

Article

Effects of Environmental Stressors on the Spring Zooplankton Community in Qinzhou Bay, China

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Abstract

Multiple environmental stressors can directly or indirectly affect zooplankton community structure in marine coastal waters. However, quantifying the relative importance of eutrophication-mediated pathways remains challenging. In this study, we surveyed zooplankton, phytoplankton, and water conditions at 24 stations in Qinzhou Bay during spring and used correlation analysis and structural equation modelling (SEM) to examine the association between eutrophication and zooplankton biomass. The results showed that zooplankton biomass increased from the Inner Bay to the Outer Bay; whereas, zooplankton evenness decreased. Biomass was significantly negatively correlated with both the eutrophication index and zooplankton evenness; a single small copepod numerically dominated the assemblage, so high biomass and low evenness co-occurred as expressions of dominance. The SEM showed an acceptable fit and linked eutrophication to lower zooplankton biomass mainly through heavy-metal enrichment, community dominance (low evenness), and reduced phytoplankton density. The total association between eutrophication and biomass was -0.40 , primarily indirect rather than through a significant direct path (-0.13 , $p = 0.51$), with heavy-metal enrichment and community dominance (low evenness) as the main statistical mediators. Because the data come from a single spring survey of 24 stations, these path coefficients should be interpreted as correlational associations requiring multi-season confirmation.

Keywords: marine coastal waters; eutrophication; heavy-metal pollution; structural equation modelling; direct and indirect associations



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1. Introduction

Zooplankton are central components of marine food webs, playing a key role in energy flow and nutrient cycling [1]. They also respond rapidly to environmental stressors, making them sensitive indicators of coastal marine ecosystem health [2]. Recent work links zooplankton communities to co-occurring stressors, especially eutrophication and heavy-metal contamination [3–5]. Eutrophication can deplete dissolved oxygen, creating hypoxic or anoxic waters that directly imperil zooplankton survival [6], and it can also shift phytoplankton community composition, thereby indirectly reshaping zooplankton

assemblages [7]. Heavy metals can cause oxidative stress and cellular damage, directly harming zooplankton [8], and can suppress phytoplankton growth and reproduction, indirectly affecting the zooplankton communities that depend on them [9]. Together, in situ surveys and controlled experiments show that these stressors can strongly shape marine zooplankton communities.

Current research increasingly focuses on interactions between eutrophication and heavy metals. Where the two stressors co-occur, their joint impact is more intricate than that of either acting alone [9]. Eutrophication drives phytoplankton overgrowth, and the ensuing senescence and decomposition of blooms modify seawater physiochemistry, thereby increasing the bioavailability of heavy metals [10,11]. Eutrophication also promotes heavy-metal adsorption onto phytoplankton, so that zooplankton grazing on contaminated cells may experience elevated mortality and reduced community diversity [12].

Most studies identify environmental stressors affecting zooplankton communities using statistical approaches such as multiple regression [13], redundancy analysis (RDA) [14], or generalized additive models [15]. However, few studies have quantitatively separated direct from indirect effects, limiting our ability to quantify the differential influence of individual stressors and to achieve a mechanistic understanding of ecological responses in coastal systems. Structural equation modelling (SEM) addresses this gap by providing a framework to distinguish direct and indirect effects. SEM has been used to quantify the direct and indirect associations between seawater eutrophication and zooplankton richness, and to separate the influences of river runoff and seasonal variation on zooplankton diversity [16]. As an *a priori* framework, SEM combines a measurement model (linking latent to measured variables) with a structural model (specifying relationships among latent variables). Grounded in ecological theory, SEM enables the specification of causal pathways among variables and the quantification of their direct and indirect statistical associations [17].

Qinzhou Bay is a semi-enclosed bay in the northern Beibu Gulf, Guangxi, receiving domestic sewage, industrial discharges, and intensive aquaculture effluents [18]. These inputs have generated an environmental gradient in which eutrophication and heavy-metal pollution co-occur [19], making the bay a suitable site for examining the ecological effects of multiple marine environmental stressors. However, the effects of this stressor combination on spring zooplankton communities in Qinzhou Bay remain insufficiently characterized. Spring is the principal season of river-driven nutrient pulses and phytoplankton bloom development in Qinzhou Bay, when eutrophication pressure and phytoplankton–zooplankton coupling are most pronounced; this season therefore offers a sensitive window for detecting stressor–zooplankton relationships [19]. During spring, we characterized zooplankton and phytoplankton assemblages, along with ambient seawater quality, across Qinzhou Bay. Using correlation analysis and structural equation modelling, we examined direct and indirect associations between multiple marine environmental stressors and zooplankton communities, aiming to provide a preliminary scientific basis for the ecological assessment of nearshore areas in spring. We hypothesized that (H1) eutrophication and heavy-metal pollution are negatively associated with zooplankton biomass; (H2) these associations are partly indirect, mediated by phytoplankton density and zooplankton community structure (evenness); and (H3) the inner-to-outer estuarine gradient structures the spring assemblage.

2. Materials and Methods

2.1. Study Area and Sampling

Trumpet-shaped in outline, Qinzhou Bay is partitioned into three zones: the Inner Bay, the Bay Neck, and the Outer Bay [20]. The Inner Bay (NW), at the northern apex, receives freshwater from the Qinjiang and Maoling rivers, the Bay Neck (WJ) connects the Inner

and Outer Bays, and the Outer Bay (WW) is strongly influenced by seawater exchange with the open Beibu Gulf. Industrial wastewater and aquaculture discharges along the coastline introduce nutrients and heavy metals, which preferentially accumulate under weak hydrodynamic exchange, generating a spatial pattern of combined enrichment [19,21].

Sampling stations were selected to cover the entire Qinzhou Bay and capture spatial variation in environmental conditions (Appendix A). Field samples were obtained from 24 stations (Figure 1). At each station, a uniform sampling and analytical protocol ensured reliable, mutually comparable data. Because water-quality and plankton samples were collected simultaneously, environmental and biological data correspond station-by-station without cross-station matching. Sampling was conducted in spring 2022, when algal blooms were most likely to occur. Net phytoplankton were sampled with a shallow-water type-III net (mesh $\sim 20\ \mu\text{m}$), which targets the net phytoplankton fraction enumerated by the Utermöhl method. Mesozooplankton were sampled with a shallow-water type-II net (mesh size $\sim 160\ \mu\text{m}$), the standard gear specified in national marine survey specifications [22]. A $\sim 160\ \mu\text{m}$ net retains mesozooplankton and may under-sample the smaller microzooplankton and large, fast-swimming taxa [23]. Each net was towed vertically from about 2 m above the seabed to the surface. Abundance estimates, therefore, integrate the entire water column, and densities were standardized to individuals per cubic metre using the filtered-water volume recorded by the flow metre (Hydrobios, model 438115, with back-run stop) [23]. Collected material was transferred to 500 mL polyethylene bottles, fixed with formaldehyde to a final concentration of 5%, and stored in darkness to preserve sample integrity for subsequent laboratory analysis [24].

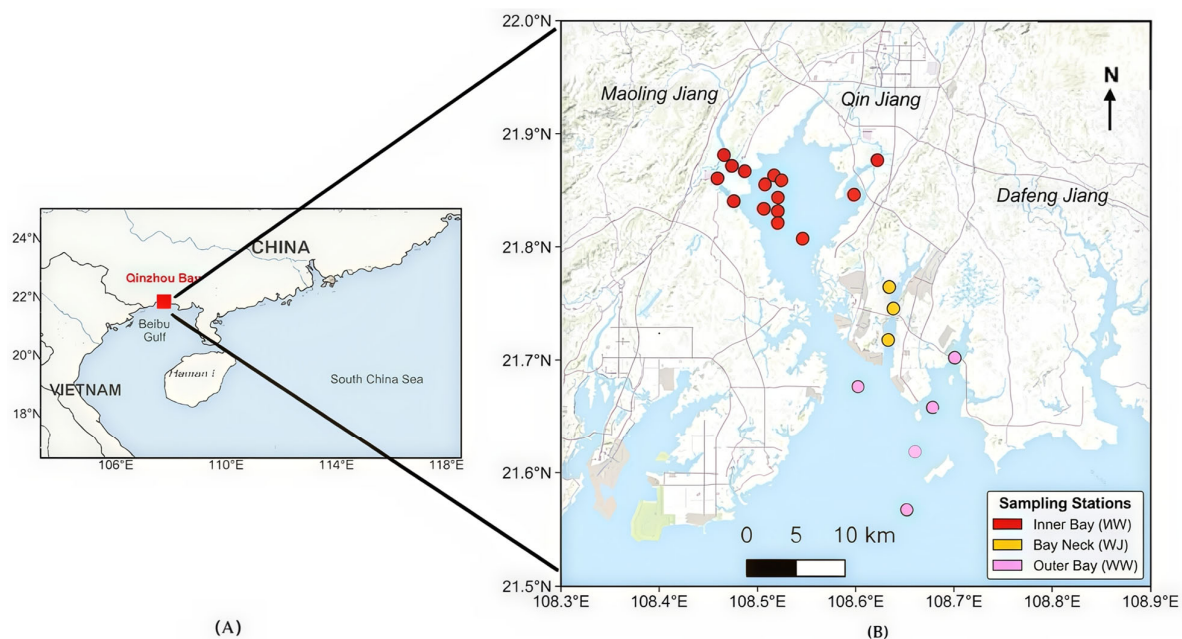


Figure 1. Layout of sampling stations in Qinzhou Bay. (A) Map indicating the position of the research area. (B) Map of sampling stations in Qianzhou Bay.

