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Environmental Heterogeneity and Salinity Gradient Impacted the Alpha and Beta Diversities of Diatom Assemblages in a Coastal Delta Wetland

Nurhayat Dalkıran [1,*] and Burcu Zünbülgil-Ünsal [2]

[1] Biology Department, Art and Science Faculty, Bursa Uludağ University, Bursa 16059, Türkiye
[2] Graduate School of Natural and Applied Science, Bursa Uludağ University, Bursa 16059, Türkiye; burcuzunbulgil@gmail.com
* Correspondence: dalkiran@uludag.edu.tr; Tel.: +90-224-2941866

Abstract: The coastal deltas are ecologically diverse and complex ecosystems that can contain different habitat types. The effect of environmental heterogeneity on diatom beta diversity is a poorly understood research topic. Freshwater (floodplain forest, river) and brackish (three lagoons) water bodies in the study area construct distinct environmental heterogeneity at a small spatial scale. The connection of the lagoons with an inland sea caused a high salinity gradient. All water bodies in the wetland were determined as hypereutrophic. CCA, Cluster, ANOSIM, and SIMPER analysis clearly explained the distribution of diatom assemblages according to salinity gradient and environmental heterogeneity. The environmental heterogeneity resulted in the presence of freshwater, brackish, and marine diatom species in the studied wetland. Diatom assemblages generally consist of freshwater species with euryhaline character adapted to wide salinity gradients. We determined the rapid replacement and richness difference in diatom assemblages due to environmental heterogeneity and salinity gradient causes high overall alpha, beta, and gamma diversity. Unlike many other studies, the high beta diversity mainly consists of the richness difference rather than species replacement. The high overall beta diversity showed low similarity between the habitats, while high overall alpha diversity exposed high species diversity at the local scale in the study area.

Keywords: diatoms; beta diversity; alpha diversity; environmental heterogeneity; salinity gradient; delta wetland

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1. Introduction

Deltas are pieces of land that are formed due to sedimentation at the mouths of the rivers. They are complex ecosystems with a high salinity gradient containing diverse and important wetland habitats since they constitute transition zones between marine and inland waters. Salinity, nutrients, hydrology, and habitat diversity support many organisms and cause substantial biodiversity. The salinity gradient is an important limiting environmental factor for diatoms and many other living organisms. This gradient is crucial in diatom distribution, as they show different tolerance to salinity [1]. Some diatom species can exhibit a broad tolerance to salinity (markedly euryhaline), while others can live either only in marine or only in freshwater (stenohaline) [2]. In estuary areas, freshwater input, precipitation, groundwater recharge rate, tides, and water temperature changes cause salinity to vary temporally and spatially, creating a salinity gradient. This change in salinity is the most critical environmental factor that determines and affects species richness and diversity, especially in estuary areas. Consequently, the diversity of diatom species is relatively high in estuary areas and coastal wetlands [3].

Determining the factors affecting the diversity of species and the spatial and temporal variation of diversity among communities is one of the leading research topics of ecology. Biodiversity can be measured spatially in three components: alpha (local or within sites),

beta (between sites), and gamma (regional) [4,5]. Alpha diversity indices are well-known and widely used in ecology since they provide general information about local diversity and apply to each sampling site. Beta diversity measures the variation of species diversity from one environment to another. In other words, it estimates the number of dissimilar species in two different environments. It is a key concept for understanding ecosystem function and managing biodiversity [6].

Recently, Podani and Schmera [7] divided beta diversity into two components: species replacement and richness difference. Legendre and De Caceres [8] developed an alternative method to explain the causes of variation in beta diversity at the local and regional scale by dividing total beta diversity into two components: Local Contributions to the Beta Diversity (LCBD) and Species Contributions to the Beta Diversity (SCBD). These developed beta diversity indices, like alpha diversity indices, provide the opportunity to compare each sampling site with each other in terms of species turnover and richness. The most important benefit of these new approaches is that they can be helpful tools for investigating the spatial and temporal variation of environmental and ecological gradients affecting beta diversity. For this reason, the examination of beta diversity variation in different organism groups against environmental and ecological gradients has become an increasingly developing research topic in recent years [9–17].

There are 112 lagoons with an area of approximately 39,000 hectares on the Anatolian coast, a peninsula rich in deltas and coastal lagoons [18]. However, studies on diatom species richness in these lagoons and coastal transitional water bodies are limited [19]. The Kocaçay Delta, one of the important protected wetland areas in Türkiye, with high environmental heterogeneity, contains three coastal lagoons, a floodplain forest, and different habitats associated with them.

This study aimed to investigate the spatial and temporal variations of diatom species diversity of the Kocaçay Delta in different habitats using alpha and beta diversity components and to determine their changes against the salinity gradient and environmental heterogeneity. We aimed to test different hypotheses simultaneously. We evaluated together Podani and Schmera's [7] and Legendre and De Caceres's [8] beta diversity approaches. The main reason is to determine whether the beta diversity indices determined by both approaches give similar results against environmental variables, environmental heterogeneity, and salinity gradient. In addition, we hypothesized that high beta diversity would mainly be attributable to the richness difference (aka nestedness) rather than species replacement. We also investigated whether environmental heterogeneity and salinity gradient are the main ecological factors that primarily affect the diatom assemblages.

2. Materials and Methods

2.1. Study Area and Sampling Sites

Deltas are ecologically diverse and complex ecosystems comprising different habitat types. The Kocaçay Delta is a protected wetland area. It is at the point where all the water draining from the Susurluk River Basin spills into the Marmara Sea. Since the river basin has a large drainage area of 24,299 km^2, the Kocaçay Delta can be affected by all polluting sources of the basin [20]. Kazancı et al. [21] classified the delta as a wave-dominated river delta. The delta has a coastal length of 21 km, and its width from west to east at its widest point is 3.5 km. The delta area is approximately 170 km^2 and Kocaçay (Çapraz Çay), had a length of approximately 4.5 km. It flows in a narrow channel in the middle of the delta and divides it into two parts. Dalyan and Poyraz lagoons are located on the west side of the river mouth, and Arapçiftliği (Ekinli) Lagoon is on the east side (Figure 1). According to Karacabey meteorological station data, the average annual precipitation was 611 mm and the average annual humidity was 74.93%. The monthly average temperature was determined in the range of 6.3 °C (December 2018) to 26.1 °C (July 2018). The most important sources of freshwater recharge in lagoons are precipitation and groundwater input. Since the water levels rise in Arapçiftliği and Dalyan lagoons, especially in heavy rain seasons, the dunes between the Marmara Sea and the lagoons are opened with construction

machines regularly, and canals are created to prevent floods in the lagoons. These canals constitute the primary sources of seawater inflow into lagoons. However, these canals are naturally closed because of waves.

