

Spatially Well Structured Mangroves Fish Communities of the Persian Gulf; a Functional Perspective

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Research Article

Keywords: Biodiversity, Mangal ecosystems, Western Indian Ocean, Conservation, Functional diversity

Posted Date: June 13th, 2023

DOI: https://doi.org/10.21203/rs.3.rs-3023864/v1

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Version of Record: A version of this preprint was published at Wetlands on August 24th, 2023. See the published version at https://doi.org/10.1007/s13157-023-01721-3.

Abstract

Functional diversity is one of the most important aspects of biodiversity studies. In this work, the functional diversity of two mangrove-associated fish communities in the Persian Gulf is evaluated, including 34 species from the estuary community and 23 species from the creek/mud community. For each community, three functional diversity indices were calculated, namely, FD (Functional Diversity, representing functional richness), MPD (Mean Pairwise Distance, representing dispersion), and MNTD (Mean Nearest Taxon Distance, representing evenness). The comparison between the observed values and the expected values indicates the low functional diversity of the estuary community, whereas, the functional diversity of the species inhabiting creeks and mud flats was not significantly lower or higher than the expected functional diversity. Moreover, the dispersion of functional traits in creek/mud species was higher and the evenness was lower than the estuaries community. This can be related to the more homogenous habitat of the estuary environment, in comparison with the creeks and mudflats. Also, we can attribute the low functional diversity of the estuary community to both the homogenous structure and the preliminary situation of the Persian Gulf. Dendrogram-based analyses show four functional guilds in both communities and were used to the recognition of the most important species for the functional diversity in each community. We found that the most important functional traits that explain the functional diversity in the estuary community were the general traits of size and position in the vertical column in water, however, in creek/mud communities more specialized traits such as the feeding habit and the migratory status explain most of the diversity.

Introduction

Biodiversity studies are one the most important analyses for understanding the ecological structure of marine ecosystems and their conservation status. Numerous studies introduced several diversity concepts based on species richness (Scott et al., 1987), genetic and phylogenetic relationships between species (Coates et al., 2018; Faith, 2018), and functional traits (Petchey & Gaston, 2002). Functional diversity analyses are based on sets of traits in understudied organisms that have ecological impacts on the environment (Cornelissen et al., 2003; Hooper et al., 2005; Loreau & Hector, 2001) and ecological service of a region (Diaz 2007). Currently, function-based approaches have an increasing role in the study of different systems such as microbial communities (Bhattacharyya et al., 2023), fungi (Plett et al., 2023), plants (Wang et al., 2023), invertebrates (Head et al., 2018; Zhang et al., 2022), and vertebrates (Ausprey et al., 2022; Mao et al., 2021; Walsh et al., 2022; Whitfield et al., 2022). Integrating functional diversity with other concepts in biodiversity (for instance, phylogenetic diversity and species richness) can produce novel conclusions about the history and assemblage of understudied communities (Flynn et al., 2011; Lin et al., 2021; Tucker et al., 2018). In particular, the relationship between functional and phylogenetic diversity is controversial (Saito et al., 2015). On the one hand, some studies suggest that phylogenetic diversity can be used as a proxy for functional diversity, therefore, in the presence of phylogenetic data, it is not advisable to investigate functional diversity (Molina-Venegas et al., 2021; Owen et al., 2019). On the other hand, some other studies indicate that different species have a different contribution to each

diversity measure (Pool et al., 2014) and phylogenetic diversity cannot efficiently captures the functional diversity, especially in communities in which their trait diversity is not phylogenetically conserved (Mazel et al., 2018; Palmer & Fischer, 2022; Swenson & Enquist, 2009). In addition, functional diversity studies can be used to evaluate the ecological processes, ecological service, and the conservation status of a region (Cadotte et al., 2011; Shah Esmaeili et al., 2022). Numerous indices have been defined to calculate different facets of functional diversity (Pla et al., 2012a; Schleuter et al., 2010). Among them, dendrogram-based indices are one of the oldest and still one of the most used indices in functional ecology studies. The first introduced dendrogram-based index in these studies is simply called FD (Functional Diversity), and is the sum of the branch length of the trait dendrogram of the community (Petchey et al., 2007; Petchey & Gaston, 2006). Other indices comprise convex hull, which is a hyper-volume of trait ranges and the position of each species in the trait space (Barber & Dobkin, 1996; Cornwell et al., 2006), whereas, other concepts have been formulated in functional diversity studies, based on richness, evenness, and divergence (Villéger et al., 2008). Nevertheless, when we want to choose appropriate indices we should be cautious, for among the diverse functional diversity indices, many of them are strongly correlated with each other and are basically redundant (Swenson, 2014b).

