Exploring the Community Structure of Plankton in the Maricultures Sites of Kodek Bay, Lombok Island

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Abstract

Mariculture is considered a future economic source for Indonesia. However, this practice may degrade the surrounding ecosystem by decreasing the water quality, including the plankton community. This study aimed to determine the community structure of plankton (phytoplankton and zooplankton) in the mariculture sites. Study sites were selected based on the mariculture activities of the Research Center for Marine and Terrestrial Bioindustry (PRBILD-BRIN) located in Kodek Bay, Lombok Island. Samplings were conducted in February 2021, zooplankton samples were collected horizontally by towing a 100 μm plankton net using a boat, whereas phytoplankton was collected using a 20 μm plankton net horizontally. The plankton samples were preserved with 4% formaldehyde, identified, and counted in a Sedgwick Rafter cell counter using an Olympus CX21 (10x). Results demonstrated that zooplankton was dominated by genera from the Subclass Copepoda (*Temora* sp*., Microsetella* sp*., Euterpina* sp*., Oithona* sp*., Acartia* sp*.,* and *Onceae* sp.) that were significantly more abundant at Sites 1 and 2 than those at Sites 3 and 4. The diversity levels were moderate at all sites, except at site 1, which *Temora* dominated. Phytoplankton was mainly composed of Bacillariophyceae, followed by Dinophyceae, Chlorophyceae, and Conjugatophyceae, with no significant difference in abundance at all sites. The diversity levels were low for all phytoplankton taxa at all sites except at site 2, where Bacillariophyceae and Dinophyceae equally composed the community. It is suggested that the mariculture organisms may shape these phytoplankton and zooplankton community structures by recycling particular nutrients.

Keywords: Community Structure, Kodek Bay, Mariculture, Phytoplankton, Zooplankton

INTRODUCTION

The potential for mariculture in Indonesian waters is approximately 4.58 million ha, with only 2% being used so far, urging the Indonesian government to support the mariculture practices as a future economic source for the nation (Ministry of Marine Affairs and Fisheries, 2020). However, these activities must be monitored since they may degrade the surrounding environment by decreasing the water quality and introducing invasive species. Fecal production and uneaten food highly determine the water quality status (Demir *et al.*, 2001). Thus, it affects the community structure of phytoplankton and zooplankton through the dynamic of nutrients in the water column and sediment directly through changing the physical and chemical water qualities and indirectly through changing food availability (Guo & Li, 2003). As the phytoplankton swifts, so the zooplankton communities do.

Phytoplankton is the base of all food webs in the marine ecosystem (Yan *et al.*, 2012). Its growth rate is strongly determined by the nutrient status in the surrounding environment, whereas consecutively, it proliferates the growth of herbivorous zooplankton. Studies revealed that the high nutrient concentration produced by intensive aquaculture shifted the phytoplankton communities from Diatom dominance to Dinoflagellate dominance (Liang *et al.*, 2019). However, the nutrient is not the only factor affecting phytoplankton's abundance and community structure. Environmental variables such as temperature, day length, and grazing can

also induce community change. Zooplankton grazing reduces the abundance of small-sized phytoplankton, increasing the survival of large-sized phytoplankton. Therefore, grazing by zooplankton can substantially change phytoplankton's composition and community structure (Gislason & Silva, 2012).

Kodek Bay in West Lombok Regency has high productivity and protected areas with the potential for mariculture. Therefore, for years some areas have been utilized for the cultivation of various marine organisms, such as pearl oysters, sea cucumbers, and lobsters, by the PRBILD. As plankton is the energy source for all marine organisms, it is essential to understand the dynamic response toward environmental change. Sutomo (2013) and Cokrowati *et al*. (2014) reported data on phytoplankton's community structure in this area. Conversely, the data on zooplankton's community structure remains limited. Hence, this study aimed to determine the phytoplankton and zooplankton community structures in the mariculture sites of Kodek Bay to provide primary data on the dynamic of plankton community structure in Kodek Bay.