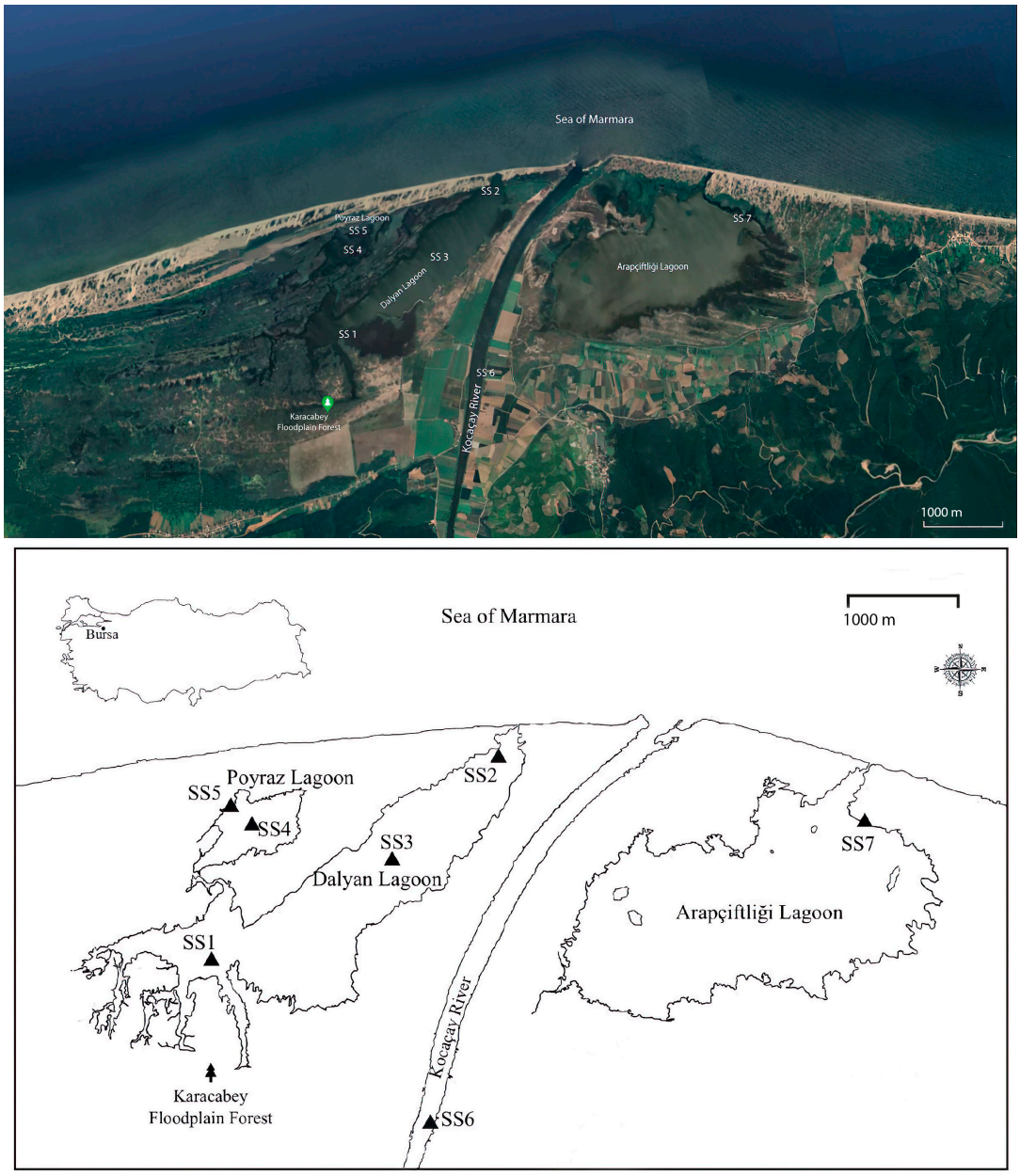

Figure 1. Map of sampling sites of Kocaçay Delta (SS1: 40°22′53.3″ N 28°28′13.3″ E; SS2: 40°23′36.1″ N 28°29′40.9″ E; SS3: 40°23′11.9″ N 28°29′04.4″ E; SS4: 40°23′23.7″ N 28°28′21.5″ E; SS5: 40°23′33.4″ N 28°28′17.6″ E; SS6: 40°22′15.4″ N 28°29′16.2″ E; SS7: 40°23′02.5″ N 28°32′00.6″ E).

There is a high environmental heterogeneity in terrestrial and aquatic habitats in the Kocaçay Delta. According to the EUNIS Habitat Classification System, 16 different habitat types, 8 of which are main types, have been identified in the delta wetland area. Mixed riparian floodplain and gallery woodland forests (G1.2) and permanent inland saline and brackish lakes, ponds, and pools (C1.5) are the dominant habitat types [20]. Due to these different feeding and discharge characteristics, the Kocaçay Delta has various habitats, including streams, brackish lagoons, swampy areas, dunes, and floodplain forest habitats. Karacabey Floodplain Forest is one of the largest floodplain forests in Türkiye. Different habitats in the wetland area also support biological richness. Studies have shown that

339 plants (6 of which are endemic), 29 fish (2 of which are endemic), more than 250 birds, and 28 mammal species inhabit the area [20]. The Kocaçay Delta Wetland was accepted as a Wetland of National Importance on 9 August 2018 due to its habitat diversity and high biological richness, and the wetland boundaries were registered. In December 2020, the Kocaçay Delta Wetland Management Plan went into effect for five years. Seven study sites were determined in five different water bodies (three lagoons, floodplain forests, and the river) and different salinity ranges in the Kocaçay Delta. Study sites and their coordinates are shown in Figure 1. The first study site (SS1) is located on the shore of the floodplain forest, and this site has shown freshwater characteristics. The floodplain forest mainly consists of ash and alder. *Nymphaea alba* L. and *Azolla filiculoides* Lam. periodically form a cover on the water surface. The second study site (SS2) is in the coastal zone where a sand bar separates Dalyan Lagoon from the Marmara Sea. In a location close to this site, a canal is opened with the help of construction machinery to drain the excess water, filled with heavy precipitation, into the Marmara Sea. In addition, due to the overflow of stormwater and wave movements in winter, seawater enters the lagoon from the littoral sand bar, so the area close to the sea becomes more saline. The third study site (SS3) is in the open water zone of Dalyan Lagoon, where the water is saline and seawater input is extensive. While the fourth study site (SS4) is also in the open water zone of Poyraz Lagoon, the fifth study site (SS5) is located in the benthic zone of Poyraz Lagoon, extending into the floodplain forest. Dalyan and Poyraz lagoons are surrounded by dense reed beds consisting of *Phragmites austrialis* L. The depth of both lagoons varies between 0.6 to 1.8 m depending on the seasons [20]. The sixth study site (SS6) is on the edge of the Kocaçay River (Çapraz Çay). The seventh study site (SS7) was determined to be in the area separated by dunes on the benthic zone of the Arapçiftliği Lagoon close to the Marmara Sea. In a location close to this sampling site, a canal is opened by using construction equipment to drain the excess water of the lagoon. Dunes surround the lagoon, and its edges and bottom are swampy. *Phragmites austrialis* is found regionally in the sampled area. The depth of Arapçiftliği lagoon varies between 0.30 and 1.2 m depending on the season [20].

2.2. Sampling, Enumeration, and Identification

Water and diatom samples were collected at monthly intervals from 7 study sites of 5 different water bodies between April 2018 and March 2019 for 11 months. Water temperature (T), pH, electrical conductivity (EC), and dissolved oxygen (DO) were measured in situ during the field study using a Lovibond multiprobe. Major nutrient analyses of the collected water samples were carried out according to standard methods [22]. These analyses were performed according to the following methods: nitrate nitrogen (NO_3-N) cadmium reduction method (APHA 4500-NO3 E.); total nitrogen (TN), alkaline persulfate digestion (APHA 4500-N C.), after cadmium reduction method; phosphate phosphorus (PO_4-P), ascorbic acid method (APHA 4500-P E.); total phosphorus (TP), persulfate digestion (APHA 4500-P B.), after ascorbic acid method.

Epipelic, epilithic, and epiphytic diatoms were collected only at study sites SS1, SS2, SS5, SS6, and SS7. According to the shallow character of the water bodies of the Kocaçay Delta, tychoplanktonic diatom species dominate in the water column, and euplanktonic species are represented by a few species. Tychoplankton samples (77 samples) were taken from the open water zone and near the littoral zone with the direct sampling method, dipping the 250 mL sample container into the surface water. Epiphytic, epipelic, and epilithic diatom samples were collected from macrophytes, natural stones, pebbles, and/or mud surfaces in the benthic zones of the study sites. The periphyton samples were collected according to Kelly et al. [23]. Collected samples were fixed and stored by adding buffered 4% formaldehyde solution during the field studies. An acid-burning method was applied to remove the organic material in the samples by adding equal volumes of nitric acid and sulfuric acid and boiling them in a fume hood in the laboratory [24]. For the enumeration and identification, three permanent slides of each sample were prepared according to Kelly et al. [23]. Firstly, 0.05 mL subsamples were dropped using a micropipette (approximate

amount corresponding to one drop of a Pasteur pipette) on the slides to ensure standardization in all samples. After this standard application, the slides were reviewed again. If the sample is very dense, it is necessary to dilute the sample to prevent the diatom frustules from overlapping. On the contrary, if the number of diatom frustules was low in the prepared slides, more drops were added to the slide. In other words, 0.01–0.2 mL of samples were used in the preparations of the slides, depending on the density of the diatom frustules. The dropped amount used was noted in all prepared slides. This procedure is important to ensure standardization, especially if the unit area/biovolume calculations are to be made. Since planktonic and benthic samples were compared together, an evaluation was made based on relative abundance or presence–absence data to ensure standardization in all samples. Taxonomic identifications of diatoms were made according to various books [25–32]. The current names of diatom species were updated according to the AlgaeBase [33] and environmental preferences of diatom species were updated according to the AlgaeBase [33] and DiatomBase [34] databases.

2.3. Statistical Analysis

The data set was designed in four different approaches. In the first approach, alpha and beta diversity indices based on tychoplankton and periphyton microhabitats (epipelic, epiphytic, and epilithic diatom communities) were estimated separately. In the second approach, each of five different water bodies, representing a distinct habitat type (lacustrine and riverine habitats), the alpha and beta diversity indices were applied apart for the 7 study sites. In the third approach, epiphyton, epipelon, and tychoplankton diatom communities were included in the analysis together. In other words, the study was designed according to the presence of three different microhabitats within seven sites. A different methodology was applied to examine the distribution of diversity indices in the fourth approach. Microhabitat differences were eliminated when the data sets were combined this way. In this approach, even if species A were identified in all microhabitats in each sample, we considered this species to have been observed once. In this combined data, the dataset consisted of 77 subsamples. The results of this approach were given in a Supplementary data file (Figure S5, Tables S1 and S2).