Connecting to the Gulf of Oman, by the Strait of Hormoz, the Persian Gulf is a recently formed shallow basin with a maximum depth of 100m and an average of 35m (Barth & Khan, 2008). This biogeographical and physical setting causes high salinity and temporal fluctuations and results in a considerably harsh and undesirable environment for its native fauna and flora (Bayani, 2016; Sheppard et al., 2010). However, studies on the species composition and richness of several taxa in this area suggest that there is a noticeable taxonomic distinctness in this region, surprisingly with various endemic species (i.e. Naderloo, 2017; Price & Izsak, 2005). Mangrove forests of this region are young ecosystems with two tree species, Avicennia marina and Rhizophora mucronate, which have been both naturally grown and artificially planted along the coastlines of the Persian Gulf and the Gulf of Oman (Zahed et al., 2010). Avicennia marina is the most dominant and widely distributed where accounting around 97% of the coverage, while R. mucronata is just naturally grown in Gaz mangroves. These forests are the subject of negative human activity in these areas, however, sustainable development and management of mangrove ecosystems with works on their biodiversity and conservational status have been fruitful and increased these mangrove forests in recent years (Milani, 2018). Recently, increasing attention is paid to the assessment of biodiversity concepts (other than species richness) in the mangrove ecosystems of the Persian Gulf. The focus is mostly on the functional diversity of macrobenthic communities (Delfan et al., 2021; Hajializadeh et al., 2020, 2022; Nozarpour et al., 2023) and phylogenetic diversity of invertebrates such as brachyuran crabs (Raeisbahrami & Naderloo, 2023). Also, mangrove vertebrates have been the subject of biodiversity studies, though these works are mainly limited to the faunistic surveys with little attention to the preliminary analyses of species richness and abundance, not functional or phylogenetic diversity assessments (Behrouz, 2014; Braulik & Ranjbar, 2009; Ghasemi et al., 2012).

Mangrove forests are stable habitats for many marine and terrestrial species (Nagelkerken et al., 2008). Fish are one of the most important taxa among the vertebrate communities of the mangrove forests. They use mangrove ecosystems as nursery beds (Nagelkerken, 2009; Sheridan & Hays, 2003) and have a

major role in the sustainability of the food web in this region (Shahraki et al., 2014; Shahraki, 2015). Moreover, ecosystem service and fisheries have a strong linkage in mangrove ecosystems (Manson et al., 2005). In addition, fish community markedly contributes to the movement of external organic material sources from adjacent habitats to the mangrove forests (Igulu et al., 2013; Kruitwagen et al., 2010). A recent checklist reported 743 fish species from 131 families in the Persian Gulf (Eagderi et al., 2019). Biodiversity studies of the fish species in mangrove forests of the Persian Gulf were conducted in Jask, Khalasi, Gabrik (Kamrani et al., 2016; Hashemi, unpublished MSc thesis), as well as Gaz creek (Zahedi et al., 2019), Qeshm, Khamir (Hashemi, unpublished PhD thesis), Tiab, Kolahi, Koleghan (Hashemi, unpublished MSc thesis), and Gwatr and Bahookalat (Zarei, 2006). 193 species from 69 families are reported from these mangrove ecosystems in the Persian Gulf. There are two communities of mangroveassociated fish in the Persian Gulf including species inhabiting shallow and narrow creeks or mudflats and other species living in the outer estuaries of the mangrove forests. Noteworthy, there are three mudskipper species (Periophthalmus waltoni, Boleophthalmus dussumieri, and Scartelaos tenuis) in the first community that are burrower in mud, therefore, have a noticeable impact on physical, chemical, and ecological structure of the ecosystem (Clayton & Snowden, 2000; Colombini et al., 1996; Ravi, 2013). The second community is relatively more homogenous, with more species than the former group.

In this study, we examined the functional diversity of both creek/mud and estuary fish species of the mangrove forests of the Persian Gulf. We calculated the alpha diversity of each community and the beta diversity between them. Moreover, we investigated the functional structure of these two groups to understand the role of each species in the functional composition of each community. Also, we determined the most important functions and species responsible for the stability of the ecosystem and its functional diversity. Our goal is to explain the difference of estuaries and creek/mud fish communities in respect of their functional structure and composition.

Material and Methods

Data collection

Based on mangrove fish checklists of the Persian Gulf, abundance tables, and sampling sessions conducted in shallow creeks, we provided a list of 193 species from 12 mangrove forests scattered in the Iranian coastline of the Persian Gulf. These mangrove forests are located in Khamir, Qeshm, Koleghan, Tiab, Kolahi, Gaz, Jask, Khalasi, Gabrik, Gwatr, and Bahookalat (Fig. 1).

All the stations are located in the marine protected areas. Khamir and Qeshm (26°57′5.49″N/55°36′45.70″E and 26°56′10.15″N/55°43′45.65″E, respectively) are adjoining Mangrove forests located in the northwestern part of the Strait of Hormuz. They are parts of the Hara Protected Area, covering approximately 267 km² (with 32% mangrove coverage). Kolahi, Tiab, and Koleghan located in the Hormuz Strait include three main areas (27°02′38.05″ N/56°50′02.54″ E (with 6% mangrove coverage), 27°04′57.79″ N/56°48′21.42″ E (with 11% mangrove coverage), and 27° 9′20.73″ N/56°38′34.46″ E (with 20% mangrove coverage), respectively) with total covering of approximately 161

km². Gaz creek located in most western part of the Gulf of Oman (26°15′04.00″N/57° 07′38.03″E) covering roughly 46 km² (with 17% mangrove coverage). The dominant tree *Avicennia marina*, however, is mixed with *Rhizophora mucronata*which is mainly grown on the creek sides with around 39% coverage. Jask, Khalasi and Gabrik mangroves compromised scattered areas in the middle part of the Gulf of Oman's Iranian coastline (25°36′47.64″ N/58°01′01.95″ E (with 22% mangrove coverage), 38°25′35″ N/48°20′58″ E (with 11% mangrove coverage), and 25°42′00.12″ N/57°40′10.82″ E (with 11% mangrove coverage), respectively). Their covering area is near to 94 km² and are located in the Gabrik and Jask Hara protected area. Gwatr Bay and Bahookalat mangroves are located at the far northeastern end of the Gulf of Oman (25°10′36.18″ N/61°31′30.96″ E (with 21% mangrove coverage) and 25°10′36.18″ N/61°31′30.96″ E (with 17% mangrove coverage), respectively) with the covering area of approximately 25 km² in total. Adjoining mangrove forests were considered as single sites. Therefore, five stations were specified including Jask/Khalasi/Gabrik (station J), Qeshm/Khamir (station Q), Tiab/Kolahi/Koleghan (station T), Gaz creek (station A), and Gwatr Bay/Bahookalat (station G).

