INTRODUCTION

Habitat degradation is one of the most important driving factors that pose serious threats to global biodiversity (Aguilar et al., 2008; Arroyo-Rodriguez et al., 2017; Laurance et al., 2002). For example, 52% of the biodiversity declined between 1970 and 2010, and this loss in the freshwater ecosystems was even greater than in the marine or terrestrial ecosystems (WWF, 2014). Additionally, for many communities, the response of other freshwater communities to environmental change is largely unknown (Celik et al., 2019; Gomes 2021).
et al., 2019). Therefore, knowledge of accurate biodiversity estimates is important for effective conservation and management of natural resources (Dudgeon et al., 2006).

Zooplankton play an important role in the biogeochemical cycling of carbon (C) and nitrogen (N) and aid the stability of food webs in freshwater ecosystems (Walsh et al., 2018). Zooplankton are useful indicators of environmental stressors because they are sensitive to external perturbations such as climate change, habitat degradation, and organic pollution (Stefanni et al., 2018). Therefore, the biomass and species of zooplankton have been widely used in biological water monitoring (Stefanni et al., 2018). However, knowledge of the effect of environmental change on zooplankton communities is hindered by traditional taxonomy challenges (Djurfhus et al., 2018; Machida et al., 2009). Traditional species identification methods and morphology-based individual counting methods are costly and time-consuming, requiring trained personnel with expertise in identifying zooplankton, especially in large-scale environmental investigations and monitoring programs (Ren et al., 2019). Traditional biomonitoring methods apply only to species that are easily observed (Walczyska et al., 2019). For some taxonomic groups, it is difficult or almost impossible to identify the species through morphological methods (Choquet et al., 2018). Therefore, it has become evident that morphological methods do not meet the increasing demand for biodiversity monitoring used in conservation and management decisions.

DNA metabarcoding is an approach that has gained significant traction by allowing ecosystem conservation and management (Goldberg et al., 2016; Taberlet et al., 2012; Thomsen & Willerslev, 2015), and has the potential to greatly reduce cost and time (Thomsen & Willerslev, 2015). Recently, DNA metabarcoding has been widely used for the detection of many taxa in freshwater ecosystems (Deiner et al., 2015; Hänfling et al., 2016; Lopes et al., 2017; Thomsen et al., 2012; Valentini et al., 2016). To date, compared to traditional monitoring, DNA metabarcoding research has demonstrated higher detection capability and cost-effectiveness (Sigsgaard et al., 2015), and it has provided the power to detect invasive and rare species (Dejean et al., 2012; Elbrecht et al., 2018; Piaggio et al., 2014; Sigsgaard et al., 2016). Therefore, DNA metabarcoding may solve the traditional taxonomy challenges of zooplankton and reduce cost and time in large-scale environmental investigations and monitoring programs (Jacchei et al., 2017; Pawlowski et al., 2020; Thomsen & Willerslev, 2015), yet the limitations of the approaches to acquiring data and the existing geographical bias need to be considered (Belle et al., 2019; Bucklin et al., 2016; Rey et al., 2020; Stoeckle et al., 2016).

Poyang Lake, the largest freshwater lake in China, is one of two lakes connected to the Yangtze River, and is a biodiversity hotspot of freshwater species (Huang et al., 2013; Jin et al., 2012). It plays an important role in maintaining and supplementing freshwater biodiversity for the Yangtze River because of extremely abundant aquatic organisms (Jin et al., 2012; Li et al., 2019; Liu, Liu, et al., 2019; Liu, Qin, et al., 2019). Poyang Lake is also a dynamic wetland system, forming a large lake covering more than 3000 km² with a high water level in the rainy season of summer and covering <1000 km² with a low water level in the dry season of winter (Jin et al., 2012; Li et al., 2019). However, in recent years, this lake has been confronted with shrinkage and environmental problems due to anthropogenic habitat disturbances, resulting in the decline of aquatic biodiversity (Huang et al., 2013; Jin et al., 2012; Li et al., 2019). Poyang Lake has suffered from water quality degradation with significantly increasing eutrophication (Liao et al., 2017; Liu et al., 2020). The lake area has declined from 5200 km² in 1949 to 3287 km² in the 21st century (Han et al., 2014; Li et al., 2019). Due to the Three Gorges Dam reducing discharge, seasonal water shortages also occurred frequently (Lai et al., 2014), and affected the survival of freshwater species (Min & Zhan, 2012). In recent years, the fluctuations in water level changed dramatically and occurred an early seasonal drying in lake areas (Feng et al., 2016; Mei et al., 2016). To understand these degradation issues, it is imperative to assess the status of the ecosystem. Previous research points to the seasonal and spatial variability in zooplankton diversity using traditional monitoring methods in Poyang Lake Basin (Chen et al., 2020; Lu et al., 2021; Lv, 2019), but no study used DNA metabarcoding to analyze the seasonal and spatial variability in zooplankton diversity. Here, we aimed to analyze the seasonal and spatial variability in zooplankton diversity using DNA metabarcoding and to explore the correlation between environmental parameters and zooplankton community composition. We test whether it had significantly seasonal and spatial variability in zooplankton diversity using DNA metabarcoding, and whether it had differed from those traditional monitoring methods? This study provides an important reference for the management of aquatic ecosystem health and conservation of aquatic biodiversity.

