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MEIOFAUNA IN THE ORGANIC SHRIMP FARMS OF MANGROVE FOREST, CA MAU PROVINCE

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ABSTRACT

Meiofaunal communities in the organic shrimp farms (OSF) of Ca Mau province was investigated in 8 ponds (Tam Giang Commune, Nam Can District). Results showed that the meiofauna, especially Nematode communities at the Tam Giang's organic shrimp farms (TGOSF) in Ca Mau mangrove express high densities and biodiversity and Nematoda dominate numerically in the mangrove meiofauna (73.69 to 96.2 %). In total, 15 major taxa were found with the dominant taxa belonged to three dominant groups: Nematoda, Copepoda, and Rotifera. The densities of meiofauna ranged from 287 ± 132.9 to 3,129 ± 1,388.6 inds.10 cm^{-2}. Seventy fifth nematode genera belonging to 24 families with the most important typifying genera were *Terschellingia*, *Daptonema*, *Parodontophora*, *Ptycholaimellus*, *Sabatieria*, *Hopperia*, *Anoplostoma*, *Pseudolella*, *Gomphionema*. The TGOSF in the study area was characterized by homogeneity and stabilization.

Keywords: mangrove, meiofaunal communities, nematode biodiversity, bioindices.

1. INTRODUCTION

Management practices for the organic shrimp farms in Ca Mau province (Southeastern Vietnam) introduces specific requirement to an organic standard. They are based on the holistic agriculture management, environmentally friendly and sustaining biodiversity. All input materials shall be natural products, avoid using synthetic products and any genetically modified organisms or genetic engineering. In order to maintain the specific qualities of organic status, this management shall be practiced throughout the production chain [1]. However, despite the biggest area of mangrove forests and mangrove – shrimp farms, there are lack of information about Ca Mau mangrove forests and benthic invertebrate in the OSF. In Vietnam, several studies on meiofaunal assemblage from mangroves habitats have been carried out, with diverse topics: Ecological data on meiofaunal assemblage from mangroves [2], biodiversity of meiofauna in the intertidal Khe Nhan mudflat, Can Gio mangrove forests with special emphasis on free living Nematoda [3].

The goal of this study was to survey the meiofaunal assemblage with special focus on free - living nematode communities in the TGOSF of Ca Mau province by assessing their composition, densities, diversity and distribution. The present study is the first of its kind concerned with the community structure and biodiversity of meiofauna in OSF and Ca Mau's mangrove forests. The received information will be valuable for sustainable development of the organic shrimp farms in Vietnam.

2. MATERIALS AND METHODS

2.1. Study area

To survey meiofaunal assemblage in OSF, the field investigations were carried out in March, 2015 (middle of the dry season). Meiofauna samples were collected at 8 ponds in TGOSF (Tam Giang Commune, Nam Can District, Ca Mau Province) and coded (P1, P2, P3, P4, P5, P6, P7 P8). The coordinate of sampling transect located at 8°46'52.5''N - 8°50'48.1''N, 105°05'32.9''E - 105°11'19.6''E in Ca Mau mangrove forests (Figure 1).

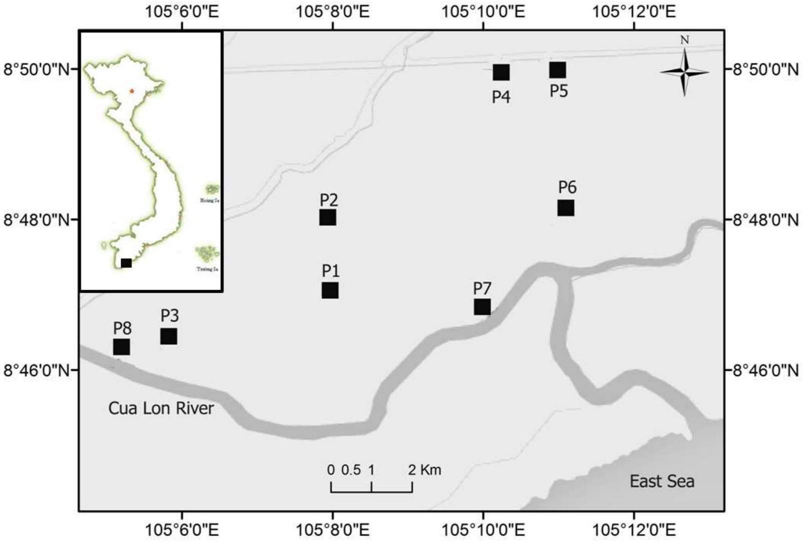

Figure 1. Map of the study area and sampling stations.

