Distribution of Meiofaunal biodiversity and abundance in relation to development stage of the Mangrove Forest

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Abstract

Mangrove ecosystems constitute a valuable economic resource harbouring a wide diversity of organisms and operating an essential provider of nutrients for adjoining marine ecosystems. The meio-benthic fauna (i.e. small benthic invertebrates) plays an important role in the food chain and has proven to be a useful indicator on environmental stressors within the mangrove forest. This study is conducted to investigate the relationship between meio-benthic fauna and mangrove development stage. The distribution, density and biodiversity were measured in the Longhai Mangrove Nature Reserve, southwest of Xiamen, China. Three replicate samples were collected from three planted mangrove forests at different age stages. Additionally, a control site was chosen, constituted by a mudflat with no observed vegetation. Significant patterns were recognized regarding biodiversity, which increased from the lower age to the higher, at a level of $p = 0.004$ ($R^2 = 0.616$). Nematodes constituted the most abundant group >90 %, followed by oligochaetes 1.5-5.6 %. The control site appeared to have the lowest number of groups observed (total 3) and was found in significantly lower level of biodiversity compared to the highest age of the mangrove sites. Considering older mangrove forests indicate higher biodiversity this may indicate the importance of preserving the presence of aging mangrove ecosystems.

Keywords: Mangrove, Meiofauna, Development stage, Biodiversity
Introduction

Mangrove forests are located in subtropical and tropical intertidal regions within the 20°C isotherm. They usually consist of only a few plant species but can nevertheless contain an immense biomass. Mangroves grow in saline regions along sediment shores, mainly in embayment and estuaries but can also be found far inland, however never isolated from the sea. The vegetation is well adapted to extreme environmental conditions of wind, water, tides and salinity. The mangrove ecosystem is detritus based and due to its rapid decomposition and nutrient cycling, while located this close to the sea, it contributes with nutrients to the coastline and adjoining ecosystems, for example, seagrass beds, coral reefs and marine organisms. Their root system provides a substrate for sessile marine organisms and also a nursing ground for marine species that may find protection from predation. The canopy also maintains a shaded and moist environment during low tide, protecting other benthic organisms living in the sediment (Aksornkoae et al., 2004; Alongi, 2009; Gutiérrez et al., 2011; Mitra, 2013).

Mangrove forests constitute one of the world’s most productive sites, being a high producer of organic carbon in excess of the ecosystem requirements, it is contributing significantly to the global carbon cycle. Furthermore it functions as flood control barrier and a protector of coastal landmass from high winds, cyclones and tidal bores (Mitra, 2013). Mangrove forests also hinder coastal erosion, and were even shown to have a marked protection against the tsunami of December 2004 compared to deforested areas (Kaiser et al., 2011). According to Mitra (2013) there are several references suggesting that the mangrove partly dispersed the force of the tsunami 2004, while also catching debris washed up by it. In this occasion it also managed to save human lives as it prevented people from being pulled out to the sea by the backwash.

Approximately one-third of the world’s mangrove forests have been lost due to anthropogenic activities during the last period of 50 years. Ironically, such big losses have reflected the importance of the mangrove forest and its economical values as nursery site for many organisms (Alongi, 2002). The main causes of destruction are establishment of shrimp aquaculture ponds but also urban development, human settlement and a number of overexploitations such as of timber, fish, shellfish and crustaceans. Furthermore, the global climate change also has a negative impact on mangroves quality (Alongi, 2009; Mitra, 2013). Similarly, Lunstrum and Chen (2014) presented that China has lost much of its historical mangrove cover, of which less than a third remained in 2009. However, in the early 1990s, the Chinese government began to invest in mangrove reforestation to regain the ecosystem services that the mangrove forest provides.

Benthos can be found in a wide diversity within the mangrove forest. The meiobenthic fauna constitute one of the most diversified groups found in the marine realm and contribute on a large scale to the ecosystem function due to their high abundance, rapid generation time and fast metabolic rate. They serve an important role in the benthic food chain both as food resource for macrobenthic organisms as well as decomposers by consuming detritus material, algae and diatoms (Zeppelli et al., 2015; Zhou et al., 2015).

Studies on meiofaunal biodiversity and distribution in mangrove ecosystems have been conducted previously in many countries (Zhou et al., 2015). Benthic fauna in general have been used as an indicator on environmental change during a long time, although mainly
macroinfauna have been targeted due to it can readily be counted and identified. Less attention has been focused on the smaller meiobenthic fauna (Liu et al., 2011). However, Zeppelli et al. (2015) propose that meiobenthic fauna can be particularly valuable as bioindicator compared to other benthic communities due to the variety and high abundance, although it is cost-effective and remains a challenge in taxonomic identification.

