Copepoda	4.47E-05	9.36E-05	4.93E-05	0	0	0

OTUID	Taxonomy	CopP1	CopP2	CopP3	CopP4	CopP5	CopP6
denovo645	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria; D6_Arthropoda; D7_Crustacea; D8_Maxillopoda; D9_Copepoda	4.47E-05	0	9.85E-05	0	0	0
denovo665	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria; D6_Arthropoda; D7_Crustacea; D8_Maxillopoda; D9_Copepoda; D10_Calanoida; D11_Eurytemora pacifica	0	0	0	0	8.00E-05	8.22E-05
denovo702	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria; D6_Arthropoda; D7_Crustacea; D8_Maxillopoda; D9_Copepoda	4.47E-05	0	4.93E-05	4.14E-05	0	0
denovo741	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria; D6_Arthropoda; D7_Crustacea; D8_Maxillopoda; D9_Copepoda	4.47E-05	0	4.93E-05	0	8.00E-05	0
denovo748	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria; D6_Arthropoda; D7_Crustacea; D8_Maxillopoda; D9_Copepoda; D10_Harpacticoida	0	0.000281	0	0	0	0
denovo794	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria; D6_Arthropoda; D7_Crustacea; D8_Maxillopoda; D9_Copepoda; D10_Harpacticoida	0	0	0.000148	0	0	0
denovo820	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria; D6_Arthropoda; D7_Crustacea; D8_Maxillopoda; D9_Copepoda; D10_Calanoida; D11_Eurytemora pacifica	0	0	0	0	8.00E-05	8.22E-05
denovo888	D0_Eukaryota	0	0	0	0	0.00024	0
denovo1106	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria; D6_Arthropoda; D7_Crustacea; D8_Maxillopoda; D9_Copepoda; D10_Calanoida; D11_Eurytemora pacifica	0	0	0	4.14E-05	0	8.22E-05
denovo1193	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria; D6_Entoprocta; D7_Coloniales; D8_Barentsiidae; D9_Barentsia benedeni	0	0	0.000148	0	0	0
denovo1560	D0_Eukaryota	0	0	0	0.000124	0	0

OTUID	Taxonomy	CopP1	CopP2	CopP3	CopP4	CopP5	CopP6
denovo1573	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria; D6_Arthropoda; D7_Crustacea; D8_Maxillopoda; D9_Copepoda	0	0.000281	0	0	0	0
denovo22	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria; D6_Arthropoda; D7_Crustacea; D8_Maxillopoda; D9_Copepoda	4.47E-05	0	4.93E-05	0	0	0
denovo37	D0_Eukaryota	8.93E-05	0	0	0	0	0
denovo80	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria; D6_Arthropoda; D7_Crustacea; D8_Maxillopoda; D9_Copepoda; D10_Cyclopoida; D11_uncultured eukaryote	8.93E-05	0	0	0	0	0
denovo85	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria; D6_Arthropoda; D7_Crustacea; D8_Maxillopoda; D9_Copepoda; D10_Calanoida	0	0.000187	0	0	0	0
denovo101	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria; D6_Arthropoda; D7_Crustacea; D8_Maxillopoda; D9_Copepoda	0	0	9.85E-05	0	0	0
denovo142	D0_Eukaryota	8.93E-05	0	0	0	0	0
denovo232	Unclassified	8.93E-05	0	0	0	0	0
denovo276	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria; D6_Arthropoda; D7_Crustacea; D8_Maxillopoda; D9_Copepoda; D10_Calanoida; D11_Eurytemora pacifica	8.93E-05	0	0	0	0	0
denovo327	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria; D6_Arthropoda; D7_Crustacea; D8_Maxillopoda; D9_Copepoda; D10_Harpacticoida	4.47E-05	0	4.93E-05	0	0	0
denovo354	D0_Eukaryota	8.93E-05	0	0	0	0	0
denovo415	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria; D6_Arthropoda; D7_Crustacea; D8_Maxillopoda; D9_Copepoda; D10_Calanoida; D11_Eurytemora pacifica	0	0	0	0	8.00E-05	4.11E-05
denovo418	D0_Eukaryota	8.93E-05	0	0	0	0	0

OTUID	Taxonomy	CopP1	CopP2	CopP3	CopP4	CopP5	CopP6
denovo490	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria; D6_Arthropoda; D7_Crustacea; D8_Maxillopoda; D9_Copepoda; D10_Calanoida; D11_Eurytemora pacifica	0	0	0	0	0.00016	0
denovo522	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria; D6_Arthropoda; D7_Crustacea; D8_Maxillopoda; D9_Copepoda; D10_Siphonostomatoida	4.47E-05	0	0	4.14E-05	0	0
denovo586	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria; D6_Arthropoda; D7_Crustacea; D8_Maxillopoda; D9_Copepoda	0	0	9.85E-05	0	0	0
denovo609	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria; D6_Arthropoda; D7_Crustacea; D8_Maxillopoda; D9_Copepoda; D10_Siphonostomatoida	0	0.000187	0	0	0	0
denovo726	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria; D6_Arthropoda; D7_Crustacea; D8_Maxillopoda; D9_Copepoda	0	0	9.85E-05	0	0	0
denovo788	D0_Eukaryota	0	0	0	8.28E-05	0	0
denovo801	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria; D6_Arthropoda; D7_Crustacea; D8_Maxillopoda; D9_Copepoda; D10_Calanoida; D11_Eurytemora pacifica	0	0	0	0	8.00E-05	4.11E-05
denovo858	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria; D6_Arthropoda; D7_Crustacea; D8_Maxillopoda; D9_Copepoda	0	0	9.85E-05	0	0	0
denovo861	D0_Eukaryota	0	0	9.85E-05	0	0	0
denovo879	D0_Eukaryota	8.93E-05	0	0	0	0	0
denovo884	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria; D6_Arthropoda; D7_Crustacea; D8_Maxillopoda; D9_Copepoda	0	0	4.93E-05	4.14E-05	0	0
denovo891	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria; D6_Arthropoda;	4.47E-05	0	0	4.14E-05	0	0