For the creek/mud community we included all the observed and sampled species for the analysis. Regarding the estuary community, as an efficient and common practice, we selected either the most abundant species that compromise 80% of the total abundance (Grime, 1998) or species that was reported in three or more than three stations. Eventually, 34 species from the estuary community and 23 species from the shallow creek/mud were selected with 6 common species (Table 1). For a better analysis of null models and random estimation, 38 additional species were included. These added species were recorded from at least 2 stations. However, we did not calculate functional diversity indices and the results of other analyses for these additional species.

Functional Traits

Functional traits were chosen based on their contribution and importance for ecosystem service (Pla et al., 2012b). These traits represent multitude aspects of the ecological influence of each species on its environment. We defined five sets of traits (size, feeding habit, migration habit, vertical position in column water, and reproduction pattern) with at least two modalities for each trait to cover the life cycle, position in the food web, and effect on the abiotic environment of the ecosystem. Ultimately, we examined the diversity and the structure of 15 modalities for the communities under consideration (Table 2).

We used a mixed coding approach to assign modalities to each species. For 13 trait modalities we used the fuzzy coding approach, as species can display two or more modalities of a functional trait simultaneously, with various intensities (Chevene et al., 1994). In this approach, we assigned a score, ranging from 0 to 3, to each trait and species (Supplementary table 1). If a species shows a trait during its whole life, we assigned the score of 3. And if there is no affinity, the score of 0 was assigned. Intermediate states were represented by 1 or 2 according to the affinity of the species to the considered modality. Only for the reproduction type we used binary coding (representing oviparity and viviparity). Traits and modality data were collected from FishBase online database (Froese and Pauly 2000), peer reviewed literatures and personal expert consultations.

Data Analysis

Dendrogram based and distance matrix based indices

Trait dendrograms were constructed based on our trait data matrix, for each community and total species (Fig. 2). As we had mixed trait variables in our data set, Gower distance was used to assemble a trait distance matrix (Gower, 1971). UPGMA method was used to construct trait dendrograms for the species. To edit and visualize the dendrogram, we used FigTree v1.4.4 (FigTree 2016). The constructed tree was used for the calculation of FD as one of the most basic and common tree-based indices of functional diversity (Petchey et al., 2007). This index represents the range of functional traits in our community; therefore, it can be interpreted as the functional richness of the community (Pla et al., 2012a). FD can be calculated using the below equation:

$$FD = \sum_{i=1}^{n} l_i$$

In this equation, l_i is the branch length of species i in the trait dendrogram of a community composed of n species.

Other indices of functional diversity that were calculated based on the Gower distance matrix were MPD (Mean Pairwise Distance) and MNTD (Mean Nearest Taxon Distance), which respectively can be used as the proxies for functional dispersion and functional evenness of a community (Pla et al., 2012a). MPD is calculated through the following equation:

$$\mathbf{MPD} = \frac{\sum_{i}^{n} \sum_{j}^{n} \delta}{n}$$

In this equation, δ is the trait distance between species *i* and *j* in a community composed of *n* species.

Similarly, the MNTD index can be calculated by the below equation:

$$\mathbf{MNTD} = \frac{\sum_{i}^{n} \min \delta}{n}$$

In this equation, min δ represents the minimum trait distance of species j and other species in a community composed of n species.

Beta diversity analysis

For the functional Beta diversity between the two aforementioned communities, we used D_{pw} (pairwise trait distance) and D_{nn} (Nearest neighbor trait distance) measures (Swenson, 2014d). Both indices are the modified versions of Beta diversity concepts introduced in Rao (1982). D_{pw} index measures the dissimilarity of functional diversity between each species of the two communities. Calculating D_{pw} is based on the below equation:

$$D_{pw} = \frac{\sum_{i}^{n(c1)} \sum_{j}^{n(c2)} \delta(ij)}{n(c1) * n(c2)}$$

In this equation $n(c_1)$ and $n(c_2)$ are the number species in the communities c_1 and c_2 . And $\delta(ij)$ stands for the trait distance between species i in the c_1 community and species j in c_2 community.

 D_{nn} index measures the difference of the most similar species between two communities. D_{nn} was calculated based on the following equation:

$$\mathsf{D}_{\mathsf{nn}} = \frac{\sum_{i}^{n(c1)} \min\!\delta(\mathrm{ic2}) + \sum_{j}^{n(c2)} \min\!\delta(\mathrm{jc1})}{n(c1) + n(c2)}$$

Here, $\min\delta$ (ic2) is the minimum trait distance between species i in the c_1 community and all the species of c_2 community. Likewise, $\min\delta$ (ic2) is the minimum trait distance between species j in the c_2 community and all the species of c_1 community.

Statistical analyses and random models

After excluding the reproduction type, due to its binary nature, four moments of the distribution of trait modalities (mean, standard deviation, skewness, and kurtosis) were calculated for each community (Table 3). Test of normality was conducted for the distribution of each trait. Based on the normality test results, Mann-Whitney Test were performed to compare the distribution of traits in both communities. P-value of the differences are reported.

Also, a principal component analysis was conducted on the trait database to determine the contribution of each trait in the functional diversity of its respective community and the most important functions of each species composition. Eigenvalues of functional traits with each component were calculated to understand the functional composition of communities. Scree plots were produced for each community. Statistical tests and PCA were conducted through IBM SPSS Statistics (Version 26).

