Taxonomic Diversity of Fish Assemblages in the Pearl River Estuary, Southern China

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ABSTRACT

The Pearl River Estuary (PRE), an important place provides natural spawning ground and migration channel to multiple fish species located in the northern South China Sea. Keeping in mind limited data available on the taxonomic diversity of fishes from this region, we compiled time-series data on fish species from the PRE collected since the 1980s, and analyze diversity at different taxonomic levels using an inclusion index at the taxonomic level, and indexes of taxonomic diversity. Species inventory includes 18 orders, 79 families and 167 genera. Average numbers of (families, genera, species), (genera, species), and (species) per order, family, and genus, (4.39, 9.28, 14.94), (2.11, 3.41), and (1.61) were recorded. An average taxonomic distinctness of 75.0, and variation in taxonomic distinctness 99.8 were calculated. Whereas, an average taxonomic distinctness reveals genetic relationships between PRE fish species to be closer than in the East China Sea continental shelf (65.7) and Daya Bay (62.2), and more distant for the Dongsha Islands (55.2). Based on the overall results of the present study it is concluded that species abundance and taxonomic diversities in the PRE reflects healthy ecosystem of PRE.

INTRODUCTION

Estuarine ecosystems are important ecological transitional zones characterized by high productivity and strong environmental gradients (Simier *et al*., 2006). They are also vulnerable to human disturbance such as by overfishing, habitat degradation, water eutrophication, and pollution (Crooks and Turner, 1999; Cai *et al*., 2021; Kutir *et al*., 2022; Xu *et al*., 2022). Estuarine salinity increases from freshwater river habitat, to transitional brackish waters, to fully saline marine conditions (Zhao, 1989). Estuarine habitat is ecologically important to fish which complete their entire life history in these environments, or use them as nursery and/or feeding grounds, or even as migration channels (Malavasi *et al*., 2004; Steel *et al*., 2013).

Generally, closely related species have similar habitat requirements (Miranda *et al*., 2005). Because of the highly heterogeneous nature of estuarine habitat (Shen, 2010; Gomes-Goncalves and Araujo, 2022), considerable differences in demand for certain habitat types should exist and these should be reflected in genetic relationships between species. If this assumption holds true, then estuarine fish communities should comprise species that are more distantly related to each other than those of more homogeneous environments.

Traditional measures of fish community diversity include Pielou's evenness (Pielou, 1975), Shannon–Wiener diversity (Shannon and Wiener, 1949), and Margalef's species richness (Margalef, 1958) indexes. However, these indexes are limited by sampling technique and sample size, and do not reflect the diversity of an entire system. The taxonomic diversity index is a statistical method that does not measure how much it deviates from an expected value, and its response to environmental changes is

not monotonic. The taxonomic diversity index changes drastically with different habitat types (Xu *et al*., 2005).

The taxonomic diversity index measures genetic relationships between species in a community by considering the number of species in a community and relationships between them based on taxonomic hierarchy. Taxonomic diversity indexes include taxonomic diversity, taxonomic distinctness, average taxonomic distinctness, and variations in taxonomic distinctness. Such indexes have been previously applied to analyze fish communities (Warwick and Clarke, 1995; Clarke and Warwick, 1998, 2001).

Most fish species in the Pearl River Estuary (PRE) are small and either coastal or estuarine dwellers that are tolerant of high temperatures and reduced salinity (Li *et al*., 2002). Within the PRE, fish communities change seasonally throughout five water areas (Wang and Lin, 2008). Assessments of ecological diversity in the PRE have revealed characteristics of fish community structure (Li, 2008), but not genetic relationships between species.

To test our hypothesis that genetic relationships between fish species in estuarine waters are more distant than those in more homogeneous environments, we compare taxonomic characteristics of fish communities within the PRE with those from outside of it. Additionally, we report diversity characteristics from different level, and provide a scientific basis on which these fish communities can be protected.