2 | MATERIALS AND METHODS

2.1 | Study area

Poyang Lake is the largest freshwater lake in China and is connected to the middle reaches of the Yangtze River (Figure 1; Jin et al., 2012). The Poyang Lake Basin has a total area of 16.2 $\times 10^4$ km², an average annual precipitation of 1350–2150 mm, and a surface runoff of 1457 $\times 10^8$ m³. In this study, we considered habitat variation and anthropogenic activities for the selection of sampling areas in the Poyang Lake Basin. We established six sampling sections in the Poyang Lake Basin in April (spring), July (summer), October (autumn) 2019, and January (winter) 2020: the Yangtze River (CJ: 1–3); the connected river channel of Poyang Lake (TJ: 4–9); the main lake area of Poyang Lake (PY: 10–20); Nanjishan area of Poyang Lake (NJ: 21–25); Junshan Lake (JS: 26–30) and Qinglan Lake (QL: 31–35); for anthropogenic activities and substrates details see Table 1. Due to rapid water flow in the connected river channel of Poyang Lake, we did not collect the water samples of zooplankton in the spring and summer of 2019.
2.2 | Sample collection

At per sampling site, 20 L quantitative water samples of zooplankton were collected using 64 µm mesh size net from a bottom depth, just above the sediment, and at the surface (i.e., 0.5 m) were passed in the field. In the laboratory, three quantitative samples of zooplankton from the Yangtze River were further mixed and filtered through 5-µm microporous filter paper (Millipore) in April (spring), July (summer), October (autumn) 2019, and January (winter) 2020, respectively. Filter membranes were then placed in a 5-ml centrifuge tube. Finally, a total of four samples from the Yangtze River were used for DNA metabarcoding analysis and stored at −20°C until extraction of DNA (Table S1). Similarly, for other sampling sections, we used the same methods to obtain samples used for DNA metabarcoding analysis (Table S1). Therefore, a total of 22 samples from the Poyang Lake Basin were used for DNA metabarcoding analysis.

2.3 | DNA extraction, PCR amplification, and high-throughput sequencing

Genomic DNA from the 22 samples was extracted using the TIANamp Marine Animals DNA Kit (TianGen). The concentration and quality of DNA were estimated using a Nanodrop 2000 spectrophotometer (Thermo Scientific) and agarose gel electrophoresis.