Additionally, using randomized functional dendrograms and trait matrices, we compared the observed functional diversity indices (FD, MPD, and MNTD) to the expected values in creek/mud and estuary fish communities (Swenson, 2014c). Randomization of the functional trait dendrogram and matrix was performed with 10,000 iterations. And the expected mean and standard deviation values of FD, MPD, and MNTD were calculated for each species composition. Observed values of these indices in each community were calculated as well (Table 3a). The P-value of the difference between the observed and expected indices is reported.

Moreover, to determine the contribution of each species to the functional richness of both communities we eliminated the species in consideration from the trait dendrogram and calculated the updated FD metric of the new community. Then we compared the new FD with both the observed and expected functional richness of the original community.

All the analyses concerning functional diversity indices were carried out through R software v.4.2.2 (R Development Core Team (2011). The calculation of FD, MPD, and MNTD was conducted through ape v.5.7-1 (Paradis & Schliep, 2019) and picante v.1.8.2. (Kembel et al., 2010) packages. We used "comdist" and "comdistnt" functions in picante to calculate the D_{pw} and D_{nn} indices respectively. The elimination of species, for the sake of assessing the functional value, was accomplished by using "drop.tip" function in ape package.

Results

Species Composition

51 species from 31 families were studied in this work (Table 1). Gobiidae and Leiognathidae have the most species among all the families (4 species in each family). *Eleutheronema tetradactylum* (Family: Polynemidae) and *Acentrogobius dayi* (Gobiidae) are the species that were recorded from all five sampling sites. However, 11 species were observed in four sampling sites including *Chanos chanos* (Chanidae), *Cociella crocodilla* (Platycephalidae), *Nematalosa nasus* (Dorosomatidae), *Otolithes ruber* (Sciaenidae), *Periophthalmus waltoni* (Gobiidae), *Planiliza klunzingeri* (Mugullidae), *Platycephalus indicus* (Platycephalidae), *Pseudorhombus arsius* (Paralichthyidae), *Scomberoides commersonnianus* (Carangidae), *Sillago sihama* (Sillaginidae), and *Upeneus sulphureus* (Mullidae). Most species are reported from Qeshm and Khamir (43 species), which is mainly due to the more extensive sampling from these sites.

Traits Moments of Distribution and PCA

Comparing the distribution of functional traits between the two communities indicates significant difference (p-value < 0.05) in some trait modalities (Supplementary table 3). Migratory status is significantly higher in estuary species (p-value = 0.04). Also, carnivorous feeding habit is significantly lower in creek/mud community (p-value = 0.02). In addition, it can be seen that limnivores feeding habit and small size are more common in creek/mud community.

Principal component analysis (PCA) was conducted for both communities. Six components were recognized in creek/mud species, explaining the 80% of the variance in data. Also, five principal components were recognized for estuary communities that explain 80% of variance in the data. In the creek/mud species (Supplementary table 4), the most important traits based on their eigenvalues are limnivore feeding habit and mud dwelling for the first component, small body size and migration status for the second component, top dwelling (with positive association) and bottom dwelling (with negative contribution) for the third component, reproduction types for the fourth component, and herbivory and medium body size for the fifth component. In estuary species composition, traits have evener eigenvalues for each principal component (Supplementary table 5). Nevertheless, the most important traits of the components are the reproduction types, migratory status, and very large body size for the first component, small body size and carnivorous and limnivorous feeding habits for the second component,

large body size (negative), top dwelling habit for the third component, middle dwelling and for the fourth component, and, finally, middle and large size for the last component. Traits associated with feeding habit and habitat are more important in creek/mud species. On the other hand, position in water column, size, and migratory status are more important to explain the trait variance in estuary community.

Functional Diversity Metrics

To calculate and interpret FD, we considered polytomies in the resulted dendrogram tree similar to polytomies in phylogenetic trees (Swenson & Worthy, 2018). FD was calculated for both creek/mud (FD = 3.18) and estuary (FD = 3.19) communities. Considering the different species numbers of these two communities, these similar FD values need a plausible explanation. Compared with creek/mud species, observed MPD and MNTD was lower in the estuary community. In comparison with null models, observed FD, MPD, and MNTD were all higher than their respective expected values in the creek/mud community (Figs. 3a, 4a, 5a). However, the differences were not statistically significant in these cases. On the other hand, the observed FD, MPD, and MNTD values of the estuary community were significantly lower (p-value < 0.05) than their expected values (Figs. 3b, 4b, 5b).

Beta Functional Diversity

Despite assessing the functional diversity of each community and comparing the observed values with the expected ones, analyzing the differences between these two communities can provide valuable information. D_{pw} (representing the overall similarity of two communities) in this study equals to 0.28, and D_{nn} (representing the similarity between the most similar species in two communities) is 0.06. This result shows that the overall similarity between the two communities is not considerably high. Also, there are species with distinct functional traits in both communities (Table 3b).

Functional Value

As a measure of functional richness, we considered the effect of species elimination on FD. MPD and MNTD were not considered in this analysis due to their insensitivity to species numbers (Swenson, 2014c). The most important species for the functional richness of the creek/mud communities were *Chanos chanos, Hemiramphus archipelagicus, Tylosurus crocodilus, Acentrogobius dayi,* and *Arius arius,* in order of priority. It should be noted that the elimination of the three mudskipper species in this community, has a substantial influence on the functional richness of creek/mud species (decreasing from FD = 3.18 to FD = 2.69). For the estuary community, *Maculabatis gerrardi, Gerres oyena, Epinephelus coioides, Plectorhinchus pictus,* and *Scomberoides commersonnianus* were recognized as the most important species for functional diversity (Table 4).