2.2. Sample collection and processes

The meiofaunal samples were collected using plastic cores of 3.5 cm diameter (10 cm^2 surface area) and 30 cm height. The cores were pushed down into the sediment to depth of 10 cm. At each pond, 3 replicates were taken and collected in plastic bottles. The samples were fixed in hot (60 ^oC) formalin solution (4 %) and gently stirred. In the laboratory, samples were sieved through a 38 µm mesh [4] and extracted by flotation with Ludox - TM50 (specific gravity of 1.18) [5]. Samples were stained with 3 – 5 mL 1 % Rose Bengal solution. All individual numbers were counted and expressed as its densities in area of 10 cm^2, one hundred nematodes were used for making slides and identification. Meiofauna in each sample slide were identified to taxon level based on pictorial keys of Higgins and Thiel [6]. Nematoda were identified at genus level with the help of the taxonomy literatures for identification of Warwick et al. [7], Zullini [8] and the NeMys online identification key [9].

2.3. Data analyses

Data were analyzed using univariate and multivariate techniques. At each pond, biodiversity was expressed as the Shannon-Wiener Index (H'($\log_2$)), Margalef diversity (d), Hill indices (N_1, N_2, N_{inf}) were calculated by means of the PRIMER VI software and used as univariate measures of the communities' structure. The significant differences in the univariate measures between sampling ponds were tested by the parametric test (ANOVA) and the non - parametric test (Kruskal -Wallis test), using the software STATISTICA 7.0. To test the assumption of homogeneity of variances, Levene's tests were applied and where necessary using log (x) transformed data. Turkey's HSD Post - Hoc and multiple comparison tests were used to detect significant among ponds ($p < 0.05$). The SIMPER analysis (SIMilarity PERcentages) was applied for identifying the taxa that are responsible for similarities and dissimilarities in each pond.

3. RESULTS

3.1. Meiofauna assemblage

3.1.1. Meiofaunal major taxa and densities

The meiofauna assemblage in the TGOSF, Ca Mau province mainly included of 15 major taxa: Nematoda; Copepoda; Turbellaria; Polychaeta; Oligochaeta; Amphipoda; Tardigrada; Ostracoda; Rotifera; Sarcomastigophora; Kinorhyncha; Isopoda; Halacaroidea; Thermosbaenacea; and Cladocera. In general, most individuals belonged to three dominant groups: Nematoda, Copepoda, and Rotifera. The first was the most dominant taxon and accounted for 73.69 ± 13.25 % - 96.20 ± 1.74 % of the total meiofaunal abundance. The second dominant taxon and constituted with range of 1.85 ± 0.36 % - 7.04 ± 4.78 %. The latter with range of 0.61 ± 0.28 % - 10.42 ± 9.94 % in this pond. Other common taxa are Polychaeta, Oligochaeta, and Sarcomastigophora which occur in high numbers in some ponds. Some taxa such as Turbellaria, Amphipoda, Tardigrada, Ostracoda, Kinorhyncha, Isopoda, Halacaroidea, Thermosbaenacea, and Cladocera were only recorded with a very small number of individuals. These constituted less than 1 % of the meiofauna. Small differences in total number of taxa were found between the different pond: The number of taxa was highest in P6 and lowest in P1.

In general, average densities (inds.10 cm^{-2}) ranged from 287 ± 132.9 in P7 to 3,129 ± 1,388.6 in P6. Other high densities ponds are P4, P8, P5, and P1 (from 2,221 ± 519.5; 2,116 ± 591.9; 1,647 ± 1,414.7; 1,628 ± 1,196.9, respectively). Ponds P2 and P3 had intermediate densities (998.7 ± 185; 1001 ± 365, respectively) (Table 1). The significant difference of meiofaunal densities between ponds was shown by one way ANOVA analysis, the meiofaunal densities was significantly highest at P6 ($p = 0.0316$). Kruskal-Wallis test was also used to test the significance of difference in densities of dominant taxa separately like Nematoda, Copepoda, and Rotifera but their denisities no significant different ($p > 0.05$) between ponds. Only the subhigh taxa (Oligochaeta) were different for the different ponds ($p = 0.04$).

3.1.2. Meiofaunal diversity

Biodiversity of meiofaunal assemblage was calculated as Shannon - Wiener (H') and Hill indices (N_1, N_2 and N_{inf}). The diversity indices show that P7 and P6 were the ponds that presented the higher diversity than other whereas the diversity value was generally lowest in the P4 (Figure 2). In addition, a Kruskal - Wallis test confirmed no significant differences between pond for meiofauna diversity ($p > 0.05$).

Table 1. Mean density (inds.10 cm^{-2}) and standard deviation (in parenthesis) of meiofauna higher taxa in the TGOSF, Ca Mau province.

