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Distribution pattern of macrobenthic assemblages along a salinity gradient in the Hangzhou Bay and its adjacent waters

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Abstract

It is widely acknowledged that the distribution of macrobenthos is affected by salinity, but the degree of influence varies in different areas. To explore the distribution pattern of macrobenthic assemblages in the Hangzhou Bay, 12 stations were sampled to collect macrobenthos and the corresponding bottom water. Changes in the general characteristics of macrobenthos along the salinity gradient in the Hangzhou Bay and its adjacent waters were considered. Three dominant species were identified, including the polychaetes *Sternaspis chinensis*, the crustacea *Oratosquilla oratoria* and the echinoderm *Ophiuroglypha kinbergi* . And the macrobenthic assemblages showed a zonal distribution along with the salinity change. The correlation analyses showed that salinity, depth, temperature, suspended solids and dissolved oxygen had concurrent significant correlations with carnivorous group, Margalef species richness (d), Brillouin index (H) and Shannon-Wiener diversity index (H'). In light of the strong correlation between salinity and Changjiang River diluted water, which produces considerable disturbances by freshwater inflows, the deposition of suspended solids and the resuspension of seabed sediments, the combined environmental disturbances, instead of salinity alone, should be adopted to explain the zonation distribution pattern of macrobenthic assemblages.

Key words: macrobenthos, dominant species, functional groups, environmental disturbances

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1 Introduction

Estuaries are among the most productive aquatic systems and are also known as variable ecosystems, changing continually in relation to the interactions among physical, geological, chemical and biological factors (Elliott and Whitfield, 2011). The complex environments are vital to the life history and development of many aquatic species by providing nursery and feeding habitat. And freshwater inputs make estuaries have a salinity that is different from that of the adjacent open ocean and create a characteristic biota (Elliott and Whitfield, 2011). Macrobenthic communities are key components in the functioning of estuarine systems (Gaston et al., 1998). They participate in most of the physical and chemical processes in the sediment, especially in the water-sediment interface, through life activities such as feeding, burrowing, and breathing (Shou et al., 2009). Their relative immobility makes them vulnerable and at risk of habitat disturbance (Izegaegbe et al., 2020), therefore distribution of macrobenthos has been extensively studied (Armonies, 2021). And these studies are the necessary prerequisites for understanding the functions and processes of estuarine ecosystems (Reiss et al., 2011).

Salinity, accompanied by changes in other physical and chemical factors, is a major feature of estuaries (Hobbie, 2000). The importance of salinity in determining the distribution patterns of estuarine benthic fauna has long been recognized, and numerous studies have investigated the relationship between salinity and macrobenthos (Chainho et al., 2006; Gaston et al., 1998; Holland et al., 1987; Teske and Wooldridge, 2003; Ysebaert and Herman, 2002). In most cases, macrobenthic species richness, average density and trophic diversity increase with salinity, but the proportion of feeding guild subsurface-deposit feeders decreases with salinity (Gaston et al., 1998; Weslawski, 1999). Nonetheless, different observations also exist, some research found that macrobenthic density, species richness and abundance did not change significantly among sites with different salinities (Teske and Wooldridge, 2001). And tropical and temperate estuarine benthos respond differently to salinity (Dittmann et al., 2015). Differences also exist between estuarine systems in the Southern and Northern Hemisphere (Teske and Wooldridge, 2003). The control of salinity on benthic fauna may be related to the location and type of estuaries. More data and analysis are needed to demonstrate the effects of salinity on macrobenthos.

In this study, we analyzed the changes in the general characteristics (abundance, biomass, dominant species, and diversity)

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of macrobenthos along the salinity gradient in the Hangzhou Bay and its adjacent waters. This special investigated estuary is located in the northern East China Sea and ranges from permanently open estuaries with high freshwater inputs (strong horizontal salinity gradients) to freshwater-deprived sea areas. The hypothesis was suggested that the macrobenthic assemblages will indicate certain distribution patterns with increasing salinity. Other environment variables (depth, temperature, suspended solids and dissolved oxygen concentrations) were also recorded to determine whether salinity was the most important factor affecting the distribution of macrobenthos. The main goal of this paper is to present new data on macrobenthos obtained during the period of 2012–2019 to verify or disprove this hypothesis.

2 Materials and methods

2.1 *Study area and macrobenthos sampling*

The Hangzhou Bay is a funnel-shaped inlet of the East China Sea, bordered by Zhejiang Province and the municipality of Shanghai, China. With depths less than 15 m, the entire bay is relatively shallow. Tidal bores or tidal surges are quite common here due to the special seabed geomorphology and funnel-shaped features of the bay (Compilation Committee of Chinese Gulf, 1993). The Qiantang River flows into the Hangzhou Bay from the west, and the Yongjiang River flows into the bay from the south. Furthermore, the Hangzhou Bay also receives freshwater from the Changjiang River, which has an annual mean discharge of 30 400 m^3/s (Qiu and Zhu, 2013). Under the influence of freshwater inputs from these rivers, the Hangzhou Bay displays a distinct west-east salinity gradient. All these factors result in a complicated and volatile environment. Because of the high tide and huge tidal range in Hangzhou Bay, it is quite difficult to collect sediment and macrobenthos there (Shou et al., 2012). Therefore, only a small scale and few stations have been involved in limited previous studies (Liu et al., 2008a), and it is difficult to fully expatiate the community structure and species composition here (Hu et al., 2006), let alone the coupling relationship between environmental factors and macrobenthos.