OTUID	Taxonomy	CopP1	CopP2	CopP3	CopP4	CopP5	CopP6
denovo912	D7_Crustacea; D8_Maxillopoda; D9_Copepoda; D10_Harpacticoida; D11_Tachidius triangularis D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria; D6_Arthropoda; D7_Crustacea; D8_Maxillopoda; D9_Copepoda; D10_Calanoida; D11_Eurytemora pacifica	0	0	9.85E-05	0	0	0
denovo952	D0_Eukaryota	8.93E-05	0	0	0	0	0
denovo978	D0_Eukaryota	8.93E-05	0	0	0	0	0
denovo983	D0_Eukaryota	0	0	0	8.28E-05	0	0
denovo992	D0_Eukaryota	0	0	0	8.28E-05	0	0
denovo993	D0_Eukaryota	0	0	9.85E-05	0	0	0
denovo1019	D0_Eukaryota	8.93E-05	0	0	0	0	0
denovo1056	Unclassified	0	0.000187	0	0	0	0
denovo1058	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria; D6_Arthropoda; D7_Crustacea; D8_Maxillopoda; D9_Copepoda; D10_Harpacticoida	0	0	0	0	0	8.22E-05
denovo1221	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria; D6_Arthropoda; D7_Crustacea; D8_Maxillopoda; D9_Copepoda; D10_Calanoida; D11_Eurytemora pacifica	0	0	0	4.14E-05	8.00E-05	0
denovo1228	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria; D6_Arthropoda; D7_Crustacea; D8_Maxillopoda; D9_Copepoda	4.47E-05	0	0	4.14E-05	0	0
denovo1240	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria; D6_Arthropoda; D7_Crustacea; D8_Maxillopoda; D9_Copepoda; D10_Calanoida; D11_Eurytemora pacifica	0	0	4.93E-05	0	0	4.11E-05
denovo1288	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria; D6_Arthropoda; D7_Crustacea; D8_Maxillopoda; D9_Copepoda; D10_Cyclopoida; D11_Paracyclopina nana	4.47E-05	9.36E-05	0	0	0	0
denovo1309	D0_Eukaryota	0	0	0	8.28E-05	0	0

OTUID	Taxonomy	CopP1	CopP2	CopP3	CopP4	CopP5	CopP6
denovo1372	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria; D6_Arthropoda; D7_Crustacea; D8_Maxillopoda; D9_Copepoda; D10_Calanoida; D11_Eurytemora pacifica	0	0	0	0	0	8.22E-05
denovo1498	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria; D6_Arthropoda; D7_Crustacea; D8_Maxillopoda; D9_Copepoda; D10_Harpacticoida; D11_Tachidius triangularis	4.47E-05	0	0	4.14E-05	0	0
denovo1545	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria; D6_Arthropoda; D7_Crustacea; D8_Maxillopoda; D9_Copepoda	4.47E-05	0	0	4.14E-05	0	0
denovo1586	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria; D6_Arthropoda; D7_Crustacea; D8_Maxillopoda; D9_Copepoda; D10_Calanoida; D11_Eurytemora pacifica	4.47E-05	0	0	0	8.00E-05	0
OTUID	taxonomy	LSUCopD21	LSUCopD22	LSUCopD23	LSUCopD24	LSUCopD25	LSUCopD26
denovo438	D0_Eukaryota	0.656131	0.6	0.849713	0.814198	0.799886	0.967107
denovo214	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa	0.00885	0	0.000547	0.000667	0.149269	0.001586
denovo1117	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria	0.020228	0.1475	0.072543	0.062823	0.013066	0.018614
denovo1429	D0_Eukaryota	0	0.0025	0.006296	0.07882	0.000284	0
denovo641	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria	0.192162	0.0475	0.0219	0.001166	0.002841	0.000317
denovo309	D0_Eukaryota	0.003161	0	0.000274	0.000333	0.021446	0.000423
denovo1339	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria	0.046144	0.04	0	0.010998	0	0.000317
denovo1336	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria	0.022756	0.0075	0.018341	0.004333	0.000568	0.000317
denovo651	D0_Eukaryota	0.000632	0	0.000274	0.000333	0	0.005606
denovo587	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria	0.001264	0.0075	0.004654	0.002666	0.000142	0.000423
denovo1416	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria	0.001896	0.0025	0.004654	0.001166	0.000284	0.000317

OTUID	Taxonomy	CopP1	CopP2	CopP3	CopP4	CopP5	CopP6
denovo1340	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria	0.012642	0.005	0.001642	0	0.000284	0
denovo237	D0_Eukaryota	0.013274	0.005	0.000274	0	0.000426	0.000212
denovo292	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria	0.001264	0.005	0.005749	0	0.000142	0.000106
denovo458	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria	0	0.0075	0.003011	0.001666	0	0
denovo442	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa	0	0.0475	0	0.000167	0	0.000106
denovo1010	D0_Eukaryota	0	0	0	0	0.002556	0
denovo1245	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria	0.000632	0	0.000547	0.0015	0.000284	0.000212
denovo498	D0_Eukaryota; D1_Opisthokonta	0.003793	0	0.000547	0.001	0	0
denovo425	D0_Eukaryota	0	0	0	0	0.001846	0
denovo960	Unclassified	0	0	0	0.002166	0	0
denovo752	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria	0	0	0.000821	0.000167	0.000426	0.000529
denovo773	D0_Eukaryota	0.000632	0.0075	0	0	0.000994	0
denovo1018	D0_Eukaryota	0	0	0	0.001833	0	0
denovo1060	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa	0	0	0	0.001	0	0.000529
denovo595	D0_Eukaryota	0	0	0	0.001666	0	0
denovo1345	D0_Eukaryota	0.001264	0	0.00219	0	0	0
denovo69	D0_Eukaryota	0	0	0	0.001333	0	0
denovo738	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa	0	0	0	0.000833	0	0.000317
denovo964	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria	0	0	0.000274	0.000333	0.000284	0.000212
denovo720	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria	0	0	0.001095	0	0.000142	0.000106
denovo1318	D0_Eukaryota	0.000632	0	0.000274	0	0.000568	0
denovo219	D0_Eukaryota	0	0.0025	0	0.000167	0.000284	0.000106