Sampling ponds	P1	P2	P3	P4	P5	P6	P7	P8
Nematoda	1,563.7 (1,179.5)	856 (218.7)	847.3 (266.9)	2,136.7 (505.2)	1,402.7 (1,408.4)	2,539.3 (1,403.3)	221.7 (122.1)	1,924.7 (461.3)
Oligochaeta	10 (4.6)	27.33 (16.6)	17.3 (10.3)	13 (2.7)	49 (40.9)	19 (13.8)	4 (3)	27.3 (6)
Polychaeta	1.3 (2.3)	21.33 (17.2)	50 (67.6)	6 (5.6)	32.67 (45.4)	9 (10.6)	3.67 (0.6)	26.5 (12)
Copepoda	29 (11)	27 (6.9)	43 (23.9)	44.3 (41.4)	65 (29.1)	191 (168.4)	23 (22.9)	39.7 (15.3)
Rotifera	12 (4.2)	52 (31.8)	19.7 (31.5)	12.67 (3.2)	39.3 (33.3)	327.7 (534.8)	21.3 (7.8)	89.7 (125.9)
Sarcomastigophora	3.33 (1.2)	1.7 (2.9)	2.3 (2.5)	0.7 (0.6)	35.5 (27.6)	42.5 (38.9)	2.7 (1.5)	8 (2.7)
Amphipoda	-	-	6.7 (11.6)	-	23.4 (40.4)	-	-	-
Tubellaria	-	-	-	-	-	-	-	0.3 (0.6)
Ostracoda	4.7 (4.5)	1.7 (2.9)	8 (9.9)	6.3 (6.5)	7 (5.6)	11.3 (5.7)	7.67 (4)	2.7 (4.6)
Kinorhyncha	8.7 (14.2)	10.7 (12.4)	5.7 (8.1)	1.3 (2.3)	3.7 (5.5)	1.7 (2.1)	2.67 (1.5)	16.3 (14.2)
Isopoda	-	0.3 (0.6)	-	-	-	1 (1.7)	-	-
Halacaroidea	-	0.7 (1.2)	-	-	0.3 (0.6)	0.3 (0.6)	-	-
Thermosbaenacea	-	-	0.3 (0.6)	-	-	-	-	-
Tardigrada	-	-	0.7 (1.2)	-	0.3 (0.6)	-	0.3 (0.6)	0.33 (0.6)
Cladocera	-	-	-	-	-	0.3 (0.6)	-	-
Total	1,628.67 (1,196.9)	998.67 (185)	1,001 (365)	2,221 (519.5)	1,647 (1,414.8)	3,129 (1,388.6)	287 (132.9)	2,126.7 (591.9)

- means absent of taxa.

3.1.3. Analysis of meiofaunal communities by SIMPER

A SIMPER analysis showed the average similarity was very high in P3, P2, P8, P4 (from 72.2; 79.5; 81.1; 82.9 %, respectively). Meanwhile, the average similarity in the remaining ponds rather lower (44.1 to 61.6 %) and the lowest similarity was found in P1. Nematoda is the most dominant and mainly on a similarity contribution. However, contribution to the similarity was not only dominant taxa such as Nematoda, but also subdominant such as Copepoda and Rotifera (Table 2).

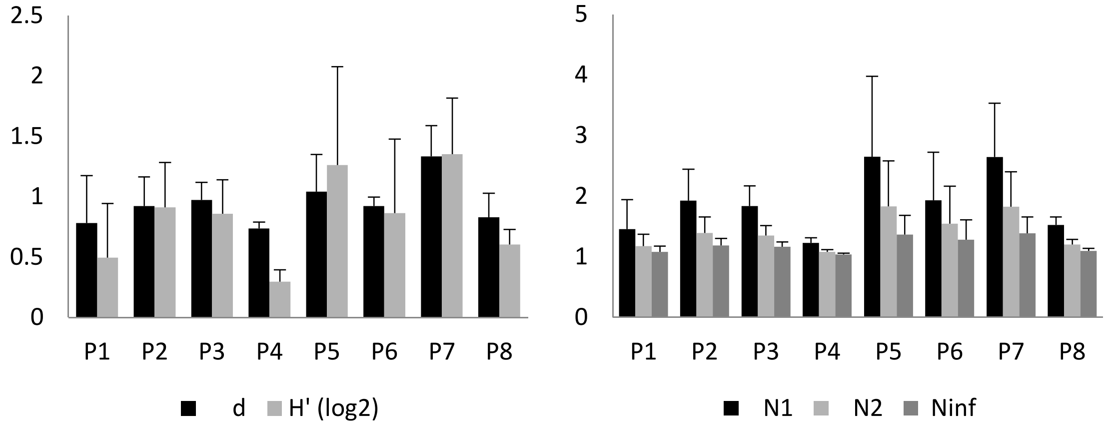

Figure 2. Meiofauna diversity.