This research was carried out annually in the Hangzhou Bay and its adjacent waters in the northern East China Sea. Sediment samples were collected from a total of 12 stations in the northern East China Sea every August from 2012 to 2019 (Fig. 1). The sampling depths ranged from 9.0 m (M3) to 49.0 m (H4) in the offshore region of the northern East China Sea. The sampling regime followed the design of a salinity gradient in the following three areas: the Hangzhou Bay (salinity: 10–20), Zhoushan Islands (salinity: 20–30) and the offshore region (salinity: >30). Another four stations were sampled in inner Hangzhou Bay, with salinities from 0 to 10. However, no calculable data were collected (no macrobenthos were found), and these four stations were discarded and are not shown in Fig. 1. At each station, two samples were collected using a 0.1 m^2 Van Veen grab. The samples were washed *in situ* through a mesh screen (0.5 mm) to collect all macrobenthos, and the filtered macrobenthos were preserved in 95% ethanol for further analysis in the laboratory. They were identified to the species level on the basis of morphological characteristics, and then quantified (for abundance, ind./m^2) and weighed (for biomass, gram wet weight for biomass, gwwt/m^2).

2.2 *Sample analysis and data processing*

Bottom water samples were also collected *in situ* for further analysis. The salinity, depth, temperature, suspended solids and dissolved oxygen concentrations of the ambient seawater were measured onsite using a Yellow Springs Instruments water quality meter (YSI, Ohio, USA).

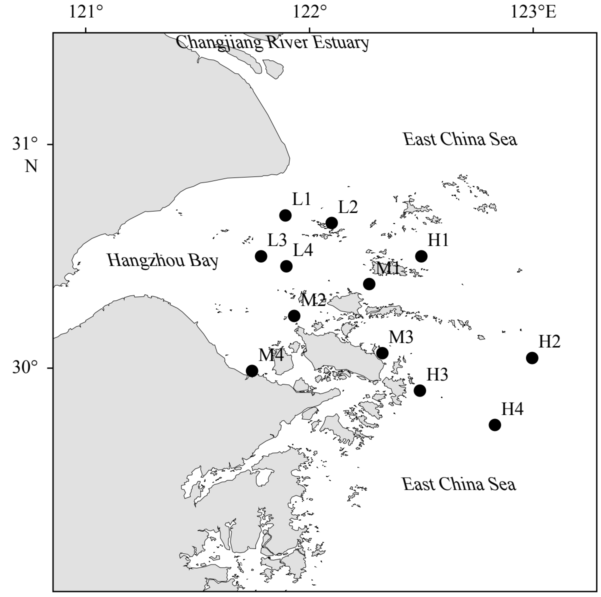

Fig. 1. Locations of the stations in the northern East China Sea investigated from 2012 to 2019. L1–L4 are in the low-salinity area (salinity: 10–20); M1–M4 are in the medium-salinity area (salinity: 20–30); H1–H4 are in the high-salinity area (salinity: >30).

A multivariate technique was applied to evaluate spatial and temporal changes in species abundance, using the Primer 6.0 ecological software package developed by the Plymouth Marine Laboratory. Univariate diversity indices, including total species (S), total individuals (N), Margalef species richness (d), Pielou's evenness (J'), Brillouin index (H) and Shannon-Wiener diversity index (H'), were calculated using the DIVERSE program of Primer 6.0. The formulae are as follows:

$$d = (S - 1)/\ln N, \qquad (1)$$

where S is the number of total species, N is the number of total individuals.

$$H' = -\sum_{i=1}^{s} P_i \ln P_i, \qquad (2)$$

where P_i is the ratio of the numbers of one species to the numbers of all species.

$$J' = H'/\ln s, \qquad (3)$$

$$H = N^{-1}\log_e[N!/(N_1!N_2!\ldots N_s!)], \qquad (4)$$

where N_1, N_2, ···, N_s are the numbers of each species.

Macrobenthic abundance data were fourth-root transformed to reduce the contribution of prevalent taxa and therefore increase the importance of less abundant species before all subsequent analyses. A similarity matrix was constructed using the Bray-Curtis similarity index after calculating the relative contributions of each species to the average similarities of these groupings. Ordination was computed via hierarchical cluster analysis (CLUSTER) using group-average sorting and tested by similarity profile routine (SIMPROF). And analysis of Similarities (ANOSIM) was used to compare between-group similarity. The index of relative importance (IRI) (Hacunda, 1981; Carlson et al., 1997; Wang et al., 2021) was used to determine the dominant species of macrobenthos, and calculated using the following formula:

$$\mathrm{IRI} = (N_i + W_i)F_i, \tag{5}$$

where N_i is the numerical percentage of species *i*, W_i is the weight percentage of the species *i*, and F_i is the frequency of occurrence percentage of the species *i*. A species with IRI > 750 would be considered to be the dominant species.

A functional group can be defined as a set of organisms that exploit food resources through a similar intake mechanism, independent of their phylogenetic relationship (Fauchald and Jumars, 1979; Manokaran et al., 2013). The assignment of functional groups for all macrobenthos were listed in Appendix. The distribution pattern of benthic communities can be analyzed from the perspective of functional groups, to enhance our understanding of the benthic ecosystem. The macrobenthos involved in this study can be classified into the following five functional groups (Zhu and Lu, 2003): the planktophagous group (Pl), phytophagous group (Ph), carnivorous group (C), omnivorous group (O) and detritivorous group (D).

One-way ANOVA and Pearson's bivariate correlations between macrobenthos (functional groups, dominant species and diversity indices) and environmental variables (salinity, depth, temperature, suspended solids and dissolved oxygen concentrations) were calculated using the PASW 18.0 package.