DNA metabarcoding of mitochondrial COI 313 bp region was used to analyze the seasonal and spatial variability in zooplankton diversity. PCR amplification of the cytochrome c oxidase subunit I (COI) genes was performed using the forward primer sequence miCOlntF (5'-GGWACWGGWTGAACWGTWTAYCCYCC-3'), and the reverse primer sequence HCO700DY2 (5'-TAAACTTCAGGGTGACCAAAAAATCA-3') (Leray et al., 2013). Sample-specific 7-bp barcodes were incorporated into the primers for multiplex sequencing at the library preparation part. The PCR
| Parameters       | Yangtze River Mean ± SD | Connected river channel of Poyang Lake Mean ± SD | Main lake area of Poyang Lake Mean ± SD | Junshan Lake Mean ± SD | Qinglan Lake Mean ± SD | Nanjishan area of Poyang Lake Mean ± SD |
|------------------|-------------------------|-----------------------------------------------|-------------------------------------|------------------------|-----------------------|----------------------------------------|
| WD (m)           | 13.83 ± 4.06            | 8.96 ± 1.31                                  | 5.9 ± 1.01                          | 5.03 ± 0.47            | 3.45 ± 1.22            | 1.67 ± 0.45                            |
| V (m/s)          | 0.38 ± 0.09             | 0.31 ± 0.04                                  | 0.21 ± 0.04                         | 0.15 ± 0.03            | 0.17 ± 0.04            | 0.10 ± 0.02                            |
| Turb (NTU⁺)      | 13.5 ± 4.39             | 26.5 ± 6.15                                  | 13.16 ± 0.75                        | 6.55 ± 3.68            | 30.67 ± 18.16          | 73.72 ± 21.83                        |
| T (°C)           | 19.85 ± 2.96            | 19.72 ± 3.63                                 | 19.63 ± 4.08                        | 20.29 ± 4.33           | 21.43 ± 3.94           | 19.31 ± 3.95                          |
| Sal (mg/L)       | 0.13 ± 0.03             | 0.05 ± 0.01                                  | 0.04 ± 0.01                         | 0.08 ± 0.03            | 0.06 ± 0.01            | 0.05 ± 0.01                           |
| DO (mg/L)        | 8.75 ± 0.11             | 8.71 ± 0.05                                  | 8.16 ± 0.25                         | 8.46 ± 0.31            | 7.66 ± 0.38            | 7.56 ± 0.23                          |
| Chl- a (μg/L)    | 5.11 ± 1.56             | 17.08 ± 1.99                                 | 16.69 ± 4.08                        | 10.28 ± 3.72           | 37.98 ± 11.88          | 25.28 ± 4.97                         |
| pH               | 6.8 ± 0.31              | 6.67 ± 0.11                                  | 6.83 ± 0.12                         | 7.32 ± 0.41            | 7.09 ± 0.27            | 7.21 ± 0.25                           |
| TN (mg/L)        | 1.92 ± 0.03             | 1.75 ± 0.12                                  | 1.65 ± 0.17                         | 1.98 ± 0.48            | 0.92 ± 0.12            | 1.74 ± 0.2                           |
| TP (mg/L)        | 0.15 ± 0.03             | 0.16 ± 0.02                                  | 0.16 ± 0.01                         | 0.22 ± 0.05            | 0.11 ± 0.01            | 0.18 ± 0.01                          |
| Anthropogenic activities | Sand mining, industrial pollution, and urban development | Sand mining and urban development | Sand mining and overfishing | Aquaculture | Aquaculture and overfishing | Aquaculture |
| Substrates       | Sand                   | Hard mud, sand, and silt                     | Hard mud, sand, and silt            | Silt                  | Silt and sand          | Silt                                  |

Abbreviations: Chl- a, chlorophyll-a; DO, dissolved oxygen; Sal, salinity; T, water temperature; TN, total nitrogen; TP, total phosphorus; Turb, turbidity; V, water velocity; WD, water depth.
reaction was carried out in a 25 μl volume containing 5 μl of 5 × buffer, 14.75 μl of ddH2O, 1 μl of 10 μM forward primer, 1 μl of 10 μM reverse primer, 2 μl of 2.5 mM deoxyribonucleotide triphosphates, 0.25 μl fast pfu DNA polymerase, and 1 μl of genomic DNA. Triplicate PCR reactions were performed for each sample to minimize the potential bias of the PCR. Sterile water was used as a negative control in the study and the strategies were employed in sterile operating table of the laboratory to prevent DNA contamination. The PCR amplifications were conducted for an initial denaturation at 98°C for 5 min, followed by 27 cycles of 98°C for 30 s, annealing temperature of 50°C for 30 s, 72°C for 45 s, and a final extension at 72°C for 5 min. PCR products were detected on a 2% agarose gel, and fragments from the gel were purified with Agencourt AMPure Beads (Beckman Coulter). After purification on the gel, products of PCR were quantified using the PicoGreen dsDNA Assay Kit (Invitrogen).