A SIMPER analysis also showed that the average dissimilarity is high (50 – 81.3 %) in some pairs and the highest dissimilarity in pair of 6 & 7. However, the average dissimilarity between ponds were quite low (< 50 %) in most pairs, and the lowest dissimilarity in pair of 4 & 8 (15 %). Because Nematoda, Copepoda, Rotifera and Polychaeta were present in high densities and dominant in all ponds; therefore, their responsible for those dissimilarities. Many pairs of pond only Nematoda to be the taxa that cause dissimilarity (Table 3).

Table 2. Similarity and abundance of meiofaunal communities.

Ponds	Average similarity (%)	Average abundance (inds.10 cm^{-2})
P1	44.1	Nematoda (1,563.7)
P2	79.5	Nematoda (856) Rotifera (52)
P3	72.2	Nematoda (847.3)
P4	82.9	Nematoda (2,136.7)
P5	47.43	Nematoda (1,402.7) Copepod (65)
P6	56.1	Nematoda (2,539.3)
P7	61.6	Nematoda (221.67) Rotifera (21.33) Copepod (23)
P8	81.1	Nematoda (1,924.7)

Table 3. Dissimilarity of meiofaunal communities between each pond to the others.

Group	Average dissimilarity (%)	Abundance taxa (pond)
1 & 2	44.8	Nematoda (1), Rotifera (2)
1 & 3	45.2	Nematoda (1), Polychaeta (2)
2 & 3	19.7	Nematoda (2), Polychaeta (3)
1 & 4	32.6	Nematoda (4)
2 & 4	42.7	Nematoda (4)
3 & 4	44.1	Nematoda (4)
1 & 5	48.7	Nematoda (1), Copepod (5)
2 & 5	37.5	Nematoda (5)
3 & 5	37.9	Nematoda (5)
4 & 5	45.9	Nematoda (4)
1 & 6	45.1	Nematoda (6), Rotifera (6)
2 & 6	50	Nematoda (6), Rotifera (6)
3 & 6	51.2	Nematoda (6), Rotifera (6)
4 & 6	28.4	Nematoda (6), Rotifera (6)
5 & 6	50.2	Nematoda (6), Rotifera (6)
1 & 7	61	Nematoda (1)
2 & 7	58.2	Nematoda (2)
3 & 7	58.4	Nematoda (3)
4 & 7	78.7	Nematoda (4)
5 & 7	62.3	Nematoda (5)
6 & 7	81.3	Nematoda (6), Rotifera (6)
1 & 8	33.51	Nematoda (8), Rotifera (8)
2 & 8	38.3	Nematoda (8), Rotifera (8)
3 & 8	40.7	Nematoda (8), Rotifera (8)
4 & 8	15	Nematoda (4), Rotifera (8)
5 & 8	45	Nematoda (8), Rotifera (8)
6 & 8	29.4	Nematoda (6), Rotifera (6)
7 & 8	77	Nematoda (7)

3.2. Free-living Nematoda assemblage

3.2.1. Composition and densities

Results of study showed that free-living nematoda communities in the TGOSF consist of 75 genera, belonging to 24 families and 7 orders (Araeolaimida, Chromadorida, Desmodorida, Enoplida, Monhysterida, Mononchida, Plectida). Linhomoeidae was of highest abundance with 25.4 %, followed by Xyalidae, Axonolaimidae and Chromadoridae (17.8; 12.9; 11.7 %, respectively). The percentage of the remaining families ranged from 0.04 % to 7.6 % in which Ceramonematidae, Paramicrolaimidae, Plectidae, Trefusiidae were the lowest density. Cyatholaimidae and Chromadoridae were the families that presented the higher number of genera than other in the TGOSF (10 and 8, respectively). Besides, many families had number of genera for one (such as Rhabdolaimidae, Selachinematidae, Ceramonematidae, Paramicrolaimidae, Plectidae, Anoplostomatidae, Trefusiidae and Mononchulidae).

Regarding meiobenthic densities, the results of the one – way ANOVA tests show that both the number of genera and the density of Nematoda did not differ significantly along the TGOSF ($p > 0.05$). Average densities of Nematoda were summarized in Table 1. They occurred in high densities (> 1,000 inds.10 cm^{-2}) in the P6, P4, P8, P1, and P5 with a mean annual density range from 1,402.7 ± 1,408.4 to 2,539.3 ± 1,403.3 inds.10 cm^{-2}. In addition, lowest densities in the P7 with a density of 221.7 ± 122.1 inds.10 cm^{-2}.