MATERIALS AND METHODS

The study sites were determined according to mariculture activity in each site (Fig. 1). Site 1 is at the mariculture cages for the rearing of sand lobster (*Panulirus homarus*) with a depth of 25 m with the substrate being sand muddy. It is cultured in a 6 x 15 m mariculture cage from a non-pigmented post-larva stage to adult lobster. There were 126 individuals with weights ranging from 50 to 140 kg. This mariculture has been operated since 2015. The organism is fed every day with fish meat. Site 2 was at the pontoon; a 4 x 4 m floated wood installation was built to clean up and select the cultured pearl oyster. Site 3 and 4 were located at pearl oyster culture areas where 976 pearl oysters with various lengths were cultured using a 100 m longline. Each site was within the 200 m range. The pearl oysters culturing in this water was started in 2005.
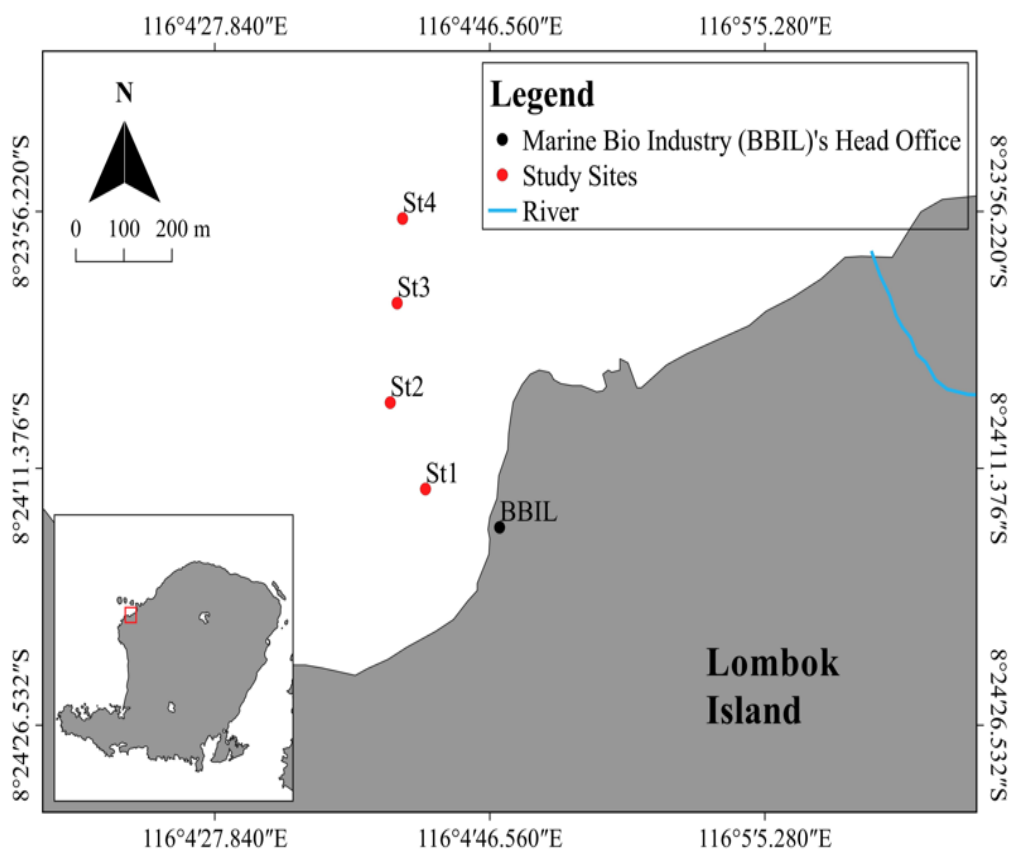

Figure 1. Map of study sites

Sampling of Zooplankton

The sample was collected according to purposive random sampling. Zooplankton's sample was taken using a plankton net with a mesh size of 100 μm, whereas phytoplankton was collected using a 20 μm mesh size plankton net with three replications at each site. Both nets were towed horizontally for 5 min in the morning. Samples for sites 1 and 2 were taken on a different day from those in sites 3 and 4. The study sites were approximately 300 m away from the coastal areas.

Sample fixation and identification

Samples were kept in a 100 ml bottle sample and preserved in a 4% formaldehyde. Plankton was identified as a genus referred to by Conway *et al*. (2003) and Yamaji (1979).

Measurement of water quality parameters

Sea surfaces water quality parameters such as pH, temperature, and salinity were measured. The temperature was measured using a bar thermometer, pH was measured using a handheld meter, and salinity was measured using a refractometer. All parameters were determined in each site for three replications.

Data Analysis

The abundance of Phytoplankton and Zooplankton

The abundance of zooplankton and phytoplankton was measured in a Sedwick Rafter Cell (Eaton *et al*., 2005).

$$K = \frac{N}{Ac} \; x \; \frac{At}{Vs} \; x \; \frac{Vt}{As}$$

Note: K = abundance (ind/l); N = the number of zooplankton or phytoplankton counted (ind/l), Ac = Sedgwick-Rafter Counting Cell's field of view (mm^2), At = Sedgwick-Rafter Counting Cell's field of view (mm^2); Vs = concentrate volume of Sedgwick-Rafter Counting Cell (ml); Vt = volume's filtered sample; As = volume's filtered water (l).