MATERIALS AND METHODS

Study area

The Pearl River catchment area 415,000 km² (Zong *et al*., 2009) is the third largest river in China, with a total river basin length of 3215 km, and discharge ~326 billion m³ (Zhao, 1990). Its annual sediment load is ~3.74 million tons, accounting for 61% of the total runoff of the Pearl River. Lingding Bay, into which the Pearl River discharges, has two relatively deep troughs the east trough (Fanshi fairway) and West Trough (Lingding fairway), boarded by

the east, middle and west shoals, each shallower than 5 m (Wu *et al*., 2014). Our study area includes Lianhuashan–Humen channel, Lingding Bay waters, and the PRE within 40 m depth (Fig. 1) bound by coordinates 21°43–22°45'N, 113°7–114°38'E (Fig. 1).

Data sources

Historical fish survey data within PRE waters (Ma, 1995; Wang, 2006; Li, 2008; Wang and Lin, 2008) was collated, and reported fish species were systematically sorted (Meng, 1996; Nelson *et al*., 2016) (Table I). Only taxa identified to species were included in analysis. Following the Nelson classification system, freshwater species were excluded.
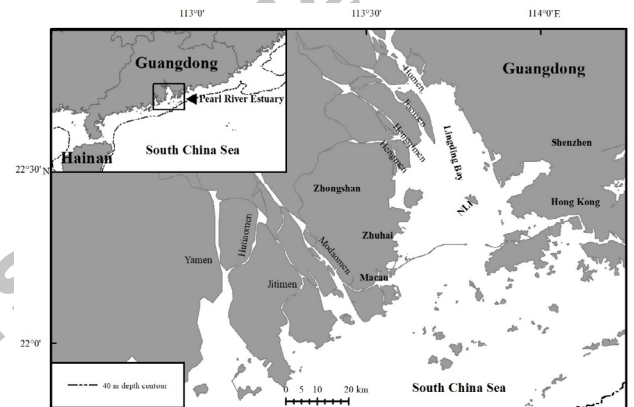

Fig. 1. Map of survey area. NLI, Neilingding Island.

The inclusion index at taxonomic level (TINCL_i)

To explain genetic relationships between fish species, we analyzed the degree of concentration of each level using $TINCL_i$ (Li *et al*., 2011). The higher the *TINCL_i* value, the more species level (families, genera, species) belonging to the higher order class, indicating that the distributions of species are more concentrated, and that relationships between them are closer.

Table I. Historical fisheries research data from Pearl River estuary.

Investigation year	Sample mode	Investigation months	Investigation area	Number of stations
1980–1981	Agassiz trawl	Season survey	Offshore area	27
1986–1987	Bottom trawl	Monthly survey	Humen channel to offshore area	18
1990–1991	Bottom trawl	March, October	Mainly offshore area, part of brackish water area	25
1997–1998	Lift net, pointed fishnet	Monthly survey	Near Neilingding Island	5
2003	Bottom trawl	March, April, May, August, September, October, November	Humen channel to Lingding Bay	6

$$TINCL_i = \frac{1}{N_i} \sum_{j=1}^{N_i} C_{kj} \ (k < i) \ ...(1)$$

N_i represents the number of i-th taxonomic level, and C_{kj} is the number of j-th k- taxonomic level. We compared $TINCL_i$ values for different sea areas.

Taxonomic diversity

Warwick and Clarke (1995) and Clarke and Warwick (1998) proposed two concepts of taxonomic diversity. These two concepts and TINCL$_i$ provide standards to use to identify relationships between species abundance and species relatedness in communities. Average taxonomic distinctness (Δ^+), based on differences in taxonomic levels of species, and their presence or absence, is used to assess species diversity within a community; this index eliminates the need to appraise diversity based on species richness. Δ^+ refers to the path length of the average taxonomic rank between any two randomly selected species in a community. It is simple weighting of dominant and common species within a community, and its average value is not affected by sample size or the nature of sampling (Warwick and Clarke, 1995; Clarke and Warwick, 1998; Xu *et al*., 2005; Li, 2013). The Λ^+ value is a theoretical average value of deviation from Δ^+, which reflects the uniformity in distribution of related fishes in a community; it can also be regarded as an index of the complexity of the classification tree (Mouillot *et al*., 2005). The value of Λ^+ is small only when there are very few species (Graham *et al*., 2007). These two indexes are calculated as follows.