The PCR amplification products were sequenced using the Illumina MiSeq platform from the Shanghai Personal Biotechnology Co., Ltd (Degnan & Ochman, 2012). Libraries were prepared using Illumina’s TruSeq Nano DNA LT Library Prep Kit. The PCR amplification products were pooled to form a library for sequencing. Equimolar PCR products from each sample were used to ensure an equal contribution of each community in the final sequencing library. An Illumina MiSeq platform was used based on a paired-end 300 bp sequence read run after library preparation.

### 2.4 | Bioinformatics

The paired-end sequences were assembled using the FLASH software (http://ccb.jhu.edu/software/FLASH/; Magoc & Salzberg, 2011). Raw FASTQ files were demultiplexed and quality filtered using QIIME 2 (Bolyen et al., 2019), and reads of low quality (mean quality <20, scanning window = 50; contained ambiguous ‘N’; sequence length: ≥150 bp) were discarded. Mothur software (Edgar, 2010; Quast et al., 2013) was used to cluster operational taxonomic units (OTUs) of zooplankton with a 97% similarity cutoff, and QIIME2 (Bolyen et al., 2019) was used to generate rarefaction curves. According to a reference database (NCBI nucleotide database in Genbank; Greengenes database (Release 13.8, http://green genes.secondgenome.com/), DeSantis et al., 2006; RDP (Ribosomal Database Project) database (Release 11.1, http://rdp.cme.msu.edu/), Cole et al., 2009; Silva database (Release132, http://www.arb-silva.de), Quast et al., 2013; UNITE database (Release 7.0, https://unite. ut.ee/). Koljalg et al., 2013), we used the Statistical Assignment Package (SAP version 1.3.2; Munch et al., 2008) to assign the representative sequence from each zooplankton OTU to a specific taxonomic group. SAP was used to retrieve homologs in each query sequence. The phylogenetic trees, taxonomy compositions, and abundances were visualized using MEGAN (Huson et al., 2011). The posterior probability was calculated for the query sequence to belong to a taxonomic group at phylum, class, order, family, genus, and species levels of zooplankton, respectively. The assignments at a significance level of 60% (posterior probability) were accepted, and SAP to retrieve 100 homologs at >80% sequence similarity was allowed. Alpha diversity indices, such as Chao1 richness estimator, ACE metric (Abundance-based Coverage Estimator), Shannon diversity index, and Simpson index, were calculated using the combined OTU-tables of the same species table of zooplankton in Mothur software (Edgar, 2010; Quast et al., 2013). The non-metric multidimensional scaling (NMDS) ordination plots were used to assess the variation in the zooplankton community among sampling sections. The Bray–Curtis resemblance matrix of the zooplankton community from sampling sections was generated and represented by the NMDS ordination plots. The NMDS ordination plots and Bray–Curtis resemblance matrix were generated using R version 2.13.1 (R Development Core Team, 2011) and the VEGAN package (Oksanen et al., 2015). One-way analysis of variance (ANOVA) was used to detect differences in the OTUs, alpha diversity indices, and environmental factors between each section and each season. We used post hoc tests to make further comparisons. We used Tukey’s honestly significant difference tests for these comparisons, but in cases of persistent heteroscedasticity (i.e., when Levene’s test was significant) we used Games–Howell tests because they do not assume equal variances between groups. SPSS version 22.0 was used to perform the ANOVA tests.

### 2.5 | Measurement of physicochemical parameters

We used four water quality variables to analyze changes in the environmental factors in the Poyang Lake Basin in April (spring), July (summer), October (autumn) 2019, and January (winter) 2020. We used a YSI 650MDS (YSI) multiparameter meter to measure the water temperature (°C), dissolved oxygen (mg/L), pH, salinity (mg/L), and turbidity (NTU”). Chlorophyll-a concentration (mg/L) was measured using a chlorophyll meter (PCH-800). A velocity meter (FP111, Global Water, 0.1 m/s accuracy) was used to measure the water velocity, and a digital sonar system (H22px handheld sonar system) was used to measure the water depth (m). In addition, concentrated sulfuric acid (H2SO4) was used to preserve the collected water samples. These collected water samples for nutrient analysis were then refrigerated and transported to the Nanchang University laboratory. The total nitrogen (TN; mg/L) and total phosphorus (TP; mg/L) content were analyzed using ultraviolet spectrophotometry (Huang et al., 1999; Wei et al., 1989).