Water temperature (WT), dissolved oxygen (DO), and salinity (SA) were recorded *in situ* with a YSI ProDSS multi-parameter sonde (USA), with each sensor calibrated according to standard procedures [24]. For chemical oxygen demand (COD), 250 mL of seawater per station was sampled and immediately frozen at $-20\ ^\circ\text{C}$.

For dissolved metals, $\sim 500\ \text{mL}$ aliquots for As and Hg were taken in glass vials and preserved with H_2SO_4 . For Cu, Cd, Cr, Pb, and Zn, $\sim 500\ \text{mL}$ aliquots were collected in PE vials, filtered through a $0.45\ \mu\text{m}$ filter, and preserved with nitric acid. These filtered,

acidified surface seawater samples yielded the dissolved heavy-metal concentrations (Cu, Zn, Pb, Cd, Hg, As) reported here. All physicochemical, nutrient and dissolved heavy-metal variables were determined on surface-layer (0–0.5 m) seawater from the same stations.

2.2. Laboratory Analysis

In the laboratory, COD was quantified by the standard dichromate oxidation procedure [25,26]. The four dissolved nutrients—ammonium (NH_4^+), phosphate (PO_4^{3-}), nitrate (NO_3^-) and nitrite (NO_2^-)—were quantified on a Technicon AA3 Auto-Analyzer (Bran + Luebbe, Norderstedt, Germany) by established colorimetric assays [27,28]. DIN and DIP denote dissolved inorganic nitrogen (the sum of NO_3^- , NO_2^- and NH_4^+) and dissolved inorganic phosphate (PO_4^{3-}), respectively.

Dissolved heavy metal concentrations in the filtered, acidified seawater samples were determined as follows: As and Hg were analyzed using atomic fluorescence spectrometry [29]; Zn was digested with nitric acid and determined by flame atomic absorption spectrometry [30]; Cu, Cd and Pb were quantified by flameless graphite furnace atomic absorption spectrometry at their respective wavelengths [31].

Phytoplankton subsamples were left to settle in a sedimentation column for 24–48 h [32]. Cell counts were then performed using an inverted microscope (Motic AE2000, Barcelona, Spain) at 400× or 200× magnification, according to standard protocols [32]. Phytoplankton density was reported as cells L^{-1} .

Zooplankton samples were concentrated to a known volume in the laboratory (approximately 50 mL; recorded individually for each station). Large and rare individuals (e.g., hydromedusae, chaetognaths, decapod larvae) were picked from the whole concentrated sample and counted. The remaining sample was thoroughly homogenized. This ensured that large, sparse taxa were fully enumerated, regardless of subsequent subsampling [33]. At least 1% of the total concentrated volume was then drawn with a calibrated Stempel pipette and transferred to a plankton counting frame (Bogorov chamber, DHI, Hørsholm, Denmark). Identification and quantification were performed under a stereomicroscope (Motic SMZ-168, Hong Kong, China) at 40–100× magnification [32].

A minimum of 300–500 individuals was counted per subsample to achieve a counting precision of approximately ± 10 –20% (95% confidence) [24,33]. When a single 1% aliquot yielded fewer than 300 individuals, additional aliquots were examined until the target was met. Zooplankton were identified to the lowest practicable taxon. Calanoid and cyclopoid copepods were identified to species; harpacticoid copepods to genus; chaetognaths, cladocerans, tunicates and pelagic poly-chaetes to species; copepod nauplii were pooled as ‘holoplankton’; and meroplanktonic larvae (barnacle nauplii/cyprids and brachyuran zoeae) were identified to type [34]. Copepodite stages (CI–CV) that could be reliably assigned to species were included in the species count. Those that could not be identified were recorded separately as ‘unidentified copepodites’ and were included in the total abundance and biomass, but not in species richness.

Zooplankton biomass was determined by the wet-weight method [22,24]. The remaining (uncounted) fraction of each sample was filtered onto a pre-weighed 160 μm nylon mesh. It was briefly rinsed with distilled water to remove adherent salt and formalin, gently blotted from beneath with absorbent paper to remove interstitial water, and weighed to 0.01 g on an analytical balance [34]. Biomass was expressed as wet weight (mg) per m^3 , standardized to the filtered water volume recorded by the flow metre. Every experimental treatment included blanks and was run in triplicate. The difference between duplicate measurements was kept below 10% [33]. Analytical quality was assured by the concurrent analysis of certified reference materials [22]. Agreement between replicate and reference analyses was acceptable throughout, with discrepancies staying under 10%. Before use, all

glassware and plasticware were soaked in 10% HNO₃ (*v/v*) for at least 2 days and then rinsed with deionized water [34]. All reagents were of analytical grade (Merck, Darmstadt, Germany). The complete checklists of identified phytoplankton and zooplankton taxa are provided in Appendices B and C, respectively.

2.3. Data Analysis

We used three ecological indicators to characterize the coastal ecosystem: the eutrophication index (Ei), the comprehensive heavy-metal pollution index (WQI), and three descriptors of plankton community structure—the Shannon–Wiener diversity index (*H'*), the Pielou evenness index (*J*), and the Margalef richness index (*D*). Ei reflects nutrient enrichment [35], WQI indicates the ecological risk posed by heavy metals [36], and *H'*, *J*, and *D* describe plankton community structure [37]. Ei integrates COD, DIN, and DIP into a single, widely used, cross-comparable nutrient-enrichment metric [35]. WQI summarizes multi-element exposure relative to the national seawater quality standard [36]. *H'*, *J*, and *D* are standard, complementary descriptors of community structure [37]. For WQI, each element is normalized to its own national Class-I seawater quality standard [37], so the equal-weighted mean reflects differences in toxicity across standards rather than treating raw concentrations as equivalent. These toxicity-based criteria are markedly stricter for highly toxic metals such as Hg and Cd than for Cu or Zn [37]. As a result, the index condenses correlated metals into a single, low-dimensional, cross-comparable predictor suited to the parsimonious SEM and RDA, but it cannot resolve toxicological synergy or antagonism, bioavailability and speciation, or element-specific effects beyond those encoded in the standards. The results indicate that only Hg varied significantly, the composite is Hg-dominated. We therefore note that toxicity-weighted schemes, such as a potential ecological risk index with metal-specific toxic-response factors, could refine future assessments.

Ei was calculated as:

$$E_i = \frac{COD \times DIN \times DIP}{b} \times 10^6 \quad (1)$$

where Ei is calculated from COD, DIN, and DIP, with *b* = 4500 [35]. $E_i \geq 1$ indicates eutrophication.

WQI was calculated as:

$$WQI = \frac{1}{n} \sum_{i=1}^n \frac{C_i^s}{C_i^n} \quad (2)$$

where WQI is the heavy-metal pollution index, with C_i^s the measured concentration of metal *i* and C_i^n the national first-class seawater quality standard.

The community structure of plankton is characterized by the Shannon–Wiener diversity index (*H'*), Pielou evenness index (*J*), and Margalef richness index (*D*), with the formulas outlined as follows:

$$H' = - \sum_{i=1}^S (P_i \times \log_2 P_i) \quad (3)$$

$$J = H' / H_{max} \quad (4)$$

$$D = (S - 1) / \log_2 N \quad (5)$$

$$Y = \frac{N_i}{N} \times f_i \quad (6)$$

Here, *Y* is species dominance; a species is dominant if $Y \geq 0.02$. *N_i* = individuals of species *i*, *N* = total individuals, *f_i* = occurrence frequency of species *i*, *S* = species richness, $P_i = N_i / N$, and $H_{max} = \log_2 S$.

2.4. Statistical Analysis

RDA and SEM serve complementary roles in this study. RDA is an exploratory form of constrained ordination that identifies which measured environmental variables account for significant variance in the multivariate community and portrays the leading gradients. However, RDA cannot separate direct from indirect pathways. SEM, in contrast, is confirmatory: for a pre-specified path structure it decomposes the association between a stressor and zooplankton biomass into direct and indirect parts [17].

For the redundancy analysis (RDA), we tested whether plankton community descriptors were significantly structured by the measured environmental variables. The response variables were grouped into zooplankton descriptors—biomass (ZCB), density (ZCT), diversity (ZCH), evenness (ZCJ), and richness (ZCD)—and phytoplankton descriptors—density (PCT), densities of the two dominant groups (dinoflagellates and diatoms), diversity (PCH), evenness (PCJ), and richness (PCD). The environmental variables were WT, SA, DO, COD, DIN, DIP, and dissolved heavy metals (Cu, Zn, Cd, Hg, and As). Pb and Cr were excluded because they fell below the detection limit at most stations. Response variables were standardized. The significance of the global constraint was assessed with a permutation test (999 permutations).