Purpose and hypothesis
The purpose of this study is to (i) do a survey of the meiofaunal fauna in the Longhai Mangrove Nature Reserve for the College of the Environment and Ecology, Xiamen University. (ii) Investigate the establishment of meiofaunal faunal communities over time by studying planted mangroves of different ages. If the mangrove has had more time to grow and facilitate its surroundings, meiofauna should have had increased opportunity to immigrate and establish.

I therefore hypothesize that (i) older mangroves will have an increased meiofaunal faunal diversity, and (ii) the planted mangroves will have a higher meiofaunal faunal diversity than the mudflats (the non-mangrove control site). This study is done in conjunction with the study by Jacobsen (2017), having the same purposes and hypothesis, but focusing on macrobenthic fauna.

2. Methods
2.1. Study area
The Longhai Mangrove Nature Reserve is located on the southern banks of the Jiulongjiang River with its outflow south of Xiamen, south eastern China. Within the area, mangroves of the species Kandelia candel has been planted during the last decades (Hu, H. 2017, pers. comm.; Tam, 2004). Site L is 17 years old (24°23'21.5"N, 117°54'6.5"E), Site M is 30 years old (24°23'40"N, 117°54'36.5"E), and Site H is 53 years old (24°23'37.5"N, 117°55'31"E) (Fig 1). To reach resembling abiotic factors, a control site C was chosen in the same area as other sites. The control site is constituted by a mudflat with similar sediment particle size but contained little or no vegetation, (24°23'39.5"N, 117°54'25"E) (Fig. 1).

Sampling was carried out mid day during low tide on the 7th and 24th of March 2017. This time of year is considered spring season in Xiamen. Several shrimp farms constitute surrounding environment.

2.2. Sampling procedure
At each site three replicate samples were taken using a cut-off syringe (Φ=2.9 cm) to a depth of 10 cm into the sediment. The tube was pushed down into the sediment and the plunger was used to extract the sample. The sample was transferred to a plastic jar and brought back to the laboratory. Back in the laboratory all samples were fixed with 10 % formalin (Zhou et al., 2015). Using this technique the samples reached a core of 5-8 cm depending on the texture of sediment at each site. According to the study of Mokievsky et al. (2011) 90 % of the meiofaunal fauna inhabit the upper 1 cm of the sediment. Therefore, we assume that the
lower parts of each core (5-8 cm) and differences between samples will not contain considerable amounts of meiofauna to affect the abundance and the outcome of this study.

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2.3. Identification

The samples were washed and sieved through a 500 μm mesh size sieve on top of a 42 μm mesh size sieve. Material remaining on the smaller mesh size was collected and meiofauna was separated from sediment by a flotation technique using Ludox (TM-50) solution \((D=1.15 \text{ g/cm}^3)\). Washed samples were stained with rose bengal to ease the identification procedure (Zhou et al., 2015). The meiofauna was then counted into major groups (exemplified in Appendix) under a stereoscopic microscope and put in 75% ethanol for preservation (Higgins et al., 1988; Platt and Warwick, 1983).

2.4. Data analysis

Since small sample sizes were collected from an endless population, normal distribution was assumed.

Meiofaunal biodiversity was calculated by Shannon Wiener biodiversity index:

\[
H' = - \sum_{i=1}^{R} p_i \ln p_i
\]

To test significance in biodiversity between sites and investigate which sites were significant to control site a one-way ANOVA post hoc Tukey was used.
To measure whether biodiversity and abundance can be related to age, regression was used in combination with scatter dot graphs. Same procedure was used to investigate differences in number of individuals from the most abundant groups (Nematoda, copepoda, polychaeta and oligochaeta) between sites, to analyse whether there may be one group affecting the outcome of the whole site.

3. Results

3.1. Meiofaunal taxa composition

At least 7 meiofaunal taxa were found in Longhai Mangrove Nature Reserve: Nematoda, Copepoda, Polychaeta, Oligochaeta, Amphipoda, Insecta and Halacoridea. Organisms that could not be identified to phyla level were grouped as “others” (Table 1). The total abundance appeared to be highest at L site (17 years) and lowest at H site (53 years). However, the amount of species found was the same as well as highest from L and H sites, although H site proved to have higher Shannon Wiener diversity index (Table 2.). Nematodes clearly dominated at all sites (93.0-98.4 %), followed by oligochaetes as the second largest group (1.5-5.3 %) (Fig. 2).