Average taxonomic distinctness (Ludwig *et al*., 1988)

$$\Delta^+ = \left(\sum\sum_{i<j} \omega_{ij} \sum_{i<j} \omega_{ij} \right) / [S(S-1)/2]$$

Variation in taxonomic distinctness (Ludwig *et al*., 1988).

$$\Lambda^+ = \left(\sum\sum_{i<j} \omega_{ij} \sum_{i<j} (\omega_{ij} - \Delta^+)^2 \right) / [S(S-1)/2]$$

Where ω_{ij} is the path length of the i-th and j-th species in a taxonomic tree, and S is the number of species. Because all fish are chordates, our five taxonomic levels are class, order, family, genus, and species. We obtained Δ^+ and Λ^+ values using TACDTEST in the PRIMER5 software package (Ricotta and Avena, 2002; Li, 2013). Differences in Δ^+ and Λ^+ among sea areas are regarded to be insignificant ($P > 0.05$), significant ($0.05 \leq P < 0.01$), or extremely significant ($P \leq 0.01$) (Table II).

Relative abundance index

The number of species in a community is called species richness. Our objective is to analyze fish species abundance in the PRE at a supraspecific level. To achieve this, we use the relative abundance index to characterize relative proportions of fish among different families/orders from the family/order level. The relative abundance index (Li *et al*., 2011) was calculated by the following equation:

$$R = S_i \times 100 / S$$

Where S_i is the number of fish species of the i-th genus (family, order), and S is the number of corresponding fish genera (family, order) recorded in a sea area. Because the relative abundance index of each taxonomic level reflects basically the same influence trend, we only calculate relative abundance of family and order-level taxa the average number of species of the i-th family/order possessed by taxonomic order.

Table II. Branch weight on species for each taxonomic level.

Taxon level	ω_{ij} relationship amongst species	ω_{ij} branch weight
Species	Species belong to the same genus	16.667
Genus	Species belong to the same family and different genera	33.333
Family	Species belong to the same order and different families	50.000
Order	Species belong to the same class and different orders	66.667
Class	Species belong to the same phylum and different classes	83.333

Similarity index

In communities with similar species, a comprehensive index of the total number of species and the number of common species a community similarity index could be used to express degrees of similarity in species composition. We use the Sorenson community similarity index to calculate similarity in fish species and family taxonomy between the East China Sea continental shelf (ECSCS), Daya Bay, and Dongsha Islands. The similarity index (Zhang and Zhang, 1998) can be expressed as:

$$C = (2S_{xy}) / (S_x + S_y)$$

Where S_x is the number of fish orders (family, genus, species) recorded in sea area A, S_y is the number of fish orders (family, genus, species) recorded in sea area B, S_{xy} is the number of fish orders common to the two areas (families, genus, species), and C is the Czekanowski coefficient. When species in two areas are identical the Czekanowski coefficient equals 1, and when the species in the two areas differ completely, this coefficient equals 0.

RESULTS

Fish species composition

Fish recorded from the PRE in the 1980s comprise 18 orders, 79 families, 167 genera, and 269 species, including 3 orders, 5 families, and 5 genera of cartilaginous fishes, and 15 orders, 74 families, and 162 genera of bony fishes (Table III). Order level analysis reveals the Perciformes as dominant (37 families, 82 genera), followed by the Clupeiformes (3 families, 14 genera). Family level analysis reveals fish species richness in PPE waters to be relatively high, with the top five families ranked by decreasing richness being the Gobiidae, Sciaenidae, Clupeidae, Carangidae, and Engraulidae.