OTUID	Taxonomy	CopP1	CopP2	CopP3	CopP4	CopP5	CopP6
denovo336	D0_Eukaryota	0	0	0	0.000667	0	0.000106
denovo382	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa	0	0	0	0.000333	0.000284	0.000106
denovo518	D0_Eukaryota	0.001264	0.005	0.000274	0	0	0
denovo656	D0_Eukaryota	0	0.005	0	0	0.000426	0
denovo697	D0_Eukaryota	0	0	0	0.000833	0	0
denovo825	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria	0	0	0.000821	0	0.000284	0
denovo1556	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia)	0	0	0	0.0005	0	0.000212
denovo227	D0_Eukaryota	0	0	0	0.0005	0.000142	0
denovo295	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia)	0.000632	0.0025	0	0.000333	0	0
denovo512	D0_Bacteria; D1_Proteobacteria; D2_Alphaproteobacteria; D3_Rhodobacterales; D4_Rhodobacteraceae; D5_HIMB11; D6_uncultured Rhodobacteraceae bacterium	0.001264	0	0	0	0.000142	0.000106
denovo623	D0_Eukaryota	0	0	0.000274	0	0.000142	0.000212
denovo816	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa	0	0.0025	0.000274	0	0	0.000212
denovo898	D0_Eukaryota	0	0.01	0	0	0	0
denovo1250	D0_Eukaryota	0	0.01	0	0	0	0
denovo1251	D0_Eukaryota	0	0.005	0	0	0	0.000212
denovo107	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa	0	0.0075	0	0	0	0
denovo374	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria	0	0	0	0.000333	0.000142	0
denovo539	D0_Eukaryota	0	0.005	0.000274	0	0	0
denovo559	D0_Eukaryota	0	0	0	0.0005	0	0
denovo626	D0_Eukaryota	0	0	0.000274	0.000167	0.000142	0
denovo722	Unclassified	0	0	0	0.0005	0	0
denovo1092	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria	0.001264	0	0	0	0.000142	0

OTUID	Taxonomy	CopP1	CopP2	CopP3	CopP4	CopP5	CopP6
denovo1110	D0_Eukaryota	0	0	0	0	0.000426	0
denovo1131	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria	0.001264	0	0.000274	0	0	0
denovo1295	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria	0	0.0025	0.000547	0	0	0
denovo1471	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa	0	0	0.000274	0	0.000142	0.000106
denovo1486	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria	0	0	0	0.0005	0	0
denovo1494	D0_Eukaryota	0	0	0	0.0005	0	0
denovo63	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria	0.001264	0	0	0	0	0
denovo98	D0_Eukaryota	0	0	0	0.000333	0	0
denovo111	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria; D6_Arthropoda	0	0.005	0	0	0	0
denovo146	D0_Eukaryota	0	0	0	0.000167	0.000142	0
denovo149	D0_Bacteria; D1_Proteobacteria; D2_Alphaproteobacteria; D3_Rhodobacterales; D4_Rhodobacteraceae; D5_Ruegeria; D6_Ruegeria lacuscaerulensis	0	0	0	0	0	0.000212
denovo153	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa	0	0	0	0.000333	0	0
denovo167	D0_Eukaryota	0	0	0	0	0.000284	0
denovo173	D0_Eukaryota; D1_Opisthokonta	0	0	0	0.000333	0	0
denovo176	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria	0	0	0	0.000333	0	0
denovo250	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa	0	0	0	0	0.000284	0
denovo301	D0_Eukaryota	0	0	0.000274	0	0	0.000106
denovo360	Unclassified	0	0	0	0	0	0.000212
denovo370	D0_Eukaryota	0	0	0	0	0.000284	0
denovo556	Unclassified	0	0	0	0	0	0.000212
denovo751	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria	0	0	0	0.000333	0	0

OTUID	Taxonomy	CopP1	CopP2	CopP3	CopP4	CopP5	CopP6
denovo780	D0_Eukaryota	0.001264	0	0	0	0	0
denovo822	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa	0	0	0.000274	0.000167	0	0
denovo848	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria	0.001264	0	0	0	0	0
denovo859	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria	0	0	0	0	0	0.000212
denovo990	D0_Eukaryota	0.000632	0	0	0	0.000142	0
denovo1029	D0_Eukaryota	0	0	0	0.000333	0	0
denovo1037	D0_Eukaryota	0	0	0	0.000333	0	0
denovo1102	D0_Eukaryota	0	0	0.000547	0	0	0
denovo1127	D0_Eukaryota	0	0.005	0	0	0	0
denovo1236	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria	0.001264	0	0	0	0	0
denovo1364	D0_Eukaryota	0	0	0	0	0.000284	0
denovo1477	Unclassified	0	0	0	0	0.000142	0.000106
denovo1503	D0_Eukaryota	0	0	0	0.000333	0	0
denovo1541	D0_Eukaryota	0	0	0	0	0	0.000212
OTUID	taxonomy	Uni18S1	Uni18S2	Uni18S3	Uni18S4	Uni18S5	Uni18S6
denovo115	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria; D6_Annelida; D7_Polychaeta; D8_Scolecida; D9_Spionida	0.03886	0.232323	0.201814	0.224299	0.101877	0.054422
denovo674	D0_Bacteria; D1_Actinobacteria; D2_Actinobacteria; D3_Micrococcales; D4_Microbacteriaceae; D5_ML602J-51; D6_uncultured bacterium	0.095855	0.080808	0.104308	0.105919	0.091153	0.122449
denovo315	D0_Bacteria; D1_Proteobacteria; D2_Alphaproteobacteria; D3_Rhodobacterales; D4_Rhodobacteraceae; D5_HIMB11; D6_uncultured Rhodobacteraceae bacterium	0.101036	0.090909	0.090703	0.093458	0.096515	0.108844
denovo119	D0_Bacteria; D1_Proteobacteria; D2_Alphaproteobacteria; D3_Rhodobacterales; D4_Rhodobacteraceae; D5_Marivita; D6_uncultured bacterium	0.106218	0.075758	0.07483	0.077882	0.080429	0.102041
denovo611	D0_Bacteria; D1_Actinobacteria; D2_Actinobacteria; D3_PeM15	0.088083	0.055556	0.061224	0.090343	0.058981	0.072562