3 *Results*

3.1 *Species composition, abundance and biomass*

A total of 615 specimens were collected across the whole sampling period from 2012 to 2019, comprising 64 species, 58 genera, 49 families and 7 phyla. Polychaeta was the group had the most species, with 27 taxa (42.19%), followed by Crustacea with 13 taxa (20.31%), Mollusca with 12 taxa (18.75%), Echinodermata with 4 taxa, Chordata with 4 taxa, Cnidaria with 2 species, and Nemertinea with 2 species. The total average abundance of macrofauna was 32.03 ind./m^2 across the whole sampling period. Polychaeta was the most abundant taxon with 17.76 ind./m^2 (55.45%) on average, followed by Crustacea with 4.48 ind./m^2 (13.98%), Mollusca with 4.38 ind./m^2 (13.66%), Echinodermata with 2.71 ind./m^2 (8.46%), and the others with 2.71 ind./m^2 (8.46%). The total average biomass of macrobenthos was 4.13 g/m^2. Polychaeta was the most dominant taxon with 1.04 g/m^2 (25.18%) on average, followed by Crustacea with 0.93 g/m^2 (22.52%), Echinodermata with 0.87 g/m^2 (21.07%), Mollusca with 0.75 g/m^2 (18.16%), Chordata with 0.45 gwwt/m^2 (10.90%), and the others with 0.09 g/m^2 (2.18%). The four leading contributors to the total biomass were *Diopatra chiliensis* and *Sternaspis chinensis* of Annelida, *Ctenotrypauchen chinensis* of Chordata and *Oratosquilla oratoria* of Crustacea. These four species comprised 46.32% of the total biomass across the whole sampling period. One-way ANOVA showed that the abundance and biomass in the high-salinity area were significantly higher than those in the medium- and low-salinity areas ($P < 0.05$).

According to the IRI values, three dominant species were identified, including the polychaetes *S. chinensis* (IRI = 652.01), the Crustacea *Ophiura oratoria* (IRI = 166.61) and the echinoderm *Ophiuroglypha kinbergi* (IRI = 286.41).

The results of the cluster analyses showed the samples could not be divided into more than one group in each year (SIMPROF test, $P > 0.05$). However, more often than not, samples with large resemblance were located in the same salinity gradient (Fig. 2).

When all samples were pooled together across the whole sampling years, stations along salinity gradient differ from each other more significantly (Fig. 3). All the low salinity samples were divided into the same group, as were all the high-salinity samples (SIMPROF test, $P < 0.05$). Therefore, to a certain extent, the macrofaunal assemblages structure were dissimilar in three salinity levels, presenting a change along with the increase in salinity. The above results were also confirmed by the analysis of Similarities (ANOSIM) results. ANOSIM indicated all dissimilarities between macrofaunal assemblages structure of different salinity levels were larger than any among samples within either salinity level ($R = 0.197$, $P = 0.1\% < 0.001$).

3.2 *Species diversity of macrobenthic assemblages*

As illustrated by Fig. 4, the number of species in high-salinity area is always larger than in low- and medium-salinity area from 2012 to 2019, and more often than not, the number of species in medium-salinity is larger than in low-salinity area. The same pattern appeared in the number of individuals and diversity indices *d*, *H* and *H*′. The *J*′ of three salinity levels changed irregularly over time.

3.3 *Functional groups*

The species found at all sampling stations could be divided into four functional groups: Pl, C, O, and D group; the Ph group was not identified in this study. The order of abundance of each functional group across the whole sampling period was C group (47.32%) > D group (41.63%) > O group (6.18%) > Pl group (4.88%).

The abundance of four functional groups changed along the salinity gradient (Fig. 5). C and D groups appeared at all stations, and their abundance increased along the salinity gradient. O group appeared at 3 low-salinity stations, 1 medium-salinity station and 4 high-salinity stations. The average abundance of O group was the highest (32.50 ind./m^2) in high-salinity area and the lowest (1.25 ind./m^2) in medium-salinity area. Pl group's average abundance (32.50 ind./m^2) and frequency of occurrence (1.00) were the highest in high-salinity area.

From 2012 to 2019, the C group in the high-salinity area is always the most abundant (Fig. 6a). The abundance differences of other functional groups at different salinities were not as significant as those of C group (Figs 6b, c and d). It seems that C group is more closed related to salinity than other functional groups.

3.4 *Correlation analysis*

The results of the correlation analysis were shown in Table 1. Correlation analyses among macrobenthic functional groups and salinity showed that salinity had significant positive correlations with carnivores ($P < 0.01$), detritivores ($P < 0.05$), and planktophagous ($P < 0.01$) group. Contrary to salinity, temperature and dissolved oxygen concentration had significant negative correlations with carnivores ($P < 0.01$), detritivorous ($P < 0.05$) and planktophagous ($P < 0.01$) group. Depth and suspended solids concentration were positively and negatively correlated with carnivorous (both $P < 0.01$), respectively. No significant relationship between environment variables and omnivorous was determined using bivariate correlation analyses.

O. kinbergi is the only dominant species that was significantly associated with environmental variables. It had positive correlations with salinity ($P < 0.05$) and negative correlations with temperature ($P < 0.05$) and dissolved oxygen ($P < 0.01$).