**Table III. Pearl River estuary fish order, family, and genus composition.**

Class/ Order	Family %	Genus %
Elasmobranchii		
Orectolobiformes	1.3	0.6
Carcharhiniformes	1.3	0.6
Myliobatiformes	3.8	1.8
Osteichthyes		
Perciformes	46.8	49.1
Anguilliformes	8.9	7.2
Scorpaeniformes	5.1	6.0
Pleuronectiformes	5.1	6.6
Tetraodontiformes	5.1	4.2
Clupeiformes	3.8	8.4
Mugiliformes	3.8	5.4
Beloniformes	2.5	1.2
Gasterosteiformes	2.5	3.0
Siluriformes	2.5	1.2
Myctophiformes	2.5	1.8
Elopiformes	1.3	0.6
Salmoniformes	1.3	1.2
Gadiformes	1.3	0.6
Atheriniformes	1.3	0.6

Inclusion index at taxonomic level

Average numbers of (families, genera, species), (genera, species), and (species) per order, family, and genus are (4.39, 9.28, 14.94), (2.11, 3.41), and (1.61), respectively. These values are compared with those from the Dongsha Islands (Shi *et al.*, 2009), ECSCS (Li, 2005), and Daya Bay (Li *et al.*, 2011) (Table IV).

Taxonomic diversity

For the PRE, the Δ^+ value is 62.3, and Λ^+ 99.8, whereas theoretical average value of Δ^+ (dotted line in Fig. 2A) changes little with an increase in fish species richness. Figure 2B reveals Λ^+ values to be small only when there are fewer than 10 fish species, but for Λ^+ to remain largely constant when the number of fish species exceeds 10.
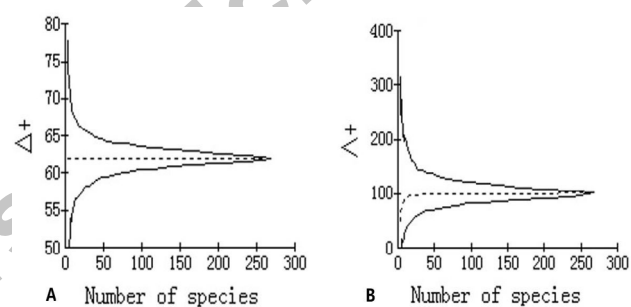
Fig. 2. The 95% probability funnels for Δ^+ (A) and Λ^+ (B) based on the total fish species list in Pearl River Estuary.

Relative abundance index

Perciformes dominate, followed by Clupeiformes, Pleuronectiformes, and Tetraodontiformes (Table V). Within the PRE, six fish families contain more than 10 species: Perciformes (Gobiidae, Sciaenidae, Carangidae), Clupeiformes (Engraulidae, Clupeidae), and Pleuronectiformes (Cynoglossidae). The relative abundance index for the Gobiidae was greatest, followed by Sciaenidae, Clupeidae, Engraulidae, Carangidae, and Cynoglossidae.

Table IV. Inclusion index at taxonomic level for Pearl River estuary fishes and other sea areas in China.

Area	Latitude	Number of species	S/G	S/F	S/O	G/F	G/O	F/O
East China Sea continental shelf	26°00′–33°00′ N	350	1.48	2.92	12.07	1.97	8.16	4.13
Daya Bay	22°30′–22°50′ N	320	1.55	3.40	14.55	2.19	9.36	4.27
Pearl River Estuary	21°43′–22°45′ N	269	1.61	3.41	14.94	2.11	9.28	4.39
Dongsha Island	20°33′–21°10′ N	514	7.45	24.48	3.09	10.14	3.29	2.41

S, species; G, genus; F, family; O, order.

Table V. Relative numbers of orders of fish in Pearl River estuary.

Order	Rr	Order	Rr
Perciformes	761.1	Beloniformes	27.8
Clupeiformes	166.7	Myliobatiformes	22.2
Pleuronectiformes	116.7	Siluriformes	11.1
Tetraodontiformes	94.4	Salmoniformes	11.1
Anguilliformes	77.8	Gadiformes	5.6
Mugiliformes	61.1	Atheriniformes	5.6
Scorpaeniformes	55.6	Orectolobiformes	5.6
Gasterosteiformes	33.3	Carcharhiniformes	5.6
Myctophiformes	27.8	Elopiformes	5.6

Similarity index

Similarity indexes of fish families and species in the PRE, Daya Bay, ECSCS, and Dongsha Island waters are presented in Table VI. At the family level, fishes in Daya Bay are most similar to those in the PRE, followed by fishes in the ECSCS, then Dongsha Islands. At the species level, the fish fauna of the PRE is most similar to that of Daya Bay, followed by the ECSCS, then Dongsha Islands.