3.2. Biodiversity

The lowest biodiversity value was found for the control site (Table. 2). However, only H had significantly higher biodiversity than the control site ($p=0.023$). H even showed a significant difference to L ($p=0.014$), while M remained too close in value to show significance to any other site (Fig. 3.). A correlation between age and biodiversity (which did not include the control site as it is not qualified as a mangrove ecosystem) suggested that biodiversity increased with time ($R^2 = 0.616$) (Fig. 4.). From site L the biodiversity increased significantly in order (L, M, H) to the highest age ($t=3.8$, $df=1$, $p=0.004$ $y = -0.004+0.006x$) (Fig. 4.).

3.3. Abundance

When separating the groups and plotting them in individual graphs, nematodes seemed to decrease in abundance from L to H, although this was non-significant. Copepoda and polychaeta on the other hand both showed a positive development but the correlation was not strong enough to be significant. However, oligochaeta increased significantly ($t=4.5$, $df=1$, $p=0.001$ $y = -6.331+1.4x$) from lowest sample number noted at L site (8 individuals) to highest noted at H site (87 individuals) (Fig. 5.).
**Table 1.** Number of individuals of each meiofaunal taxa found at each site. Marked samples (*) were collected the 24th of March, samples without label were collected 2 weeks previous, the 7th of March.

<table>
<thead>
<tr>
<th></th>
<th>Control = mudflat</th>
<th>Low age = 17 years</th>
<th>Middle age = 30 years</th>
<th>High age = 53 years</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>C1*</td>
<td>C2*</td>
<td>C3*</td>
<td>L1</td>
</tr>
<tr>
<td>Nematoda</td>
<td>1584</td>
<td>735</td>
<td>2646</td>
<td>841</td>
</tr>
<tr>
<td>Copepoda</td>
<td>2</td>
<td></td>
<td></td>
<td>3</td>
</tr>
<tr>
<td>Polychaeta</td>
<td>39</td>
<td>15</td>
<td>10</td>
<td>29</td>
</tr>
<tr>
<td>Oligochaeta</td>
<td></td>
<td></td>
<td></td>
<td>3</td>
</tr>
<tr>
<td>Amphipoda</td>
<td></td>
<td></td>
<td></td>
<td>3</td>
</tr>
<tr>
<td>Insecta</td>
<td></td>
<td></td>
<td></td>
<td>3</td>
</tr>
<tr>
<td>Halacaroidea</td>
<td></td>
<td></td>
<td></td>
<td>3</td>
</tr>
<tr>
<td>Others</td>
<td></td>
<td></td>
<td></td>
<td>3</td>
</tr>
<tr>
<td>Total density</td>
<td>1625</td>
<td>750</td>
<td>2656</td>
<td>876</td>
</tr>
</tbody>
</table>

**Table 2.** Summary of sample data from each site. Presented here are total abundance, total amount of species and a biodiversity index calculated by Shannon Wiener Diversity index, where the higher value represent higher level of biodiversity.

<table>
<thead>
<tr>
<th></th>
<th>Mean total abundance</th>
<th>Total amount of species</th>
<th>Mean Shannon Wiener diversity index</th>
</tr>
</thead>
<tbody>
<tr>
<td>C Mudflat</td>
<td>1677.00</td>
<td>3</td>
<td>0.0818</td>
</tr>
<tr>
<td>L 17 years</td>
<td>2267.20</td>
<td>6</td>
<td>0.0889</td>
</tr>
<tr>
<td>M 30 years</td>
<td>1637.33</td>
<td>5</td>
<td>0.1880</td>
</tr>
<tr>
<td>H 53 years</td>
<td>1388.33</td>
<td>6</td>
<td>0.2976</td>
</tr>
</tbody>
</table>
Fig. 2. The relative proportion of each taxonomic group at the four different sites. C = control, L = 17 years, M = 30 years and H = 53 years.

Fig. 3. Biodiversity (Shannon Wiener Diversity Index) presented from each site. C = control, L = 17 years, M = 30 years and H = 53 years. H is significantly higher to C ($p = 0.023$) and to L ($p = 0.014$).
**Fig. 4.** Biodiversity (Shannon Wiener Diversity Index) development over time. The dots represent the value from each sample collected at each site: L = 17 years, M = 30 years and H = 53 years.

**Fig. 5.** Abundance of nematoda (A), copepoda (B), polychaeta (C) and oligochaeta (D) presented in relation to age. The dots represent number of individuals found in each sample.
4. Discussion

The results of this study indicate that the meiofaunal biodiversity in the mangrove ecosystem increases significantly with the age of the forest. Significant results also show that the biodiversity is higher for H site compared to control site. No significant differences were found in biodiversity between control and L and M, respectively. The study of Schratzberger et al., (1998) investigated how nematode communities in two different estuaries were affected by the content of organic matter. The outcome suggests that the nematode abundance is in fact reduced when exposed to high content of organic matter. This conclusion can possibly support the significance between control and H site in present study, since the nematode abundance should be reduced within the mangrove area and therefore increase the meiofaunal biodiversity harbouring mangrove areas compared to mudflats. When reviewing the total nematode abundance from each site, it appears that L site had the highest amount of nematodes (2244 individuals) followed by control site (1655 individuals) and then decreased in order M to H. However, the variety of taxonomic groups found at the control site was very low, which in itself affected the biodiversity index negatively.