OTUID	Taxonomy	CopP1	CopP2	CopP3	CopP4	CopP5	CopP6
denovo943	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria; D6_Arthropoda; D7_Crustacea; D8_Maxillopoda; D9_Copepoda; D10_Calanoida; D11_Eurytemora pacifica	0.020725	0.010101	0.036281	0.024922	0.150134	0.099773
denovo1204	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria; D6_Annelida; D7_Polychaeta; D8_Scolecida; D9_Spionida; D10_Polydora haswelli	0.204663	0.045455	0.029478	0.003115	0.024129	0
denovo967	D0_Bacteria; D1_Proteobacteria; D2_Alphaproteobacteria; D3_Rhodobacterales; D4_Rhodobacteraceae	0.023316	0.055556	0.038549	0.05296	0.024129	0.038549
denovo554	D0_Bacteria; D1_Actinobacteria; D2_Actinobacteria; D3_Corynebacteriales; D4_Mycobacteriaceae; D5_Mycobacterium	0.049223	0.030303	0.038549	0.018692	0.037534	0.038549
denovo1148	D0_Bacteria; D1_Proteobacteria; D2_Alphaproteobacteria; D3_Rhodobacterales; D4_Rhodobacteraceae; D5_Ruegeria	0.033679	0.050505	0.043084	0.05296	0.037534	0.013605
denovo1568	D0_Bacteria; D1_Actinobacteria; D2_Actinobacteria; D3_Micrococcales; D4_Microbacteriaceae; D5_Candidatus Aquiluna; D6_uncultured bacterium	0.020725	0.020202	0.036281	0.018692	0.034853	0.018141
denovo1081	D0_Bacteria; D1_Bacteroidetes; D2_Bacteroidia; D3_Flavobacteriales; D4_Flavobacteriaceae; D5_Formosa	0.018135	0.025253	0.034014	0.031153	0.010724	0.020408
denovo324	D0_Bacteria; D1_Bacteroidetes; D2_Bacteroidia; D3_Cytophagales; D4_Cyclobacteriaceae; D5_Algoriphagus; D6_Algoriphagus marincola DSM 16067	0.010363	0.035354	0.020408	0.009346	0.021448	0.015873
denovo1376	D0_Bacteria; D1_Actinobacteria; D2_Actinobacteria; D3_PeM15	0.012953	0.010101	0.00907	0.015576	0.016086	0.018141
denovo1497	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria; D6_Rotifera; D7_Monogononta; D8_Ploimida; D9_uncultured eukaryote	0	0	0.004535	0	0	0.049887
denovo55	D0_Bacteria; D1_Bacteroidetes; D2_Bacteroidia; D3_Flavobacteriales; D4_Flavobacteriaceae; D5_NS3a marine group; D6_uncultured marine bacterium	0.012953	0.015152	0.006803	0.006231	0.010724	0.006803
denovo834	D0_Bacteria; D1_Proteobacteria; D2_Alphaproteobacteria; D3_Rhodobacterales; D4_Rhodobacteraceae	0.002591	0.020202	0.011338	0.006231	0.008043	0.00907

OTUID	Taxonomy	CopP1	CopP2	CopP3	CopP4	CopP5	CopP6
denovo53	D0_Bacteria; D1_Proteobacteria; D2_Gammaproteobacteria; D3_Alteromonadales; D4_Pseudoalteromonadaceae; D5_Pseudoalteromonas	0.005181	0.010101	0.00907	0.003115	0.008043	0.006803
denovo75	D0_Bacteria; D1_Actinobacteria; D2_Actinobacteria; D3_PeM15; D4_uncultured bacterium	0	0.015152	0.013605	0.003115	0	0.011338
denovo1210	D0_Bacteria; D1_Bacteroidetes; D2_Bacteroidia; D3_Flavobacteriales; D4_Flavobacteriaceae; D5_Tenacibaculum; D6_Tenacibaculum aiptasiae	0.007772	0	0.002268	0.003115	0.008043	0.00907
denovo546	D0_Bacteria; D1_Actinobacteria; D2_Actinobacteria; D3_PeM15; D4_uncultured actinobacterium	0.002591	0	0.002268	0.009346	0	0.011338
denovo592	D0_Bacteria; D1_Bacteroidetes; D2_Bacteroidia; D3_Flavobacteriales; D4_Flavobacteriaceae; D5_Polaribacter 4; D6_uncultured bacterium	0.002591	0	0.002268	0.009346	0	0.011338
denovo1495	D0_Bacteria; D1_Bacteroidetes; D2_Bacteroidia; D3_Flavobacteriales; D4_Flavobacteriaceae; D5_Maribacter; D6_Maripseudobacter aurantiacus	0.002591	0	0.006803	0.003115	0.002681	0.006803
denovo121	D0_Bacteria; D1_Bacteroidetes; D2_Bacteroidia; D3_Flavobacteriales; D4_Flavobacteriaceae; D5_Hanstruepera; D6_Hanstruepera neustonica	0	0	0.006803	0.006231	0.002681	0.004535
denovo1297	D0_Bacteria; D1_Actinobacteria; D2_Actinobacteria; D3_Corynebacteriales; D4_Mycobacteriaceae; D5_Mycobacterium	0	0	0.004535	0.012461	0	0.004535
denovo116	D0_Bacteria; D1_Proteobacteria; D2_Alphaproteobacteria; D3_Rhodobacterales; D4_Rhodobacteraceae; D5_Tabrizicola; D6_uncultured bacterium	0.010363	0.005051	0	0	0	0.004535
denovo589	D0_Bacteria; D1_Proteobacteria; D2_Alphaproteobacteria; D3_Rhodobacterales; D4_Rhodobacteraceae	0	0	0.002268	0.015576	0	0.002268
denovo733	D0_Eukaryota; D1_SAR; D2_Alveolata; D3_Ciliophora; D4_Intramacronucleata; D5_Conthreep; D6_Oligohymenophorea; D7_Peritrichia; D8_Zoothamnium; D9_uncultured eukaryote	0	0	0	0	0.018767	0
denovo873	D0_Bacteria; D1_Proteobacteria; D2_Alphaproteobacteria; D3_Rhodobacterales; D4_Rhodobacteraceae	0.005181	0.005051	0.002268	0	0	0.006803