We fitted an observed-variable path model, a structural equation model without a latent measurement component, so the generic measurement-model equations linking latent to observed variables do not apply here [17,38]. Each path, therefore, connects directly measured indicators within an a priori structure. Previous studies show that zooplankton communities respond to phytoplankton, COD, DIN, DIP, and heavy metals [39,40]. We therefore included these as measured variables. To avoid multicollinearity, we aggregated environmental factors into two ecologically meaningful indices: the eutrophication index (Ei) and the heavy-metal pollution index (WQI). This allowed us to quantify the direct and indirect associations of environmental factors with zooplankton holistically. The model assumed that: (1) eutrophication and heavy metals are directly associated with zooplankton biomass [2]; (2) eutrophication and heavy metals are associated with zooplankton evenness, thereby being indirectly related to biomass [41]; and (3) eutrophication and heavy metals are associated with phytoplankton density or evenness, which in turn are indirectly related to zooplankton biomass. The recursive path model was fitted to standardized variables using Python 3.12 (statsmodels). Because the model contains only observed variables and no reciprocal paths, each structural equation was estimated by ordinary least squares. Given the modest sample size ($n = 24$), the significance of individual path coefficients was assessed using two-tailed t -tests, and 95% confidence intervals for the indirect and total effects were obtained via nonparametric bootstrapping (5000 resamples). Four standard indices judged model fit: the Tucker–Lewis index (TLI), the comparative fit index (CFI), the standardized root mean square residual (SRMR), and the root mean square error of approximation (RMSEA) [42]. Good fit requires $SRMR < 0.09$ and $RMSEA < 0.05$ [43].

3. Results

3.1. Spatial Characteristics of Water Quality Factors

Most water-quality factors showed significant regional differences ($p < 0.05$; Table 1). Salinity, by contrast, was greatest in the Outer Bay and lowest in the Inner Bay ($p < 0.05$). DIN and DIP both peaked in the Inner Bay, with DIN exceeding levels in the Bay Neck and Outer Bay and DIP exceeding the Outer Bay ($p < 0.05$). These elevated DIN and DIP levels in the Inner Bay indicate that the Qinjiang and Maoling rivers are the primary nutrient sources there. Stations in the Inner Bay also had the highest WT and COD, which significantly surpassed Outer-Bay levels ($p < 0.05$). DO also peaked in the Inner Bay, above Bay-Neck values ($p < 0.05$).

Table 1. Spatial characteristics of seawater factors in Qinzhou Bay. “*” represents significant differences ($p < 0.05$), and “**” represents highly significant differences ($p < 0.01$). The different lowercase letters “a” and “b” in the same column indicate significant differences ($p < 0.05$), while the same lowercase letters indicate insignificant differences ($p > 0.05$).

Sampling Area	WT (°C)	SA	DO (mg/L)	COD (mg/L)	DIN (mg/L)	DIP (mg/L)
NW	26.51 ± 1.60 a	14.66 ± 2.55 b	7.16 ± 0.62 a	2.14 ± 0.60 a	0.72 ± 0.37 a	0.04 ± 0.02 a
WJ	25.90 ± 1.45 ab	27.45 ± 1.37 a	6.33 ± 0.28 b	1.54 ± 0.27 ab	0.23 ± 0.04 b	0.03 ± 0.01 ab
WW	24.30 ± 0.67 b	29.61 ± 1.12 a	6.99 ± 0.34 ab	1.14 ± 0.42 b	0.19 ± 0.06 b	0.02 ± 0.01 b
F-value	3.58 **	110.02 **	4.44 *	6.72 **	8.32 **	4.97 **

The spatial distribution of heavy metals differed by element (Table 2). Hg concentration showed significant spatial variation ($p < 0.05$), with the highest value in the Inner Bay and the lowest in the Outer Bay; the maximum-to-minimum ratio was approximately 3.0, indicating a threefold difference. Hg was the only element with a significant spatial contrast. For the other heavy metals, no statistically significant spatial variation was detected, indicating relatively uniform distributions. The maximum-to-minimum ratios were Cr (2.58), Cd (1.5), Zn (1.25), As (1.23), Cu (1.08), and Pb (1).

Table 2. Spatial characteristics of heavy metal content in Qinzhou Bay. “*” represents significant differences ($p < 0.05$), and “**” represents highly significant differences ($p < 0.01$). The different lowercase letters “a” and “b” in the same column indicate significant differences ($p < 0.05$), while the same lowercase letters indicate insignificant differences ($p > 0.05$).

Sampling Area	Cu (µg/L)	Pb (µg/L)	Zn (µg/L)	Cd (µg/L)	Cr (µg/L)	Hg (µg/L)	As (µg/L)
NW	0.78 ± 0.31 a	0.12 ± 0.05 a	11.09 ± 3.69 a	0.10 ± 0.09 a	0.31 ± 0.37 a	0.06 ± 0.02 a	1.48 ± 0.30 a
WJ	0.79 ± 0.52 a	0.14 ± 0.09 a	13.82 ± 2.66 a	0.12 ± 0.10 a	0.12 ± 0.27 a	0.03 ± 0.02 b	1.40 ± 0.32 a
WW	0.73 ± 0.35 a	0.14 ± 0.11 a	12.65 ± 1.03 a	0.08 ± 0.05 a	0.27 ± 0.31 a	0.02 ± 0.01 b	1.20 ± 0.14 a
F-value	0.04	0.19	1.45	0.27	0.59	9.34 **	1.54

The Ei showed significant spatial variation ($p < 0.05$; Table 3). The Inner Bay recorded the highest value, indicating a prominent eutrophication risk; several stations had already reached a eutrophic state ($Ei \geq 1$). The heavy-metal pollution index (WQI) declined from the Inner Bay to the Bay Neck and then to the Outer Bay, with significant spatial variation ($p < 0.05$). Overall, WQI values remained low, indicating mild heavy-metal pollution. Because Hg was the only metal with significant spatial contrast, the WQI signal is substantially driven by Hg; this limitation is discussed in Section 4.3.

Table 3. Seawater pollution risk index in different sampling areas of Qinzhou Bay. “*” represents significant differences ($p < 0.05$), and “**” represents highly significant differences ($p < 0.01$). The different lowercase letters “a” and “b” in the same column indicate significant differences ($p < 0.05$), while the same lowercase letters indicate insignificant differences ($p > 0.05$).

Sampling Area	Ei	WQI
NW	13.49 ± 10.61 a	0.31 ± 0.08 a
WJ	2.28 ± 0.63 b	0.29 ± 0.09 ab
WW	1.14 ± 1.27 b	0.20 ± 0.04 b
F value	5.15 **	4.87 *

3.2. Characteristics of Plankton Communities

Diplostraca, tunicate and polychaete were less well represented, each accounting for 7.7% of the total species richness (Figure 2).

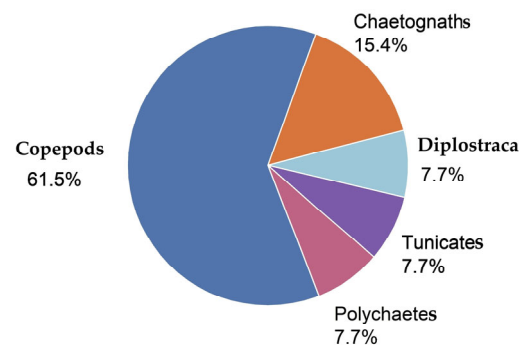


Figure 2. Zooplankton community composition in Qinzhou Bay.

Zooplankton biomass varied among regions, averaging 317 mg m^{-3} across the study area (Figure 3). Biomass was highest in the Outer Bay and lowest in the Inner Bay, increasing steadily toward the Outer Bay. Across zooplankton assemblages, Shannon–Wiener values ranged from 0.93 to 1.98, and evenness from 0.59 to 0.99. Evenness varied significantly ($p < 0.05$); whereas, the Shannon–Wiener index showed little spatial variation. Both indices reached their lowest values in the Bay Neck (WJ) region.

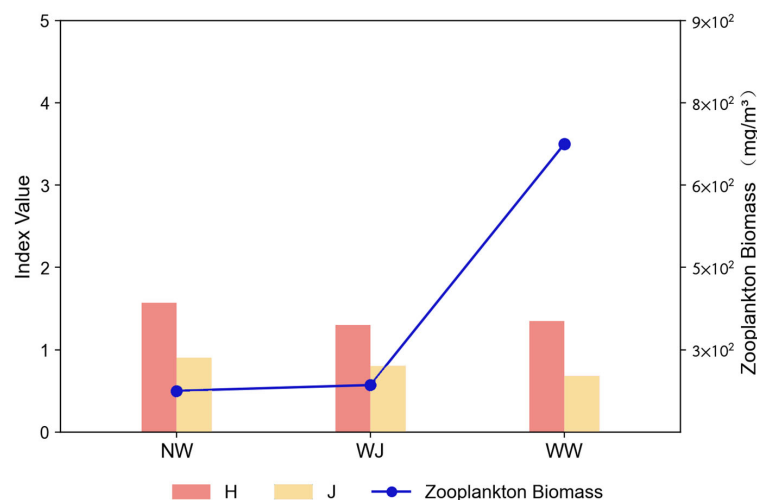


Figure 3. Zooplankton community structure in different sampling area of Qinzhou Bay. H: Shannon–Wiener diversity index, J: Pielou evenness index; NW: Inner Bay, WJ: Bay Neck, WW: Outer Bay.