The abundance of meiobenthic fauna may in general be affected by several factors such as salinity, sediment particle size, water temperature, organic matter content etc. (Hua et al., 2009; Schratzberger et al., 1998; Zhou et al., 2015). Due to that neither pollutants nor other factors mentioned above were investigated in the present study, there is no certainty to that meiofaunal biodiversity is strictly affected by development stages of the mangrove forest, even though significance was found. Since meiofauna is known for its sensitivity to environmental changes (Zeppelli et al., 2015), the impact of abiotic factors may have affected the outcome of meiofaunal distribution from this area. Previous studies suggest that some nematode species are less affected or can even be favoured by pollutants and environmental changes compared to other meiofaunal groups (Raffaelli et al., 1981; Zeppelli et al., 2015). However, neither can development stage of the mangrove be excluded as an affecting factor on the meiofaunal community. Similar study have been conducted on nematode communities in Xiamen, China previously, which indicated that the abundance decreases towards older mangrove while the diversity in contrast increases (Guo, 2008).

When analysing the abundance from the separate groups, the oligochaeta is distinguished from the others by having significant increase dependent on age. According to those results one can assume that the main indicator of the mangrove development stage may be oligochaeta. The numbers found in both copepods and particularly polychaetes are low as well as inconsistent within the sites, which entails that the groups neither can show a significant result, nor represent a population high enough to use as an indicator for mangrove development stage in this survey. Conversely, the nematode abundance is distinctively higher and seemed to decrease according to age, but referring to Guo (2008) this may be a common phenomenon. While identifying nematodes to lower taxa, there seem to be a change in dominant species located in different habitats. According to this, one may have reached a better overview of the meiobenthic faunal distribution if the nematodes had been identified to lower taxa than phyla, since there may be species within the group of nematodes that are in fact increasing while others are decreasing more rapidly. Furthermore, comparing groups identified to equal taxonomic level would present a more particular view over the meiofaunal distribution and most abundant groups.
The 42 µm sieve used for washing sample L1 and L2 was partly clogged with ludox solution from previous users. Due to this the water did not flow freely through the pores and parts of the sample had to be transferred to a bucket while washing. This may have caused a loss of organisms in the process. In consultation with my supervisor Dr. Hongyou Hu and Prof. Lizhe Cai from Xiamen University, it was decided to collect new samples from those two locations the 24th of March. For the remaining samples as well as the retake (L1* and L2*) a new sieve was used which caused no issues in the washing procedure. All samples have been included in the data analysis since there is no certainty on loss of organisms from the first samples collected. However, this must still be presented as a potential source of error affecting the results. Sampling carried out the 24th brings a second source of error due to the later date and the possibility of parameters (salinity, pH etc.) changing within 2 weeks time. Meiofauna responds quickly to environmental changes and therefore we have to assume that the abundance as well as the number of groups present may have been affected during this time (Zhou et al., 2015).

Due to a limited amount of time the replicate samples in this survey are few and only one site from each age is presented. Unfortunately, this entails difficulties in interpreting the results and for further studies it is therefore suggested to increase replicate samples and particularly the number of sites. In addition it would be an advantage to measure other environmental parameters, such as salinity, pH and sediment particle size, since multistressor experiments will strengthen scientific interpretations. Nevertheless, meiofauna have shown to be good indicators on environmental changes in mangroves (Zeppelli et al., 2015), which is also indicated by the results from this study, and it may be an asset for further research on mangrove development to determine whether meiofauna can be related to age.

5. Conclusion

Older mangroves seem to have an increased meiofaunal biodiversity compared to younger. The oldest mangrove site showed to have significantly higher biodiversity compared to control. Further improved studies including other environmental stressors such as salinity, pH and seasonal variations are necessary to support the indications presented in this survey.
Acknowledgements

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References


Appendix

The taxonomic information was collected from *World Register of Marine Species*

Phylum: Nematoda

Widespread in all ages and samples.
Phylum : Arthropoda
Subphylum : Crustacea
Superclass : Multicrustacea
Class : Hexanauplia
Subclass : Copepoda

Found at all ages, although, very few from age 17 and control site.
Phylum: Annelida
Class: Polychaeta

Found in all ages but control site.
Phylum: Annelida
Class: Clitellata
Subclass: Oligochaeta

Found in all samples