Ecology Indices

Ecology indices in this study consisted of diversity and dominance indices. The diversity index was calculated according to Shannon and Weiner's diversity index (H) given by the equation:

$$H' = -ln \sum_{i=1}^{s} \; (\frac{ni}{N} ln \; \frac{ni}{N})$$

Where H' is the diversity index, i = Counts denoting the ith species ranging from 1 – n, n= the species represents several individuals, and N = the total number of individuals in the sampling space.

The dominance index was determined using the Simpson dominance index (D) given by the equation:

$$D = -\sum_{i=1}^{s} \; (\frac{ni}{N})^2$$

Where D = Simpson dominance index; n$_i$ = number of individual species-ith; N = total number of individuals; S = number of genera.

Statistical Analyzes

One-way ANOVA was used to test the differences between zooplankton and phytoplankton abundances among study sites. Normality and homogeneity tests were conducted before this test to meet the assumption for the One-Way ANOVA test. The sites that make the differences were analyzed by using the Least Difference Test. All these statistical tests were conducted using IBM SPSS Statistics 22.

RESULTS AND DISCUSSION

The average water quality parameters are presented in Table 1. The average sea surface temperature, pH, and salinity at all sites were relatively similar. These data were collected almost identically, except the sea surface temperature at site three was higher because the measurement was conducted at noon. The salinity at all sites was relatively low and was likely related to the rainy season when sampling.

Community Structure of Phytoplankton and Zooplankton

The relative abundance and composition of phytoplankton recorded in the study sites are shown in Fig. 2 and Table 2. Quantitatively, the phytoplankton was dominated by Bacillariophyceae followed by Dinophyceae, Chlorophyceae, and Conjugatophyceae in that order (Bacillariophyceae > Dinophyceae > Chlorophyceae > Conjugatophyceae). As shown by its higher relative abundances at all sites, Bacillariophyceae was the main constituted of the

phytoplankton community, mainly dominated by genera *Thallasiosira* and *Nitzschia* (Table 2). The higher relative abundance of Bacillariophyceae is also indicated by the higher dominance index in all sites, except at Site 2, where along with Dinophyceae, it constitutes the diversity (Table 3). It also resulted in a low level of diversity in the plankton community structure at all sites. However, the abundance of these phytoplankton classes composing the community was no significant difference among study sites (Fig. 3. A).

The abundance of *Thallasiosira* and *Nitzchia* at all sampling sites revealed their natural ability to adapt. *Nitzchia* is the second largest genus of Diatom (Mann, 1986) and can be composed of more than 30 to 100% Diatom community (Grady *et al*., 2020; Sitoki *et al*., 2013), whereas *Thallassiosira* ranges in size to fit the available nutrient in the environment. Therefore, these genera strive in freshwater, brackish water, and seawater (Lange-Bertalot *et al.,* 2017; Lobban *et al.*, 2019). The second-largest phytoplankton abundance is Dinophyceae, which mainly consists of mixotrophic dinoflagellates. This genus might indicate high productivity in the environment in the forms of small ciliates, bacteria, and other tiny diatoms. The higher relative abundance of Bacillariophyceae in all sites, except in Site 2, might be related to the surrounding water's nutrient levels. Though this study did not measure the nutrient concentration in the waters, it is assumed that the cultured organisms in each mariculture site (Sites 1, 3, and 4) regulate the recycling of nutrients for the surrounding water through their metabolism waste and uneaten food. This finding agrees with the studies by Gaertner-Mazouni *et al.* (2012), Lacoste *et al*. (2014), and Lacoste and Gaertner-Mazouni (2016) that mariculture activities, such as pearl oyster longlines culture, may contribute to the growth of phytoplankton through recycling the nutrients in the water column. However, there was no significant difference in the average total phytoplankton abundance among mariculture sites (Fig. 3. A). It is argued that the ranges between the study sites are relatively close, so they have similar water quality parameters and nutrient profiles, leading to approximately equal plankton community structures.

Conversely, the average of the total phytoplankton abundance in all sites in this study is higher than those reported by Sutomo (2013) and Cokrowati *et al*. (2014), who sampled in the same areas. The differences might come from the mesh size and sampling method. Sutomo (2013) used an 80 μm mesh size, whereas Cokrowati *et al.* (2014) used a similar mesh size to this study but towed the plankton net vertically. Only two taxa groups were observed in Kodek bay (Bacillariophyceae and Dinophyceae).