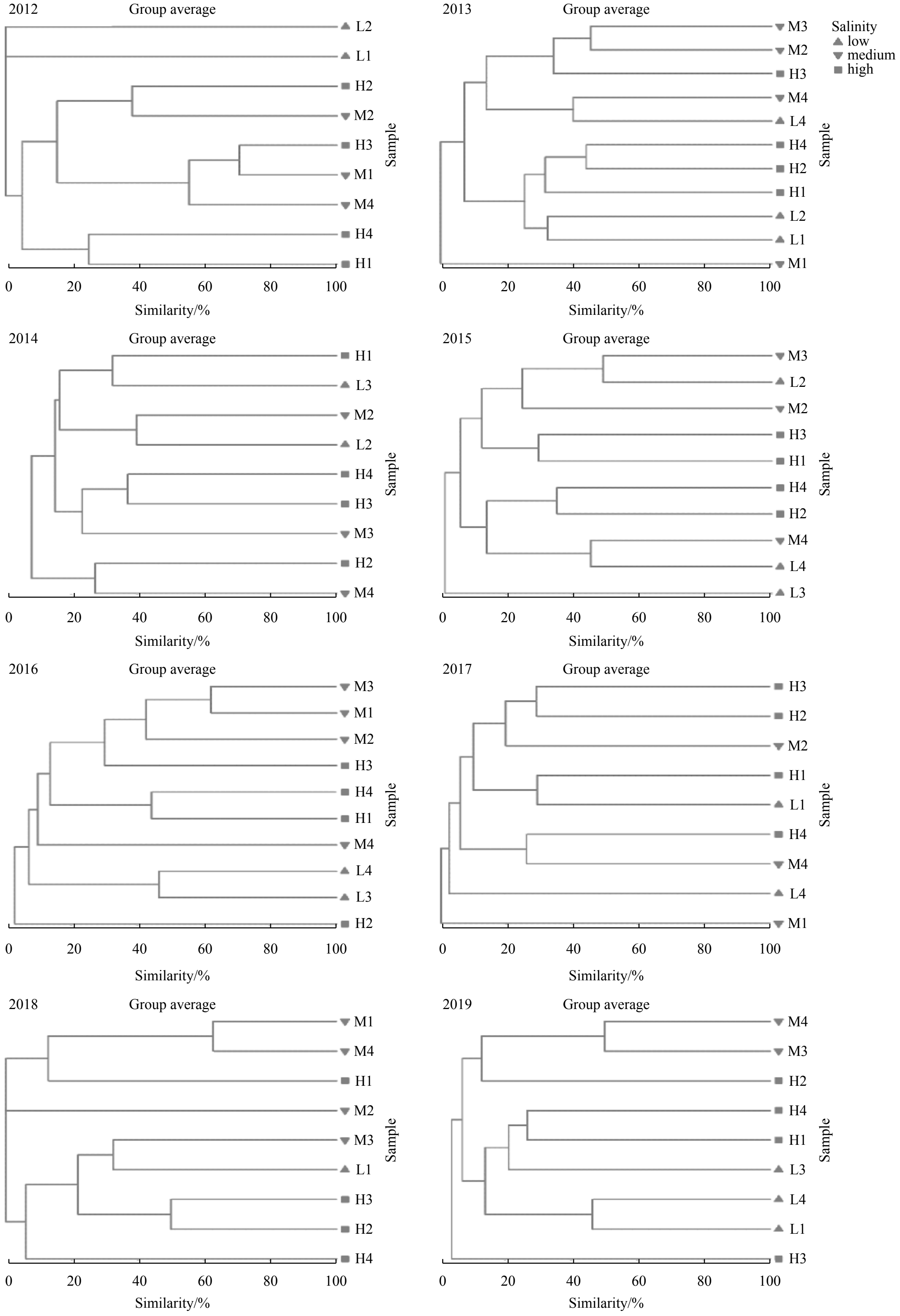

Fig. 2. Cluster analysis of macrofaunal assemblages during 2012–2019.

The correlation analyses also showed that both salinity and depth had concurrent significant positive correlations with *d*, *H*, *H′* while temperature, suspended solids and dissolved oxygen were concentrations negatively correlated with all of the above

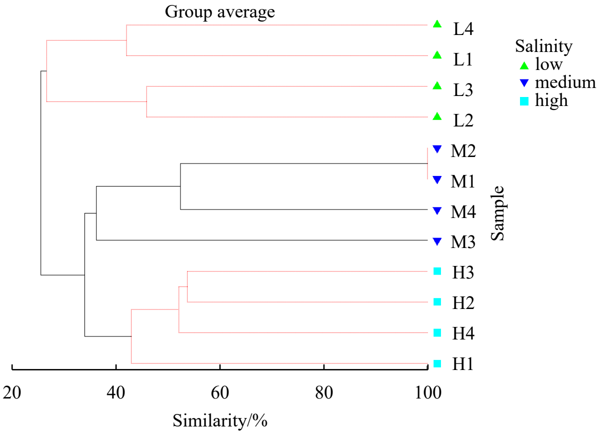

Fig. 3. Cluster analysis of macrofaunal assemblages across the whole sampling period.

diversity indices.

4 Discussion

4.1 *Distribution pattern of macrobenthic species in Hangzhou Bay and its adjacent waters*

The Hangzhou Bay located in the densely populated Changjiang River Delta, providing prominent ecosystem services to humans (O'Higgins et al., 2010). Hence the Hangzhou Bay has always been a hot spot of marine ecological research. Under the strong influence of human activities, the environment quality of the Hangzhou Bay was poor at the end of the 20th century (Jia et al., 2014). The survey during 1992 to 2012 (spring only) showed that the macrobenthic assemblages in the Hangzhou Bay were single, and the Shannon-Wiener diversity index was only 0–0.81 (Jia et al., 2014), which was significantly lower than that of this study. Seasonal variation of macrobenthic community may be responsible for the difference, because another study showed that the benthic diversity of the Hangzhou Bay was higher in summer than in spring (Shou et al., 2012). Additionally, the number of sampling stations also affects the survey results of biodiversity (Yan et al., 2019). The government's continuous working of marine environmental protection has also restored the diversity of benthos (Wang and Pan, 2017), which may be another reason for making the diversity of this study higher than that of previous studies. However, it is a difficult process to restore the ecological environment. Bao et al. (2021) showed that the species of benthos in the Hangzhou Bay was still decreasing from 2003 to 2015.

