



RESEARCH ARTICLE

Intertidal meiofaunal communities in relation to salinity gradients in the Ba Lai river, Vietnam

Quần xã động vật đáy cỡ trung bình trong mối liên hệ với độ mặn trên sông Ba Lai, Việt Nam

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In order to reveal the characteristics of meiofaunal communities (MC) (specifically freshwater meiofauna) and their relationship with salinity gradients, meiofauna samples were collected in September 2015 in Ba Lai river (BLR) in the Mekong Delta region, Vietnam. A total of 14 meiofaunal taxa were identified. The most dominant group was Nematoda, followed by Nauplii and Rotifera. The MC (specifically nematodes) in BLR were characterized by high abundances and diversities. The characteristics of MC in the downstream site (marine habitats) may be considerably different from those in the upstream site (fresh habitats). Abundances and diversities of nematode communities in the downstream site were much higher than those observed in the upstream site, especially for abundances. Regarding MC, their abundance in the downstream site was also considerably higher than those in upstream site, whereas their diversity was lower. Furthermore, the Ba Lai dam (BLD) has the ability to change salinity gradients in BLR, while MC were in strong correlation with salinity. Specifically, nematode abundances, diversities and meiofaunal abundances were in strong positive correlation with salinity gradients. By contrast, meiofaunal diversities were significantly negatively correlated with salinity. Therefore, the MC and their correlation with environmental variables can be considered as a good tool for the assessment of dams' impact on river's ecosystems.

Để xác định các đặc điểm của quần xã động vật đáy cỡ trung bình (đặc biệt là nhóm nước ngọt) và mối liên hệ giữa chúng với độ mặn, mẫu động vật đáy được thu thập vào tháng 09 năm 2015 trên sông Ba Lai, thuộc hệ thống sông Mekong, Việt Nam. Tổng cộng 14 nhóm động vật đáy được ghi nhận, ưu thế nhất là Nematoda, sau đó là Nauplii và Rotifera. Quần xã động vật đáy trên sông Ba Lai có mật độ và đa dạng cao và đặc điểm nhóm nước ngọt (trong đập Ba Lai) khác biệt với nhóm nước mặn (ngoài đập). Mật độ và đa dạng của nhóm Nematoda ngoài đập cao hơn trong đập. Trong khi đó, đa dạng quần xã động vật đáy trong đập cao hơn bên ngoài, mật độ thì ngược lại. Ngoài ra, đập Ba Lai làm biến đổi độ mặn trên sông Ba Lai, trong khi độ mặn có tương quan chặt chẽ với quần xã động vật đáy. Cụ thể, mật độ, đa dạng của quần xã tuyến trùng và mật độ của quần xã động vật đáy cỡ trung bình có tương quan thuận với độ mặn. Ngược lại, độ đa dạng quần xã động vật đáy cỡ trung bình có tương quan nghịch với độ mặn. Cho nên, quần xã động vật đáy có thể sử dụng làm chỉ thị cho tác động của đập chắn lên hệ sinh thái thủy vực.

Keywords: Ba Lai river, biomonitoring, dam effects, meiofaunal communities, Mekong river, nematodes, salinity

1. Introduction

The term "meiofauna" or "meiobenthos" was first utilized by Mare (1942) to describe small sediment-dwelling organisms with phylogenetic representation from almost all the invertebrate phyla. Generally, they are defined as benthic metazoans with intermediate size between the macro- and microfauna. The size of meiobenthic organisms is between 500 μm and 40-64 μm (Higgins and Thiel, 1988). They have a ubiquitous distribution in aquatic sediments worldwide and correspond to 60% of total metazoan abundance on Earth (Coull, 1999; Danovaro, 2010). Thus, they are the most

abundant and diverse metazoan group in any aquatic habitat (Danovaro, 2010). Meiofauna can be categorized into: a) permanent meiofauna, which are small organisms that spend their complete life cycle without reaching sizes greater than 1 mm (such as Nematoda, Rotifera, Copepoda, Ostracoda, Turbellaria, Tardigrada and so on) and b) temporary meiofauna, which are usually larvae of macrofauna and only become part of meiofauna during juvenile stages (e.g., Oligochaeta, Mollusca and insect larvae) (Hentschel and Jumars, 1994).

Meiofaunal communities play a crucial role in the benthic ecosystem processes: (i) MC are an important component

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in benthic food web as trophic link between the microfauna and larger fauna: the main food sources of meiofauna are organic detritus, bacteria, and benthic diatoms while they can provide food for a variety of predators especially many juvenile fish, prawns, and shellfishes (Montagna et al., 1995; Liu et al., 2005; Liu et al., 2014). (ii) MC play a crucial role in nutrients, materials cycling, and energy flow in aquatic ecosystems: several studies have warned that the mineralization of organic matter is enhanced and microbial production is stimulated in the presence of meiofauna. Thus, MC can promote nutrients recycling (Montagna et al., 1995; Semprucci et al., 2013). Recently, the biomass of MC in benthic ecosystems is similar (or even higher) than the biomass of macrofauna communities, which makes them important in global biogeochemical cycles (Platt and Warwick, 1980; Heip et al., 2000). (iii) MC are considered as important indicators in marine environmental quality monitoring and ecosystem health assessment because of high species richness, ubiquitous distribution, high fecundity, short life history, and respondent rapidly to natural and anthropogenic disturbances (Vassallo et al., 2006; Schratzberger and Ingels, 2016).

The diversity and ecology of MC have been studied in many parts of the world (for details, see Ngo et al., 2007) and marine meiofauna has received much attention from ecologists (Schmid-Araya, 2000). However, the studies of freshwater meiofauna are not yet fully focused in comparison to marine meiofauna (Radwell and Brown, 2008). Although there is a vast body of literature dealing with nematode communities (Tran et al., 2018c), the basic information regarding the ecological attributes and the composition of MC is still largely lacking in Vietnam. Only a few papers deal with the composition of MC and their correlation with environmental characteristics has been investigated in Can Gio mangrove forest (Ngo et al., 2007), Mekong estuaries (Ngo et al., 2010, 2013), and Ca Mau mangrove forest (Tran et al., 2018a). Clearly, these estimates have been carried out in marine habitats. To the authors' knowledge, there have been no studies done on the MC in freshwater habitats in Vietnam.