The low species richness (13 species) is attributable to four factors. (i) Gear selectivity: because the $\sim 160 \mu\text{m}$ net targeted mesozooplankton, the richness represents that size spectrum rather than the full zooplankton assemblage. (ii) Season: a single spring survey misses warm-season cladoceran and meroplankton pulses. (iii) Environmental stress: the eutrophic, low-salinity, hydrodynamically stressed Inner Bay favours a few tolerant, opportunistic taxa, as shown by *P. crassirostris* dominance. (iv) Consistency: prior Qinzhou Bay spring surveys have also reported copepod-dominated, low-richness assemblages [44–46].

A total of 205 phytoplankton species were identified, belonging to 70 genera across seven phyla (Figure 4; full checklist in Appendix C). Diatoms showed the highest species richness, with 142 species across 33 genera, accounting for 69.3% of the total. Dinoflagellates ranked second, with 23 species across 12 genera, and accordingly represented 11.2%. Chlorophytes comprised 21 species across 14 genera, and therefore accounted for 10.2%.

Euglenophytes had eight species across three genera (3.9%). Cyanophytes included seven species across five genera (3.4%). Cryptophytes had three species across two genera (1.5%). Chrysophytes had one species across one genus (0.5%).

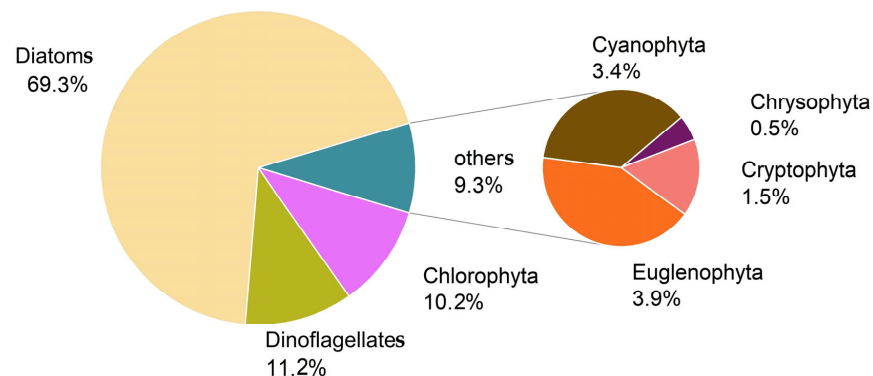


Figure 4. Phytoplankton community composition in Qinzhou Bay.

Species with $Y \geq 0.02$ were considered dominant [34]. The six dominant species were *Skeletonema costatum* (0.14) and *Cyclotella striata* (0.03) from *Bacillariophyta*; *Prorocentrum minimum* (0.03) from *Dinophyta*; *Chroomonas acuta* (0.06) and *Cryptomonas erosa* (0.07) from *Cryptophyta*; and *Lepocinclis playfairiana* (0.09) from *Euglenophyta*.

The total average phytoplankton density in the study area was 8.93×10^4 cells L^{-1} , with spatial variation (Figure 5). The Outer Bay recorded the highest density (6.79×10^5 cells L^{-1}) and the Inner Bay the lowest (2.42×10^5 cells L^{-1}). Phytoplankton density rose steadily from the Inner Bay toward the Outer Bay. This pattern shows that phytoplankton richness was considerably greater than zooplankton richness. Phytoplankton were enumerated to species from bottle samples and comprise many small primary producers occupying numerous micro-niches; whereas, the 160 μm net samples only the mesozooplankton size class at a higher trophic level. The size–diversity and trophic-pyramid relationships predict far higher producer than consumer richness, a gap widened here by the coarse zooplankton mesh [34]. For phytoplankton, Shannon–Wiener diversity spanned 0.39 to 4.12 (mean 2.53), evenness 0.10 to 0.86 (mean 0.55), and Margalef richness 1.37 to 2.85 (mean 2.15). Spatially, diversity and richness varied significantly; whereas, evenness showed less variation. All three indices reached their lowest values in the Outer Bay (WW) region, underscoring it as the least diverse area.

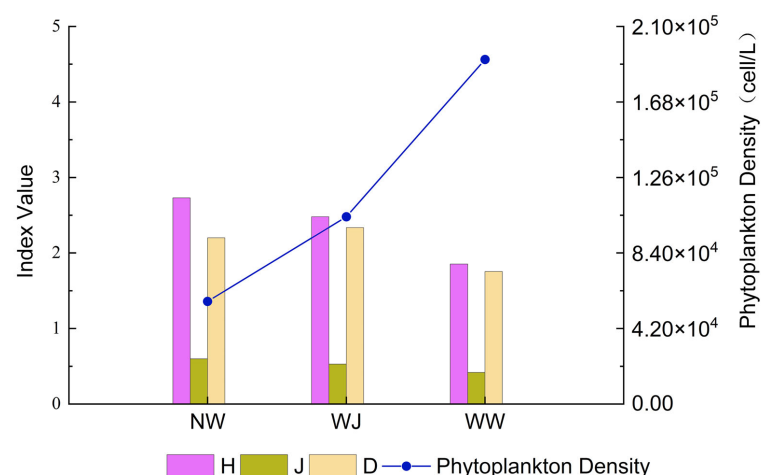


Figure 5. Phytoplankton community structure in different sampling area of Qinzhou Bay. H: Shannon–Wiener diversity index, J: Pielou evenness index, D: Margalef richness index; NW: Inner Bay; WJ: Bay Neck; WW: Outer Bay.

3.3. Correlation Analysis Between Planktonic Community and Water Quality Factors

Correlation analysis (Figure 6) showed a significant negative correlation between phytoplankton density and both the phytoplankton diversity and evenness indices, indicating that high-biomass phytoplankton communities were dominated by a few species, resulting in simplified species composition. Phytoplankton density also showed a significant inverse relationship with the eutrophication index. Among the phytoplankton community indices, the diversity index was significantly positively correlated with evenness and richness, and evenness was significantly positively correlated with richness. Zooplankton biomass was significantly negatively correlated with zooplankton evenness, consistent with the co-occurrence of high biomass and low evenness in zooplankton communities. A significant inverse correlation was likewise observed between zooplankton biomass and the eutrophication index. The eutrophication index was positively correlated with the heavy-metal pollution index, suggesting either a common terrestrial source or a shared transport and enrichment process.

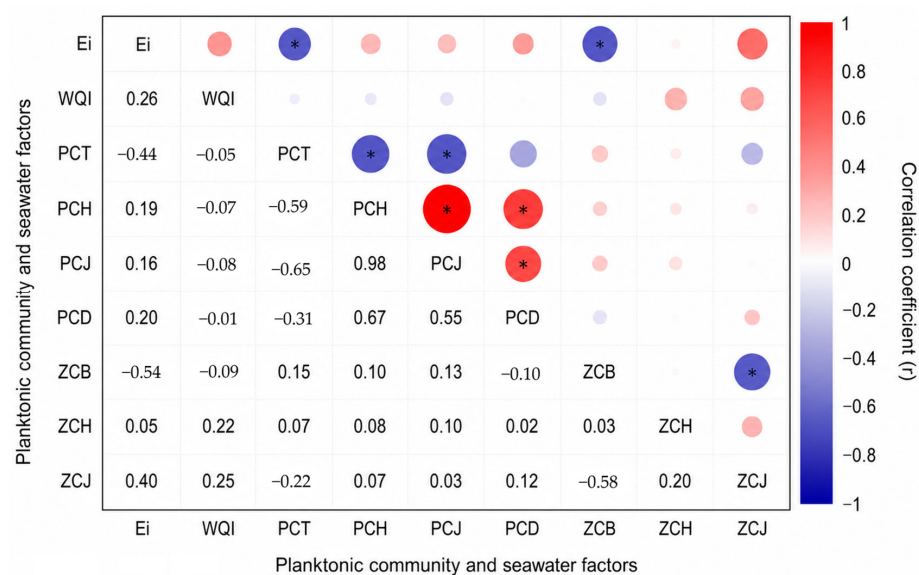


Figure 6. Correlation between planktonic community and seawater factors in Qinzhou Bay. * indicates a highly significant correlation at the 0.01 level. ZCB: Zooplankton community biomass; ZCH: Zooplankton community Shannon–Wiener diversity index; ZCJ: Zooplankton Pielou evenness index; Ei: Eutrophication index; WQI: Heavy metal pollution index; PCT: Phytoplankton community density; PCH: Phytoplankton community Shannon–Wiener diversity index; PCJ: Phytoplankton Pielou evenness index; PCD: Phytoplankton Margalef richness index.

3.4. Results of the Redundancy Analysis (RDA)

Redundancy analysis explained 61.0% of the total variance in the plankton community descriptors, and the global constraint was significant (permutation test, 999 permutations, $p = 0.011$), indicating that the measured environmental variables were associated with the spring assemblage rather than sampling noise. The first two constrained axes captured the dominant structure, accounting for 23.3% (RDA1) and 15.1% (RDA2) of the total variance. In the response space, zooplankton biomass (ZCB) and zooplankton total density (ZCT) projected onto the saline, Outer-Bay end of RDA1; whereas, zooplankton evenness (ZCJ) and phytoplankton evenness and diversity (PCJ, PCH) aligned with the nutrient- and metal-rich Inner-Bay end. Overall, the ordination shows that salinity was the primary gradient, with nutrient enrichment and As/Hg contamination also shaping the community; high zooplankton biomass remained concentrated in the more saline, less-eutrophic Outer Bay (Figure 7).