Salinity can produce unstable habitats and benthic disturbance and is associated with community stability (Van Diggelen and Montagna, 2016). All organisms inhabiting estuary areas can be divided into two groups: stenohaline marine organisms and euryhaline marine species. Stenohaline marine organisms are restricted to salinities close to seawater or freshwater, whereas some euryhaline marine species were able to penetrate further up estuaries. In this study, almost all macrobenthic species collected from the low salinity area (salinity from 10 to 20) could also be found at other stations with higher salinity (salinity > 20),

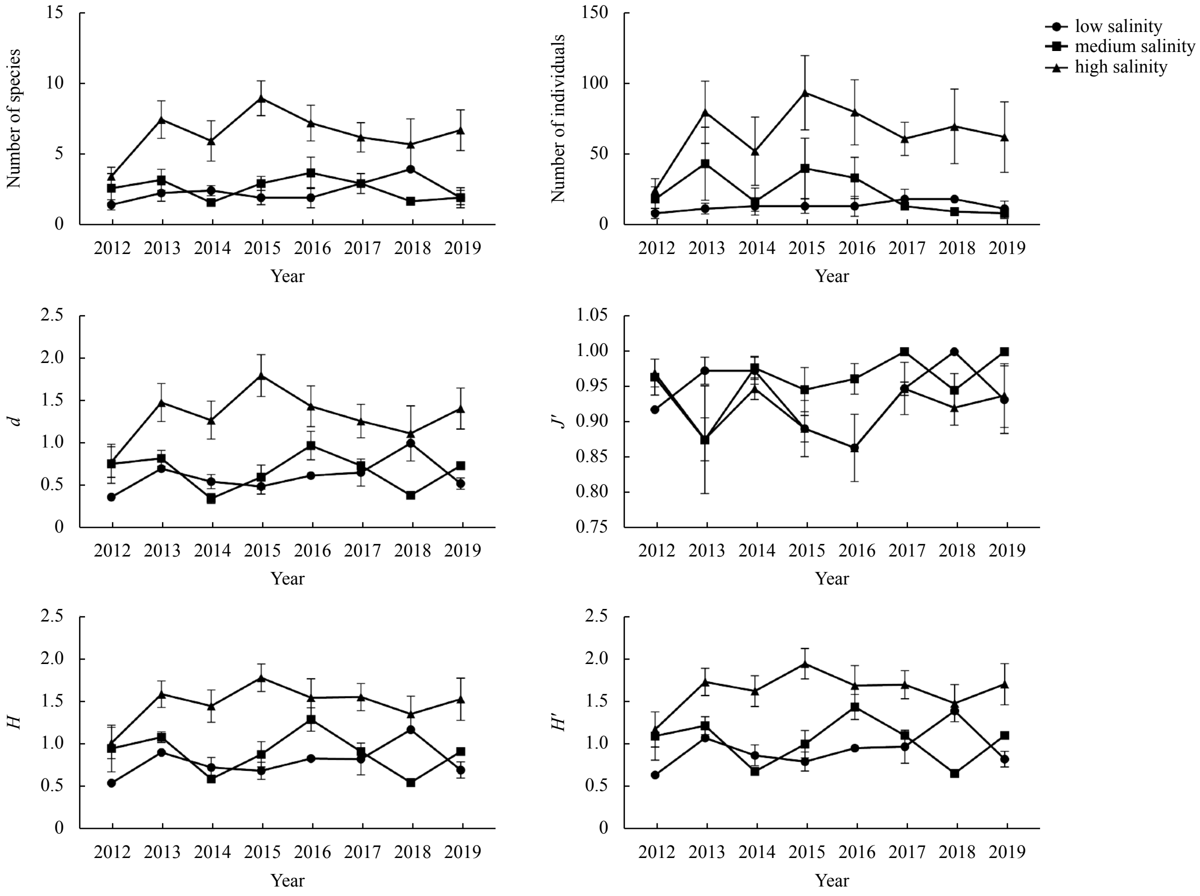

Fig. 4. The microbenthic diversity indices during 2012–2019. The following abbreviations were used in the figure: Margalef species richness (*d*), Pielou's evenness (*J*′), Brillouin index (*H*), and Shannon-Wiener diversity index (*H*′).