Discussion

Functional structure

Considering the functional trait dendrogram of each community, we can determine four functional guilds in both communities (Fig. 1). However, *Maculabatis gerrardi* and *Chanos chanos* cannot be included in any definitive functional guild in estuary community. Functional values of these two species support this exclusion, as the elimination of *Maculabatis gerrardi* has the most negative influence on the FD value of this community, and *Chanos chanos* is among the most important species for functional richness. In comparison with the estuary community, creek/mud functional guilds are more distinct from each other, with the distinguished group of mudskippers (*Boleophthalmus dussumieri, Periophthalmus waltoni*, and *Scartelaos tenuis*) plus the small and burrower species, *Acentrogobius dayi*. Due to the specific habit of burrowing in mud bottoms, this distinction is completely expected. In fact, as was noted before, the elimination of these four species has a huge detrimental impact on the functional richness of this community. Limnivory (FL) and mud dwelling (HI) represent this burrow making behavior and it can be seen that these modalities have a considerable contribution in principal component analysis for the creek/mud community.

PCA shows that other than the burrow dwelling habit, migration type has a considerable contribution to the functional structure of the fish species inhabiting creeks and muds. The results support the importance of resource delivery from outside of mangrove forests to this ecosystem (Kruitwagen et al., 2010). Also, PCA results suggest that more general and variable traits such as body size modalities and vertical position are the most important functional traits in estuary fish species. In addition, the dispersion of traits and their contribution to each principal component in estuary community is more uniform in comparison to creek/mud species. This can be attributed to the more homogenous environment of the estuaries. Although species from the creek/mud community inhabit various habitats such as shallow creeks, deep creeks, near the tree roots, and mudflats, we cannot see this heterogeneity in the habitat of mangrove-associated species sampled from estuaries (Ellison, 2019; Hongwiset et al., 2021). The lower FD index of functional richness for this species supports the explanation.

Functional Diversity Measures

Despite the larger species number of the estuary community (34 species in contrast with 23 creek/mud species) comparison of the FD index, as a measure of functional richness, between the two communities shows a slight difference. Two different hypotheses can explain this similarity, namely, 1) the high functional richness of creek/mud species, or 2) the low functional richness of the estuary community. Comparing the observed FD values of each community with its expected value indicates the second explanation. The observed FD for creek/mud species does not have a significant difference from the expected value. However, this is not the case for the estuary community, which its observed FD is significantly lower than the expected value.

In addition, the comparison of the observed values of other functional diversity indices (MPD and MNTD) with their respective expected values implies the low functional diversity of the estuary community. Recent studies show that the accumulation of functional diversity is non-identical with species diversity and mainly depends on the age of the area (Jarzyna & Stagge, 2023; Oliveira et al., 2016). Knowing the young status of the Persian Gulf and its ecosystems, therefore, the lack of proper time for the formation

of separate niches, we can account this for the low functional diversity of fish in mangrove associated estuaries. As mentioned earlier, creek and mudflat environments in mangrove forests have more diverse and separate habitats, therefore, there will be more completely separate niches in these regions. Hence, we expect the functional diversity of their fish inhabitants reach its optimum sooner.

Considering MPD and MNTD indices, as measures of functional dispersion and evenness, the results suggest that the dispersion of functional traits in the estuary community is significantly low (observed MPD is lower than the expected value). We can attribute this result to the harsh environment of the mangrove associated regions in the Persian Gulf (Bayani, 2016). A recent study suggests the larger contribution of environmental filtering than the competition for the assembling process of mangrove crabs in this region (Raeisbahrami & Naderloo, 2023), therefore, we can expect the species in the Persian Gulf occupy restricted preliminary niches that results in a cluster of trait values (Peres-Neto, 2004). In homogenous environments, such as mangrove estuaries habitats, this process can produce communities with a limited functional richness and dispersion (Biswas & Mallik, 2011). The lack of significant difference in the aforementioned functional diversity indices in the creek/mud community shows a rather neutral assembly in these regions. Also, we should bear in mind the more heterogeneous and separated niches in this area which can produce a community with varied and distinct functional traits.

The Beta diversity D_{pw} index shows a relatively high difference between the two communities (D_{pw} <0.3). Also, D_{nn} indicates the existence of species with a rather distinct functional role in both communities (this can be shown by the D_{nn} < 0.3). This result is caused due to the species with completely distinct functions in creek/mud species. Mudskippers are the most obvious examples, for they have a complete set of functional traits that cannot be found in estuary species.

Functional Value

In this study, the contribution of each species to the functional richness of the communities was calculated. The five most important species for the functional diversity of the creek/mud community are representatives from the four distinct functional guilds. Surprisingly, from three species of mudskippers, none of them were among the most important species. This we can relate to the substitution of each species with the functional role of another mudskipper. For instance, the elimination of *Periophthalmus waltoni* can be compensated by the existence of *Scarlateus tenuis* or *Boleophthalmus dussumieri*. However, the elimination of *Acentrogobius dayi* causes a significant decrease in the functional richness of the creek/mud community. This species is among the burrow dwelling species of tree covered zone, yet is not a mudskipper, which are mainly in non-vegetated nearby mud flats. Therefore, its deletion cannot be completely compensated by the mudskippers. *Hemiramphus archipelagicus* and *Tylosurus crocodilus* are both carnivores, with large or very large body sizes. Hence, they are key species in the food web of these region. *Arius arius* and *Chanos chanos* are both migratory species, therefore, have a substantial influence on the transmission of resources for mangroves and adjacent ecosystems.