Ba Lai river (BLR) is one of the four branches of the Tien river (the main northern tributary of the Mekong river) discharging directly into the East Sea. In 2002, an irrigation dam was built across the river to stop the infiltration of salt water. Henceforth, the BLR was divided into two sections: the section upstream dam with freshwater conditions, while the section downstream the dam referred to salinity conditions. Therefore, BLR is a "great case" study for MC in both habitats: freshwater and marine.

The objectives of this paper are: (i) to survey the MC by assessing their composition, abundance, and diversity, and (ii) to determine the correlation between the characteristics of MC and the salinity gradients in BLR. The

data gathered from the study could be used as baseline data for future research of MC in Vietnam. Also, this study provides one of the first baseline surveys of MC in freshwater habitats in Vietnam.

2. Materials and methods

2.1. Study area

The Ba Lai River (Vietnamese: *Sông Ba Lai*) is a river in Ben Tre province, Mekong Delta region, Vietnam. The river has a length of 55 km, width from 200 to 300 m, depth from 3 to 5 m. This river plays a pivotal role in supplying freshwater for agriculture, industry, domestic applications, as well as other economic activities such as navigation, tourism, aquaculture (Thach and Doan, 2001). In 2002, an irrigation dam (the Ba Lai dam - BLD) was built across the river to stop the infiltration of salt water and preserve fresh water for 100,000 hectares of farmland in the Ben Tre province. Several recent studies have claimed slight disturbances as soft-bottom sediment layers have already been deposited in river-estuarine, and the reason of that seems to be BLD (Nguyen and Nguyen, 2011; Tran et al., 2018b).

2.2. Sampling

The study was carried out in September 2015 (wet season) at eight different stations distributed throughout the major stream of BLR in Ben Tre province, Vietnam (Figure 1). The stations B1–B3 were distributed downstream of BLD (D side), while the stations B4–B8 were distributed upstream of BLD (U side). The geographical coordinates of the sampling stations are given in Table 1.

Table 1. Sampling stations with coordinates

Stations	Geographical locations	
	Latitude	Longitude
BL1	10°01'52.61"N	106°41'23.65"E
BL2	10°05'19.96"N	106°41'60.25"E
BL3	10°08'28.69"N	106°37'58.45"E
BL4	10°08'48.09"N	106°37'37.86"E
BL5	10°11'37.71"N	106°34'10.46"E
BL6	10°13'28.04"N	106°30'24.00"E
BL7	10°15'47.23"N	106°26'36.73"E
BL8	10°17'16.27"N	106°23'20.41"E

Salinity concentration in BLR was measured *in situ* using a Multiparameter Water Quality Meter Model WQC22A. Cowardin et al. (1979) classified water into five categories based on salinity concentration, ranging from fresh (0 to 0.5‰) to hyperhaline (>40‰). They further subdivided the brackish habitat types (0.5 to 30‰) into: oligohaline (0.5 to 5‰), mesohaline (5 to 18‰), and polyhaline (18 to 30‰).

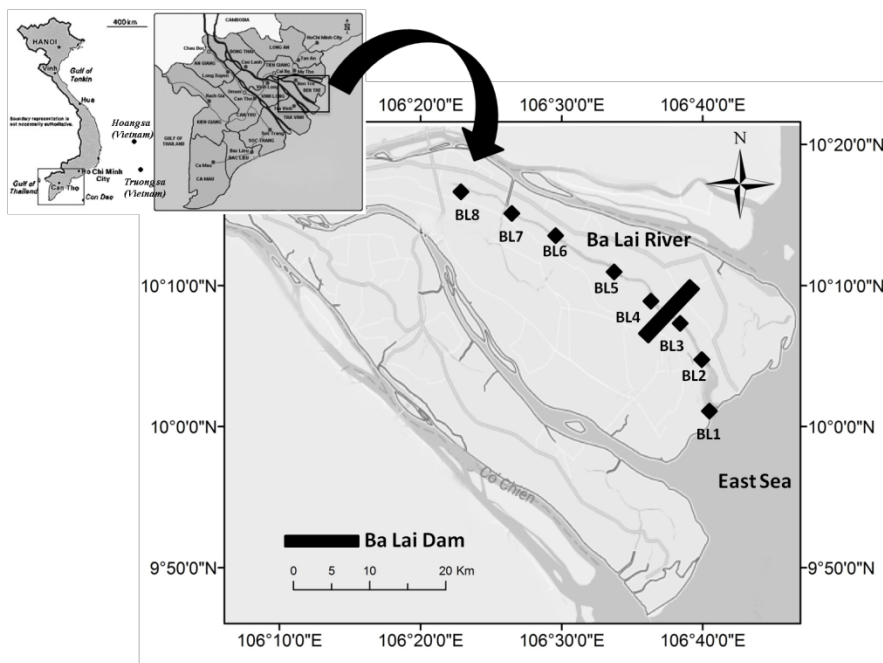


Figure 1. Maps of the sampling sites in Ba Lai river (adapted from Tran et al., 2018c). Note: ♦ Sampling stations

Three replicates were taken at each station and intertidal sediment sample was collected with cores of 3.5 cm in diameter (10 cm² surface area) and 30 cm in length. All the samples were fixed with 10% buffered formaldehyde solution and gently stirred. In the laboratory, the sediment samples for meiofauna were stained with 3-5 ml Rose Bengal (1%) for > 24h, followed by sieving with 0.5 mm and 0.040 mm meshes. Meiofauna was extracted by flotation technique with Ludox - TM50 solution (Ludox™, Aldrich Chemical Company) with a specific gravity of 1.18 g.cm⁻³ (Vincx, 1996). The procedure was repeated three times and each sample was washed into a lined petri dish. All meiofauna were counted under a stereomicroscope and identified to taxon level based on pictorial keys of Higgins and Thiel (1998). Each time, two hundred nematodes per sample were randomly picked out and transferred into separate embryo dishes for processing by three types of De Grisse solutions before making permanent slides for identification. Nematodes were identified to genus level by using the following taxonomy literature: Platt & Warwick (1983, 1988), Warwick et al. (1988), Zullini (2005), Nguyen (2007) and the NEMYS database of the Marine Biology Section, Ghent University, Belgium (Bezerra et al., 2018) (www.nemys.ugent.be).