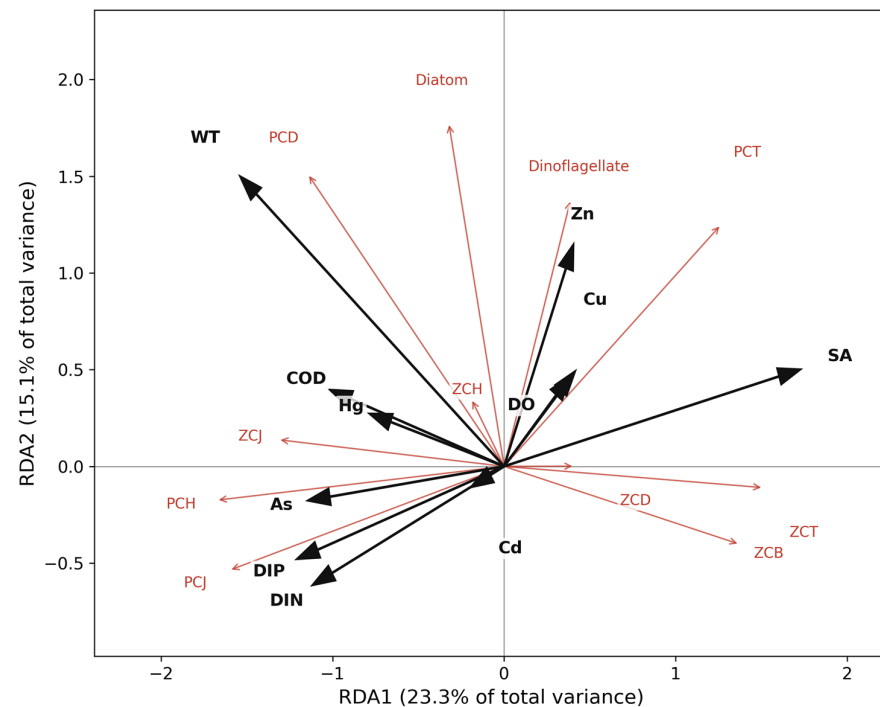


Figure 7. Redundancy analysis (RDA) biplot of plankton community descriptors constrained by the measured environmental variables in Qinzhou Bay. Black arrows, environmental variables; red arrows, community descriptors. Cu: copper; Zn: zinc; Pb: lead; Cd: cadmium; Cr: chromium; Hg: mercury; As: arsenic; WT: water temperature; DO: dissolved oxygen; SA: salinity; COD: chemical oxygen demand; DIN: dissolved inorganic nitrogen; DIP: dissolved inorganic phosphate; ZCT: zooplankton total density; ZCB: zooplankton biomass; ZCH: zooplankton Shannon–Wiener diversity index; ZCJ: zooplankton Pielou evenness index; ZCD: zooplankton Margalef richness index; PCT: phytoplankton total density; PCH: phytoplankton Shannon–Wiener diversity index; PCJ: phytoplankton Pielou evenness index; and PCD: phytoplankton Margalef richness index.

3.5. Results of Structural Equation Modelling

Model fit was good: the SEM explained 57.6% of the variance in zooplankton biomass and 40.1% of that in zooplankton evenness (Table 4). The model resolved the two composite stressors—the eutrophication index (Ei) and the heavy-metal pollution index (WQI)—into direct and indirect statistical associations with phytoplankton density, zooplankton evenness and zooplankton biomass (Figure 8).

Table 4. Results of goodness-of-fit tests for SEM.

	<i>p</i> Value	TLI	CFI	SRMR	RMSEA
Result	0.03	0.99	0.99	0.06	0.01
Standard	<0.05	≥0.90	≥0.90	≤0.08	≤0.08

Higher zooplankton evenness was statistically associated with lower biomass ($\beta = -0.51$, $p = 0.017$). This relationship reflects the numerical dominance of a few taxa—high biomass with low evenness—rather than a causal effect of evenness on biomass. Consequently, the dominant statistical mediation ran from eutrophication through heavy-metal enrichment and community dominance (low evenness) to reduced biomass. This chain was the single largest indirect route (-0.14); the aggregate indirect effect (-0.27) was estimated with lower precision at this sample size.

The heavy-metal pollution index had a weak, non-significant direct path to biomass ($\beta = -0.19$, $p = 0.39$), indicating that its influence was mediated mainly through zooplank-

ton evenness rather than direct toxicity. The other direct paths were also non-significant: phytoplankton density to zooplankton evenness ($\beta = -0.31$) and biomass ($\beta = 0.21$), and eutrophication to zooplankton evenness ($\beta = -0.19$). Thus, the stressor–biomass associations were negative and of similar magnitude to the RDA gradient, but the pattern suggests an indirect pathway via reduced phytoplankton density and altered zooplankton evenness rather than a direct effect. Because all analyses are based on a single spring survey of 24 stations, interpret these path coefficients as correlational rather than causal associations.

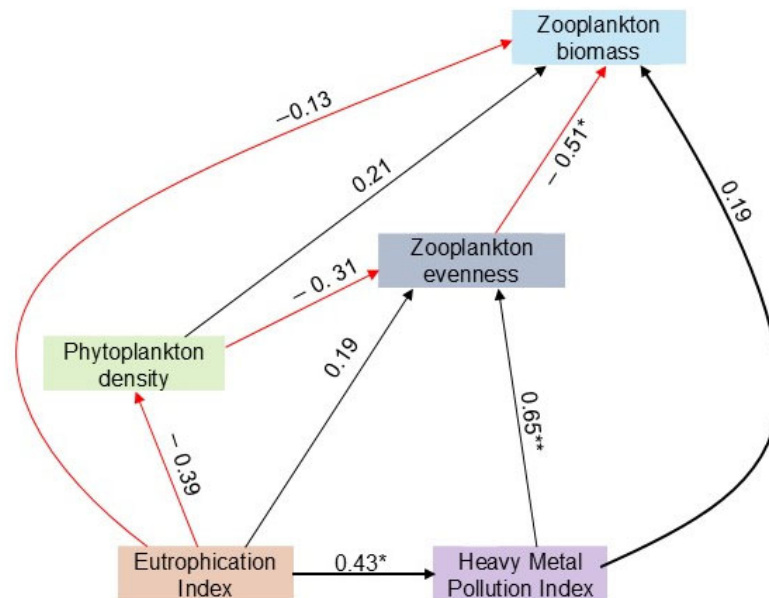


Figure 8. Simulation result of the effect of environmental factors on the zooplankton community. The black arrow indicates positive effects and the red arrow indicates negative effects. In the path diagram, the values on the lines connecting the variables represent the standardized path coefficients. “*” represents significant differences ($p < 0.05$), and “**” represents highly significant differences ($p < 0.01$).

4. Discussion

4.1. Spatial Distribution of Zooplankton Communities

These findings point to a consistent ecological pattern: copepods serve as the core group within zooplankton communities in subtropical estuaries and bays. The dominant species during spring was *Parvocalanus crassirostris*, with a dominance index of 0.54. The community structure of zooplankton showed pronounced spatial variation. Zooplankton biomass increased gradually from the Inner Bay to the Outer Bay, forming a ‘low inside, high outside’ pattern consistent with observations reported by Lan et al. (2015) from 2011 to 2012 surveys [46].

Compared with data from a decade ago, zooplankton biomass in Qinzhou Bay has risen markedly. Zooplankton evenness decreased from the Inner Bay to the Outer Bay, creating a “high biomass, low evenness” pattern. This trend matches zooplankton miniaturization observed in other eutrophic coastal systems, such as Xiangshan Bay [47], and suggests a shift toward smaller-bodied, opportunistic taxa in Qinzhou Bay. Similar responses to nutrient enrichment and multiple stressors have also been reported in European and other coastal and transitional systems, including the loss of zooplankton functional diversity under hyper-eutrophication and stressor-driven community change in coastal ecosystems [7,48]. This indicates that the trajectory inferred for Qinzhou Bay aligns with a broader, cross-regional pattern.

At the species level, the spring assemblage was numerically dominated by the small calanoid copepod *Parvocalanus crassirostris* (dominance index 0.54), with barnacle (*Balanus*)

larvae and copepod nauplii as subdominants. *P. crassirostris* is a small-bodied, estuarine-tolerant copepod favoured by warm, nutrient-enriched, lower-salinity water. Together with the prevalence of meroplanktonic larvae, its dominance marks a community shifted toward small, opportunistic, eutrophication-tolerant taxa in the Inner Bay. Reading the community through such indicator species, rather than broad taxonomic groups alone, links the observed Inner-Bay pattern to the traits of the taxa that actually drive it.