In the estuary community, the elimination of *Maculabatis gerrardi* has the most negative impact on the functional richness of the community. This is due to its peculiar set of functional traits, because the

species is a large stingray that swims over sandy and mud bottoms. Again, *Chanos chanos* is among the most functionally important species of the community. It should be noted that *Chanos chanos* is the only living representative species of the family Chanidae, so it has a special phylogenetic status in this community as well as its functional situation. This concurrency can be due to the much important role of environmental filtering in the assembling process of the community, and a sign of a strong phylogenetic signal in fish communities (Swenson, 2014a), a result which is reported from the studies on the brachyuran crabs of this region (Raeisbahrami & Naderloo, 2023). Future comparative phylogenetic studies can reveal more about the ecological and evolutionary structure of the mangrove fish communities in the Persian Gulf.

Conclusion

There are two different fish communities in the Persian Gulf mangrove forest in estuaries and creek/mud habitats. Functional diversity analysis of these communities reveals two distinct functional compositions in estuaries and creek/mud communities. Functional diversity of estuaries species is relatively low, due to its homogenous environment and its preliminary stage of formation. However, the functional diversity of creek/mud community is in the range of the expected values. Functional structure of the both communities reveal four functional guilds that are in creek/mud species are based on more specified traits (feeding habit and habitat), despite the more general based guilds in estuaries species. Therefore, we can infer that fish communities in shallow creeks- muddy substrate have reached their optimum functional diversity. Also, important species were specified based on their contribution on the functional diversity of each community. Considering these results, conservation policies can be made to protect the mangrove ecosystem of the Persian Gulf which have a harsh environment and are the subject of many biodiversity threats in this region.

Declarations

Acknowledgments

We appreciate Seyyed Hassan Hashemi (Department of environment, University of Hormozgan) for providing fish species data from his unpublished theses in Qeshm and Jask. Also, we thank Parima Hajializadeh (University of Tehran, Iran), and Seddigh Azizi (University of Hormozgan, Iran) for helping us to have access to the reports and references in the University of Hormozgan library. We thank Pezhman Maghsoodi (University of Tehran) for the maps and data on the mangrove forests of the Persian Gulf. We are grateful to Kiarash Farahmandrad who substantially assisted us to provide figures in this paper. We also thank Samaneh Pazoki and Neda Fahimi for helping us to conduct statistical analyses. Financial support was partly provided by the Research Council, University of Tehran.

Funding: The authors declare that no funds, grants, or other support were received during the preparation of this manuscript.

Conflict of Interest: The authors have no relevant financial or non-financial interests to disclose.

Data availability: The datasets generated and analyzed during the current study are available from the corresponding author on reasonable request.

Sampling and field studies: All necessary permits for sampling have been obtained by the authors from the competent authorities and are mentioned in the acknowledgements.

Consent to Participate: The authors agree to participate in this research project.

Consent to Publish: The authors agree to publish all data in this manuscript.

Ethical approval: No animal testing was performed during this study.

Authors Contribution: All authors contributed to the study conception and design. RN supervised the project. The first draft of the manuscript was written by AR and all authors commented on previous versions of the manuscript. AR and FS fabricated the species samples and trait data. AR and FS analyzed the data and performed the calculations. All authors read and approved the final manuscript.

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Tables

Table 1. Species composition of the estuaries and creek/mud communities. Asterisks (*) represents the existence of the species in the related community. Station codes for each species represent Jask/Khalasi/Gabrik (J), Qeshm/Khamir (Q), Tiab/Kolahi/Koleghan (T), Gaz (A), and Gwatr Bay/Bahookalat (G).

Family	Species	Estuary	Creek/Mud	Stations
Ariidae	Arius arius		*	G
Belonidae	Strongylura strongylura	*		JQG
	Tylosurus crocodilus		*	Q
Carangidae	Carangoides malabaricus		*	JQ
	Scomberoides commersonnianus	*		JQAG
Chanidae	Chanos chanos	*	*	JQAG
Dasyatidae	Maculabatis gerrardi	*		JQA
Dorosomatidae	Anodontostoma chacunda		*	А
	Nematalosa nasus		*	JQAG
	Sardinella albella	*		Q
Drepaneidae	Drepane longimana	*		JQA
Engraulidae	Thryssa vitrirostris	*		JAG
	Thryssa whiteheadi	*		Q
Gerreidae	Gerres filamentosus	*		JQA
	Gerres oyena	*		Q
Gobiidae	Acentrogobius dayi		*	JQTAG
	Boleophthalmus dussumieri		*	Q
	Periophthalmus waltoni		*	JQAG
	Scartelaos tenuis		*	J
Haemulidae	Plectorhinchus pictus	*		JQAG
	Pomadasys furcatus	*		А
	Pomadasys kaakan	*		JQA
Harpadontinae	Saurida tumbil		*	JQA
Hemiramphidae	Hemiramphus archipelagicus		*	JQ
Leiognathidae	Deveximentum indicium	*		Q
	Equulites lineolatus		*	JQT
	Leiognathus brevirostris	*		JAG
	Nuchequula gerreoides	*		Q

Mugilidae Minimugil cascasia * * (JQA Q Q JQTA
	Q
Osteomugil perusii *	·
	JQTA
Planiliza klunzingeri *	
Mullidae Upeneus sulphureus *	JQAG
Paralichthyidae Pseudorhombus arsius *	JQAG
Platycephalidae Cociella crocodilla *	JQAG
Platycephalus indicus *	JQAG
Plotosidae Plotosus lineatus *	JQA
Polynemidae Eleutheronema tetradactylum * *	JQTAG
Pristigasteridae Ilisha megaloptera *	JQA
Ilisha melastoma *	JQA
Scatophagidae Scatophagus argus *	JQG
Sciaenidae Otolithes ruber * *	JQAG
Serranidae Epinephelus coioides *	JQA
Sillaginidae Sillago sihama *	JQAG
Soleidae Brachirus orientalis * (Q
Sparidae Acanthopagrus arabicus *	Q
Acanthopagrus latus *	JAG
Terapontidae Terapon jarbua *	JQA
Tetraodontidae Lagocephalus guentheri *	J
Triacanthidae Triacanthus biaculeatus *	JQG

Table 2. Functional traits and modalities used for the calculation of functional diversity metrics. A brief description for each trait and how codes are assigned to each modality is given.