OTUID	Taxonomy	CopP1	CopP2	CopP3	CopP4	CopP5	CopP6
denovo1396	D0_Bacteria; D1_Planctomycetes; D2_Planctomycetacia; D3_Planctomycetales; D4_Rubinisphaeraceae; D5_Planctomicrobium; D6_uncultured bacterium	0.005181	0	0	0	0.005362	0.006803
denovo1575	D0_Bacteria; D1_Proteobacteria; D2_Gammaproteobacteria; D3_Vibrionales; D4_Vibrionaceae; D5_Vibrio	0.002591	0.005051	0.004535	0.003115	0	0.004535
denovo24	D0_Bacteria; D1_Actinobacteria; D2_Actinobacteria; D3_Corynebacteriales; D4_Nocardiaceae; D5_Rhodococcus; D6_Rhodococcus erythropolis	0	0	0	0.006231	0.005362	0.004535
denovo550	D0_Bacteria; D1_Proteobacteria; D2_Alphaproteobacteria; D3_Rhodobacterales; D4_Rhodobacteraceae	0.002591	0	0.004535	0	0.002681	0.004535
denovo769	D0_Bacteria; D1_Proteobacteria; D2_Alphaproteobacteria; D3_Rhizobiales; D4_Rhizobiaceae; D5_Nitratireductor; D6_Nitratireductor basaltis	0.002591	0.005051	0.002268	0	0.005362	0.002268
denovo948	D0_Bacteria; D1_Bacteroidetes; D2_Bacteroidia; D3_Flavobacteriales; D4_Cryomorphaceae; D5_Phaeocystidibacter; D6_Coccinistipes vermicola	0.002591	0	0.004535	0.003115	0.002681	0.002268
denovo1023	D0_Bacteria; D1_Proteobacteria; D2_Deltaproteobacteria; D3_PB19; D4_uncultured bacterium	0	0	0	0.003115	0.008043	0.004535
denovo1059	D0_Bacteria; D1_Proteobacteria; D2_Alphaproteobacteria; D3_Rhodobacterales; D4_Rhodobacteraceae	0	0.010101	0	0.003115	0.002681	0.004535
denovo529	D0_Bacteria; D1_Bacteroidetes; D2_Bacteroidia; D3_Flavobacteriales; D4_Flavobacteriaceae	0	0	0.004535	0.006231	0	0.002268
denovo1052	D0_Bacteria; D1_Bacteroidetes; D2_Bacteroidia; D3_Flavobacteriales; D4_Flavobacteriaceae; D5_Seonamhaeicola; D6_uncultured bacterium	0.005181	0	0.004535	0	0	0.002268
denovo20	D0_Bacteria; D1_Bacteroidetes; D2_Bacteroidia; D3_Flavobacteriales; D4_Flavobacteriaceae; D5_Winogradskyella; D6_uncultured bacterium	0	0.010101	0	0.003115	0.002681	0
denovo144	D0_Bacteria; D1_Bacteroidetes; D2_Ignavibacteria; D3_OPB56	0	0	0.002268	0	0.002681	0.004535
denovo240	D0_Bacteria; D1_Planctomycetes; D2_Planctomycetacia; D3_Planctomycetales; D4_Rubinisphaeraceae; D5_Planctomicrobium; D6_uncultured bacterium	0.002591	0.005051	0	0	0.002681	0.002268
denovo277	D0_Bacteria; D1_Proteobacteria; D2_Gammaproteobacteria; D3_Gammaproteobacteria Incertae Sedis; D4_Unknown Family; D5_Marinicella; D6_Marinicella litoralis	0	0	0	0	0.002681	0.006803