2.3. Data analysis

The characteristics of nematode communities in BLR such as abundances, species richness, and diversity indices (Shannon diversity index, Hill index) have been described by Tran et al. (2018c). The abundance of the MC was standardized for a 10 cm² area, which is a generally recommended unit in meiofaunal research (Pfannkuche and Thiel, 1988). The diversity of the MC was measured using indices such as the taxa richness (S), the Shannon diversity index (H'(log₂)) (Shannon, 1948); the Hill index (N_i)

(Hill, 1973). All the data of MC was presented as an average ± standard deviation.

Statistical analyses were performed with STATISTICA software version 7.0 which was used for one-way ANOVA analysis (parametric test) with assumptions of homogeneity tested by Levene's test. In case that homogeneity of variances was not fulfilled (even not after log transformation of the data), the Kruskal-Wallis test (non-parametric test) was applied (Statistica, 2004). An Analysis of similarities (ANOSIM) was applied for comparing the characteristics of MC and salinity between upstream and downstream stations. Additionally, the SIMPER analysis (SIMilarity PERcentages) was used for identifying the taxa responsible for similarities and dissimilarities between downstream and upstream stations. The ANOSIM and SIMPER were performed using PRIMER v6.1.6 (Clarke, 2006).

Non-parametric Spearman rank correlation coefficients were used (p < 0.05) to identify correlations between salinity variables and characteristics of the MC (abundance, S, H', N₁). The regression procedure was applied to construct a statistical model describing the relation of a single quantitative factor (salinity variables) on a single dependent variable (characteristics of the MC). The correlation and regression analysis was performed using the software Statgraphic Centurion XV version 15.1.02, for finding the best regression model. The model with the highest R-squared was chosen because it explains the largest percentage of the variation in the response variable (Stat, 2005).

3. Results

3.1. The characteristics of meiofauna communities in Ba Lai river

3.1.1. Meiofaunal composition

The meiofauna communities of the eight stations in BLR were composed of 14 taxa: Nematoda, Nauplii, Copepoda,

Rotifera, Oligochaeta, Polychaeta, Ostracoda, Sarcostomastigophora, Cnidaria, Amphipoda, Insecta, Kinorhyncha, Halacaroidea, and Cladocera. Nematoda was always the most dominant taxa, whereas Nauplii and Rotifera were subdominants. By contrast, the Sarcostomastigophora, Cnidaria, Amphipoda, Insecta, Kinorhyncha, Halacaroidea, and Cladocera were only represented by a very small number of individuals (Table 2).

Table 2. Composition and densities (inds/10cm²) of meiofauna communities in Ba Lai river (Average ± SD)

	BL1	BL2	BL3	BL4	BL5	BL6	BL7	BL8
Nematoda	4580 ± 1533	3435 ± 470	1466 ± 394	356 ± 43.4	83.0 ± 17.0	114 ± 28.5	218 ± 160	203 ± 73.3
Nauplii	32.7 ± 16.74	42.7 ± 7.64	57.7 ± 32.3	91.7 ± 92.2	147 ± 46.7	38.7 ± 35.5	76.7 ± 31.7	52.3 ± 29.0
Copepoda	21.7 ± 18.2	28.0 ± 20.8	37.7 ± 36.7	10.3 ± 11.9	2.50 ± 0.71	6.00 ± 1.00	5.00 ± 3.00	2.67 ± 1.53
Rotifera	6.33 ± 7.09	11.3 ± 7.37	72.7 ± 57.3	25.7 ± 22.0	74.0 ± 39.6	31.0 ± 24.3	34.7 ± 31.3	28.0 ± 17.3
Oligochaeta	3.00 ± 2.65	2.00 ± 2.00	0.67 ± 0.58	5.33 ± 7.51	0.50 ± 0.71	3.33 ± 4.93	0.67 ± 0.58	0.33 ± 0.58
Polychaeta	12.7 ± 8.50	3.67 ± 3.79	2.00 ± 1.73	0.33 ± 0.58	7.00 ± 7.07	0.33 ± 0.58	0.33 ± 0.58	1.33 ± 1.53
Ostracoda	7.67 ± 9.29	4.33 ± 2.52	7.33 ± 10.21	1.00 ± 1.00	0.50 ± 0.71	5.33 ± 4.04	0.33 ± 0.58	8.67 ± 11.0
Sarcostomastigophora	2.00 ± 2.00	1.00 ± 1.00	0 ± 0	0.67 ± 0.58	0.50 ± 0.71	0 ± 0	0 ± 0	0 ± 0
Cnidaria	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0.33 ± 0.58	0.33 ± 0.58	0 ± 0
Amphipoda	2.00 ± 3.46	0 ± 0	1.00 ± 1.00	0.33 ± 0.58	0 ± 0	0 ± 0	0 ± 0	0 ± 0
Insecta	0.33 ± 0.58	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0
Kinorhyncha	1.00 ± 1.73	1.00 ± 1.00	0 ± 0	0.33 ± 0.58	0 ± 0	0 ± 0	0 ± 0	0 ± 0
Halacaroidea	0 ± 0	0 ± 0	0 ± 0	0.33 ± 0.58	0 ± 0	0 ± 0	0 ± 0	0 ± 0
Cladocera	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0.33 ± 0.58	0 ± 0

The results of the SIMPER analysis confirmed that the average similarity within station was high and varied from 60.46% (BL7) to 90.47% (BL2). Nematoda was the main taxa contributing to similarities in all stations, from 30.21%

(BL5) to 98.78% (BL1). Except for BL5, Nauplii was the main group contributing to similarities. Furthermore, Rotifera seem to be the taxa significantly contributing to the similarities of BL5, BL6, and BL8 (Table 3).