Multivariate ordination analyses were applied to determine the relationship between diatom taxa and measured physicochemical variables. To determine the gradient length, DCA analysis was run with 235 diatom taxa and nine physicochemical variables. Since the gradient length was determined to be above 3, CCA analysis was applied. Both ordination analyses were performed using CANOCO 4.5 package program according to presence–absence data and log + 1 transformation of the data.

Analysis of Variance (One-way ANOVA) was performed in the SPSS28 statistical package program to determine the difference in physicochemical variables at sampling sites. Analysis of Similarities (ANOSIM) and Similarity Percentage Analysis (SIMPER) (between and within groups) were performed to determine the diatom communities' similarity and percent contribution of each taxon to the similarity, according to study sites and different microhabitats. SIMPER analysis was applied to support the beta diversity results, as it is an analysis to identify the diatom species that contribute to the percent (dis)similarity at the study sites based on relative abundance data. Cluster analyses were performed using the Bray–Curtis distance measure in accordance with Ward's method. ANOSIM, SIMPER, and Cluster analysis were performed by the CAP 4.1.3 statistical package program [35].

Shannon–Wiener diversity index (H') (alpha diversity) was used to determine the spatial and temporal (sites) variation of taxonomic and functional alpha diversity in different habitat types in diatom communities. This sensitive index is frequently used for diversity measurement, especially for rare species [36]. As observed in Kocaçay Delta's diatom communities, it is suitable to measure diatom species diversity, most of which consist of rare species [37]. Alpha (H' and species richness) coefficients were estimated by the SDR 4.1.2 package program [38].

To estimate overall beta diversity, two approaches were applied. Firstly, beta diversity was calculated using the beta.div function in the R package 'adespatial' [39,40] according to Podani and Shmera's [7] approach. This function estimates the total beta diversity (hereafter referred to as BDtot) from the total variance in the community data matrix Y, based on Hellinger's method based on presence–absence data and derived from local contribution to beta diversity (LCBDindex) and species contribution to beta diversity (SCBDindex) statistics. When this function is used, the more the species composition of the sampling sites differs, the closer the BDtot value is to 1. BDtot is 1 if all sampling sites are different from each other [40].

Secondly, to estimate beta diversity with Legendre and De Caceres [8] approach, beta diversity was estimated using the functions of beta.div.comp and LCBD.comp in the R package "adespatial" in Rstudio [39,40]. These functions decomposed to total beta diversity (hereafter referred to as LCBDtot) in species replacement (LCBDrepl) and richness difference (LCBDrich) components. Jaccard-based from the Podani family indices were used to estimate beta diversity based on presence–absence data. Using this function, the beta diversity value is calculated from 0 to 0.5. Low beta diversity values (0) mean that the same species are present at all sites [8]. Values close to the highest value, 0.5, indicate that no common species are shared between sites. For estimation of the LCBDrepl and LCBDrich indices components, it is determined how the composition of each sample differs from the virtual mean sample [8]. The sum of the beta diversity indices at all sampling sites equals 1. Therefore, each site's spatial and temporal contribution rate to beta diversity can be determined. A distance-based ordination technique, Non-metric Multi-dimensional Scaling (NMDS) analysis, was performed to demonstrate spatial differences in beta diversity indices. The NMDS analysis was performed in the CAP 4.1.3 statistical package program. Finally, Spearman rank correlation analysis was applied in the SPSS 28 package program to determine the relationship of alpha and beta diversity indices with each other and environmental variables.

3. Results

3.1. Water Chemistry

The annual mean, minimum, and maximum values of measured environmental variables are given in Table 1. Graphs of some measured physicochemical variables are given in the Supplemental data (Figure S1). All water bodies in the wetland area are hypereutrophic according to TN (>1.5 mg/L) and TP (>0.1 mg/L). pH values changed from neutral to alkaline (6.92 to 9.03). Although the mean annual dissolved oxygen was 7.17 mg/L, the oxygen concentration was determined in a wide range of spatial and temporal variances. Salinity showed spatial and temporal variation (0.16 to 28.89 ppt) during the sampling period (Table 2). One-way ANOVA analysis revealed a statistically significant difference in salinity at sampling sites. (F: 12.98, $p < 0.001$.) SS1 and SS6 study sites constituted one group, and the other five sites formed the other group regarding salinity.

Table 1. The descriptive statistics of some measured environmental variables (n: 77).

		Mean ± SE	**Min–Max**
T	°C	18.36 ± 0.85	4.55–34.0
pH		8.28 ± 0.05	6.92–9.03
EC	mS/cm	10.76 ± 1.08	0.33–44.70
Sal	ppt	6.42 ± 0.67	0.16–28.89
DO	mg/L	7.17 ± 0.24	1.60–11.9
NO_3-N	mg/L	0.26 ± 0.38	0.03–1.74
PO_4-P	mg/L	0.08 ± 0.01	0.01–0.37
TP	mg/L	0.27 ± 0.04	0.05–2.83
TN	mg/L	4.01 ± 0.25	1.59–16.37

Table 2. Salinity variation according to study sites.

Sampling Sites	Mean ± SE	Min–Max
SS1	0.352 ± 0.053	0.159–0.690
SS2	9.647 ± 1.281	3.582–14.016
SS3	8.662 ± 1.472	1.238–14.016
SS4	6.701 ± 1.317	1.055–12.181
SS5	6.638 ± 1.235	1.071–11.849
SS6	0.348 ± 0.025	0.214–0.470
SS7	12.59 ± 2.097	5.345–28.892

3.2. The Variation of Diatom Species Richness and Diversity

A total of 357 diatom taxa (γ-diversity) were identified in the wetland area. Of these, 60 were observed in only one of 182 samples, while 119 were observed with occurrence rates of 3 and less than 3. The highest species number was determined in the epipelon (291) and the freshwater habitat floodplain forest site (SS1) (266) (Table 3).

Table 3. Species richness and diversity results according to microhabitat types and study sites.

Microhabitat Types		Species Richness		Alpha Diversity	Beta Diversity				SIMPER Within
	n_{samp}	n_{taxa}	Mean (Min–Max)	H′ ± Jackknife SE	$LCBD_{repl}$	$LCBD_{rich}$	$LCBD_{tot}$	BD_{tot}	Average Sim (%)
Epipelon	49	291	35.27 (2–103)	4.303 ± 0.184	0.206	0.231	0.437	0.76	11.653
Epilithon	6	110	25.667 (1–90)						3.747
Epiphyton	50	261	25.90 (1–92)	4.225 ± 0.126	0.171	0.287	0.458	0.825	8.504
Tychoplankton	77	288	24.04 (1–151)	4.439 ± 0.296	0.199	0.259	0.458	0.828	8.042
Study Sites									
SS1	36	266	37.17 (1–151)	4.482 ± 0.085	0.147	0.289	0.436	0.756	12.842
SS2	29	203	27.62 (1–74)	3.496 ± 0.138	0.182	0.265	0.447	0.788	9.859
SS3	11	58	9.91 (2–16)	3.148 ± 0.339	0.214	0.202	0.416	0.526	13.931
SS4	11	68	10.00 (1–29)	2.16 ± 1.289	0.201	0.271	0.472	0.884	7.267
SS5	32	227	29.53 (1–85)	4.078 ± 0.12	0.169	0.279	0.448	0.791	9.607
SS6	32	210	31.03 (2–90)	3.798 ± 0.086	0.186	0.237	0.423	0.713	16.167
SS7	31	192	23.61 (2–73)	3.885 ± 0.242	0.18	0.273	0.453	0.803	9.689
All samp. indices:	182	357	27.63 (1–151)	4.604 ± 0.056	0.187	0.269	0.456	0.821	7.77

As a result of the DCA analysis, the gradient lengths were determined at 3.424 and 3.122 for the first two axes, respectively. After the step-wise forward selection analysis, salinity (F: 3.26, *p*: 0.002), NO_3-N (F: 1.49, *p*: 0.002), water temperature (F: 1.39, *p*: 0.004), and PO_4-P (F: 1.26 *p*: 0.034) were found significantly correlated with diatom assemblages (Figure 2). The first (F: 3.379; *p*: 0.002) and all axes (F: 1.865; *p* 0.002) were found to be significant under 499 permutations. These four physicochemical variables explained 9.4% of the total variance (total inertia 3.372). SS1 and SS6, which show freshwater character, are grouped on the left side of the diagram, while the other five sampling sites (lagoon sites) were found to be associated with salinity on the right side. It is seen that nutrients are associated with SS6 (Kocaçay River), which carries the pollution load of the basin (Figure 2).