OTUID	Taxonomy	CopP1	CopP2	CopP3	CopP4	CopP5	CopP6
denovo427	D0_Bacteria; D1_Proteobacteria; D2_Gammaproteobacteria; D3_Betaproteobacteriales; D4_Rhodocyclaceae; D5_Azoarcus	0.002591	0	0.004535	0	0.002681	0
denovo439	D0_Bacteria; D1_Bacteroidetes; D2_Bacteroidia; D3_Flavobacteriales; D4_Flavobacteriaceae	0	0.005051	0.002268	0	0.002681	0.002268
denovo608	D0_Bacteria; D1_Proteobacteria; D2_Alphaproteobacteria; D3_Rhodobacterales; D4_Rhodobacteraceae	0.002591	0	0.002268	0.003115	0.002681	0
denovo671	D0_Bacteria; D1_Proteobacteria; D2_Alphaproteobacteria; D3_Rhodobacterales; D4_Rhodobacteraceae	0	0.005051	0	0	0.002681	0.004535
denovo706	D0_Bacteria; D1_Proteobacteria; D2_Gammaproteobacteria; D3_Xanthomonadales; D4_Xanthomonadaceae; D5_Stenotrophomonas	0	0.010101	0	0	0.002681	0.002268
denovo940	D0_Bacteria; D1_Proteobacteria; D2_Gammaproteobacteria; D3_Alteromonadales; D4_Idiomarinaceae; D5_Idiomarina; D6_Idiomarina maritima	0	0	0	0.009346	0	0.002268
denovo1124	D0_Bacteria; D1_Bacteroidetes; D2_Bacteroidia; D3_Flavobacteriales; D4_Flavobacteriaceae; D5_Pseudozobellia; D6_uncultured bacterium	0	0	0.002268	0.006231	0	0.002268
denovo1263	D0_Bacteria; D1_Proteobacteria; D2_Alphaproteobacteria; D3_Rhodobacterales; D4_Rhodobacteraceae	0	0	0.002268	0	0	0.006803
denovo1351	D0_Bacteria; D1_Bacteroidetes; D2_Rhodothermia; D3_Balneolales; D4_Balneolaceae; D5_Balneola; D6_uncultured Bacteroidetes bacterium	0	0	0.002268	0.003115	0.002681	0.002268
denovo1502	D0_Bacteria; D1_Proteobacteria; D2_Alphaproteobacteria; D3_Rhodobacterales; D4_Rhodobacteraceae; D5_Rhodobaculum; D6_uncultured bacterium	0.002591	0.005051	0	0	0.002681	0.002268
denovo1553	D0_Bacteria; D1_Proteobacteria; D2_Gammaproteobacteria; D3_Gammaproteobacteria Incertae Sedis; D4_Unknown Family; D5_Marinicella; D6_Marinicella litoralis	0.002591	0	0.004535	0.003115	0	0
denovo14	D0_Bacteria; D1_Proteobacteria; D2_Gammaproteobacteria; D3_Legionellales; D4_Legionellaceae; D5_uncultured; D6_uncultured gamma proteobacterium	0.002591	0	0.004535	0	0	0
denovo16	D0_Bacteria; D1_Proteobacteria; D2_Gammaproteobacteria; D3_Pseudomonadales; D4_Pseudomonadaceae; D5_Pseudomonas; D6_Pseudomonas fulva	0	0	0.002268	0.003115	0.002681	0

OTUID	Taxonomy	CopP1	CopP2	CopP3	CopP4	CopP5	CopP6
denovo141	D0_Bacteria; D1_Proteobacteria; D2_Gammaproteobacteria; D3_Pseudomonadales; D4_Moraxellaceae; D5_Acinetobacter; D6_Acinetobacter venetianus	0.005181	0	0.002268	0	0	0
denovo151	D0_Bacteria; D1_Proteobacteria; D2_Gammaproteobacteria; D3_Steroidobacteriales; D4_Woeseiaceae; D5_Woeseia; D6_uncultured bacterium	0	0	0	0	0.002681	0.004535
denovo192	D0_Bacteria; D1_Bacteroidetes; D2_Rhodothermia; D3_Rhodothermales; D4_Rhodothermaceae; D5_uncultured D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa	0	0	0.002268	0.003115	0	0.002268
denovo251	(Animalia); D4_Eumetazoa; D5_Bilateria; D6_Rotifera; D7_Monogononta; D8_Ploimida; D9_uncultured eukaryote; D10_; D11_	0	0	0	0	0	0.006803
denovo269	D0_Bacteria; D1_Bacteroidetes; D2_Bacteroidia; D3_Flavobacteriales; D4_Flavobacteriaceae; D5_Muricauda; D6_uncultured bacterium	0.002591	0	0.002268	0	0.002681	0
denovo300	D0_Bacteria; D1_Proteobacteria; D2_Alphaproteobacteria; D3_Rhodobacteriales; D4_Rhodobacteraceae	0.002591	0	0.002268	0.003115	0	0
denovo459	D0_Bacteria; D1_Bacteroidetes; D2_Bacteroidia; D3_Cytophagales; D4_Spirosomaceae; D5-Taeseokella; D6_Lacihabitans sp. MCCC 1A00733	0	0	0.002268	0.003115	0	0.002268
denovo491	D0_Bacteria; D1_Bacteroidetes; D2_Bacteroidia; D3_Flavobacteriales; D4_Flavobacteriaceae; D5_Wenyngzhuangia; D6_Flavobacteriaceae bacterium RC2-3	0	0	0	0.003115	0.002681	0.002268
denovo600	D0_Bacteria; D1_Proteobacteria; D2_Alphaproteobacteria; D3_Rhodobacteriales; D4_Rhodobacteraceae	0.002591	0.005051	0	0	0	0.002268
denovo620	D0_Eukaryota	0	0	0	0.003115	0.002681	0.002268
denovo663	D0_Bacteria; D1_Proteobacteria; D2_Gammaproteobacteria; D3_Enterobacteriales; D4_Enterobacteriaceae	0.002591	0.005051	0	0	0.002681	0
denovo951	D0_Bacteria; D1_Bacteroidetes; D2_Bacteroidia; D3_Flavobacteriales; D4_Flavobacteriaceae; D5_Aureimarina; D6_uncultured bacterium	0.002591	0	0	0.003115	0.002681	0
denovo1040	D0_Bacteria; D1_Cyanobacteria; D2_Oxyphotobacteria; D3_Chloroplast; D4_Nannochloropsis gaditana	0	0	0	0	0.002681	0.004535