Table 3. Average similarity and major meiofaunal taxa contributing to similarity within the station in Ba Lai river. Cut off for low contributions: 90.00% (Av.Si: average similarity-%; Con: contribution-%)

Stations	Av.Si (%)	Taxa (Con-%)
Downstream	BL1	80.73 Nematoda (98.78)
	BL2	90.47 Nematoda (97.94)
	BL3	78.75 Nematoda (92.72)
Upstream	BL4	77.88 Nematoda (85.74), Nauplii (9.74)
	BL5	74.60 Nauplii (48.51), Nematoda (30.21), Rotifera (19.57)
	BL6	66.89 Nematoda (71.71), Nauplii (11.00), Rotifera (10.59)
	BL7	60.46 Nematoda (65.03), Nauplii (27.69)
	BL8	70.86 Nematoda (72.58), Nauplii (16.91), Rotifera (8.82)

The SIMPER analysis also showed that the average dissimilarity between stations was fairly high. Specifically, pairwise comparison of stations in downstream (such as BL1&BL2, BL2&BL3, and BL1&BL3) indicated quite a high dissimilarity (ranged from 13.90 to 50.43%) The Nematoda served as the key players responsible for those dissimilarities. Additionally, the average dissimilarities between stations up - and downstream were considerably

high, ranged from 58.68% in the case of BL3 & BL4 to 93.40% in the case of BL1 & BL6. The taxa responsible for those dissimilarities was also Nematoda. The dissimilarities in a pairwise comparison of stations upstream between 29.85% (BL7&BL8) and 54.18% (BL4&BL5). The taxa responsible for those dissimilarities were Nematoda, Nauplii, and Rotifera (Table 4).

Table 4. Average dissimilarity and major meiofaunal taxa contributing to dissimilarity within the station in Ba Lai river. Cut off for low contributions: 90.00% (Av.Dis: average dissimilarity-%; Con: contribution-%; Cum: cumulative-%)

Groups	Av.Dis (%)	Taxa (Con-%)
Downstream stations		
BL1&2	13.90	Nematoda (93.93)
BL1&3	50.43	Nematoda (94.94)
BL2&3	40.71	Nematoda (93.85)
Up-Downstream stations		
BL1&4	83.58	Nematoda (96.81)
BL1&5	90.40	Nematoda (95.04)
BL1&6	93.40	Nematoda (97.74)
BL1&7	89.17	Nematoda (97.15)
BL1&8	89.61	Nematoda (97.66)
BL2&4	79.09	Nematoda (96.54)
BL2&5	92.46	Nematoda (94.16)
BL2&6	91.26	Nematoda (97.44)
BL2&7	85.94	Nematoda (96.90)
BL2&8	86.60	Nematoda (97.35)
BL3&4	58.68	Nematoda (86.59), Nauplii (5.08)
BL3&5	79.25	Nematoda (87.95), Nauplii (5.79)
BL3&6	79.87	Nematoda (90.59)
BL3&7	69.59	Nematoda (90.18)
BL3&8	70.80	Nematoda (90.39)
Upstream stations		
BL4&5	54.18	Nematoda (63.39), Nauplii (20.82), Rotifera (10.82)
BL4&6	51.67	Nematoda (69.11), Nauplii (18.69), Rotifera (6.19)
BL4&7	36.44	Nematoda (63.21), Nauplii (21.23), Rotifera (9.77)
BL4&8	33.51	Nematoda (59.11), Nauplii (24.02), Rotifera (7.65)
BL5&6	41.10	Nauplii (52.44), Rotifera (21.95), Nematoda (16.84)
BL5&7	39.22	Nematoda (46.09), Nauplii (30.31), Rotifera (19.00)
BL5&8	44.25	Nematoda (44.40), Nauplii (33.79), Rotifera (15.85)
BL6&7	33.87	Nematoda (49.07), Nauplii (26.41), Rotifera (17.34)
BL6&8	33.16	Nematoda (55.73), Nauplii (21.55), Rotifera (12.98)
BL7&8	29.85	Nematoda (58.85), Nauplii (18.46), Rotifera (15.13)

3.1.2. Meiofaunal densities and diversities

The total meiofaunal densities ranged from 199.33 ± 76.96 (BL6) to 4669.67 ± 1542.73 (BL1) inds/10 cm². The highest value of meiofaunal abundances was found at BL1 and those at BL2 and BL3 were also high (3529.33 ± 440.33 , 1644.67 ± 350.29 inds/10cm², respectively). Densities in the upstream stations were rather lower than downstream, ranged from 199.33 ± 76.96 to 491.67 ± 70.12 inds/10cm² (Figure 3A). The ANOVA test showed that meiofaunal densities were significant differences between sampling stations ($p < 0.0001$). Also, meiofaunal densities were significant differences between upstream and downstream with $p < 0.0001$ in ANOVA test.

The diversity of the MC was measured by the taxa richness (S), the Shanon-Wiener index (H'), and the Hill index (N₁). The species richness ranged from 8.00 ± 1.00 to 5.99 ± 1.06 and the Shanon-Wiener index ranged from 0.18 ± 0.07 to 1.71 ± 0.009 . The Hill index showed average values ranging from 1.13 ± 0.06 to 3.28 ± 0.02 for N₁ (Figures 2B-D). ANOVA/Kruskal-Wallis analysis showed there were significant differences between stations for all indices (except for S, Table 5). Furthermore, the results of an ANOSIM analysis confirmed that there were significant differences between upstream and downstream for all indices (except for S, Table 6).