Table VI. Pearl River estuary fish faunal similarities with other sea areas in China.

Region	Daya Bay (family/ species)	East China Sea continental shelf (family/species)	Dongsha Islands (family/species)
Pearl River Estuary	0.682/0.57	0.503/0.271	0.358/0.023

DISCUSSION

Ecosystem of the Pearl River Estuary (PRE) is triggered by both marine water and river runoff influences that ultimately shake salinity of the estuarine. Therefore, fish species that can adapt wider range of salinities (e.g., big head croaker *Collichthys lucidus*, Osbeck's grenadier anchovy *Coilia mystus*, Dussumier's thryssa *Thryssa dussumieri,* and Kammal thryssa *Thryssa kammalensis* dominate the populations (Wang, 2006). However, in particular years, changes in tides and currents lead to various marine fishes also occurring in the PRE, including shrimp scad *Alepes djedaba*, silver pomfret *Pampus argenteus*, orangefin ponyfish *Photopectoralis bindus*, and largehead hairtail *Trichiurus lepturus* (Chen, 1990). Compared with other estuaries in China (Yalu, Yellow, Yangtze, and Oujiang river estuaries) (Chen *et al.*, 2000; Xu, 2008; Huang, 2011), the PRE contains more brackish

water fish species (20 Gobiidae and 7 Mugilidae species). Numbers of species are consistent with a decrease in species richness with increased latitude, as similarly reported by Shi *et al.* (2009).

In addition to latitude, habitat range and runoff affect species diversity (Sambou *et al.* 2020). The PRE occurs in a low-latitude subtropical region, with an average annual water flow to the sea second only to the Yangtze River. Higher species diversity might be related to its larger catchment area. Collectively, low-latitude, high-runoff, and large water area render the PRE habitat complex and elevate its fish species richness. At the order level, more species are referable to the Perciformes than Clupeiformes, then Pleuronectiformes. At the family level, most species are referable to the Gobiidae (Perciformes), Clupeidae and Engraulidae (Clupeiformes), and Cynoglossidae (Pleuronectiformes). At the order level, the Perciformes and Cypriniformes dominate waters of the Yellow River and Yangtze River estuaries (Zheng *et al.*, 2014), while Perciformes, Clupeiformes and Pleuronectiformes taxa dominate those of the PRE.

Table VII. Summary of indices of taxonomic diversity for fish species in the East China Sea continental shelf, Daya Bay, Pearl River Estuary, and Dongsha Islands.

Area	Latitude	Δ^+	Λ^+
East China sea continental shelf	26°00′–33°00′ N	65.7	120
Daya Bay	22°30′–22°50′ N	62.2	110
Pearl River Estuary	21°43′–22°45′ N	62.3	100
Dongsha Islands	20°33′–21°10′ N	55.2	110

Table VIII. Significance of △+ for fish species in Pearl River Estuary, Daya Bay, East China Sea continental shelf, and Dongsha Islands (t-test).

Region	Daya Bay	East China Sea continental shelf	Dongsha Islands
Pearl River Estuary	4.172**	4.815**	9.823**

Note: **extremely significant difference ($P < 0.01$).

The PRE Δ^+ (62.3) value is greater than that for Daya Bay, and Dongsha Islands (Table VII), indicating that PRE fish species are more closely related to each other than elsewhere, and that the composition of fish species in this estuary is also more complex. The PRE taxonomic diversity index differs significantly from those of the other three areas (Table VIII, $P < 0.01$). Of 18 orders, 79 families, 167 genera and 269 species recorded from the PRE, the number of species is less than reported elsewhere. The *TINCL$_i$* of all leves in the PRE was higher than for the

ECSCS and lower than for the Dongsha Islands (Table IV). Compared with the TINCL$_i$ in Daya Bay, that in the PRE at the genus level was highest, reflecting the significant difference in numbers of species in this region compared with those elsewhere. The highest TINCL$_i$ values for different taxonomic orders occur in the PRE. Annual variation in water temperature and salinity throughout the PRE is considerable (Zhao, 1981).