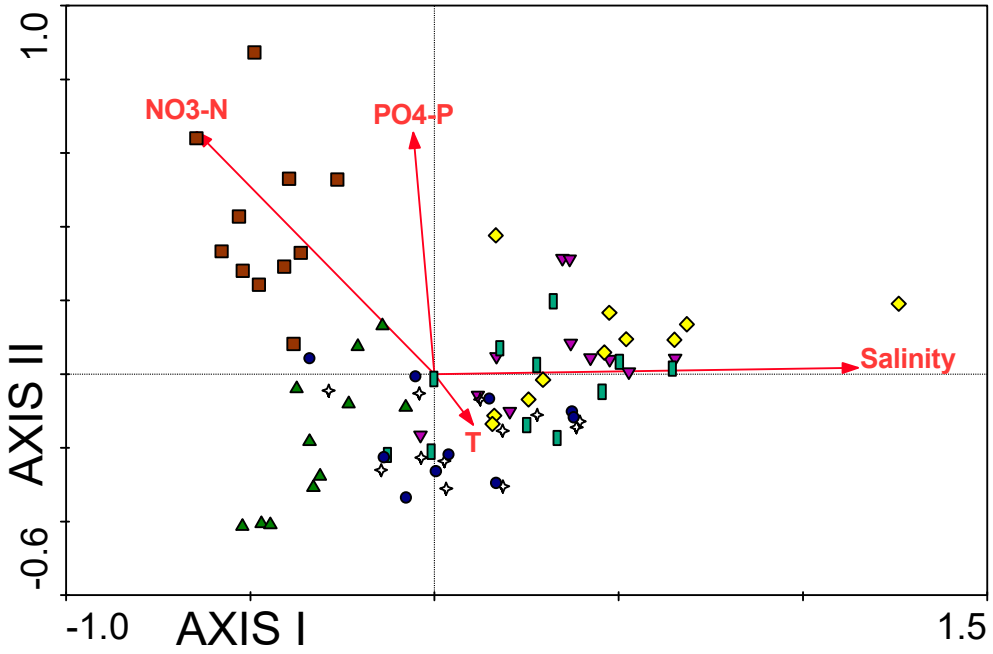

Figure 2. The CCA ordination graph between study sites and significant physicochemical variables based on diatoms presence–absence data (up triangle SS1, down triangle SS2, box SS3, star SS4, circle SS5, square SS6, and diamond SS7).

The Cluster analysis results based on the presence/absence data of diatom taxa (Figure 3) summarize the different habitat preferences of the diatoms, including the salinity gradient. SS3 and SS4 are clustered on the left side of the dendrogram. These sampling sites are in the Dalyan and Poyraz lagoons pelagic zone, respectively, and only the tychoplankton sampling was done. SS1 and SS6, which show lacustrine and riverine characters, respectively, are clustered together since they contain a high percentage of freshwater species due to their freshwater character. The study sites, including the coastal zones of the lagoons, are seen in the middle part of the dendrogram.

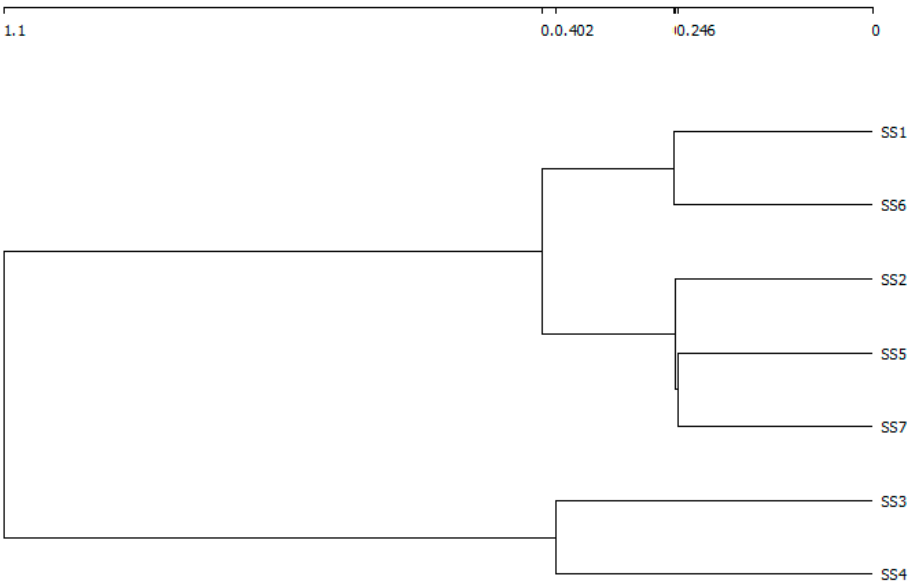

Figure 3. Dendrogram of diatom's presence/absence data according to study sites.

ANOSIM analysis applied to determine the (dis)similarity of the diatom composition between the study sites was found to be significant (Global R:0.238, *p*: 0.001, 1000 random-

izations). While there was no statistically significant difference between SS2–SS3, SS3–SS4, and SS2–SS4 in the pairwise groups, other pairwise tests were found to be significant ($p < 0.05$).

SIMPER analysis (within groups) was performed to determine the similarity rate of diatom taxa at study sites and in different microhabitats. Hereof, it was determined that the average percentage of similarity between microhabitats and sites was low (Table 3). Minimum average similarity percentage values were observed in SS5 and epilithon. SS1 (floodplain forest) and SS6 (river) have freshwater character; 266 and 210 diatom taxa were identified in these sites, respectively.

In SS1, SIMPER within analysis identified 16 taxa with a cumulative rate of 70%, *Melosira varians* being the most dominant diatom species with a contribution rate of 13% (Figure 4).

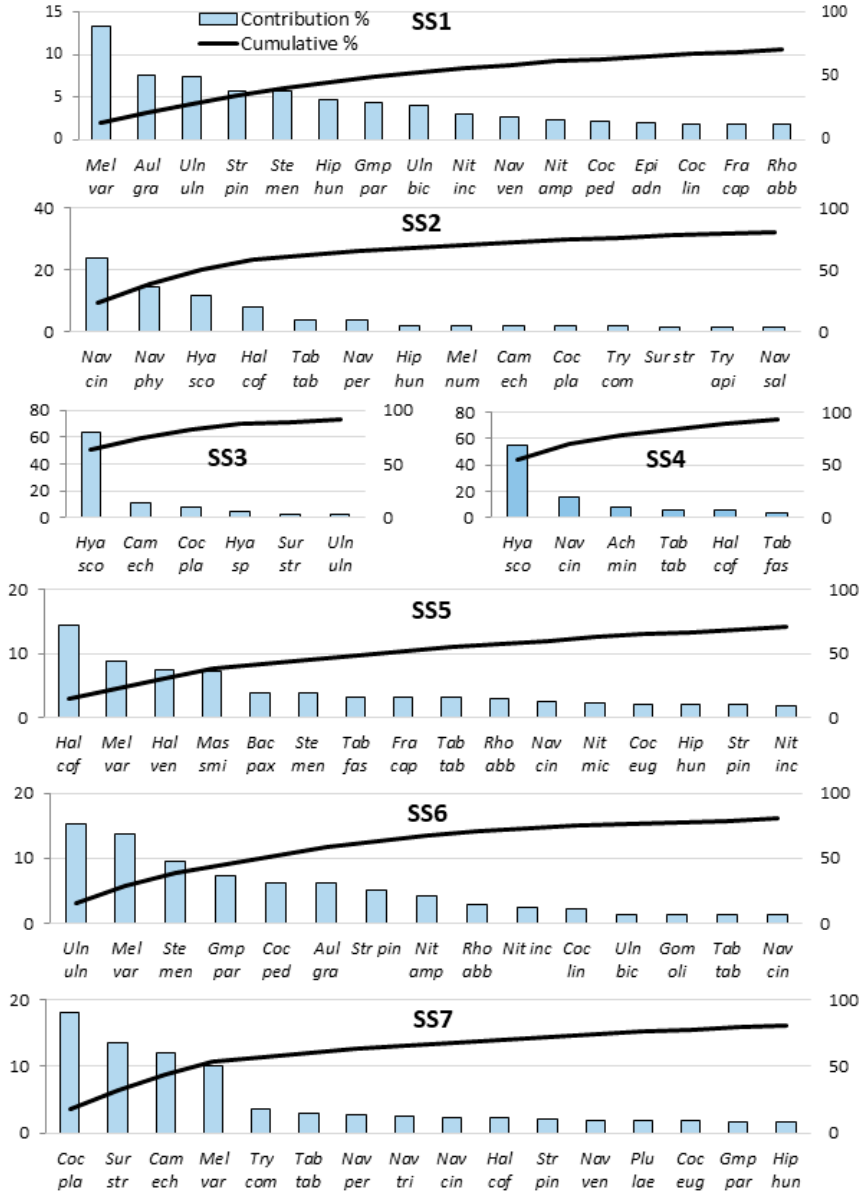

Figure 4. Contribution % and cumulative % ratios of diatom species according to SIMPER within analysis based on study sites. The acronyms of species are given in Table 4.