3.2.2. Nematoda diversity

As shown in Figure 3, Shannon - Wiener index (H'), Margalef index (d) and Hill indices (N_1, N_2 and N_{inf}) to express high biodiversity. The d index ranged from 2.7 ± 1.1 to 4.4 ± 0.4 on average, from 2.4 ± 1.1 to 3.6 ± 0.2 for H' index. Meanwhile, Hill index also showed a high diversity in all eight ponds. Regarding meiofaunal diversity, pond P1 was also classified to be in the lowest diversity depending on its diversity index. By contrast, pond P4 showed highest diversity according to H', d, N_1, and N_2 whereas N_{inf} index to express highest biodiversity for pond P8. Results of one - way ANOVA and Kruskal - Wallis test also showed no significant differences between ponds for meiofaunal diversity (Shannon - Wiener, Margalef index and Hill indices).

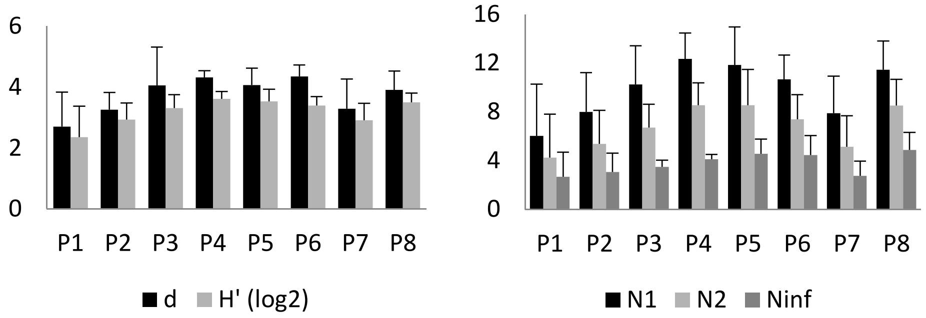

Figure 3. Nematoda diversity.

3.2.3. Nematoda communities analysed by SIMPER

Similarity percentage (SIMPER) analyses were performed to show average similarities and average dissimilarities and contribution of Nematoda genera to similarities and dissimilarities among ponds. Similarities of stations within P2 and P8 ponds (53.35; 53.75 %, respectively) were higher than remaining ponds whereas the similarity value was generally low in P1 and P3 (28.53; 26.34 %, respectively) (Table 4). *Terschellingia* and *Daptonema* were the two main genera contributing to similarities of all ponds (expect for P3). At P1 and P2, the three main genera contributing to similarities were *Terschellingia*, *Daptonema* and *Parodontophora*; meanwhile, *Ptycholaimellus*, *Sabatieria* and *Hopperia* contributed at P3. *Daptonema*, *Terschellingia*, *Anoplostoma* contributed at P5. At P7, the third genera contributing was

Sabatieria, instead of *Anoplostoma*, as seen at P5. In addition, these genera (including *Terschellingia* and *Daptonema*) such as *Pseudolella*, *Ptycholaimellus*; *Parodontophora*, *Gomphionema*, *Ptycholaimellus*; *Pseudolella*, *Parodontophora* contributing to similarities of P4, P6, P8, respectively.

Table 4. Average similarity and major genera Nematoda contributing to similarity within ponds.

Ponds	Average similarity (%)	Average abundance (inds. 10 cm^{-2})
P1	28.53	*Terschellingia* (649.71); *Daptonema* (180.9); *Parodontophora* (86.1)
P2	53.35	*Terschellingia* (340.6); *Daptonema* (149.2); *Parodontophora* (66.3)
P3	26.34	*Ptycholaimellus* (168); *Sabatieria* (147.6); *Hopperia* (36.5)
P4	44.85	*Daptonema* (469.4); *Pseudolella* (299.6); *Ptycholaimellus* (159.7); *Terschellingia* (140.6)
P5	34.14	*Daptonema* (245.2); *Terschellingia* (337.7); *Anoplostoma* (27)
P6	38.56	*Daptonema* (635.2); *Terschellingia* (356.8); *Parodontophora* (217.3); *Gomphionema* (254.8); *Ptycholaimellus* (233.1)
P7	42.38	*Terschellingia* (83.9); *Daptonema* (25.23); *Sabatieria* (21.8)
P8	53.75	*Pseudolella* (276.6); *Terschellingia* (307.7); *Daptonema* (189.8); *Parodontophora* (181.2)

Dissimilarities among ponds in the TGOSF are shown with values that range from 52.46 % between pond 6 & 7 to 85.11 % between pond 6 & 8. *Terschellingia*, *Daptonema* seem to be the genera that main cause dissimilarity between ponds. Between P1 and the other ponds, average dissimilarities were ranged from 58.28 % (1 & 2) to 80.72 % (1 & 3). A high abundance of *Terschellingia*, *Daptonema*, *Ptycholaimellus* and *Parodontophora* at P1 contributed mainly to the dissimilarities between P1 and the other ponds. *Daptonema*, *Pseudolella*, *Terschellingia* at P2 was cause dissimilarity for P2 and the other ponds. Meanwhile, *Sabatieria* and *Ptycholaimellus* contributed to dissimilarity between P3 and remaning ponds. These genera such as *Daptonema*, *Pseudolella* (at P4); *Terschellingia*, *Daptonema* (at P5) contributors to dissimilarity between two sites with the other ponds. *Daptonema*, *Gomphionema*, *Terschellingia*, *Parodontophora*, *Ptycholaimellus* appeared as the most abundant genera that main caused the dissimilarity of P6, with the other ponds. For dissimilarity between P8 and other ponds, *Pseudolella*, *Gomphionema*, *Terschellingia*, *Parodontophora* and *Daptonema* (at P8) were main responsible genera.