OTUID	Taxonomy	CopP1	CopP2	CopP3	CopP4	CopP5	CopP6
denovo1220	D0_Bacteria; D1_Chloroflexi; D2_Anaerolineae; D3_Caldilineales; D4_Caldilineaceae; D5_uncultured; D6_uncultured Chloroflexi bacterium	0.005181	0	0.002268	0	0	0
denovo1229	D0_Bacteria; D1_Bacteroidetes; D2_Bacteroidia; D3_Chitinophagales; D4_Saprosiraceae; D5_Phaeodactylibacter; D6_Phaeodactylibacter xiamenensis	0.002591	0	0	0.003115	0.002681	0
denovo1285	D0_Bacteria; D1_Proteobacteria; D2_Alphaproteobacteria; D3_Rhodobacterales; D4_Rhodobacteraceae	0.002591	0	0	0.003115	0	0.002268
denovo1287	D0_Bacteria; D1_Proteobacteria; D2_Gammaproteobacteria; D3_Oceanospirillales; D4_Nitrincolaceae; D5_Neptunomonas; D6_Neptunomonas sp. HPM-16	0.002591	0	0.002268	0	0.002681	0
denovo1387	D0_Bacteria; D1_Bacteroidetes; D2_Bacteroidia; D3_Flavobacteriales; D4_Flavobacteriaceae; D5_Tamlana; D6_Tamlana crocina	0.002591	0	0.002268	0	0.002681	0
denovo5	D0_Bacteria; D1_Bacteroidetes; D2_Bacteroidia; D3_Flavobacteriales; D4_Flavobacteriaceae; D5_Muricauda	0	0.005051	0	0	0	0.002268
denovo18	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria; D6_Arthropoda; D7_Crustacea; D8_Maxillopoda; D9_Copepoda; D10_Calanoida	0	0	0	0	0.005362	0
denovo106	D0_Bacteria; D1_Actinobacteria; D2_Actinobacteria; D3_Micrococcales; D4_Microbacteriaceae	0.002591	0.005051	0	0	0	0
denovo110	D0_Bacteria; D1_Bacteroidetes; D2_Bacteroidia; D3_Cytophagales; D4_Cyclobacteriaceae; D5_Cyclobacterium; D6_uncultured bacterium	0	0	0	0.003115	0	0.002268
denovo152	D0_Bacteria; D1_Verrucomicrobia; D2_Verrucomicrobiae; D3_Verrucomicrobiales; D4_Rubritaleaceae; D5_Rubritalea; D6_Rubritalea sabuli	0	0	0.002268	0	0.002681	0
denovo162	D0_Bacteria; D1_Planctomycetes; D2_Planctomycetacia; D3_Pirellulales; D4_Pirellulaceae; D5_Blastopirellula; D6_planctomycete MS1316	0	0	0	0	0.005362	0
denovo182	D0_Eukaryota; D1_SAR; D2_Alveolata; D3_Ciliophora; D4_Postciliodesmatophora; D5_Heterotrichea; D6_Eufolliculina; D7_uncultured eukaryote	0.005181	0	0	0	0	0

OTUID	Taxonomy	CopP1	CopP2	CopP3	CopP4	CopP5	CopP6
denovo247	D0_Bacteria; D1_Actinobacteria; D2_Actinobacteria; D3_PeM15; D4_actinobacterium GP-6	0.002591	0	0	0	0.002681	0
denovo312	D0_Bacteria; D1_Bacteroidetes; D2_Bacteroidia; D3_Flavobacteriales; D4_NS9 marine group	0.002591	0	0	0	0.002681	0
denovo313	D0_Bacteria; D1_Bacteroidetes; D2_Bacteroidia; D3_Flavobacteriales; D4_Flavobacteriaceae; D5_Mesoflavibacter; D6_uncultured bacterium	0.002591	0.005051	0	0	0	0
denovo349	D0_Bacteria; D1_Bacteroidetes; D2_Bacteroidia; D3_Flavobacteriales; D4_Flavobacteriaceae; D5_Hyunsoonleella; D6_Hyunsoonleella jejuensis	0.002591	0	0	0	0	0.002268
denovo444	D0_Bacteria; D1_Proteobacteria; D2_Alphaproteobacteria; D3_Sphingomonadales; D4_Sphingomonadaceae; D5_Sphingomonas	0.005181	0	0	0	0	0
denovo500	D0_Bacteria; D1_Proteobacteria; D2_Alphaproteobacteria; D3_Rhodobacterales; D4_Rhodobacteraceae; D5_Ruegeria; D6_uncultured alpha proteobacterium	0	0.005051	0	0	0.002681	0
denovo503	D0_Bacteria; D1_Bacteroidetes; D2_Bacteroidia; D3_Chitinophagales; D4_Chitinophagaceae; D5_uncultured; D6_uncultured marine bacterium	0.002591	0	0	0	0	0.002268
denovo601	D0_Bacteria; D1_Bacteroidetes; D2_Bacteroidia; D3_Chitinophagales; D4_Saprospiraceae; D5_uncultured; D6_uncultured marine bacterium	0	0.005051	0	0	0.002681	0
denovo603	D0_Bacteria; D1_Proteobacteria; D2_Alphaproteobacteria; D3_Rhodobacterales; D4_Rhodobacteraceae	0.002591	0.005051	0	0	0	0
denovo633	D0_Bacteria; D1_Proteobacteria; D2_Alphaproteobacteria; D3_Thalassobaculales; D4_Thalassobaculaceae; D5_Thalassobaculum; D6_Thalassobaculum salexigens DSM 19539	0	0	0.004535	0	0	0
denovo684	D0_Bacteria; D1_Planctomycetes; D2_Planctomycetacia; D3_Pirellulales; D4_Pirellulaceae; D5_Blastopirellula; D6_uncultured Planctomycetales bacterium	0	0	0	0	0.002681	0.002268
denovo691	D0_Bacteria; D1_Actinobacteria; D2_Actinobacteria; D3_PeM15; D4_uncultured actinobacterium	0	0.005051	0	0.003115	0	0
denovo708	D0_Bacteria; D1_Proteobacteria; D2_Alphaproteobacteria; D3_Rhodobacterales; D4_Rhodobacteraceae	0	0	0	0.006231	0	0