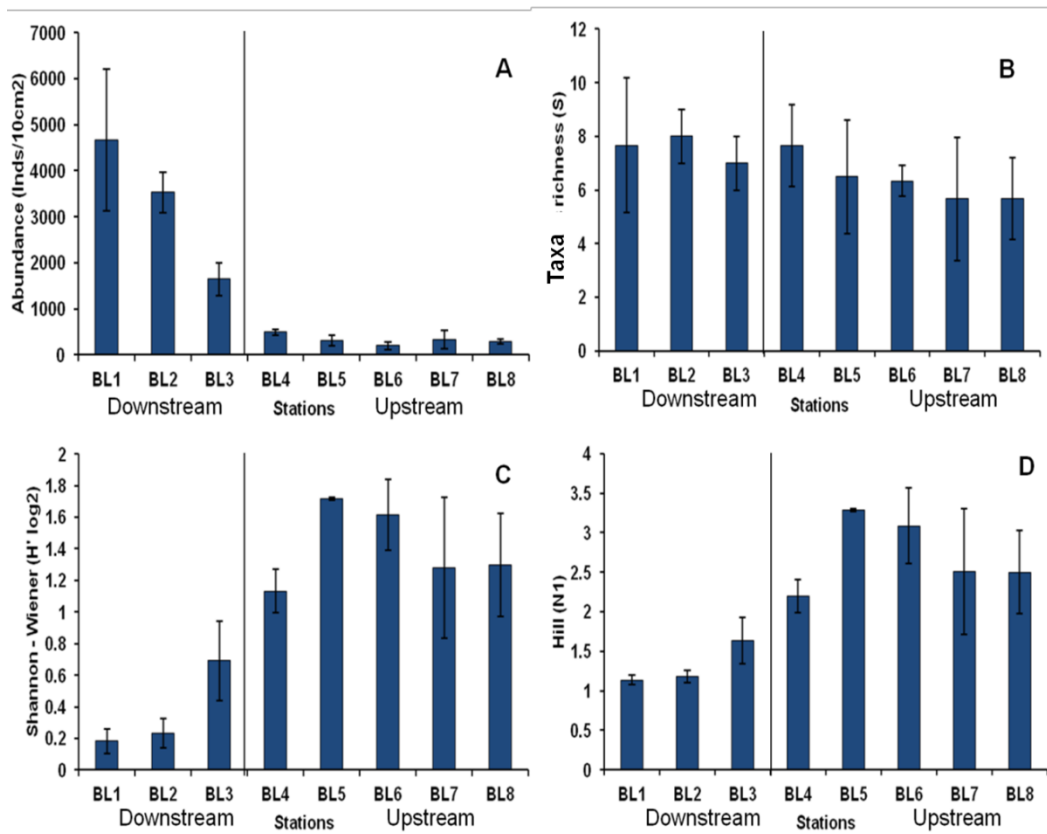


Figure 2. Characteristics of meiofauna communities. (A) Abundances (Inds/10cm²), (B) Taxa richness (S), (C) Shannon - Wiener diversity (H' (log₂)), (D) Hill indices (N₁)

Table 5. The results of an ANOVA / Kruskal - Wallis for characteristics of meiofaunal communities (between sampling stations). The significant difference was respectively indicated with bold

	Variables used	p-value	ANO/Kru
Meiofaunal communities	Ab.meio	< 0.0001	ANO
	S.meio	0.57	ANO
	H'.meio	< 0.0001	ANO
	N1.meio	0.01	Kru
Nematode communities (Modified from Tran <i>et al.</i> , 2018c)	Ab.nema	< 0.0001	ANO
	S.nema	< 0.0001	ANO
	H'.nema	0.014	Kru
	N1.nema	< 0.0001	ANO

Notes. ANO: ANOVA, Kru: Kruskal-Wallis, Ab.meio: meiofaunal abundance (inds/10cm²), S.meio: meiofaunal taxa richness, H'.meio: meiofaunal Shannon index, N₁.meio: meiofaunal Hill index, Ab.nema: nematodes abundance (inds/10cm²), S.nema: nematodes taxa richness, H'.nema: nematodes Shannon index, N₁.nema: nematodes Hill index)

Table 6. The results of an ANOSIM for characteristics of meiofauna communities (between upstream and downstream). The significant difference was respectively indicated with bold

	Variables used	Global R	p-value	Mean	
				D	U
Meiofaunal communities	Ab.meio	0.96	0.001	3128 ± 1528	328 ± 106
	S.meio	-0.024	0.53	7.55 ± 0.50	6.36 ± 0.81
	H'.meio	0.78	0.001	0.37 ± 0.27	1.40 ± 0.24
	N ₁ .meio	0.82	0.001	1.31 ± 0.27	2.71 ± 0.45
Nematode communities	Ab.nema	0.95	0.001	3160 ± 1575	195 ± 107
	S.nema	0.24	0.013	30.4 ± 3.20	22.14 ± 5.43
	H'.nema	0.23	0.014	3.83 ± 0.24	3.21 ± 0.42
	N ₁ .nema	0.26	0.008	14.5 ± 2.34	9.66 ± 2.71

3.2. Salinity gradients in Ba Lai river

The salinity concentration values ranged from 0.03 to 6.38‰, the highest value being observed at the station BL1 (6.38‰), followed by the stations BL2 and BL3 (5.35 and 3.28‰, respectively). On the other hand, the stations BL6, BL5, and BL4 were the group having low salinity concentration values (with 0.21, 0.52, and 0.43‰, respectively). The lowest salinity value was found in the station BL8 and BL7 (0.03 and 0.05‰, respectively). All stations at U side were assigned to freshwater conditions, whereas all stations on D side could be classified as oligohaline and mesohaline conditions (Figure 3).

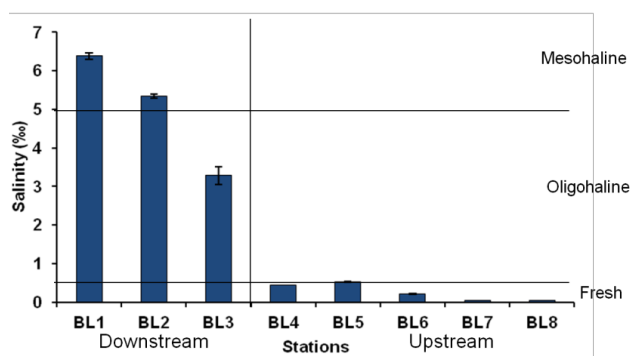


Figure 3. Salinity variability in Ba Lai river

The results of Kruskal–Wallis showed significant differences between stations for salinity concentration ($p=0.002$). Also, salinity in the D side was significantly higher than U side (mean salinity D = 5.00‰, U = 0.23‰, Global R = 0.71, $p=0.001$).