Trait	Modality	Description	ID
Body Size	Small (< 30)	Reported total size of the species. When maximum size belongs to another modality, we assigned 1 for the maximum reported modality, and	BS
	Medium (30-50)	2 for the average reported modality.	BM
	Large (50- 100)		BL
	Very large (> 100)		BVL
Feeding habit	Limnivores	The diet pattern of the organism. If the species feeds on deposits and mud or sandy bottoms, we assigned a value for FL, based on the occurrence of	FL
Habit	Carnivores	the behavior.	FC
	Herbivores		FH
Migration	Migratory	The amount of time that species spends in mangrove associated habitats.	MM
	Resident		MR
Habitat	Top dweller	The vertical position of the species in the column of water. If the species makes burrows in the mud or sandy bottoms, we assigned a value to the	HT
	Middle	HI modality	HM
	dweller Bottom		НВ
	dweller		
	Mud		HI
Reproduction	dweller Oviparous	This trait was not codded by fuzzy approach. It has a binary codding.	RO
	Viviparous		RV

Table 3. a) Results of the FD, MPD, and MNTD indices for estuaries and creek/mud communities. Expected values for each index is given in mean \pm standard deviation format. P-values represents the significancy of the difference between the observed and expected values. Asterisks (*) represent a significant difference. b) Results of beta diversity analyses. Values of D_{pw} and D_{nn} indices are given.

a) Alpha diversity indices

Index	Community	Observed value	Expected value	P value
FD	Estuary	3.19	3.65 ± 0.188	0.01*
	Creek/Mud	3.18	2.90 ± 0.211	0.91
MPD	Estuary	0.23	0.26 ± 0.014	0.03*
-	Creek/Mud	0.30	0.26 ± 0.020	0.99
MNTD	Estuary	0.06	0.07 ± 0.009	0.06
	Creek/Mud	0.10	0.09 + 0.013	0.84

b) Beta diversity indices

Index	Value between creek/mud and estuary regions		
D _{pw}	0.281		
D _{nn}	0.067		

Table 4. The importance of each species for the functional richness of estuaries and creek/mud communities. Numbers represent the FD index value of the community after the elimination of the corresponding species.

	FD After Eli	imination
Species	Estuary	Creek/Mud
Acanthopagrus arabicus	3.172222	3.183333
Acanthopagrus latus	3.194444	3.183333
Acentrogobius dayi	3.194444	3.027778
Anodontostoma chacunda	3.194444	3.161111
Arius arius	3.194444	3.027778
Boleophthalmus dussumieri	3.194444	3.116667
Brachirus orientalis	3.194444	3.072222
Carangoides malabaricus	3.172222	3.183333
Chanos chanos	3.094444	3.005556
Cociella crocodilla	3.150000	3.183333
Deveximentum indicium	3.150000	3.183333
Drepane longimana	3.172222	3.183333
Eleutheronema tetradactylum	3.127778	3.116667
Epinephelus coioides	3.038889	3.183333
Equulites lineolatus	3.194444	3.138889
Gerres filamentosus	3.194444	3.183333
Gerres oyena	2.972222	3.183333
Hemiramphus archipelagicus	3.194444	3.005556
llisha megaloptera	3.194444	3.144444
llisha melastoma	3.194444	3.183333
Lagocephalus guentheri	3.194444	3.083333
Leiognathus brevirostris	3.172222	3.161111
Lutjanus johnii	3.194444	3.183333
Lutjanus russellii	3.150000	3.183333
Maculabatis gerrardi	2.950000	3.183333
Minimugil cascasia	3.194444	3.122222
Nematalosa nasus	3.194444	3.116667

Nuchequula gerreoides	3.194444	3.161111
Osteomugil perusii	3.172222	3.183333
Otolithes ruber	3.172222	3.116667
Periophthalmus waltoni	3.194444	3.183333
Planiliza klunzingeri	3.194444	3.144444
Platycephalus indicus	3.150000	3.183333
Plectorhinchus pictus	3.038889	3.183333
Plotosus lineatus	3.194444	3.183333
Pomadasys furcatus	3.194444	3.083333
Pomadasys kaakan	3.194444	3.183333
Pseudorhombus arsius	3.172222	3.183333
Sardinella albella	3.172222	3.183333
Saurida tumbil	3.150000	3.183333
Scartelaos tenuis	3.194444	3.183333
Scatophagus argus	3.194444	3.055556
Scomberoides commersonnianus	3.061111	3.183333
Sillago sihama	3.083333	3.183333
Strongylura strongylura	3.194444	3.183333
Terapon jarbua	3.133333	3.183333
Thryssa vitrirostris	3.116667	3.183333
Thryssa whiteheadi	3.194444	3.183333
Triacanthus biaculeatus	3.194444	3.138889
Tylosurus crocodilus	3.194444	3.016667
Upeneus sulphureus	3.194444	3.183333