4.2. Analysis of Structural Equation Modelling Results

Building on the spatial patterns described above, we used the SEM to quantitatively decompose the environmental gradients resolved by the RDA. The structural equation model and the RDA offer complementary, mutually reinforcing views of the same community–environment system. The SEM adds mechanistic insight that the RDA cannot resolve: it suggests that the eutrophication–biomass association embedded in RDA is largely indirect, operating through reduced phytoplankton density and altered zooplankton evenness rather than as a direct effect. While the RDA confirms that the environmental gradient structures the assemblage, the SEM quantifies how that gradient is associated with biomass via specific pathways. Eutrophication had a negative total association with zooplankton biomass (total = -0.40). This was expressed mainly indirectly rather than as a significant direct effect ($\beta = -0.13$, $p = 0.51$), suggesting that the association between eutrophication and reduced zooplankton biomass may be mediated through multiple indirect routes. Two interpretive cautions apply. First, the phytoplankton-density-to-biomass path was weak and non-significant ($\beta = 0.21$), so the inference that lower phytoplankton density reduces zooplankton biomass remains suggestive rather than established. Second, measured heavy-metal concentrations were generally low—mild pollution overall, with only Hg showing significant spatial variation (Table 2). So the indirect heavy-metal pathway should be read as a tentative, low-magnitude signal rather than firm evidence of metal control.

The counterintuitive negative spatial association between eutrophication and phytoplankton density (Inner Bay: highest Ei, lowest phytoplankton density) highlights a key takeaway: several non-exclusive mechanisms likely explain this pattern. First, light limitation in the turbid, sediment-laden Inner Bay constrains photosynthesis despite nutrient surplus [49]. Second, the short residence time and strong riverine flushing in the Inner Bay export phytoplankton faster than they can accumulate; whereas, the more retentive Outer Bay permits biomass to build up [50]. Third, because the eutrophication index reflects nutrient loading rather than realized productivity, high inshore nutrient loading and high offshore biomass are spatially decoupled [51]. These conditions can also trigger algal blooms, whose decomposition rapidly reduces dissolved oxygen and creates hypoxic or anoxic conditions that threaten zooplankton [52]. Decomposing phytoplankton also releases ammonia nitrogen, which can become toxic to zooplankton at elevated concentrations [50]. As a result, zooplankton may face poor-quality or harmful phytoplankton, expend more energy processing low-quality or toxic food, and ultimately have inhibited growth and reproduction [53]. Certain toxic cyanobacteria can also cause developmental delays and reproductive disorders in zooplankton [54]. This provides one explanation for the low zooplankton biomass observed in bays with high eutrophication. No significant direct link emerged between heavy-metal pollution and zooplankton biomass. The ecological risks of heavy metals affect the physiological functions, growth, and reproduction of zooplankton through chronic, cumulative effects [55,56]. The SEM also revealed that eutrophication was positively associated with the heavy-metal pollution index, consistent with eutrophication enhancing the bioavailability and toxicity of heavy metals by altering metal speciation [57]. Because absolute heavy-metal concentrations were low and the direct

metal-to-biomass path was non-significant ($\beta = -0.19$, $p = 0.39$), the heavy-metal associations more likely reflect a co-varying contamination gradient than acute toxicity. Different metals may differ in their bioavailability and ecological effects despite normalization, which limits the interpretation of the composite index. In the Inner Bay, these factors may act synergistically to suppress zooplankton growth and reproduction [58], and eutrophication selects for small, fast-reproducing, tolerant taxa such as *P. crassirostris* and meroplanktonic larvae, producing the observed Inner-Bay pattern of low biomass and low evenness.

A driver not captured by our bottom-up framework is top-down predation. Zooplanktivorous predators can regulate zooplankton quantitatively by reducing standing stock and structurally by feeding selectively on larger-bodied taxa [59,60]. Size-selective predation by visually feeding planktivores removes large zooplankton and shifts assemblages toward small-bodied, fast-reproducing forms [59]. This may complement eutrophication-driven selection in explaining the numerical dominance of the small copepod *Parvocalanus crassirostris* and the community miniaturization we observed. Predators were present in our samples: chaetognaths accounted for 15.4% of the zooplankton assemblage, and hydromedusae were abundant enough to be removed and counted separately during processing. Chaetognaths and gelatinous predators (medusae, ctenophores) can consume a large fraction of the copepod standing stock in estuaries and embayments [61,62]. In eutrophic, hypoxia-prone waters, gelatinous predators may increase while copepods decline [63]. Because predation pressure covaried with the eutrophication and hypoxia gradient measured here, top-down control may help explain the inner-to-outer change in zooplankton biomass and evenness. This also suggests that the predation pathway may clarify the model's bottom-up results.

4.3. Research Limitations and Future Prospects

This study examined how zooplankton communities in Qinzhou Bay respond to various water-quality stressors, but several constraints must be acknowledged. First, the data come from a single spring cruise, which cannot capture annual variability or succession; thus, all inferences are restricted to spring conditions. Second, a uniform distribution of zooplankton in the water column was assumed for vertical tows, but some species exhibit diel vertical migration, so future studies should employ stratified sampling. Third, surface-layer water chemistry and dissolved metals were related to whole-water-column hauls, which may not capture vertically structured exposure. Fourth, with 24 stations, the SEM and RDA are necessarily parsimonious and modestly powered, so the standardized path coefficients should be interpreted as correlational associations rather than proven causal effects, and they also require multi-season confirmation. Fifth, this is a case study of a typical subtropical bay, so its conclusions are regionally specific. Sixth, top-down predation was not quantified; vertebrate and invertebrate predators can reduce zooplankton biomass through grazing and reshape evenness by selectively consuming larger-bodied taxa. Seventh, sampling gear selectivity constrains the size spectrum resolved; the ~160 μm mesh under-sampled smaller microzooplankton (e.g., rotifers, ciliates, and early copepod nauplii); whereas, active net avoidance may have under-represented large, fast-swimming taxa. Eighth, only eutrophication and heavy metals were assessed; microplastics and organic contaminants (e.g., PAHs, pesticides, and antibiotics) were not measured, and they may contribute to the observed patterns.

In the future, we plan to: (a) conduct seasonal and interannual monitoring with indicator-species analysis to capture variability and succession; (b) quantify predator fields—planktivorous fish and gelatinous predator abundance—using gut-content or molecular diet analysis, and incorporate top-down terms into the model; (c) adopt size-fractionated, stratified sampling to resolve the full plankton size spectrum, from micro-

zooplankton to macro-gelatinous taxa; and (d) add hydrodynamic and contaminant measurements to separate physical and chemical drivers. Building on these data, we aim to develop a mixed-effects model that integrates plankton growth dynamics and evaluates alternative management measures through scenario simulations.

5. Conclusions

Based on a single survey conducted in spring 2022, this study offers a preliminary exploration of relationships between water-quality factors and the zooplankton community in Qinzhou Bay. Using correlation analysis and structural equation modelling, we found an inverse relationship between total zooplankton biomass and community evenness. When a single small copepod dominated the assemblage numerically, biomass was high, and evenness was low. Thus, low evenness and high biomass co-occur as expressions of dominance, rather than evenness being directly associated with biomass. This pattern helps explain why biomass remains low in the Inner Bay, where eutrophication is high and the assemblage is more evenly distributed. Eutrophication was associated with lower zooplankton biomass mainly through indirect pathways: heavy-metal enrichment, community dominance, and reduced phytoplankton density, rather than through a significant direct effect. Neither the phytoplankton-density association nor an acute toxic effect of heavy metals was statistically significant. These results show the value of identifying pathways linking different stressors to zooplankton communities in spring, enabling more targeted management strategies. The study provides a methodological reference and baseline data for ecological assessments of similar estuarine bays, while the single-season, 24-station design means that the reported path strengths are correlational associations requiring multi-season confirmation.

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Data Availability Statement: The data presented in this study are available on request from the corresponding authors.

Conflicts of Interest: The author Li jiao Deng was employed by Beijing Zhongdihongke Environmental Technology Co., Ltd. The remaining authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

Appendix A. Sampling Stations: Coordinates and Bottom Depth

Station	Longitude (E)	Latitude (N)	Bottom Depth (m)
1	108°27'58"	21°52'53"	4.4
2	108°28'27"	21°52'19"	1.7
3	108°29'14"	21°52'02"	1.0
4	108°31'01"	21°51'48"	2.4

5	108°31'28"	21°51'33"	1.8
6	108°31'16"	21°50'38"	2.3
7	108°31'15"	21°49'54"	2.3
8	108°31'14"	21°49'17"	1.7
9	108°30'24"	21°50'02"	4.5
10	108°30'28"	21°51'20"	2.7
11	108°28'34"	21°50'26"	3.6
12	108°27'34"	21°51'39"	5.2
13	108°37'19"	21°52'37"	9.5
14	108°35'54"	21°50'47"	7.9
15	108°32'46"	21°48'27"	3.4
16	108°38'03"	21°45'53"	3.7
17	108°38'18"	21°44'45"	8.5
18	108°37'59"	21°43'05"	5.7
19	108°36'09"	21°40'36"	3.1
20	108°42'03"	21°42'08"	1.5
21	108°40'42"	21°39'30"	1.3
22	108°39'38"	21°37'07"	3.5
23	108°39'08"	21°34'02"	7.4
24	108°45'09"	21°33'55"	10.8