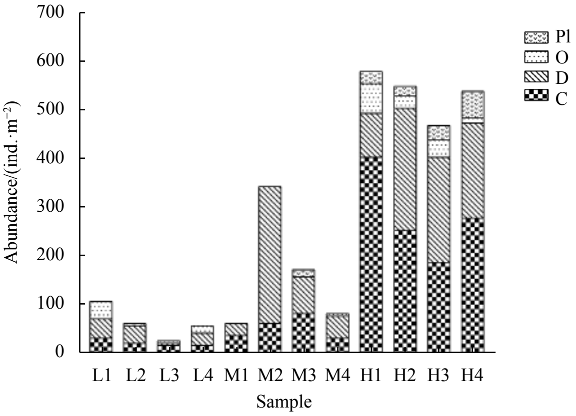

Fig. 5. The abundance of functional groups at different stations across the whole sampling period. Pl: planktophagous group; C: carnivorous group; O: omnivorous group; D: detritivorous group.

with the only exceptions being *Siliqua minima* and *Neoeriocheir leptognathus*; these species were the only two freshwater stenohaline species identified in this study. Excessive salinity fluctuations have a negative effect on their growth and survival (Chai et al., 2008; Liu and He, 2007). Moreover, the salinity of some adjacent waters of the Changjiang River is very low due to the enormous freshwater inflow from the Changjiang River, and benthos living in freshwater could be collected from coastal waters in the northern Hangzhou Bay, such as *Corbicula fluminea* (Li et al., 2006; Zheng et al., 2013). *Sternaspis chinensis* was the most predominant and common euryhaline species identified. This polychaeta is frequently misidentified as the nominally cosmopolitan species *S. scutata* in China since the 1950s (Wu et al., 2015). Tolerance to variation of salinity, temperature, depth, suspended solids and dissolved oxygen made *S. chinensis* the most abundant species in the study area. In the past studies on dominant species in Hangzhou Bay, the dominant species were judged by the dominance index *Y* (Shou et al., 2012; Yan et al., 2020), which did not consider the biomass of the species in the calculation process (Xu and Chen, 1989). In this study, the dominance index

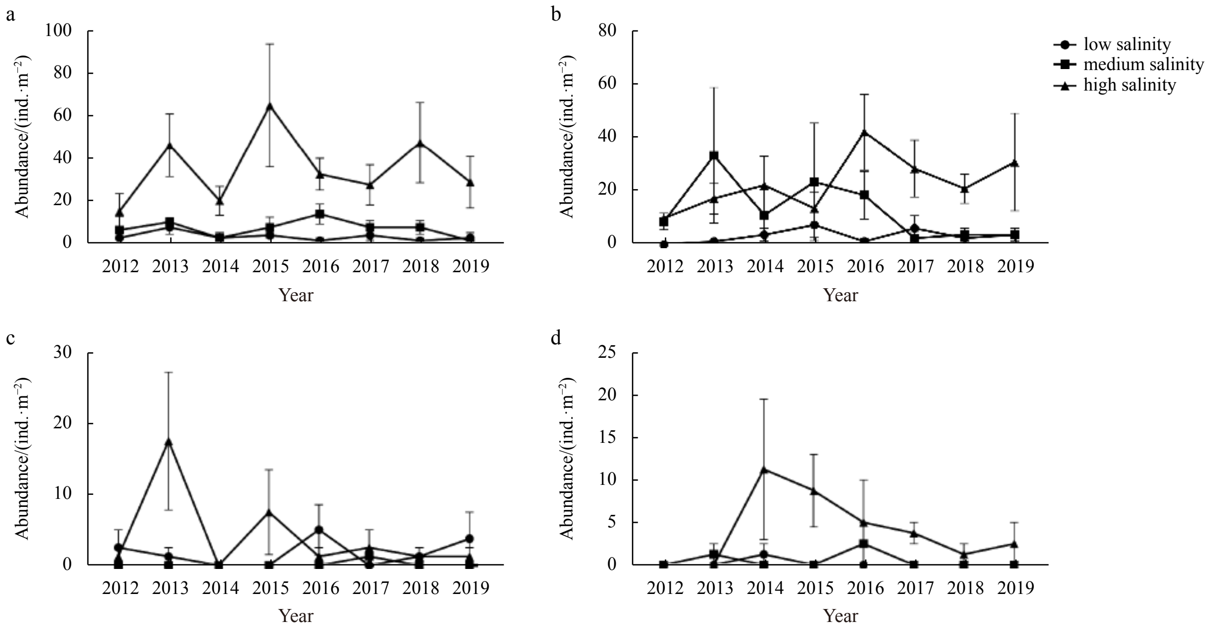

Fig. 6. The abundance of functional groups in three salinity levels from 2012 to 2019. a. Carnivorous group; b. detritivorous group; c. omnivorous group; d. planktophagous group.

Table 1. Pearson bivariate correlation analyses among macrobenthic functional groups, dominant species, diversity indices, depth, salinity, temperature, suspended solids and dissolved oxygen concentrations

	Depth	Salinity	Temperature	Suspended solids	Dissolved oxygen
Carnivorous	0.415**	0.433**	−0.437**	−0.322**	−0.282*
Detritivorous	0.189	0.295*	−0.254*	−0.085	−0.294*
Omnivorous	0.030	0.048	−0.083	−0.084	−0.077
Planktophagous	0.233	0.277*	−0.375**	−0.160	−0.350**
Sternaspis chinensis	−0.198	0.050	0.051	0.125	0.002
Oratosquilla oratoria	0.143	0.202	−0.201	−0.148	−0.111
Ophiuroglypha kinbergi	0.266*	0.227	−0.263*	−0.218	−0.336**
d	0.612**	0.646**	−0.696**	−0.383**	−0.640**
J'	−0.139	−0.186	0.156	0.060	0.076
H	0.633**	0.681**	−0.719**	−0.397**	−0.656**
H'	0.629**	0.675**	−0.713**	−0.392**	−0.661**

Note: **Correlation is significant at the 0.01 level (2-tailed); * correlation is significant at the 0.05 level (2-tailed), and the following abbreviations were used: Margalef species richness (d), Pielou's evenness (J'), Brillouin index (H), and Shannon-Wiener diversity index (H').

Y was replaced by IRI, and the high biomass of *O. oratoria* made it the dominant species.