Figure 4 shows the dominant genera in the TGOSF, such as *Terschellingia*, *Daptonema*, *Parodontophora*, *Pseudolella*, *Ptycholaimellus*, *Sabatieria*, *Hopperia* and *Gomphionema*. *Daptonema*, *Terschellingia* and *Parodontophora* were occupied at all ponds (except for *Terschellingia* and *Parodontophora*, wich was absent at P3. In addition, *Terschellingia* was the most dominant genera at all pond (expect for P3 and P6). At P3, *Ptycholaimellus*, *Sabatieria* appears with hight abundances, followed by *Daptonema* and *Hopperia*. *Gomphionema* with high numbers in P8 and P6, but was absent in remaining ponds.

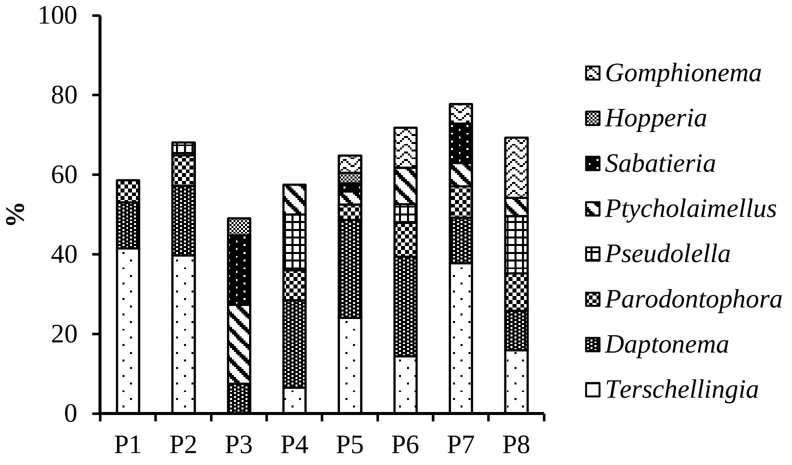

Figure 4. Dominant genera of Nematoda communities.

4. DISCUSSION

The meiofaunal communities, especially Nematoda at the TGOSF in Ca Mau’s mangrove forests were characterized by high densities and diversity.

4.1. The meiofaunal composition, densities and diversity

Meiofauna in mangrove has been studied in several areas from tropical to subtropical as well as temperate mangrove in America, Africa, Asia, especially in Australia. In Vietnam, several studies on meiofaunal assemblage from mangroves habitats have been carried out [2, 3]. However, there is a lack of information about meiofauna communities in the OSF, most probably because it has newly been introduced in Vietnam. The OSF is part of the mangrove ecosystem; therefore, it can be compared with other comparable studies in the mangrove ecosystem around the world.

Regarding meiobenthic composition, a study in the mangrove of Unguja, Zanzibar, showed that meiobenthic composition include only four groups: Nematoda, Harpacticoid copepoda, Chironomids (Diptera larvae) and Plathelminthes [10]. Seventeen taxa were recorded in mangroves of Gazi Bay, Kenya: Nematoda and Copepoda as the most dominant followed by Turbellarians, Oligochaetes, Polychaetes, Ostracods, Rotifers, which occur as the more common taxa [11]. Eight meiofaunal taxa were found in the mangrove sediment of Transkei, Southern Africa: Nematoda, Ciliates, Oligochaetes, Gastrotrichs, Polychaetes, Copepoda, Kinorhynchs, Crustacea larva [12]. As reported by Netto & Gallucci [13], in Santa Catarina (South Brazil), there were Nematoda, Polychaeta, Copepoda, Halocaridea, Kinorhyncha, Insect larvae, Ostracoda, Turbellaria, Oligochaeta. Meiofanual taxa, such as Nematoda, Polychaetes, Harpacticoids, Nauplii, Tardigrades, Gastrotrichs, Isopods, Bivalves, Kinorhynchs, Amphipods, Oligocheates, Foraminiferans, Hydrozoa, Archiannelida, Cumacea were recorded [14]. The composition of the meiofaunal community in Khe Nhan mudflat, Can Gio mangrove forests consists of some the main taxa as Nematoda, Copepoda, Sarcomastigophora, Polychaeta, Ostracoda, Oligochaeta, Tardigrada, Bivalvia larvae, Gastropoda, Gastrotricha, Nemertina, Halacaroidea, Tunicata, Kinorhyncha, Tanaidacea, Turbelaria, Insecta larvae, Nauplius [3]. According to Lai Phu Hoang [2], meiobenthic composition mainly included Nematoda, Copepoda, Nauplii, Foraminifera, Polychaetes, Oligochaetes, Kinorhynchs, Acari, Ostracods, and others less abundant group (Bivalves, Gastropods, Insect larvae, Turbellaria, Nemertinea). In general, the average number of taxa found in mangrove forests around world ranging from 4 to 18. In the present study, 15 taxa were collected which commonly also appear in other mangrove areas. Therefore, the number of meiofaunal taxa at the TGOSF is high when compared to other comparable studies.