Appendix B. Checklist of Zooplankton Taxa Identified in Qinzhou Bay, Spring 2022

No.	Group	Scientific Name
1	Chaetognatha	<i>Zonosagitta bedoti</i>
2	Chaetognatha	<i>Flaccisagitta enflata</i>
3	Tunicata (Appendicularia)	<i>Oikopleura dioica</i>
4	Diplostraca	<i>Penilia avirostris</i>
5	Copepods	<i>Euterpina acutifrons</i>
6	Copepods	<i>Parvocalanus crassirostris</i>
7	Copepods	<i>Paracalanus parvus</i>
8	Copepods	<i>Oithona similis</i>
9	Copepods	<i>Ditrichocorycaeus affinis</i>
10	Copepods	<i>Temora turbinata</i>
11	Copepods	<i>Acartia pacifica</i>
12	Copepods	<i>Microsetella norvegica</i>
13	Polychaeta	Polychaeta (trochophore larvae)

14	Holoplankton	Copepod nauplii
15	Meroplanktonic larvae	Barnacle larvae (Balanus, Cirripedia)
16	Meroplanktonic larvae	Brachyuran (crab) zoeae

Appendix C. Checklist of Phytoplankton Taxa Identified in Qinzhou Bay, Spring 2022

No.	Group	Scientific Name
1	Bacillariophyta (diatoms)	<i>Achnanthes brevipes</i>
2	Bacillariophyta (diatoms)	<i>Amphora</i> sp.
3	Bacillariophyta (diatoms)	<i>Amphora coffeaeformis</i>
4	Bacillariophyta (diatoms)	<i>Amphora proteus</i>
5	Bacillariophyta (diatoms)	<i>Amphora coffeaeformis</i> var. <i>acutiuscula</i>
6	Bacillariophyta (diatoms)	<i>Amphora ovalis</i> var. <i>pediculus</i>
7	Bacillariophyta (diatoms)	<i>Amphora grevilleana</i>
8	Bacillariophyta (diatoms)	<i>Amphora angusta</i>
9	Bacillariophyta (diatoms)	<i>Amphora exigua</i>
10	Bacillariophyta (diatoms)	<i>Amphora commutata</i>
11	Bacillariophyta (diatoms)	<i>Amphora robusta</i>
12	Bacillariophyta (diatoms)	<i>Amphora turgida</i>
13	Bacillariophyta (diatoms)	<i>Entomoneis alata</i>
14	Bacillariophyta (diatoms)	<i>Diploneis</i> sp.
15	Bacillariophyta (diatoms)	<i>Diploneis elliptica</i>
16	Bacillariophyta (diatoms)	<i>Ditylum brightwellii</i>
17	Bacillariophyta (diatoms)	<i>Ditylum sol</i>
18	Bacillariophyta (diatoms)	<i>Bacillaria paxillifera</i>
19	Bacillariophyta (diatoms)	<i>Chaetoceros</i> sp.
20	Bacillariophyta (diatoms)	<i>Chaetoceros pelagicus</i>
21	Bacillariophyta (diatoms)	<i>Chaetoceros costatus</i>
22	Bacillariophyta (diatoms)	<i>Chaetoceros diadema</i>
23	Bacillariophyta (diatoms)	<i>Chaetoceros lorenzianus</i>
24	Bacillariophyta (diatoms)	<i>Chaetoceros teres</i>
25	Bacillariophyta (diatoms)	<i>Chaetoceros curvisetus</i>
26	Bacillariophyta (diatoms)	<i>Chaetoceros laciniatus</i>
27	Bacillariophyta (diatoms)	<i>Chaetoceros pseudocurvisetus</i>
28	Bacillariophyta (diatoms)	<i>Chaetoceros paradoxus</i>
29	Bacillariophyta (diatoms)	<i>Chaetoceros decipiens</i> f. <i>singularis</i>
30	Bacillariophyta (diatoms)	<i>Cyclotella</i> sp.

31	Bacillariophyta (diatoms)	<i>Cyclotella meneghiniana</i>
32	Bacillariophyta (diatoms)	<i>Cyclotella striata</i>
33	Bacillariophyta (diatoms)	<i>Coscinodiscus</i> sp.
34	Bacillariophyta (diatoms)	<i>Caloneis permagna</i>
35	Bacillariophyta (diatoms)	<i>Cymbella</i> sp.
36	Bacillariophyta (diatoms)	<i>Cymbella ehrenbergii</i>
37	Bacillariophyta (diatoms)	<i>Cymbella perpusilla</i>
38	Bacillariophyta (diatoms)	<i>Cymbella pusilla</i>
39	Bacillariophyta (diatoms)	<i>Cymbella hustedtii</i>
40	Bacillariophyta (diatoms)	<i>Eunotogramma laevis</i>
41	Bacillariophyta (diatoms)	<i>Eunotogramma debile</i>
42	Bacillariophyta (diatoms)	<i>Fragilaria</i> sp.
43	Bacillariophyta (diatoms)	<i>Gyrosigma spencerii</i>
44	Bacillariophyta (diatoms)	<i>Gyrosigma grovei</i>
45	Bacillariophyta (diatoms)	<i>Gyrosigma tenuissimum</i>
46	Bacillariophyta (diatoms)	<i>Gyrosigma nodiferum</i>
47	Bacillariophyta (diatoms)	<i>Gyrosigma nodiferum</i> var. <i>latum</i>
48	Bacillariophyta (diatoms)	<i>Gyrosigma balticum</i>
49	Bacillariophyta (diatoms)	<i>Grammatophora undulata</i>
50	Bacillariophyta (diatoms)	<i>Hyalodiscus subtilis</i>
51	Bacillariophyta (diatoms)	<i>Leptocylindrus danicus</i>
52	Bacillariophyta (diatoms)	<i>Licmophora abbreviata</i>
53	Bacillariophyta (diatoms)	<i>Lauderia annulata</i>
54	Bacillariophyta (diatoms)	<i>Mastogloia paradoxa</i>
55	Bacillariophyta (diatoms)	<i>Mastogloia rostrata</i>
56	Bacillariophyta (diatoms)	<i>Mastogloia serrata</i>
57	Bacillariophyta (diatoms)	<i>Mastogloia composita</i>
58	Bacillariophyta (diatoms)	<i>Paralia sulcata</i>
59	Bacillariophyta (diatoms)	<i>Navicula</i> sp.
60	Bacillariophyta (diatoms)	<i>Navicula halophila</i>
61	Bacillariophyta (diatoms)	<i>Navicula marina</i>
62	Bacillariophyta (diatoms)	<i>Navicula directa</i>
63	Bacillariophyta (diatoms)	<i>Navicula longa</i>
64	Bacillariophyta (diatoms)	<i>Navicula jejuna</i>
65	Bacillariophyta (diatoms)	<i>Navicula carinifera</i>
66	Bacillariophyta (diatoms)	<i>Navicula mollis</i>
67	Bacillariophyta (diatoms)	<i>Navicula tenera</i>

68	Bacillariophyta (diatoms)	<i>Navicula crucicula</i>
69	Bacillariophyta (diatoms)	<i>Navicula cancellata</i>
70	Bacillariophyta (diatoms)	<i>Navicula membranacea</i>
71	Bacillariophyta (diatoms)	<i>Navicula pavillardii</i>
72	Bacillariophyta (diatoms)	<i>Navicula gracilis</i>
73	Bacillariophyta (diatoms)	<i>Navicula perrotettii</i>
74	Bacillariophyta (diatoms)	<i>Navicula minuscula</i>
75	Bacillariophyta (diatoms)	<i>Navicula northumbrica</i>
76	Bacillariophyta (diatoms)	<i>Navicula cryptocephaloides</i>
77	Bacillariophyta (diatoms)	<i>Navicula cryptocephala</i>
78	Bacillariophyta (diatoms)	<i>Navicula cincta</i>
79	Bacillariophyta (diatoms)	<i>Navicula corymbosa</i>
80	Bacillariophyta (diatoms)	<i>Nitzschia</i> sp.
81	Bacillariophyta (diatoms)	<i>Nitzschia hybrida</i>
82	Bacillariophyta (diatoms)	<i>Nitzschia longissima</i>
83	Bacillariophyta (diatoms)	<i>Nitzschia sigma</i>
84	Bacillariophyta (diatoms)	<i>Nitzschia paleacea</i>
85	Bacillariophyta (diatoms)	<i>Nitzschia palea</i>
86	Bacillariophyta (diatoms)	<i>Nitzschia subtilis</i>
87	Bacillariophyta (diatoms)	<i>Nitzschia frustulum</i>
88	Bacillariophyta (diatoms)	<i>Nitzschia acuminata</i>
89	Bacillariophyta (diatoms)	<i>Nitzschia angularia</i>
90	Bacillariophyta (diatoms)	<i>Nitzschia obtusa</i>
91	Bacillariophyta (diatoms)	<i>Nitzschia fasciculata</i>
92	Bacillariophyta (diatoms)	<i>Nitzschia denticula</i>
93	Bacillariophyta (diatoms)	<i>Nitzschia epithemoides</i>
94	Bacillariophyta (diatoms)	<i>Nitzschia lanceola</i>
95	Bacillariophyta (diatoms)	<i>Nitzschia salinarum</i>
96	Bacillariophyta (diatoms)	<i>Nitzschia capitellata</i>
97	Bacillariophyta (diatoms)	<i>Nitzschia microcephala</i>
98	Bacillariophyta (diatoms)	<i>Nitzschia lorenziana</i>
99	Bacillariophyta (diatoms)	<i>Nitzschia vitrea</i>
100	Bacillariophyta (diatoms)	<i>Nitzschia lorenziana</i> var. <i>densestriata</i>
101	Bacillariophyta (diatoms)	<i>Nitzschia majuscula</i> var. <i>lineata</i>
102	Bacillariophyta (diatoms)	<i>Nitzschia closterium</i>
103	Bacillariophyta (diatoms)	<i>Nitzschia marina</i>
104	Bacillariophyta (diatoms)	<i>Pleurosigma acutum</i>