OTUID	Taxonomy	CopP1	CopP2	CopP3	CopP4	CopP5	CopP6
denovo767	D0_Bacteria; D1_Proteobacteria; D2_Alphaproteobacteria; D3_Rhizobiales; D4_Rhizobiaceae; D5_Roseitalea; D6_uncultured bacterium	0	0	0.002268	0.003115	0	0
denovo771	D0_Bacteria; D1_Proteobacteria; D2_Alphaproteobacteria; D3_Rhizobiales; D4_Rhizobiaceae; D5_Pseudahrensia; D6_uncultured bacterium	0	0	0.004535	0	0	0
denovo814	D0_Bacteria; D1_Proteobacteria; D2_Alphaproteobacteria; D3_Rhodobacterales; D4_Rhodobacteraceae	0	0	0	0	0.002681	0.002268
denovo843	D0_Bacteria; D1_Proteobacteria; D2_Alphaproteobacteria; D3_Rhodobacterales; D4_Rhodobacteraceae; D5_Ruegeria; D6_uncultured alpha proteobacterium	0	0	0.002268	0	0	0.002268
denovo880	D0_Bacteria; D1_Proteobacteria; D2_Gammaproteobacteria; D3_Gammaproteobacteria Incertae Sedis; D4_Unknown Family; D5_uncultured organism	0.002591	0	0.002268	0	0	0
denovo941	D0_Eukaryota; D1_SAR; D2_Alveolata; D3_Ciliophora; D4_Intramacronucleata; D5_Litostomatea; D6_Mesodiniidae; D7_Myrionecta; D8_uncultured eukaryote	0	0	0	0	0.005362	0
denovo1048	D0_Bacteria; D1_Proteobacteria; D2_Alphaproteobacteria; D3_Rhizobiales; D4_Devosiaceae; D5_Maritalea; D6_Maritalea sp. ZJ2704	0.002591	0	0	0	0.002681	0
denovo1082	D0_Bacteria; D1_Bacteroidetes; D2_Bacteroidia; D3_Flavobacteriales; D4_Flavobacteriaceae; D5_Xanthomarina	0.002591	0	0	0	0	0.002268
denovo1140	D0_Bacteria; D1_Proteobacteria; D2_Alphaproteobacteria; D3_Rhodobacterales; D4_Rhodobacteraceae	0.002591	0	0	0	0	0.002268
denovo1160	D0_Bacteria; D1_Proteobacteria; D2_Alphaproteobacteria; D3_Rhodobacterales; D4_Rhodobacteraceae	0	0	0.002268	0	0.002681	0
denovo1161	D0_Bacteria; D1_Bacteroidetes; D2_Bacteroidia; D3_Chitinophagales; D4_Saprospiraceae	0.002591	0	0	0	0	0.002268
denovo1173	D0_Bacteria; D1_Bacteroidetes; D2_Bacteroidia; D3_Chitinophagales; D4_Saprospiraceae; D5_uncultured; D6_uncultured bacterium	0.002591	0	0	0	0.002681	0
denovo1202	D0_Bacteria; D1_Bacteroidetes; D2_Bacteroidia; D3_Flavobacteriales; D4_Flavobacteriaceae; D5_Tenacibaculum; D6_Tenacibaculum aiptasiae	0.002591	0	0.002268	0	0	0

OTUID	Taxonomy	CopP1	CopP2	CopP3	CopP4	CopP5	CopP6
denovo1279	D0_Eukaryota; D1_Opisthokonta; D2_Nucleomyces; D3_Fungi; D4_Dikarya; D5_Ascomycota; D6_Pezizomycotina; D7_Sordariomycetes; D8_Hypocreales	0	0	0	0	0.005362	0
denovo1385	D0_Bacteria; D1_Actinobacteria; D2_Actinobacteria; D3_Micrococcales; D4_Microbacteriaceae; D5_Microbacterium	0	0	0.002268	0	0.002681	0
denovo1417	D0_Bacteria; D1_Proteobacteria; D2_Alphaproteobacteria; D3_Rhodobacterales; D4_Rhodobacteraceae	0	0	0	0	0.005362	0
denovo1461	D0_Bacteria; D1_Bacteroidetes; D2_Bacteroidia; D3_Flavobacteriales; D4_Flavobacteriaceae; D5_NS5 marine group; D6_uncultured bacterium	0	0.005051	0	0.003115	0	0
denovo1484	D0_Bacteria; D1_Proteobacteria; D2_Gammaproteobacteria; D3_Betaproteobacteriales; D4_Burkholderiaceae; D5_Ralstonia; D6_Ralstonia pickettii	0	0	0	0	0.002681	0.002268
denovo1516	D0_Bacteria; D1_Proteobacteria; D2_Alphaproteobacteria; D3_Rhodobacterales; D4_Rhodobacteraceae	0.002591	0	0	0	0.002681	0
denovo1537	D0_Bacteria; D1_Proteobacteria; D2_Alphaproteobacteria; D3_Rhodobacterales; D4_Rhodobacteraceae	0.002591	0	0	0	0.002681	0
denovo1552	D0_Bacteria; D1_Actinobacteria; D2_Actinobacteria; D3_Corynebacteriales; D4_Mycobacteriaceae; D5_Mycobacterium	0	0	0.004535	0	0	0
denovo1562	D0_Eukaryota; D1_Opisthokonta; D2_Holozoa; D3_Metazoa (Animalia); D4_Eumetazoa; D5_Bilateria; D6_Arthropoda; D7_Crustacea; D8_Maxillopoda; D9_Copepoda; D10_Calanoida; D11_Acartia pacifica	0	0	0.002268	0.003115	0	0
denovo1571	D0_Bacteria; D1_Planctomycetes; D2_Planctomycetacia; D3_Planctomycetales; D4_Rubinisphaeraceae; D5_Fuerstia; D6_uncultured bacterium	0.002591	0	0.002268	0	0	0