The results demonstrated that the Phylum Arthropoda dominated the zooplankton community in all sites, Subphylum Crustacea and Subclass Copepoda (Table 2B.). The Copepoda collected at all sampling sites is shown in Fig. 4. It is primarily comprised of the genus *Temora* at Site 1 that more than 60% of the community, followed by genera *Oncaea, Microsetella, Oithona, Acartia*, and *Euterpina* in that order (*Temora > Oncaea > Microsetella > Oithona > Acartia > Euterpina*) (Fig. 2. A). This high abundance increases *Temora*'s dominance at Site 1, thus lowering the diversity of zooplankton at this site contrasts with other sites with a moderate level of zooplankton diversity (Table 4). The average total abundance of zooplankton ranged from the highest at Site 2 (98 ind/l), and it was significantly lower at Sites 3 and 4 (32 ind/l) ($P = < 0.5$).

Table 1. Mean of water quality parameters among the study sites

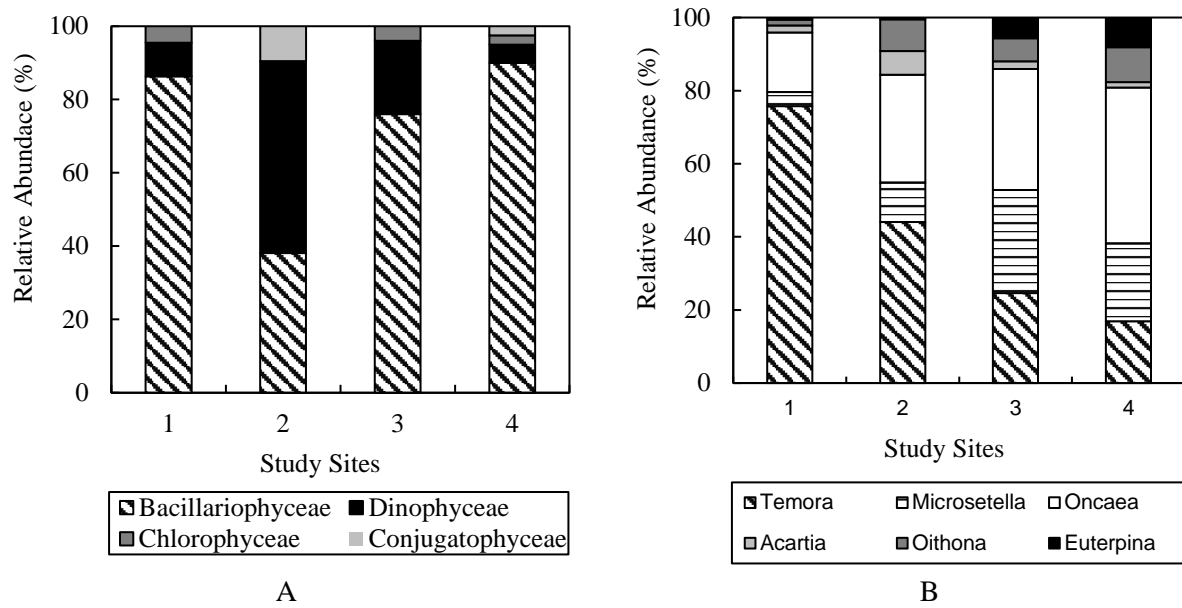| Sites	Date	Location	Temperature (°C)	pH	Salinity (ppt)
1	23 February 2021	116°4'42.17988"E 8°24'12.6"S	28.5 ± 0.1	8.2 ± 0.1	28.5 ± 0.5
2	23 February 2021	116°4'39.78012"E 8°24'7.5"S	30.0 ± 0.1	8.1 ± 0.1	29.0 ± 0.1
3	27 February 2021	116°4'40.25172"E 8°24'1.62918"S	28.1 ± 0.1	8.3 ± 0.1	29.0 ± 0.3
4	27 February 2021	116°4'40.62"E 8°23'56.64"S	28.0 ± 0.1	8.2 ± 0.1	29.0 ± 0.1

Figure 2. Relative abundance (%) of the dominant taxonomic groups of plankton in the study sites in February 2021. A. Phytoplankton. B. Zooplankton.