In the present study, Nematoda is the dominant taxon at all ponds ranging from 73.69 to 96.2 %. This percentage corresponds to the value (95 %) found in mangroves of Gazi Bay, Kenya [11], but is occasionally higher compared with the data published by Ngo Xuan Quang et al. [3] and Lai Phu Hoang [2] in Can Gio mangrove forests (84.58; 88.3 – 93 %, respectively); Dye [15] in Transkei, Southern Africa (80 %); Ali et al. [16]: 50 – 67 %; by Kondalarao [17] in India: 86 % and by Lalana - Rueda et al. [18]: 54 %. In addition, Copepoda occupied the position of the second most abundant group that were found in the studies by Ngo Xuan Quang et al. [3] and Lai Phu Hoang [2] in Can Gio mangrove forests, by Vanhove et al. [11] and Ólafsson [19].

The results of the present study showed that meiofaunal densities in the TGOSF ranging from 287 to 3,129 inds. 10 cm^{-2}, high in comparison to mangroves in the other parts of the world, such as in Americas, African, Australia and Asia. Mangrove in the Americas, by Lalana - Rueda & Gosselck [18]: 36 - 245 inds.10 cm^{-2}, by Armenteros et al. [20] recorded an average of 101 inds.10cm^{-2} and Netto & Gallucci [13] (77 – 1,589 inds.10 cm^{-2}). African mangrove is high meiofaunal densities [2]. Average total meiofauna with 2,460 inds.10 cm^{-2} [12], 1,000 inds.10 cm^{-2} [15]. Vanhove et al. [11] showed that densities of meiofauna varied maximum of 6,707 inds.10 cm^{-2} in *Bruguiera* forest, Kenia. Mangroves in Australia has been studied extensively, where densities ranging from 217 – 2,454 inds.10 cm^{-2} [21], 14 ± 8 – 1,840 ± 2,517 inds.10 cm^{-2} [14]. Hodda & Nicholas [22] reported that the highest meiofaunal densities approximately 12,058 inds.10 cm^{-2} at *Avicennia* mangrove in South - eastern Australia. In Asia, at a mangrove in Bay of Bengal (India) only 35 - 280 inds.10 cm^{-2} were found [16]. Chinnadurai & Fernando [23] study in the South - eastern coast of India, show that average densities of meiofauna from 234 to 890 inds.10cm^{-2}. Kondalarao [17] recognized that meiofaunal densities reaching 2,130 inds.10 cm^{-2} in Gautami - Godavari estuarine system. In another part of Asia, Sasekumar [24] recorded densities of meiofauna ranging from 407 to 1,109 inds.10 cm^{-2} in mangrove forests along the coast of Malaysia. In Vietnam, mangrove forests in Southern delta has been studied extensively, especially in Can Gio mangrove forests. In a study investigating the meiofauna in Can Gio mangrove forests, Lai Phu Hoang [2] recorded that average meiobenthic density ranging from 1,303 to 2,440 inds.10 cm^{-2}. In addition, Ngo Xuan Quang et al. [3] reported that meiobenthic density was 1,156 - 2,082 inds.10 cm^{-2} in Khe Nhan mudflat, Can Gio mangrove forests.

For meiofauna diversity in mangrove forests, all publications only included taxa richness instead of calculation of the biodiversity indices. However, a study investigating the meiofauna in Khe Nhan mudflat, Can Gio mangrove forests, Ngo Xuan Quang et al. [3] has calculated of the biodiversity index in detail. Diversity of meiofauna in Khe Nhan mudflat was computed in Margalef index – d (1.31 – 1.62), Shannon - wiener diversity index – H' (0.67 – 0.78) and Hill indices - N_1, N_2 and N_{inf} (1.97 – 2.22; 1.36 – 1.46; 1.17 – 1.21, respectively). In present study, the d index ranged from 0.73 to 1.33 on average, from 0.2 to 1.35 for H' index. Meanwhile, Hill index were 1.23 - 2.64, 1.08 - 1.83 and 1.03 - 1.39 (N_1; $N_{2;}$ and N_{inf}, respectively). For value of H', N_1 and $N_{2,}$ present study is higher than value in Khe Nhan mudflat. In contrast, d and N_{inf} value in present study is lower than in Khe Nhan mudflat.