4.2 *Zonation distribution pattern of macrobenthic assemblages*

When communities are not influenced by persistent stressors, such as in high-salinity areas without the influence of diluted Changjiang River water inflows or suspended solid inputs, multiple stages of succession may occur with more species available to occupy the resulting open niches, thereby increasing diversity (Van Diggelen and Montagna, 2016). The similar study in the Nueces Estuary (Ritter et al., 2005) showed that frequent salinity disturbances prevented the initial environmental conditions from being the primary mechanism in the regulation of succession. And the abundance and species composition of benthos in both tropical and temperate estuaries are significantly influenced by freshwater inputs (Ghasemi et al., 2016; Lowe et al., 2022). The situation in the Hangzhou Bay and its adjacent waters is similar. In addition to the impact of the diluted water from the Changjiang River, the huge tidal range in the Hangzhou Bay has also strengthened the changes in the hydrodynamics and sedimentary environment. The diversity levels of benthic communities increased with increasing salinity concentrations, and areas with higher freshwater inflows displayed lower levels of benthic diversity. The benthic communities in this area must be frequently disturbed.

The macrobenthic community structures in estuaries are mainly driven by salinity and two other environmental factors, depth and sediment silt-clay content (Rakocinski et al., 1997). Generally, macrobenthic abundance, biomass, and density increase with increasing salinity (Gaston et al., 1998; Udalov et al., 2004). Teske and Wooldridge (2003) noted “The reason for the structuring effect of salinity on macrobenthic communities is that the salinity gradient acts as a physiological barrier for stenohaline marine and freshwater species and places environmental stress on euryhaline marine species”. Due to this, the fauna inhabiting the upper part of the riverine estuaries is very impoverished compared to the adjacent marine and freshwater habitats. Wider fluctuations in salinity within the middle estuary heighten physiological stress and can also result in a reduction in the number of species. Some benthic macrofaunal studies have suggested different assemblages inhabit different portions of the estuarine gradient (Lu et al., 2008; Mariano and Barros, 2015). And there is every indication that the findings derived from benthic fauna are applicable both to fishes and other nekton and to plankton (Teske and Wooldridge, 2003). In the study area, the types of functional groups in each high-salinity station were more than those in medium-salinity and low-salinity stations, and more functional groups usually means richer biodiversity and more stable ecosystems (Peng and Li, 2013) in high-salinity area. These evidences all showed the zonation distribution pattern of macrobenthic assemblages along the salinity.

4.3 *The possible driving factors behind the salinity gradient*

Macrobenthos are sensitive and show profound reactions to disturbances in the benthic environment, which makes them good indicators for reflecting local environmental conditions (Qiu et al., 2018). However, many benthic taxa in estuaries are able to tolerate a wide range of salinities, especially South African estuarine species (De Villiers et al., 1999). Therefore, the distribution of many macroinvertebrates in estuaries is relatively independent of salinity. Salinity controlling the distribution of macrobenthos in estuaries may be only a symptom. Although a zonation distribution pattern was detected in this study along the salinity gradient, more complex factors were involved. Hydrodynamic factors play a vital role in in forming the distribution of macrobenthos (Donadi et al., 2015), especially in estuarine areas, because of their strong control over salinity. In the northeastern the Hangzhou Bay and southern Changjiang River Estuary, sediment suspension and sedimentation are strong due to the influence of fresh water and strong ocean currents in the Changjiang River Estuary, and the diversity and productivity of the macrobenthic community is the lowest (Hu et al., 2006).

Tides greatly influence several water parameters, especially salinity and turbidity (Cornelisen et al., 2011). Suspended solids from the Changjiang River experience rapid deposition and resuspension, controlled by tidal currents and Changjiang River outflows. There are two main sediment deposition areas in the Changjiang River, the east beach of Chongming Island in the north and the sublittoral zone of northern the Hangzhou Bay in the south (Dong, 1991). The deposited fine particles are resuspended and carried to the Hangzhou Bay by rising tide and tidal surge. The suspended sand is deposited while the deposited sand resuspends continuously, and turbidity is correlated with broad-scale resuspension and redeposition (Wlodarska-Kowalczuk et al., 2004). These highly unstable sedimentary conditions are tough for most macrobenthic organisms, and only limited brackish species independent of harsh substrate can survive here. In addition to the unstable substrate, dissolved and suspended solids create a turbid appearance and restrict light penetration (Davies-Colley and Smith, 2001). This leads to oxygen deficiency and dangerous effects on aquatic life. Turbidity can affect macrobenthos by light penetration, photoinhibition, pollutant and suspended matter migration (Lawler et al., 2006). Under these conditions, faunas in turbid environments would be less diverse (Farrow et al., 1983; Le Bris and Glémarec, 1996), especially for bivalves (Kaczmarek et al., 2005). Macrobenthic assemblages here showed a quite low diversity, extremely fragile community structure (Liu and Zheng, 2010) and low secondary productivity (Liu et al., 2008b). The offshore area at approximately 122°30′–123°30′E, eastward from Hangzhou Bay, is the intersection area of the diluted Changjiang River water and the offshore sea water. Generally, this area showed a trend of gradual macrobenthos increase from the estuary of the Changjiang River to the eastern sea area (Liu et al., 2008b). Species diversity was the highest around 124°E (Li et al., 2007). This area has been basically far away from the sediment deposition area of the Changjiang River, with a stable seabed substrate and a higher salinity than that of the estuary area, as well as a large amount of phosphorus salt brought by the invasion of the Taiwan Warm Current (Fan and Song, 2014). Macrobenthic community composition here was more complex than elsewhere in the study region, with higher biomass, habitat density and biodiversity indices (Liu et al., 2008a). The inflow of diluted water from Changjiang River reduce the salinity and bring a lot of suspended matter, caused strong correlations among salinity, turbidity and depth and other environmental variables in Hangzhou Bay. The zonation distribution pattern of macrobenthic assemblages could not be explained by any single environmental factor.