Table 2. Composition and relative abundance (%) of phytoplankton in the mariculture sites of Kodek Bay

Class	Genus	St1	St2	St3	St4
Bacillariophyceae	*Thalassiosira*	4	10	8	10
	Fragilaria	8	0	0	0
	Nitzschia	25	5	8	10
	Thallassionema	8	0	0	0
	Synedra	13	0	4	8
	Pinnularia	0	0	0	3
	Chaetoceros	0	0	0	3
	Licmophora	4	0	0	3
	Cyclotella	0	19	4	3
	Grammatophora	0	5	0	0
	Skeletonema	4	0	0	15
	Cerataulina	0	0	8	3
	Rhizosolenia	0	0	21	21
	Odontella	4	0	0	0
	Navicula	8	0	17	13
	Haslea	8	0	0	0
Dinophyceae	*Dinophysis*	0	0	8	5
	Ceratium	0	0	4	0
	Lingulodinium	8	38	4	0
	Gonyaulax	0	14	8	0
Chlorophyceae	*Scenedesmus*	0	0	0	3
	Sphaeroplea	4	0	4	0
Conjugatophyceae	*Gonatozygon*	0	5	0	0
	Cosmarium	0	5	0	0
	Closterium	0	0	0	3

The zooplankton community in all study sites is a member of Copepoda, the most dominant group composed of zooplankton in coastal areas. The dominance of the genus *Temora* at Site 1 is assumed to be related to the availability of suitable food for its feeding behavior (Klein Breteler & Koski, 2003). The food availability at Sites 1 and 2 is also suggested to reduce the abundance of zooplankton at Sites 3 and 4 as Dinophyceae predominates at Sites 3 and 4. All the Dinoflagellates observed in the study site have phycotoxin. However, all zooplankton genera recorded in these sites are omnivorous and small planktonic marine copepods because their body length is < 1 mm. It is indicated that these zooplankton depend on their food, grazing the phytoplankton in the water column and on other smaller zooplankton and copepods' fecal pellets. These small planktonic copepods can also reveal the environment's nutrient status as they proliferate in rich nutrient waters (Uye, 1994).

Moreover, the abundance and diversity of zooplankton may vary across sites and time and sampling methods, mesh size of plankton net, depth, and lunar periodicity. The mainly small Copepods obtained in this study are assumed due to the use of a 100-um plankton net, as reported in other studies (Böttger, 1987; Böttger-Schnack, 1988). The lunar periodicity is also suggested to influence the community structure of zooplankton in the water. The zooplankton sampling was conducted when the moon was in the phase of waxing gibbous that might attract the positive phototaxis species such as *Oithona helgolandica* and *Acartia negligen* or avoid the damaging phototaxis species such as *O. nana* (Böttger, 1987; Echelman & Fishelson, 1990; Vaissiere & Seguin, 1984). However, there is no data on the phototaxis species in this study.

The abundance of plankton in the study sites ensures the availability of foods for cultured biotas, such as pearl oysters and lobsters; thus, it can sustain the mariculture activities in the area. The phyllosoma lobster is an active zooplankton predator that requires more nutrition from crustacean plankton than any other prey taxa (Wang & Jeffs, 2014), while the pearl oyster can control the phytoplankton community through its suspension-feeding habit (Dame and Kenneth, 2011).

Table 3. Diversity and dominance indices of phytoplankton at the different study sites of Kodek Bay