4.2. Nematoda diversity

Table 5. Literature on Nematoda diversity from mangrove areas all over the world.

Area	Site	Habitat	Diversity	References
Vietnam	TGOSF, Ca Mau	Mangrove forests	d = 2.7 – 4.35 H' = 2.35 – 3.61 N1 = 6.03 – 12.35 N2 = 4.25 – 8.54 Ninf = 2.68 – 4.87	Present study
	Khe Nhan mudflat, Can Gio	Mangrove forests	d = 4 - 5.2 H' = 3.6 - 4.2 N1 = 12.72 - 18.9 N2 = 6.87 - 10.68 Ninf = 2.98 - 4.09	[3]
	Rach Oc creek, Can Gio	Mangrove forests	Dry season: d = 5.3 - 11.4 H' = 2 - 3.7 Rainy season: d = 5 - 11.1 H' = 1.9 - 3.6	[2]
Asia	Merbok, Malaysia	*Rhizophora, Brugiera*	H' = 2.0 - 3.2	[26]
Australia	Victoria	*Avicennia*	H' = 0.56 ± 0.084	[27]
	Cape York peninsula	Mangrove estuarine	H' = 2.02 - 2.91	[21]
		Avicennia marina mangrove mudflat	H' = 1.43 - 2.76	[28]
	Hunter river and Fullerton	Mangrove forests	H' = 1.28 - 2.76	[22]
Europe	Marennes - Oléron, France	Temperate intertidal mudflat	H' = 2.7 - 3.5	[29]
Americas	Santa Catarina, South Brazil	Mangrove forests	H' = 2.5 - 3.5	[13]
Africa	Zanzibar	Tropical mangrove	H' = 0.94 - 4.25	[19]

When compared to other comparable studies in mangrove forests of Vietnam [2, 3], the biodiversity of Nematoda in the TGOSF showed quite lower diversity index than that in the Can Gio mangrove forests. However, the range in diversity is approximately similar to those observed by Ólafsson [19] in the Zanzibar tropical mangrove (Africa). Nematoda diversity in the TGOSF is very high as compared to mangroves in the world (Table 5).

Therefore, Nematoda communities at mangrove forests in Vietnam’s Southern delta (especially in Can Gio and Ca Mau mangrove) were characterized by very high diversity. This supports the statement that Vietnam is ranked as countries with the highest biological diversity [25]. In addition, there was no significant difference between the pond for these biodiversity indices could be due to the Nematoda communities show more continuous cycle of reproduction and environmental TGOSF in Ca Mau’s mangrove forests were characterized by homogeneity and stabilization. During the operation period a famer had not yet affected the mangrove ecosystem. However, shrimp - pond is potential impacts on mangroves if we use the wrong method.

4.3. The composition of nematode communities in the TGOSF

In the present study, Nematoda were identified up to genus level. Results showed that free-living Nematoda communities in the TGOSF consist of 75 genera belonging to 24 families and 7 orders were recorded. Ngo Xuan Quang et al. [3] when studying Nematoda in Khe Nhan mudflat, Can Gio mangroves reported that the Nematoda communities was characterized by a minimum of 80 genera, 24 families, 7 orders. Lai Phu Hoang [2] showed that Nematoda communities in Rach Oc creek, Can Gio mangroves consisting of 92 genera and 36 families. The number of genera in the present study is similar to those by Ngo Xuan Quang et al. [3], but lower than those by Lai Phu Hoang [2], illustrating the high diversity of Nematoda in TGOSF.

The SIMPER analysis shows the total average similarity and dissimilarity for each pond, the responsible genera and their contribution to the average similarity and dissimilarity. The result demonstrated that the most important typifying genera at TGOSF were *Terschellingia*, *Daptonema*, *Parodontophora*, *Ptycholaimellus*, *Sabatieria*, *Hopperia*, *Anoplostoma*, *Pseudolella*, and *Gomphionema*. It was the main genera contributing to similarities and dissimilarities of all ponds in the study area.

4. CONCLUSIONS

The meiofauna at the TGOSF in Ca Mau mangrove forests is characterized by high densities and biodiversity, supporting the statement that mangrove forests in Vietnam’s Southern delta is of high biodiversity. Nematode communities dominate numerically in the mangrove meiofauna. The characteristics of nematode communities and their links with environmental factors can therefore be a good tool for environmental monitoring. Further research should be done on the nematode communities in correlation with environmental characteristics in mangrove – shrimp farms systems so that using them as an environmental monitoring tool can be validated.

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