105	Bacillariophyta (diatoms)	<i>Pleurosigma falx</i>
106	Bacillariophyta (diatoms)	<i>Pleurosigma elongatum</i> var. <i>elongatum</i>
107	Bacillariophyta (diatoms)	<i>Pleurosigma delicatulum</i>
108	Bacillariophyta (diatoms)	<i>Pleurosigma aestuarii</i>
109	Bacillariophyta (diatoms)	<i>Pleurosigma angulatum</i>
110	Bacillariophyta (diatoms)	<i>Pleurosigma decorum</i>
111	Bacillariophyta (diatoms)	<i>Pleurosigma naviculaceum</i>
112	Bacillariophyta (diatoms)	<i>Pleurosigma finmarchicum</i>
113	Bacillariophyta (diatoms)	<i>Pleurosigma intermedium</i>
114	Bacillariophyta (diatoms)	<i>Pleurosigma rigidum</i>
115	Bacillariophyta (diatoms)	<i>Pinnularia</i> sp.
116	Bacillariophyta (diatoms)	<i>Pinnularia brevicostata</i>
117	Bacillariophyta (diatoms)	<i>Pseudo-nitzschia pungens</i>
118	Bacillariophyta (diatoms)	<i>Pseudo-nitzschia delicatissima</i>
119	Bacillariophyta (diatoms)	<i>Rhizosolenia delicatula</i>
120	Bacillariophyta (diatoms)	<i>Rhizosolenia fragilissima</i>
121	Bacillariophyta (diatoms)	<i>Rhizosolenia alata</i>
122	Bacillariophyta (diatoms)	<i>Rhopalodia uncinata</i>
123	Bacillariophyta (diatoms)	<i>Skeletonema costatum</i>
124	Bacillariophyta (diatoms)	<i>Skeletonema dohrnii</i>
125	Bacillariophyta (diatoms)	<i>Skeletonema tropicum</i>
126	Bacillariophyta (diatoms)	<i>Surirella fluminensis</i>
127	Bacillariophyta (diatoms)	<i>Surirella ovata</i>
128	Bacillariophyta (diatoms)	<i>Surirella fastuosa</i>
129	Bacillariophyta (diatoms)	<i>Synedra</i> sp.
130	Bacillariophyta (diatoms)	<i>Synedra acus</i>
131	Bacillariophyta (diatoms)	<i>Synedra gaillonii</i>
132	Bacillariophyta (diatoms)	<i>Synedra formosa</i>
133	Bacillariophyta (diatoms)	<i>Synedra undulata</i>
134	Bacillariophyta (diatoms)	<i>Synedra tabulata</i>
135	Bacillariophyta (diatoms)	<i>Synedra investiens</i>
136	Bacillariophyta (diatoms)	<i>Thalassionema nitzschioides</i>
137	Bacillariophyta (diatoms)	<i>Thalassiothrix longissima</i>
138	Bacillariophyta (diatoms)	<i>Thalassiothrix delicatula</i>
139	Bacillariophyta (diatoms)	<i>Thalassiosira</i> sp.
140	Bacillariophyta (diatoms)	<i>Thalassiosira nordenskiöldii</i>
141	Bacillariophyta (diatoms)	<i>Thalassiosira rotula</i>

142	Bacillariophyta (diatoms)	<i>Plagiotropis maxima</i>
143	Dinophyta (dinoflagellates)	<i>Gonyaulax spinifera</i>
144	Dinophyta (dinoflagellates)	<i>Gonyaulax polyedra</i>
145	Dinophyta (dinoflagellates)	<i>Gonyaulax</i> sp.
146	Dinophyta (dinoflagellates)	<i>Gonyaulax verior</i>
147	Dinophyta (dinoflagellates)	<i>Gonyaulax polygramma</i>
148	Dinophyta (dinoflagellates)	<i>Gyrodinium intriatum</i>
149	Dinophyta (dinoflagellates)	<i>Gymnodinium catenatum</i>
150	Dinophyta (dinoflagellates)	<i>Heterocapsa</i> sp.
151	Dinophyta (dinoflagellates)	<i>Karenia</i> sp.
152	Dinophyta (dinoflagellates)	<i>Karenia mikimotoi</i>
153	Dinophyta (dinoflagellates)	<i>Katodinium glaucum</i>
154	Dinophyta (dinoflagellates)	<i>Lingulodinium polyedrum</i>
155	Dinophyta (dinoflagellates)	<i>Oxyrrhis marina</i>
156	Dinophyta (dinoflagellates)	<i>Prorocentrum micans</i>
157	Dinophyta (dinoflagellates)	<i>Prorocentrum donghaiense</i>
158	Dinophyta (dinoflagellates)	<i>Prorocentrum minimum</i>
159	Dinophyta (dinoflagellates)	<i>Peridiniopsis elpatiewskyi</i>
160	Dinophyta (dinoflagellates)	<i>Peridinium pusillum</i>
161	Dinophyta (dinoflagellates)	<i>Peridinium quinquecorne</i>
162	Dinophyta (dinoflagellates)	<i>Peridinium willei</i>
163	Dinophyta (dinoflagellates)	<i>Peridinium bonatum</i>
164	Dinophyta (dinoflagellates)	<i>Protoperidinium steinii</i>
165	Dinophyta (dinoflagellates)	<i>Scrippsiella trochoidea</i>
166	Chlorophyta (green algae)	<i>Ankistrodesmus</i> sp.
167	Chlorophyta (green algae)	<i>Ankistrodesmus angustus</i>
168	Chlorophyta (green algae)	<i>Ankistrodesmus falcatus</i>
169	Chlorophyta (green algae)	<i>Ankistrodesmus convolutus</i>
170	Chlorophyta (green algae)	<i>Actinastrum hantzschii</i>
171	Chlorophyta (green algae)	<i>Chlamydomonas</i> sp.
172	Chlorophyta (green algae)	<i>Chlamydomonas stellata</i>
173	Chlorophyta (green algae)	<i>Chlamydomonas striolatus</i>
174	Chlorophyta (green algae)	<i>Cladophora insignis</i>
175	Chlorophyta (green algae)	<i>Chlorella vulgaris</i>
176	Chlorophyta (green algae)	<i>Closterium kuetzingii</i>
177	Chlorophyta (green algae)	<i>Klebsormidium fluitans</i>
178	Chlorophyta (green algae)	<i>Nephroselmis olivacea</i>

179	Chlorophyta (green algae)	<i>Pyramimonas nanella</i>
180	Chlorophyta (green algae)	<i>Raphidonema longiseta</i>
181	Chlorophyta (green algae)	<i>Oocystis borgei</i>
182	Chlorophyta (green algae)	<i>Scourfieldia complanata</i>
183	Chlorophyta (green algae)	<i>Stichococcus bacillaris</i>
184	Chlorophyta (green algae)	<i>Scenedesmus</i> sp.
185	Chlorophyta (green algae)	<i>Scenedesmus quadricauda</i>
186	Chlorophyta (green algae)	<i>Trochiscia reticularis</i>
187	Cryptophyta (cryptophytes)	<i>Chroomonas caudata</i>
188	Cryptophyta (cryptophytes)	<i>Chroomonas acuta</i>
189	Cryptophyta (cryptophytes)	<i>Cryptomonas erosa</i>
190	Euglenophyta (euglenoids)	<i>Euglena gracilis</i>
191	Euglenophyta (euglenoids)	<i>Euglena polymorpha</i>
192	Euglenophyta (euglenoids)	<i>Euglena tristella</i>
193	Euglenophyta (euglenoids)	<i>Heteronema abruptum</i>
194	Euglenophyta (euglenoids)	<i>Lepocinclis playfairiana</i>
195	Euglenophyta (euglenoids)	<i>Lepocinclis texta</i>
196	Euglenophyta (euglenoids)	<i>Phacus agilis</i>
197	Euglenophyta (euglenoids)	<i>Phacus cylindrus</i>
198	Cyanophyta (cyanobacteria)	<i>Chroococcus epiphyticus</i>
199	Cyanophyta (cyanobacteria)	<i>Merismopedia minima</i>
200	Cyanophyta (cyanobacteria)	<i>Merismopedia cantonensis</i>
201	Cyanophyta (cyanobacteria)	<i>Aphanocapsa</i> sp.
202	Cyanophyta (cyanobacteria)	<i>Synechocystis thermalis</i>
203	Cyanophyta (cyanobacteria)	<i>Synechocystis minuscula</i>
204	Cyanophyta (cyanobacteria)	<i>Spirulina</i> sp.
205	Chrysophyta (haptophytes)	<i>Prymnesium parum</i>

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