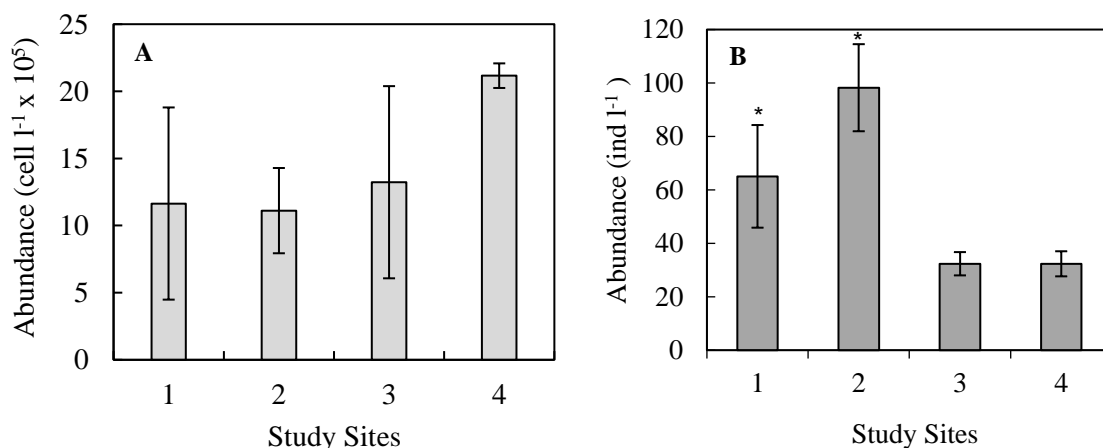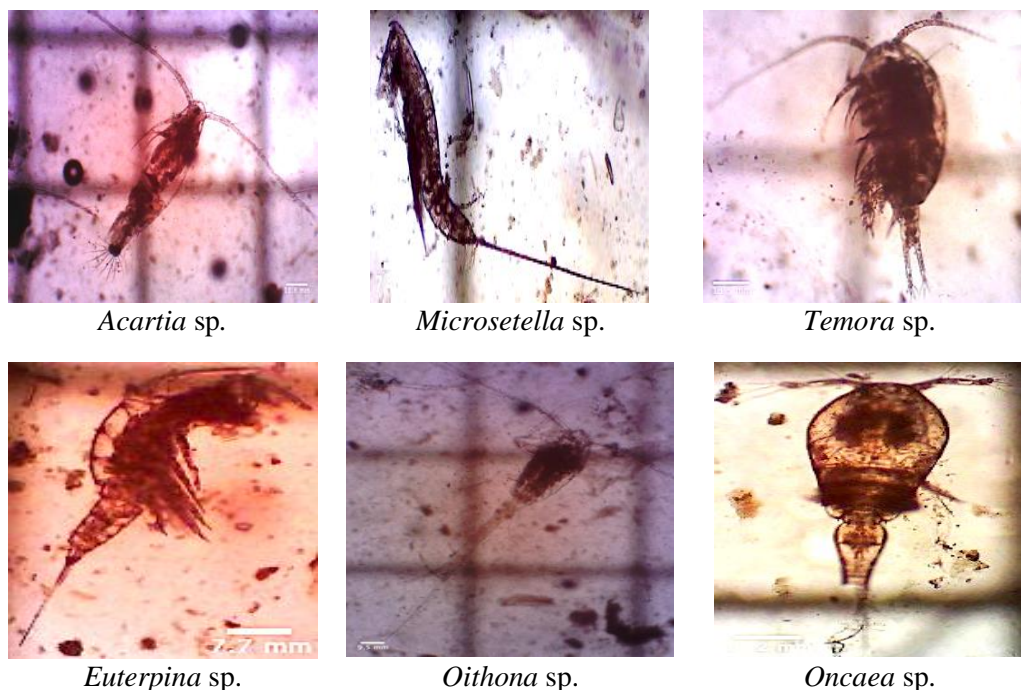|	Site 1	Site 2	Site 3	Site 4
No. of taxa	12	8	12	14
Dominance (C)	0.8	0.4	0.6	0.8
Shannon-Wiener (H')	0.5	0.9	0.7	0.4

Figure 3. The abundance of plankton in the study sites in February 2021. A. Phytoplankton. B. Zooplankton. *: Indicates significant difference ($P = 0.045$ for Site 1 and 3 and $P = 0.040$ for Site 1 and 4, Least Difference Test)

Table 4. Diversity and dominance indices of zooplankton at the different study sites of Kodek Bay

	Site 1	Site 2	Site 3	Site 4
No. of taxa	6	6	6	6
Dominance (C)	0.8	0.3	0.3	0.3
Shannon-Wiener (H')	0.8	1.4	1.5	1.5

Acartia sp.   *Microsetella* sp.   *Temora* sp.

Euterpina sp.   *Oithona* sp.   *Oncaea* sp.

Figure 4. Composition of zooplankton in the study sites using an Olympus CX21 (10x).

CONCLUSION

The diversity levels of zooplankton were moderate at all sites, except at Site 1, dominated by *Temora*. Phytoplankton was mainly composed of Bacillariophyceae, followed by Dinophyceae, Chlorophyceae, and Conjugatophyceae, with no significant difference in abundance at all sites. The diversity levels were low for all phytoplankton taxa at all sites except at Site 2, where Bacillariophyceae and Dinophyceae equally composed the community. It is suggested that the cultured organisms in these sites (sand lobster and pearl oyster) may shape these phytoplankton and zooplankton community structures by recycling nutrients. This condition can likely induce specific taxa groups' growth over other groups. The abundance and diversity of plankton may vary across sites and time and sampling methods, mesh size of plankton net, depth, and lunar periodicity.

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