In SS6, *Ulnaria ulna* with a contribution of about 15%, and *Melosira varians* with a contribution of about 14% were determined as the most dominant taxa. In SS3 and SS4, the open water zones of Poyraz and Dalyan lagoons that were used only for tychoplankton

sampling, *Hyalodiscus scoticus* made the largest contribution to average similarity, with contribution rates of 64% and 55%, respectively. At both study sites, 6 dominant taxa exceeded 90% of the percent cumulative rate (Figure 4). The coastal zone sampling sites SS2, SS5, and SS7 are located next to the dunes that separate the Dalyan, Poyraz, and Arapçiftliği lagoons from the Marmara Sea. SS2 and SS7 are more affected by seawater interference, as they are located near the canals connecting lagoons to the sea. *Navicula cincta*, with a contribution rate of 23% in SS2; *Halamphora coffeiformis*, with a contribution rate of 14.5% in SS5 and *Cocconeis placentula*, with a contribution rate of approximately 18% in SS7; were the species that made the greatest contribution to average similarity.

Although the ANOSIM analysis applied to determine the difference between the microhabitats showed a significant difference (Global R: 0.083, p: 0.001, 1000 randomizations), the R statistic was low. In the pairwise test result, each group was found to be statistically different from the other ($p < 0.05$). According to the SIMPER analysis, *Melosira varians*, *Hippodonta hungarica*, *Rhoicosphenia abbreviata*, and *Navicula cincta* were the species that contributed the most to the similarity in epipelon, with a total cumulative rate of 30%. Among the epipelic taxa, 18 taxa contributed 80% to the similarity (Figure 5).

Table 4. The SIMPER analysis, alpha, and beta diversity results of most common diatom species in Kocaçay Delta.

			SIMPER Analysis Results				Alpha D.	Beta D.
Species	**Abrr.**	**Ocurr.**	**Ave. Ab.**	**Ave. Sim.**	**Cont. %**	**Cumul. %**	**Spec H′**	**SCBDindex**
Melosira varians	*Mel var*	87	4.589	0.8	10.293	10.293	2.876	0.0242
Navicula cincta	*Nav cin*	76	3.575	0.394	5.076	15.369	2.713	0.0226
Ulnaria ulna	*Uln uln*	77	2.834	0.366	4.709	20.078	2.797	0.0176
Stephanocyclus meneghinianus	*Ste men*	79	2.252	0.322	4.14	24.218	1.971	0.0188
Halamphora coffeiformis	*Hal cof*	71	2.185	0.32	4.119	28.337	2.912	0.0144
Hyalodiscus scoticus	*Hya sco*	57	4.403	0.318	4.098	32.435	3.427	0.0222
Gomphonema parvulum	*Gmp par*	73	1.912	0.307	3.946	36.381	3.135	0.0122
Cocconeis placentula	*Coc pla*	59	3.09	0.295	3.791	40.172	2.95	0.0246
Staurosirella pinnata	*Str pin*	78	2.311	0.273	3.517	43.689	3.549	0.0148
Campylodiscus echeneis	*Cam ech*	55	3.379	0.258	3.319	47.007	3.304	0.0173
Hippodonta hungarica	*Hip hun*	77	2.242	0.244	3.136	50.143	2.842	0.013
Tabularia tabulata	*Tab tab*	61	1.998	0.233	2.996	53.139	1.987	0.0131
Cocconeis pediculus	*Coc ped*	66	2.263	0.193	2.481	55.62	2.616	0.0197
Rhoicosphaenia abbreviata	*Rho abb*	70	2.022	0.191	2.455	58.075	2.009	0.0161
Surirella striatula	*Sur str*	52	2.185	0.186	2.392	60.467	2.61	0.0121
Aulacoseira granulata	*Aul gra*	57	1.884	0.185	2.386	62.853	3.055	0.0121
Halamphora veneta	*Hal ven*	56	1.638	0.17	2.184	65.036	2.593	0.0123
Nitzschia amphibia	*Nit amp*	72	1.327	0.161	2.07	67.107	3.483	0.0123

Table 4. *Cont.*

			SIMPER Analysis Results				Alpha D.	Beta D.
Species	**Abrr.**	**Ocurr.**	**Ave. Ab.**	**Ave. Sim.**	**Cont. %**	**Cumul. %**	**Spec H′**	**SCBDindex**
Nitzschia inconspicua	*Nit inc*	69	1.039	0.161	2.07	69.176	3.33	0.009
Tabularia fasciculata	*Tab fas*	54	1.534	0.16	2.058	71.234	2.575	0.0099
Navicula veneta	*Nav ven*	61	1.124	0.14	1.797	73.032	3.278	0.0089
Achnanthidium minutissimum	*Ach min*	50	2.233	0.126	1.624	74.656	1.4	0.0111
Mastogloia smithii	*Mas smi*	51	1.74	0.124	1.592	76.248	2.234	0.0129
Cocconeis placentula var. *euglypta*	*Coc eug*	42	1.246	0.103	1.327	77.575	2.904	0.0099
Fragilaria capucina	*Fra cap*	57	1.573	0.096	1.236	78.811	2.594	0.0144
Navicula phyllepta	*Nav phy*	46	1.616	0.093	1.197	80.008	2.215	0.0075
Ulnaria biceps	*Uln bic*	55	0.871	0.09	1.153	81.161	3.035	0.0086
Tryblionella compressa	*Try com*	50	1.208	0.083	1.068	82.229	2.333	0.0133
Cocconeis lineata	*Coc lin*	48	0.923	0.081	1.046	83.275	2.417	0.0069
Nitzschia palea	*Nit pal*	52	0.606	0.069	0.884	84.158	3.3	0.0078
Gogorevia exilis	*Gog exi*	38	1.361	0.067	0.866	85.024	2.675	0.0103
Tryblionella apiculata	*Try api*	59	0.785	0.065	0.835	85.858	3.289	0.0082
Navicula tripunctata	*Nav tri*	47	0.759	0.057	0.733	86.591	2.845	0.0109
Bacillaria paxillifera	*Bac pax*	51	0.784	0.057	0.73	87.321	2.926	0.0077
Fallacia pygmaea	*Fal pyg*	41	0.891	0.051	0.655	87.976	2.722	0.008
Navicula peregrina	*Nav per*	41	0.775	0.047	0.601	88.577	2.378	0.009
Nitzschia microcephala	*Nit mic*	40	0.85	0.044	0.564	89.141	2.591	0.0088
Gomphonella olivacea	*Gom oli*	35	0.616	0.037	0.479	89.62	1.584	0.0062
Amphora pediculus	*Amp ped*	50	0.402	0.034	0.436	90.055	3.518	0.008

In epiphyton, *Melosira varians* (11%), *Cocconeis placentula* (10%), *Ulnaria ulna* (7.5%), *Cocconeis pediculus* (6%), and *Stephanocyclus meneghinianus* (5%) were the most important species. These five species provided 40% of the cumulative rate. The 16 taxa identified (Figure 5) reached a cumulative rate of about 70%. In tychoplankton, the most dominant species with a contribution rate of 11% was *Hyalodiscus scoticus*. *Campylodiscus echeneis* followed this with 10% and *Surirella striatula* with 8%. In epilithon, *Ulnaria ulna* was identified as the most remarkable diatom species, with a contribution rate of 28%. It was followed by *Rhoicosphenia abbreviata*, *Gomphonella olivacea*, and *Stephanocyclus meneghinianus*, each with a contribution rate of 10%.

Wide ranges of overall alpha and beta diversity coefficients were determined at the study sites (Table 3 and Table S1). Among the study sites, the site with the highest overall alpha diversity values is SS1 (Figure 6, Table 3 and Table S1). According to all species data, the all-sample index of alpha diversity coefficient (H′) of the wetland area was estimated as 4.604. On the other hand, tychoplankton diatom communities had the highest overall alpha diversity value. The highest number of taxa identified at a single site was 151, and it

was determined in the tychoplankton at SS1 in August. At the same study site, 103 taxa were identified in the epipelon and 92 in the epiphyton. These numbers were recorded as the highest taxa numbers determined at a single site according to these microhabitats. However, in the combined data, the total number of taxa determined in SS1 in August is 192 (Table S1). In epilithon, on the other hand, the total number of taxa determined at SS6 in April 2019 is 90.