Figures

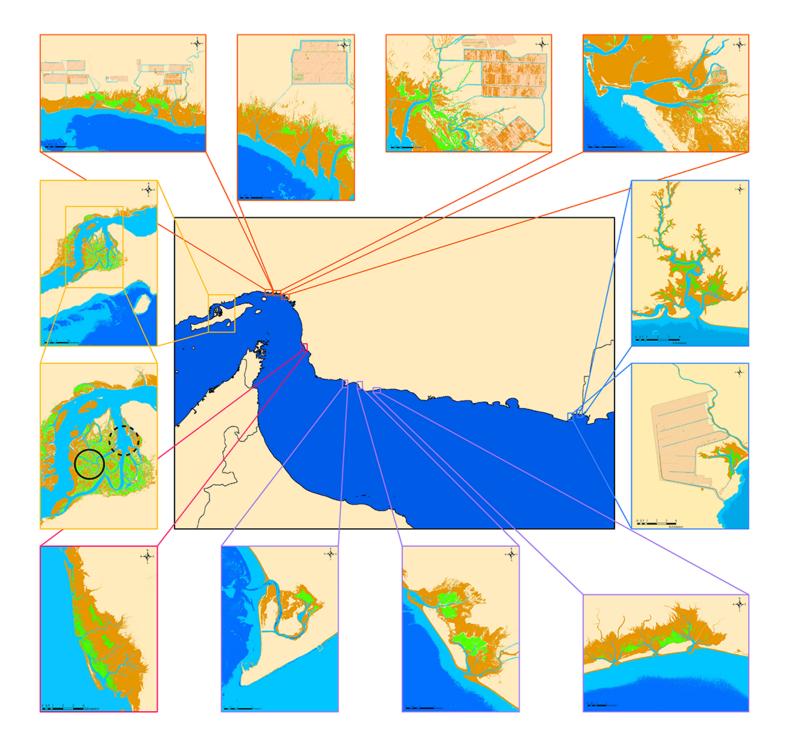


Figure 1

Mangrove forests in the Persian Gulf. Adjoining stations which were considered as a single site are represented by the same color. Example of sampling positions for estuaries community (represented by the dotted line) and creek/mud community (solid line) is shown.

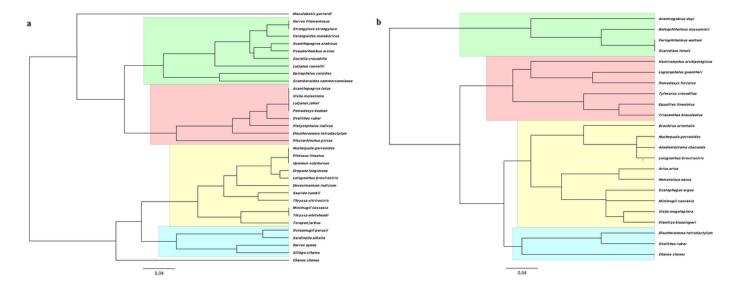


Figure 2

Dendrograms of a) estuaries, and b) creek/mud communities' functional traits. Four functional guilds are specified by different colors in both trees.

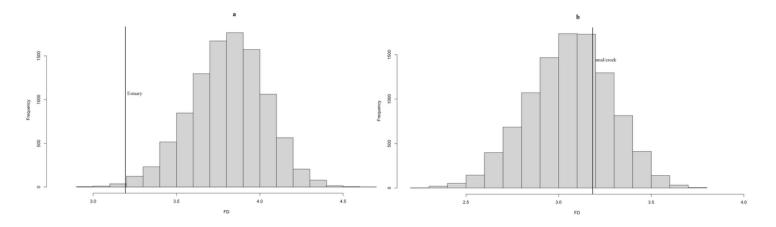


Figure 3

Histograms of random FD values for each community. a) estuaries species and b) creek/mud community. Observed FD values are represented by a black line.

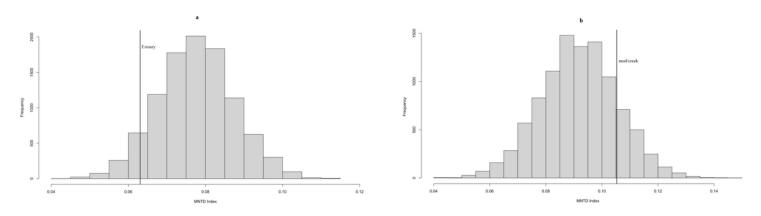


Figure 4

Histograms of random MPD values for each community. a) estuaries species and b) creek/mud community. Observed MPD values are represented by a black line.

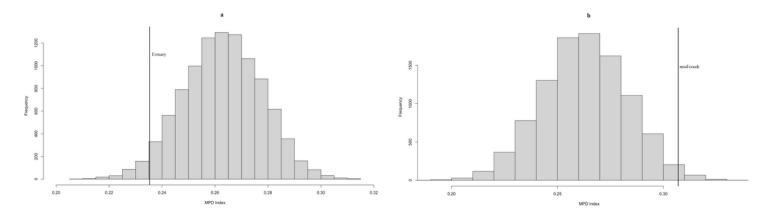


Figure 5

Histograms of random MNTD values for each community. a) estuaries species and b) creek/mud community. Observed MNTD values are represented by a black line.

Supplementary Files

This is a list of supplementary files associated with this preprint. Click to download.

- supp.1.traits.docx
- supp.2.moments.docx
- supp.3.MWUtest.docx
- supp.4.PCA.creek.docx
- supp.5.PCA.estuary.docx