In addition, the rate of salinity changes can also affect benthos significantly (Teske and Wooldridge, 2003; Chen et al., 2018). Many benthic species can adapt to large variation in salinity only if it’s slow-changing (Bassindale, 1943). In areas where salinity changes quickly, salinity data may not be “accurate” (salinity change rate is difficult to reflect) enough. Obtaining the rate of change in salinity requires high frequency monitoring, which is very difficult to implement. However, combined with the change rate of environmental variables such as salinity, the undergoing driving factors of macrobenthic distribution can be further explained.

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Appendix:

Table A1. Macrobenthos collected in the Hangzhou Bay and its adjacent waters across the whole sampling period from 2012 to 2019

Species	Phylum	Functional group
Chloeia sp.	Annelida	C
Glycera chirori Izuka, 1912	Annelida	C
Glycinde bonhourei Gravier, 1904	Annelida	C
Goniada japonica Izuka, 1912	Annelida	C
Kuwaita heteropoda (Marenzeller, 1879)	Annelida	C
Lumbrineris cruzensis Hartman, 1944	Annelida	C
Aglaophamus dibranchis (Grube, 1877)	Annelida	C
Aglaophamus sinensis Fauvel, 1932	Annelida	C
Nephtys glabra Hartman, 1950	Annelida	C
Alpheus japonicus Miers, 1879	Arthropoda	C
Eucrate crenata (De Haan, 1835)	Arthropoda	C
Neoeriocheir leptognathus (Rathbun, 1913)	Arthropoda	C
Heteropilumnus ciliatus (Stimpson, 1858)	Arthropoda	C
Charybdis japonica (A. Milne-Edwards, 1861)	Arthropoda	C
Oratosquilla oratoria (de Haan, 1844)	Arthropoda	C
Cylichna cylindracea (Pennant, 1777)	Mollusca	C
Nassarius sinarus (Philippi, 1851)	Mollusca	C
Nassarius succinctus (A. Adams, 1852)	Mollusca	C
Nassarius variciferus (A. Adams, 1852)	Mollusca	C
Neverita didyma (Röding, 1 798)	Mollusca	C
Philine kinglipini Tchang, 1934	Mollusca	C
Lineus sp.	Nemertea	C
Nemertea indet.	Nemertea	C
Diopatra chiliensis Quatrefages, 1866	Annelida	C
Caprella spp.	Arthropoda	C
Cossura dimorpha (Hartman, 1976)	Annelida	C
Metasychis gotoi (Izuka, 1902)	Annelida	C
Perinereis nuntia (Savigny in Lamarck, 1818)	Annelida	C
Filograna implexa Berkeley, 1835	Annelida	C
Ehlersileanira incisa (Grube, 1877)	Annelida	C
Palaemon carinicauda (Holthuis, 1950)	Arthropoda	C
Xenophthalmus pinnotheroides White, 1846	Arthropoda	C
Ctenotrypauchen chinensis Steindachner, 1867	Chordata	C
Odontamblyopus lacepedii (Temminck & Schlegel, 1845)	Chordata	C
Odontamblyopus rubicundus (Hamilton, 1822)	Chordata	C
Trypauchen vagina (Bloch & Schneider, 1801)	Chordata	C
Hediste japonica (Izuka, 1908)	Annelida	D
Notomastus latericeus Sars, 1851	Annelida	D
Aphelochaeta filiformis (Keferstein, 1862)	Annelida	D
Euclymene annandalei Southern, 1921	Annelida	D
Maldanidae	Annelida	D
Ophelina spp.	Annelida	D
Paraprionospio pinnata (Ehlers, 1901)	Annelida	D
Sternaspis chinensis Wu, Salazar-Vallejo & Xu, 2015	Annelida	D
Loimia medusa (Savigny in Lamarck, 1818)	Annelida	D
Amaeana occidentalis (Hartman, 1944)	Annelida	D
Paracaudina chilensis (Müller, 1850)	Echinodermata	D
Protankyra bidentata (Woodward & Barrett, 1858)	Echinodermata	D
Amphioplus (Lymanella) laevis (Lyman, 1874)	Echinodermata	D
Ophiuroglypha kinbergi (Ljungman, 1866)	Echinodermata	D
Nucula faba Xu, 1999	Mollusca	D
Yoldia similis Kuroda et Habe, 1952	Mollusca	D
Raphidopus ciliatus Stimpson, 1858	Arthropoda	O
Actiniaria	Cnidaria	O

to be continued

Continued from Table A1

Species	Phylum	Functional group
Lygdamis nesiotes (Chamberlin, 1919)	Annelida	O
Lygdamis sp.	Annelida	O
Gammaridae	Arthropoda	O
Upogebia sp.	Arthropoda	O
Oliva mustelina Lamarck, 1811	Mollusca	O
Virgularia sp.	Cnidaria	Pl
Siliqua minima (Gmelin, 1791)	Mollusca	Pl
Leptochela (Leptochela) gracilis Stimpson, 1860	Arthropoda	Pl
Moerella hilaris (Hanley, 1844)	Mollusca	Pl
Moerella iridescens (Benson, 1842)	Mollusca	Pl

Note: the following abbreviations were used: carnivorous group (C), detritivorous group (D), omnivorous group (O) and planktophagous group (Pl).