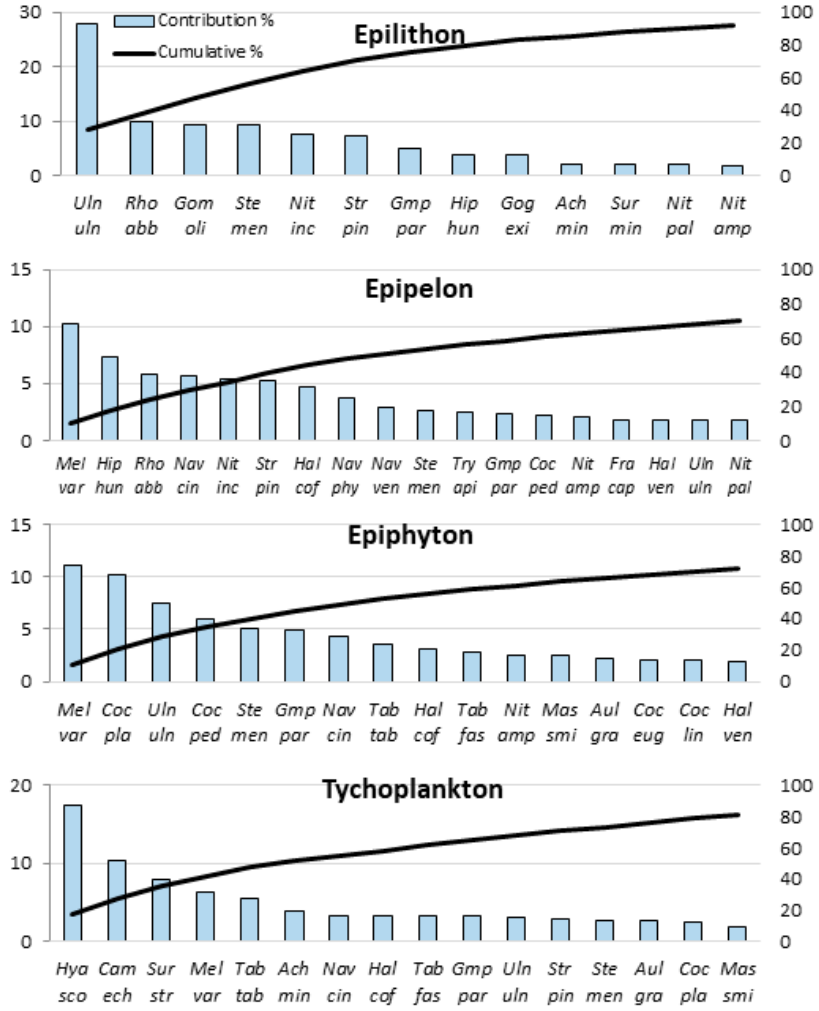

Figure 5. Contribution % and cumulative % ratios of diatom species according to SIMPER within analysis based on different microhabitats. The acronyms of species are given in Table 4.

The BDtot and LCBDtot coefficients gave similar results about beta diversity (Table 3). The overall BDtot and LCBDtot coefficients were estimated as 0.821 and 0.456, respectively. The sum of all coefficients was very close to 1 and 0.5, which are the highest values of the indices. The highest BDtot and LCBDtot coefficients were estimated in SS4 and the lowest in SS3. The overall LCBDtot coefficients equals the sum of the overall LCBDrepl and LCBDrich values. It was determined that LCBDrich coefficients were higher than LCBDrepl in all study sites, except SS3 (Table 3, Figure 7). The lowest overall species richness was found at SS3, where the highest overall LCBDrepl and the lowest LCBDrich values were estimated. In contrast, the highest overall species richness was found at SS1, where the highest overall LCBDrich and the lowest LCBDrepl values were detected (Table 3, Figure 7). The NMDS diagrams of beta diversity indices are given in Figure 8. However, in the combined data, alpha diversity values increased, and beta diversity values decreased with the increase in the number of taxa at the sampling sites (Table S1).

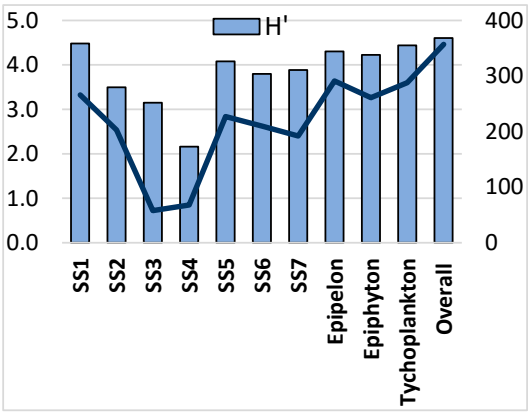

Figure 6. Alpha diversity coefficients and species richness according to study sites and microhabitats.

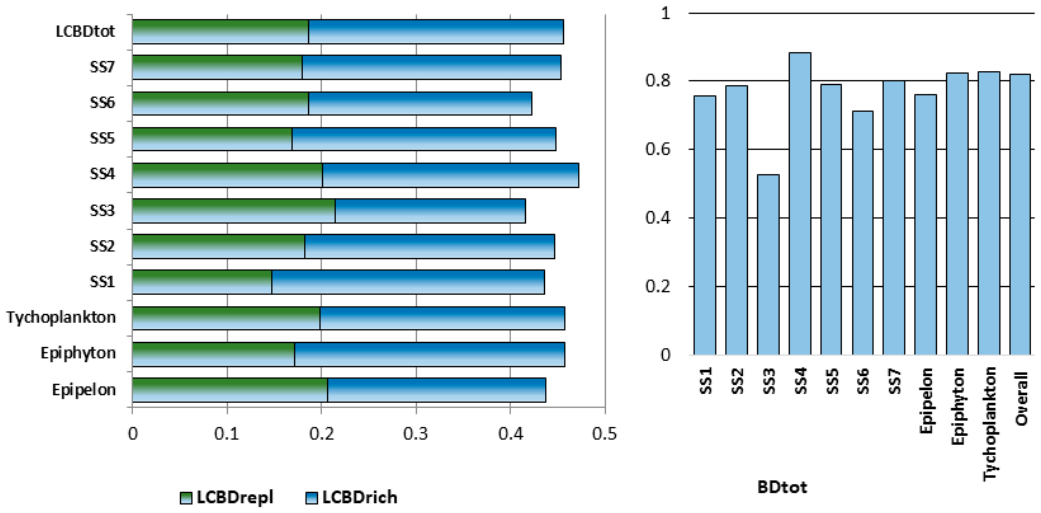

Figure 7. The partition of LCBDrepl and LCBDrich components, and BDtot coefficients.

However, no significant correlation was observed between the LCBDrepl index and species richness. In contrast, a significant negative correlation was determined between the LCBDrich index and species richness at a local scale (Table 5 and Table S2). None of the diversity indices showed a correlation with salinity, EC, and pH (Table 5 and Table S2). The beta diversity index that showed the most correlation with environmental variables was the BDtot index. LCBDrepl and LCBDrich indices showed a significant correlation only with PO_4-P (Table 5) and NO_3-N (Table S2).

Table 5. Results of Spearman rank correlation analysis between physicochemical variables and diversity indices (** correlation is significant at the 0.01 level, 2-tailed).

	BDtot Index	LCBDrep Index	LCBDrich Index	H′ Index	Sp. Rich.
BDtot index					
LCBDrep index		1			
LCBDrich index	0.345 **	−0.926 **	1		
H′ index	−0.824 **	0.236 **	−0.471 **	1	
Sp. Rich.	−0.926 **		−0.368 **	0.840 **	1
DO	0.224 **			−0.169 **	−0.221 **
T	−0.383 **			0.282 **	0.374 **
PO_4-P	−0.288 **	0.175 **	−0.245 **	0.212 **	0.255 **
TP	−0.235 **			0.166 **	0.196 **
TN	−0.356 **			0.272 **	0.314 **