Spatial and temporal environmental gradients change greatly, as does variation in species composition. However, in relatively homogeneous environments, such as tropical coral reefs, fish communities are both relatively diverse but have relatively close morphological relationships because of numerous microhabitats with limited change in temperature and salinity (Shi *et al.*, 2009).

Regional environmental differences also affect regional similarities. At the family level, the similarity between the PRE and Daya Bay is the highest (0.682), the ECSCS the second highest (0.503), and that with Dongsha Islands the lowest (0.358). At the species level, species similarity decreased between the PRE and Daya Bay, ECSCS, and Dongsha Islands. At the family level, fish faunas of PRE and Daya Bay were most similar, with families common to both including the Gobiidae, Sciaenidae, and Carangidae (Perciformes), the Engraulidae (Clupeiformes), and Tetraodontidae (Tetraodontiformes). Of these the Gobiidae is widely distributed and occurs mainly in near-shore intertidal and shallow seas with sediment and reefs, and brackish and freshwater areas of estuaries. Most Sciaenidae (e.g., miiuy croaker *Miichthys miiuy*, big head croaker *Collichthys lucidus*, Belanger's croaker *Johnius belangerii*) are coastal species, with main habitats in estuaries and bays. Engraulids (such as Osbeck's grenadier anchovy and Gray's grenadier anchovy *Coilia grayii)* can generally adapt to waters with large salinity changes, and estuaries and bays represent important feeding grounds.

Many families have similar habitats, and the similarity between PRE and ECSCS is the greatest. The similarity index between PRE and ECSCS waters is 0.503, with families common to both including (for example) the Gobiidae, Carangidae, Apogonidae, Sciaenidae, Leiognathidae, and Stromateidae (Perciformes), Engraulidae (Clupeiformes), Synodidae (Myctophiformes), and (for example) Bothidae, Soleidae, and Cynoglossidae (Pleuronectiformes), all of which mostly occur in coastal waters. The PRE and Dongsha Islands have the lowest similarity in family composition (the family similarity index is only 0.358); these families are mainly reef fish and a small number of fish that frequent coral clusters of marine species. Families common to two areas mainly include Perciformes (e.g., Serranidae, Carangidae,

Lutjanidae, Mullidae, Chaetodontidae, Gobiidae), for which main habitats are near coral or rocky reefs. There are only 9 species of fish, and the similarity index of species is only 0.023 between the PRE and Dongsha Islands. Dissimilarity in coral reef and continental shelf environments typically allows for gene exchange only where similar habitats occur. Although some coral reef ecosystems can be separated by thousands of kilometers, similarities in species composition can be higher between them than between reef and adjacent continental shelf waters (Tilman, 1996; Findley and Findley, 2002).

With increased fishing intensity and rampant fishing practices, most economic fish species in the PRE have been over-exploited. Land reclamation and other marine developments reducing spawning grounds and environmental degradation has led to ecological imbalances. Therefore, maintaining fish communities is unavoidable for ecosystem stability (Tilman, 1996; Li *et al*., 2021; Jarzyna *et al*., 2022). The taxonomic diversity index is more sensitive to environmental changes than traditional diversity indexes (Xu *et al*., 2005). Therefore, identifying changes in PRE fish communities using the taxonomic diversity index can provide a scientific basis for environmental protection by historical data and latest survey data.

CONCLUSION

Higher species diversity and higher taxonomic diversity are main characteristics of patterns in fish diversity in estuary region. By calculating the taxonomic diversity index, it is also possible to understand the degree of impact on biodiversity due to human or natural disturbances. Under the influence of global warming, overfishing and other factors, the fish in the Pearl River Estuary have been disturbed to varying degrees. Some commercial fish species have been overfished. The species have also been significantly reduced, but how do these factors affect the taxonomic diversity of fish in the estuary? The extent of the impact needs to be further studied.

IRB approval

This research as approved by South China Sea

Fisheries Research Institute Animal Welfare Committee (2021SD01).

Ethical statement

The care and use of experimental fishes were consistent with the People's Republic of China animal welfare laws, guidelines and policies. Fishes were collected by scientific surveys and the experimental conditions did not distress any fishes involved in our experiments.

Statement of conflict of interest

The authors have declared no conflict of interests.

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