3.3. The meiofauna communities in relation to salinity gradients in Ba Lai river

The correlation coefficients based on MC characters with salinity gradients are shown in Table 7. All characteristics of MC (including abundances, diversities) showed significant correlations with salinity concentration in BLR (except for S.meio). Specifically, all characteristics of nematode communities (including abundances and diversities) and meiofaunal abundance (Ab.meio) were a strong positive correlation with salinity gradients. In turn, meiofaunal diversities such as H'.meio and N1.meio were significantly negatively correlated with salinity (Table 7).

Table 7. Correlation coefficients of abundance and diversity of meiofauna communities with salinity gradients in Ba Lai river (n = 23). Significant correlations were respectively indicated with bold

Variables used	Salinity	
	r	p
S.nema	0.52	0.01
H'.nema	0.67	<0.0001
N ₁ .nema	0.67	<0.0001
Ab.nema	0.72	<0.0001
S.meio	0.41	0.06
H'. Meio	-0.66	<0.0001
N ₁ . Meio	-0.66	<0.0001
Ab. Meio	0.81	<0.0001

The Table 8 shows the results of significance tests for meiofaunal characteristics with salinity regressions. The polynomial regression of Ab.meio, Ab.nema, N₁.meio, and H'.meio with salinity was strong ($R^2>80\%$ of the variation explained). Figures 4 A1-D1 shows a plot of a fitted model of nematode communities with salinity, whereas Figures 4 A2-C2 show a plot of a fitted model of MC and salinity.

Table 8. Regression coefficients and results of fitting the regression model to describe the relationship between meiofaunal community characteristics with salinity gradients in Ba Lai river. Meiofauna characteristics and salinity were respectively indicated with bold and italic

Meiofaunal community-salinity (Sal)	Regression model	Regression coefficients			
		R ²	F	Df	p-value
S.nema & Sal	S.nema = sqrt(1.84 + 0.60*Sal ²)	34.13	10.88	1	0.003
H'.nema & Sal	H'.nema = sqrt(0.38 + 0.10*Sal)	39.40	13.66	1	0.001
N ₁ . Nema & Sal	N₁.nema = sqrt(1.00 + 0.50*Sal)	42.69	15.65	1	0.0007
Ab.nema & Sal	Ab.nema = sqrt(4.98 + 11.45*Sal ²)	92.44	256.93	1	<0.0001
H'.meio & Sal	H'.meio = (0.61 - 0.46*Sal ²) ²	89.03	170.47	1	<0.0001
N ₁ .meio & Sal	N₁.meio = 1/(1.78 + 1.70*Sal ²)	86.89	139.18	1	<0.0001
Ab.meio & Sal	Ab.meio = sqrt(6.09 + 9.94*Sal ²)	93.53	304.02	1	<0.0001