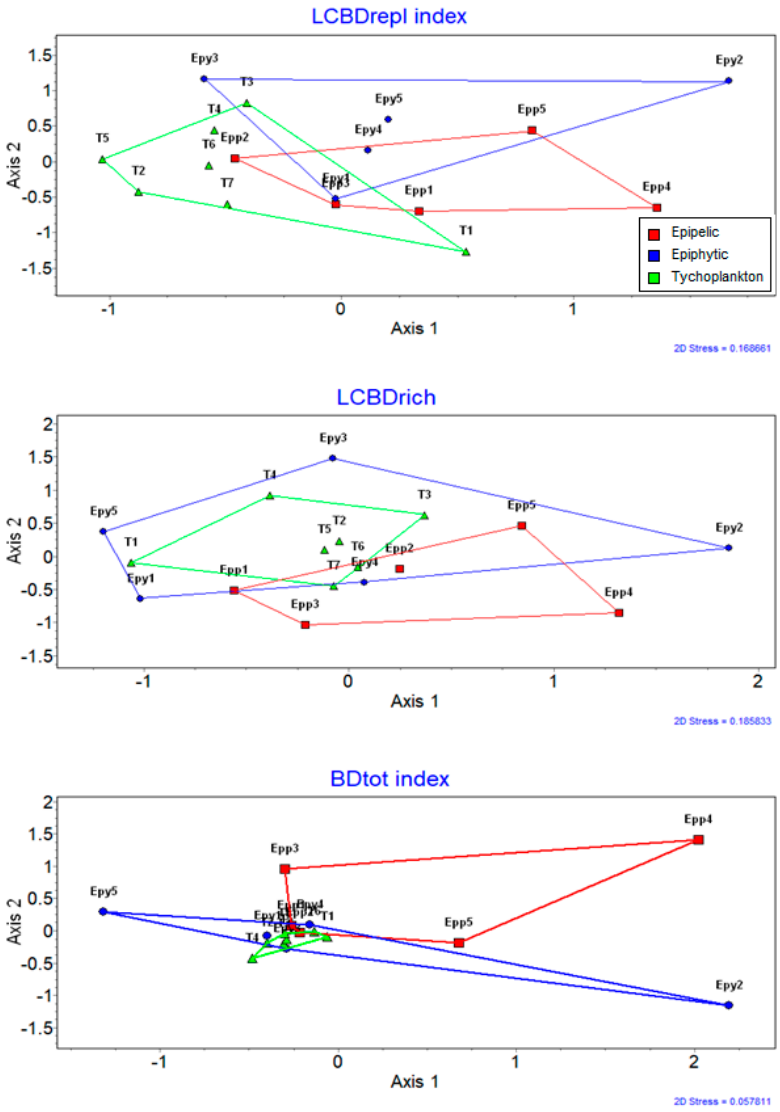

Figure 8. NMDS diagrams of beta diversity indices. 2D stress for LCBDrepl:0.168661; LCB-Drich:0.185837; BDtot: 0.057811 (T: Tychoplankton, Epp: Epipelon, Epy: Epiphyton).

SIMPER within analysis showed that 39 diatom species with a total cumulative rate of 90% were the most dominant taxa in the wetland area (Table 4). Most of these species are known as cosmopolitan and are markedly euryhaline (see Appendix A). The SCBD index coefficients of the species were found to be more consistent with the SIMPER analysis results than Shannon's H' coefficients.

The most dominant species was *Melosira varians*, which was observed in 87 samples with a contribution rate of 10.29%. *Navicula cincta* followed this with 5%, and *Ulnaria ulna*, *Stephanocyclus meneghinianus*, *Halamphora coffeiformis*, and *Hyalodiscus scoticus* with 4% each. However, the species with the highest SCBDindex value were *Cocconeis placentula*, followed by *Melosira varians*, *Navicula cincta*, and *Hyalodiscus scoticus*. The species with the highest alpha diversity (Spec H') value was *Staurosirella pinnata*, followed by *Amphora pediculus*, *Nitzschia amphibia*, and *Hyalodiscus scoticus*. The SCBDindex sum of 39 species contributing 90% to the similarity was 0.4967. This value indicates that the contribution rate of 39 species in the beta diversity is 49.67%.

4. Discussion

It has been determined that the salinity gradient and habitat heterogeneity have affected diatom species richness and diversity, and euryhaline species with wide salinity

tolerance found in freshwater, brackish, and marine environments are found in the area. Brackish habitats, transitional zones between freshwater and marine environments, are considered to be the richest areas in terms of biodiversity [3]. Desienti et al. [3], in their study of New Jersey coastal lagoons, determined that the salinity gradient is the primary factor affecting the composition of diatom assemblages.

ANOSIM and SIMPER analyses show that diatoms exhibit wide variation within and between sites and microhabitats. The low similarity between the sampling sites and microhabitats and the different % contribution ratios of varying diatom species at the sampling sites are evidence of this situation. As a result of the SIMPER analysis, 39 taxa providing a 90% cumulative rate were determined in the wetland area (Table 4). 29 of these taxa are markedly euryhaline species with wide salinity tolerance [2], and it is known that the general environment of 16 of them is only freshwater [33,34] (see Appendix A). However, these species have also been determined in lagoons with brackish water characteristics and inland seas with less salinity than oceans, such as the Baltic Sea [41], the Black Sea [42–44], and the Marmara Sea [45] (22 of 39 species).

Many diatoms, which are known as freshwater species, have high salinity tolerance and can be found in wide salinity ranges [46–48]. Various studies have shown that diatoms exhibit phenotypic plasticity to adapt to different environmental factors or stress [49,50]. Bussard et al. [51] say that diatoms change their gene expression pathways by showing phenotypic plasticity against the salinity gradient, and, in this way, they adapt to different environmental factors. For example, Leterme et al. [52] state that *Cocconeis placentula* changes the pore opening width on the frustule at different salinity ranges, and thus increases its ecological competitiveness in fluctuating environments. Determining the high number of euryhaline diatom species in the study area, generally found in freshwater habitats, reveals the importance of this adaptation mechanism. In particular, lagoons and transition zones showing brackish water characteristics are seen as suitable environments for investigating the high phenotypic plasticity of diatoms against salinity. Areas with different salinity ranges or gradients are suitable for a more detailed investigation of freshwater species' salinity tolerances.

Beta diversity studies conducted in recent years have shown significant improvement and beta diversity indices, which allow the comparison of spatial differences of sampling sites, have become available for researchers [7]. There are various approaches to separate beta diversity into components. While Legendre and De Caceres [8] estimate beta diversity by dividing it into LCBD and SCBD components, LCBD can also be estimated by dividing it into two components: species replacement and richness difference [39]. This study determined spatial and environmental heterogeneity affecting beta diversity using both approaches. Although the sampling sites are close to each other (small spatial scale), a high spatial variation was determined at the diatom assemblages. At the same time, the determination of high overall beta diversity indicates the similarity between the habitats is low. It is known that high beta diversity observed in an area indicates high spatial variation and low similarity of species compositions found at sampling sites [4]. The detection of low average similarity percentages of the sampling sites may be associated with high beta diversity. Similarly, the spatial and temporal variations observed in Shannon's H', LCBDrepl, LCBDrich, and BDtot indices further prove this situation.

Sampling sites with high beta diversity values are known as poor species richness sites [8]. Yang et al. [53] found high beta diversity with low alpha diversity in their study. Species richness was found to be low at sampling sites with low LCBDrepl index and high LCBDrich index values (Figures S2–S5). In addition, a strong negative correlation was found between the LCBDrich index, species richness, and alpha diversity (Table 5 and Table S2). It was determined that species richness, alpha, and beta diversity indices showed significant variation according to sampling sites (Table 3 and Table S1). The high variation observed in species richness was also reflected in the alpha and beta diversity values. High alpha and gamma diversity values are important indicators of high biodiversity in the area.

Virta et al. [54] showed that high alpha diversity in diatoms has a supportive effect on ecosystem productivity.

It has been determined that the SCBD coefficients of the species that contributed the most to the % similarity were higher than Shannon's H' coefficients (Table 4). H' coefficients of the diatom species with the highest % contribution, such as *Melosira varians* and *Navicula cincta*, were found to be lower than the other species (Table 4). On the other hand, the SCBD coefficients of the species were found to be more similar to the results of the SIMPER analysis. Because the SIMPER analysis measures the (dis)similarity of the compared areas (SIMPER within or between analyses) according to the Bray–Curtis dissimilarity matrix. Similarly, since beta diversity measures spatial differentiation, the results of these two analyses supported each other.

Partitioning of overall beta diversity revealed that both species replacement and richness differences were significant in forming diatom communities. In fact, unlike many studies, LCBDrich was determined at higher values than LCBDrepl (Tables 3 and S1). A similar finding was detected by Wu et al. [55], who determined that beta diversity was mainly caused by nestedness components. Valente-Neto et al. [15] found that beta diversity components equally contributed to overall beta diversity in benthic macroinvertebrate communities. The fact that the most contributing component to LCBDtot is LCBDrich in this study indicates that a diatom community may contain more species than another and may reflect the variety of ecological niches in different locations in the study area [39,56]. Also, species thinning causes nestedness, which is a type of richness difference pattern [39]. Podani et al. [56] pointed out that a high LCBDrich component indicates that one sampling site may contain more unique species. SIMPER analysis showed that different species were found in different habitats in the Kocaçay Delta wetland. We think that this uniqueness affects the LCBDrich component values. Rodríguez-Alcalá et al. [57] found that species turnover is stronger than nestedness at any spatial scale in their studied region, either along a large spatial scale in Europe or lakes at a national scale. On the other hand, many researchers have identified the LCBDrich component as low or even negligible [13,14,53,58–62].

The importance of the LCBDrepl components indicates that species tend to replace each other along ecological gradients, and the replacement rate is also a function of ecological tolerance reflecting the impact of environmental variables that control ecological gradients on community formation [39]. A high LCBDrepl coefficient also means the simultaneous increase or extinction of species due to different reasons such as competition and environmental filtering [39,56,63].

Contrary to many studies, the fact that LCBDrich was found to be higher than the LCBDrepl components to total beta diversity indicates that multiple factors are important that affect the rapid species gain, loss, and variation observed spatially and temporally in the wetland area. The hydrological connection of the lagoons with the sea, the associated salinity gradient, and high eutrophication are thought to cause significant environmental heterogeneity. Stefanidou et al. [62] state that the hydrological connection of lagoons with the sea causes high species replacement (turnover), which in turn causes high beta diversity. Significant seasonal water level fluctuations are observed in shallow lakes, which are related to precipitation and evaporation amounts. Wind-generated wave movements cause sediment to be mixed with the water column, especially in the shallow littoral zone. This causes the observation of tychoplanktonic species rather than euplanktonic species in the plankton. It should not be noted that the high LCBDrich values detected in the wetland area may be related to the high physical and chemical disturbance observed in the delta wetland, resulting in distinct environmental heterogeneity.

Szabo et al. [13] showed that spatial distance and environmental heterogeneity equally contribute to diatom community associations. It has been concluded that high environmental heterogeneity causes great variation in the number of species at each study site and the low occurrence rate of many species. Although the species diversity is high, 1/3 of the diatom species determined in the wetland area had an occurrence rate of 3 or below 3. This

finding indicates that diatom species rapidly replace (species gain and loss) in the area. It is known that the replacement of diatoms is rapid, especially in special habitats such as coastal lagoons. For instance, Stephanidou et al. [62] found that diatoms are the most diverse group in terms of species richness in their study on coastal lagoon phytoplankton.

Explaining the factors that influence the spatial variation of species composition is an important goal of community ecology studies. Many researchers consider determining the correlation between beta diversity indices and environmental variables to be a suitable tool for understanding the factors affecting beta diversity [15]. Valente-Neto et al. [15] stated that correlative methods between LCBD components and environmental variables are appropriate for understanding the driving patterns of beta diversity. They also noted that specific environmental conditions are the reason for detecting high beta diversity values at sampling sites. Although a significant correlation was not observed between salinity and beta diversity indices in this study, the salinity gradient is thought to create specific environmental conditions.

While a significant correlation was observed between the BDtot index and TN and TP, none of the diversity indices showed a significant correlation with salinity. Although no meaningful relationship could be determined between diversity indices and salinity, CCA, ANOSIM, SIMPER, and Cluster analyses explain diatom species' richness and compositional variation against salinity gradient. According to TN and TP, all sampling sites are hypereutrophic. The eutrophic character of the Marmara Sea [45] and the Susurluk River Basin and the agricultural activities around the delta area explain the source of the high eutrophication detected in the region.

It has been shown in many studies that other environmental factors, especially nutrient enrichment, are essential in the change of diatom species diversity and diversity values, besides salinity and habitat preference [64–67]. Spearman rank analysis results show that eutrophication has a positive effect on alpha diversity indices and a negative effect on beta diversity indices. This is expected because, in this study, alpha and beta diversity indices show strong negative correlations. While eutrophication observed in the wetland contributes positively to the increase in species diversity at a local scale (alpha diversity), it causes a decrease in beta diversity. However, the effect of eutrophication on beta diversity components was found to be different. The significant positive and negative correlations of LCBDrepl and LCBDrich indices with PO_4-P, respectively, indicate that eutrophication increases the species' tendency to replace each other but decreases the ordered loss of the diatom species along eutrophication gradients. Leboucher et al. [11] state that nutrient enrichment has a strong negative effect on beta diversity, especially on large spatial scales. According to their study, this is due to nutrient enrichment that eliminates specialized species and leads to an increase in physiologically plastid generalist species.

5. Conclusions

Coastal wetlands are known as highly productive and high species diversity systems due to their shallow character, being rich in seawater input and nutrients originating from the inland waters or sea to which they are connected. High alpha and gamma diversity values detected in the Kocaçay Delta pointed out the high diatom biodiversity in the area. The BDtot index is related to environmental variables, the LCBDtot and its components gives information about species replacement and richness differences ratios in the area. In light of the evidence mentioned above, although the study sites were close to each other (small spatial scale), it was concluded that the high variation in species richness observed due to the salinity gradient and environmental heterogeneity at the sampling sites caused the high variation in alpha and beta diversity components.

Biomonitoring studies using the indicator properties of diatoms have been in practice for many years. However, in lagoons where salinity gradient and habitat heterogeneity are highly observed, monitoring studies can be diversified and expanded by using the rapid gain and loss characteristics of the diatoms. Furthermore, various conservation strategies can be developed by utilizing the responses of diatoms, which show high phe-

notypic plasticity, to salinization and water level changes that occur with climate change in wetlands.

Supplementary Materials: The following supporting information can be downloaded at: https://www.mdpi.com/article/10.3390/w15193414/s1, Figure S1: The box-plot graphics of some measured physicochemical variables; Figure S2: The spatial and temporal variations of species richness, alpha and beta diversity indices of epipelon samples; Figure S3: The spatial and temporal variations of species richness, alpha and beta diversity indices of epiphyton samples; Figure S4. The spatial and temporal variations of species richness, alpha and beta diversity indices of tychoplankton; Figure S5: The spatial and temporal variations of species richness, alpha and beta diversity indices of overall combined data; Table S1: Species richness and diversity results according to study sites based overall combined data. All diversity indices were estimated according to presence absence data; Table S2: Results of spearman rank correlation analysis between some physicochemical variables and diversity indices based overall combined data.

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Data Availability Statement: The data that support the findings of this study are available from the corresponding author upon reasonable request.

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Conflicts of Interest: The authors declare no conflict of interest.

Appendix A

Table A1. List of the most common diatom species, according to their habitat preferences [32,33] and euryhalinity classes [2] (b: brackish; f: fresh; m: marine; t: terrestrial; mark eury: markedly euryhaline; some eury: somewhat euryhaline; NG: not given).

Species	AlgaeBase	DiatomBase	Euryhalinity Class
Melosira varians C.Agardh	f	f	mark eury
Navicula cincta (Ehr.) Ralfs	f, m	b, f, t	mark eury
Ulnaria ulna (Nitzsch) P.Compère	f	f	some eury
Stephanocyclus meneghinianus (Kützing) Kulikovskiy, Genkal & Kociolek	f, m	f	mark eury
Halamphora coffeiformis (C.Agardh) Mereschkowsky	b	b	mark eury
Hyalodiscus scoticus (Kützing) Grunow	m	m	mark eury
Gomphonema parvulum (Kützing) Kützing	f	f, m	mark eury
Cocconeis placentula Ehrenberg	f	f, m	mark eury
Staurosirella pinnata (Ehrenberg) D.M.Williams & Round	f	f, m	mark eury
Campylodiscus echeneis Ehrenberg ex Kützing	m	m	mark eury
Hippodonta hungarica (Grunow) Lange-Bertalot, Metzeltin & Witkowski	f	f	some eury
Tabularia tabulata (C.Agardh) Snoeijs	f, m	f, b, m	NG
Cocconeis pediculus Ehrenberg	f	f	some eury
Rhoicosphenia abbreviata (C.Agardh) Lange-Bertalot	f	f, m	mark eury
Surirella striatula Turpin	m	f, b, m	mark eury
Aulacoseira granulata (Ehrenberg) Simonsen	f	f	some eury
Halamphora veneta (Kützing) Levkov	f	f	some eury

Table A1. *Cont.*

Species	AlgaeBase	DiatomBase	Euryhalinity Class
Nitzschia amphibia Grunow	f	f	mark eury
Nitzschia inconspicua Grunow	f	f	NG
Tabularia fasciculata (C.Agardh) D.M.Williams & Round	m	f, b, m	mark eury
Navicula veneta Kützing	b	f, b	mark eury
Achnanthidium minutissimum (Kützing) Czarnecki	f	f, t	mark eury
Mastogloia smithii Thwaites ex W.Smith	f, m	f, m	mark eury
Cocconeis placentula var. *euglypta* (Ehrenberg) Cleve	f	f	mark eury
Fragilaria capucina Desmazières	f, m	f	some eury
Navicula phyllepta Kützing	f, m	f, m	mark eury
Ulnaria biceps (Kützing) Compère	f	f	NG
Tryblionella compressa (Bailey) Poulin	m	m	mark eury
Cocconeis lineata Ehrenberg	f	f	mark eury
Nitzschia palea (Kützing) W.Smith	f	f	mark eury
Gogorevia exilis (Kützing) Kulikovskiy & Kociolek	f	f	some eury
Tryblionella apiculata W.Gregory	m	f	mark eury
Navicula tripunctata (O.F.Müller) Bory	f	f, m	mark eury
Bacillaria paxillifera (O.F.Müller) T.Marsson	b	f, m	mark eury
Fallacia pygmaea (Kützing) Stickle & D.G.Mann	f	f, b	mark eury
Navicula peregrina (Ehrenberg) Kützing	b	f, b, m	mark eury
Nitzschia microcephala Grunow	f	f	mark eury
Gomphonella olivacea (Hornemann) Rabenhorst	f	f	mark eury
Amphora pediculus (Kützing) Grunow	f	f	mark eury

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