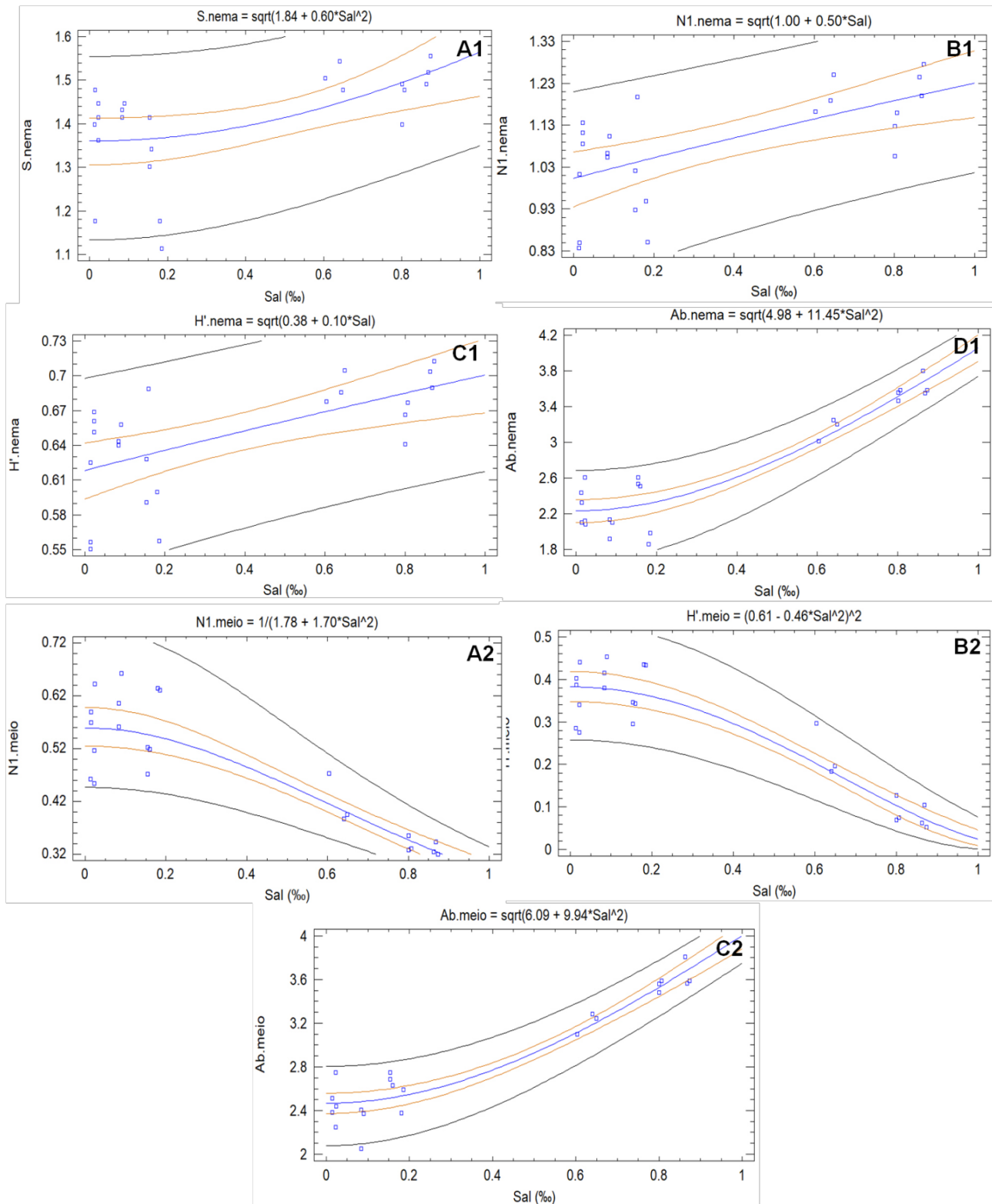


Figure 4. The plot of fitted model meiofaunal community characteristics with salinity gradients. S.nema & Sal (A1), H'.nema & Sal (B1), N1. Nema & Sal (C1), Ab.nema & Sal (D1), N1.meio & Sal (A2), H'.meio & Sal (B2), Ab.meio & Sal (C2)

4. Discussion

4.1. Saltwater intrusion in the upstream site of Ba Lai river

The BLD was constructed mainly for agricultural purposes and irrigation/water supply. Freshwater reservoirs (U areas) created by BLD provide freshwater for activities

such as irrigation, human consumption, aquaculture, and particularly in agriculture. However, our field survey confirmed saline water intrusion into “freshwater reservoirs” in U areas. The evidence for this case is the U site, which contains low salt concentration levels (mean 0.23‰).

Generally, the BLD gates open once a month in the rainy season and twice a month in the dry season, leading to saline water intrusion into U site from D site (Way-1). Also, saline water from the Tien River intrudes the U site of BLR through An Hoa canal (particularly in the dry season) (Way-2) (Figure 5). This constitutes an explanation of the saltwater intrusion in the upstream site of BLR. Monitoring of saltwater intrusion in BLR is essential to delineate the fresh-saline water interface for the protection of freshwater supply wells.

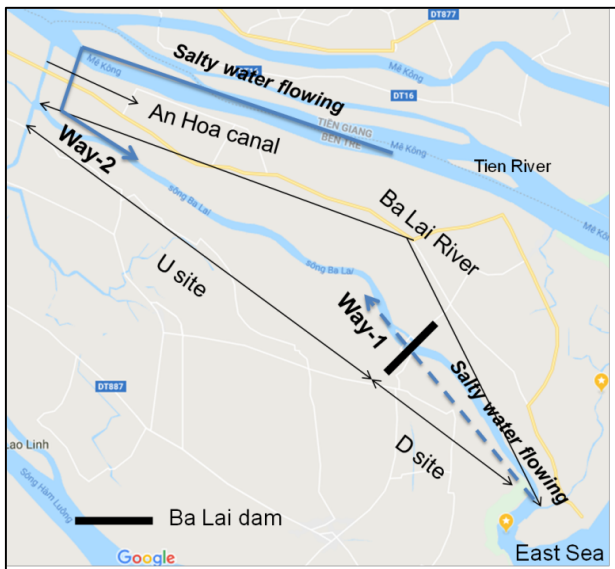


Figure 5. Schematic showing two-way of saline water into freshwater areas in the upstream site of Ba Lai river

4.2. The difference in meiofaunal characteristics with special emphasis on nematodes between fresh and marine habitats

Although U site contains low salt concentration, the stations were assigned to freshwater conditions in general, whereas all stations in D side could be classified as marine conditions. Patterns of MC structure in D site (marine habitats) may be a considerably different from those in U site (fresh habitats).

The abundances and diversities of nematode communities in D site were much higher than those observed in U site, especially for abundances (mean D = 3160.44 ± 1575.42 , mean U = 194.86 ± 106.62 inds/10cm²). Regarding MC, their abundance in D site was also considerably higher than those in U site (mean D = 3128.22 ± 1527.68 , mean U = 327.80 ± 105.58 inds/10cm²), whereas their diversity in D site was lower than estimated in U site. Generally, there is a tendency of decreased abundance from the estuary to freshwater. Similar results have been reported by Austen and Warwick (1989) and Coull (1988). Low diversities of

meiofauna in D site compared to U site could be explained by the domination of nematodes in meiofauna communities. In D site, Nematoda were the most dominant taxa (over 92% of the total meiofaunal density). Taxa Nematoda was still dominated in U site but their contribution decreased from 85.74 to 30.21%, leading to an increasing number of others taxa such as Nauplii and Rotifera.

The present study showed that Nematoda taxa were the most dominant group of BLR's meiofauna community in term of density and species number. The percentages of marine nematodes in D site ranged from 93.85 to 94.94% of the total meiofaunal density. These results were similar to those reported by Ngo et al. (2010) in Mekong estuaries, Vietnam (64-99%), Gao and Liu (2018) in Jiaozhou Bay, China (91-97%), Alves et al. (2013) in Mondego estuary, Portugal (88-95%), Stark et al. (2017) in O' Brien Bay, USA (90-98%). However, the percentages of nematodes' domination in the present study were rather high in comparison with some other studies such as Ngo et al. (2007) in Can Gio mangroves, Vietnam (84.58%), Ólafsson (1995) in an estuarine mangrove area, Eastern Africa (68-87%), and many other studies (Ali et al., 1983: 50-67%; Dye, 1983: 80%; and Lalana-Rueda et al., 1986: 54%). In U site, the percentages of nematodes varied from 30.21 to 85.74% of the total meiofaunal density. These results were higher than those observed in earlier studies such as Montagna et al. (2002) in Rincon Bayou lake, USA (84%), Yozzo and Smith (1995) in Chickahominy River, Virginia (37%), and Silva et al. (2015) in Greenwich Island, Antarctica (11%).

The density of MC in D site was higher than the density observed in other studies such as by Ngo et al. (2010, 2013), Ngo et al. (2007), Gao & Liu (2018), and Alves et al. (2013). However, our estimates in diversities of MC in D site were slightly lower than diversities of MC reported by Ngo et al. (2010, 2013) and Ngo et al. (2007) (Table 8). Because a limited number of studies exist regarding overall meiofauna community in freshwater habitats, scarce information is provided for comparison and consistent patterns of MC within freshwater.

While studies and reviews on MC in the marine environment are increasingly common, to date, few studies have assessed the characteristics of meiofauna in freshwater environments. Thus, comparing our results with other studies has been difficult. Overall, densities of MC in U site were lower than those observed in several studies such as by Montagna et al. (2002), Yozzo and Smith (1995), and Silva et al. (2015) (Table 9). A comparison of the meiofaunal community characteristics between fresh and marine habitats will help to fill the baseline knowledge gap for future research of MC in freshwater areas.

Table 9. Data from the literature on meiofaunal density and diversity from other studies over the world

Area	Densities (inds/10cm ²)	Diversities	References
Marine habitats			
Ba Lai river (D site), Vietnam	1644 ± 350 to 4670 ± 1543	H': 0.18 ± 0.07 to 0.69 ± 0.24 N _i : 1.13 ± 0.06 to 1.63 ± 0.29	Present study
Mekong estuaries, Vietnam	581 ± 400 to 3168 ± 353	H': 0.2-1.14	Ngo et al. (2010, 2013)
Can Gio mangroves, Vietnam	1156 to 2032	H': 0.67 to 0.78; N _i : 1.97 to 2.22	Ngo et al. (2007)
Jiaozhou Bay, China	912 ± 603 to 2152 ± 1062	N.A.	Gao and Liu (2018)
Mondego estuary, Portugal	25.4 ± 25.9 to 1384 ± 688	N.A.	Alves et al. (2013)
Freshwater habitats			
Ba Lai river (U site), Vietnam	199 ± 77.0 to 492 ± 70.1	H': 1.13 ± 0.13 to 1.71 ± 0.009 N _i : 2.19 ± 0.20 to 3.28 ± 0.02	Present study
Rincon Bayou lake, USA	1200	N.A.	Montagna et al. (2002)
Chickahominy River, Virginia	169 to 13832	N.A.	Yozzo and Smith (1995)
Greenwich Island, Antarctica	72.2 ± 111 to 1366 ± 2717	N.A.	Silva et al. (2015)

N.A. = not available

4.3. The dam has the ability to change salinity gradients in Ba Lai river that are the major reasons for the difference in the MC structure

There were strong relationships between meiofaunal abundances and diversities and salinity gradients in BLR. Our results showed that all characteristics of nematode communities (including abundances and diversities) and meiofaunal abundance were a strong positive correlation with salinity gradients. By contrast, meiofaunal diversities were significantly negatively correlated with salinity. When salinity concentration increases, meiofaunal abundances increase but diversities decrease, so it is suggested that abundances of meiofauna in D site were also considerably higher than those in U site, whereas their diversity in D site was lower than estimated in U site.

It is well known that the density, diversity, distribution, and functional properties of MC can be affected by several abiotic variables such as salinity, temperature, hydrodynamics, sediment grain size, oxygenation level, and food availability (Ingels et al., 2011; Cai et al., 2012; Ngo et al., 2013; Zeppilli et al., 2013; Górska et al., 2014). The basic effects of horizontal salinity gradients on MC were first reviewed by Coull (1988). Austen and Warwick (1989) have warned that there tend to be decreased abundances and the number of species from the estuarine to freshwater. Several subsequent surveys have demonstrated that salinity is one of the most common ancillary measures used in coastal and marine ecological research to monitor drivers of benthic communities (Alber 2002; Ysebaert and Herman 2002; Kimmel and Roman 2004). Van Diggelen (2016) has warned that the salinity gradients could be more important to explain diversity across multiple estuarine systems.

Natural phenomena such as tide, rain, and seasonal monsoon can change the salinity gradient of the river, leading to influences of the characteristics of MC. However, anthropogenic activities, and in particular dam

construction, have had an enormous impact on river's horizontal salinity gradients. Overall, the salinity gradients in BLR discriminated strongly between upstream (U) and downstream (D) sides of the dam, also generally decreasing from the D to U side. Clearly, BLD could be one of the major reasons why the salinity gradients in BLR discriminated. The BLD changed the salinity in BLR, while MC were a strong correlation with salinity, leading to the question: can meiofauna (with focus on nematodes) be used as a potential tool for environmental impact assessment of the dam? Worldwide, many studies on assessment of sediment condition successfully used MC (specifically nematodes) as indicators (Schratzberger et al., 2000; Austen and Widdicombe, 2006; Alves et al., 2013). Ngo et al. (2016) have demonstrated that the nematode communities in the Mekong estuarine system can be considered as a good tool for environmental monitoring. The future study should pay more attention to the relationships between the BLD, physicochemical variables in BLR affected by the BLD and the characteristics of meiofauna affected by the physicochemical variables. The answers to this relationship could help explain the impact of dams on the river's ecosystems.

5. Conclusion

The MC (specifically nematodes) in BLR were characterized by high abundances and diversities. Nematoda were the most dominant taxa, followed by Nauplii and Rotifera. The patterns of MC structure in D site (marine habitats) may be considerably different from those in U site (fresh habitats). The abundances and diversities of nematode communities in D site were much higher than observed in U site, especially for abundances. Regarding MC, their abundance in D site was also considerably higher than those in U site, whereas their diversity in D site was lower. Furthermore, BLD has the ability to change salinity gradients in BLR, while MC were a strong correlation with salinity. Thus, the characteristics of MC and their links with environmental factors can be considered as a good tool for the effects of dams on river's ecosystems.

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