### 2.6 | Correlation between environmental factors and zooplankton community structure

We performed a detrended correspondence analysis for the composition of zooplankton community to determine whether linear or unimodal ordination (Lep & Smilauer, 2003). To evaluate the correlation between environmental factors and community composition of the zooplankton, a redundancy analysis (RDA) with 499 Monte Carlo
permutations was performed using CANOCO version 4.5 (ter Braak & Verdonschot, 1995; Lep & Smilauer, 2003). All environmental factors and community composition of zooplankton were log_{10}(X + 1) transformed to meet the assumptions of multivariate normality and to moderate the influence of extreme data (Borcard et al., 2011).

3 RESULTS

3.1 The OTUs of zooplankton

A total of 1,197,035 raw sequences were generated from 22 samples (NCBI SRA Accession no. PRJNA661399). A total of 338,947 sequences (28.3%) were obtained after quality filtering and 240,053 sequences belonged to the zooplankton. The sequence number of each OTU sample was distributed in the 97% sequence similarity threshold based on Chao1 and Shannon rarefaction curves (Figure S1). The number of total OTUs per sample ranged from 72 to 355, and the number of zooplankton OTUs per sample ranged from 45 to 301 (Table 2). Significant differences were detected in the number of zooplankton OTUs in each season (ANOVA, p < .05). The number of zooplankton OTUs in spring and summer was greater than that in autumn and winter (Table 2; Table S2; Figure S2). In addition, we also found significant differences in the number of zooplankton OTUs among the same sampling area (ANOVA, p < .05). The number of zooplankton OTUs in the main lake areas of Poyang Lake were greater than those in the other sampling areas (Table 2; Table S2; Figure S2).

3.2 Seasonal and spatial variability in the diversity of zooplankton

The combined OTUs of the same zooplankton species were categorized into 92 species, 45 genera, 26 families, eight orders, four classes, and two phyla in the Poyang Lake Basin (Table S3). Of the total zooplankton species detected 52.2% were rotifera, 29.3% were copepods, and 18.5% were cladocerans. Significant differences were detected in the relative abundance of zooplankton in each season (ANOVA, p < .05). The relative abundance of rotifera in spring and summer was greater than that in autumn and winter (Figure 2; Figure S3). The relative abundance of copepods in winter and cladocerans in autumn was greater than that in other seasons (Figure 2; Figure S3). In addition, we also found significant differences in the relative abundance of zooplankton in each sampling area (ANOVA, p < .05). The relative abundance of rotifera in the Qinlan Lake and Nanjishan area of Poyang Lake was greater than that in the other sampling areas (Figure 2; Figure S3).

Significant differences were detected in the diversity of zooplankton among the different seasons (ANOVA, p < .05). The diversity of zooplankton in the summer (Simpson = 0.87; Chao1 = 207.5; ACE = 218.7; Shannon = 4.3) was greater than those in the other seasons (Table 2). We also found significant differences in the diversity of zooplankton among the sampling areas (ANOVA, p < .05). The diversity of zooplankton in the main lake areas of Poyang Lake (Simpson = 0.84; Chao1 = 180.83; ACE = 190.53; Shannon = 3.97) and Nanjishan area of Poyang Lake (Simpson = 0.89; Chao1 = 173.67; ACE = 178.40; Shannon = 4.46) were greater than those in the other sampling areas (Table 2).

3.3 Community structure of zooplankton

The Bray–Curtis resemblance matrix showed that the community structure of zooplankton in spring was divided into three areas: the first area included the Nanjishan area of Poyang Lake and Qinlan Lake, the second area included the Yangtze River and the main lake area of Poyang Lake, and the third area included the Junshan Lake (Figure 3). The community structure of zooplankton in summer was divided into three areas, in which the first area included the main lake area of Poyang Lake, Nanjishan area of Poyang Lake, and Qinlan Lake, the second area included the Yangtze River, and the third area included the Junshan Lake (Figure 3). The community structure of zooplankton in autumn was divided into four areas, in which the first area included the Qinlan Lake and the main lake area of Poyang Lake, the second area included the Junshan Lake, the third area included the Nanjishan area of Poyang Lake and the Yangtze River, and the fourth area included the connected-river channel of Poyang Lake (Figure 3). The community structure of zooplankton in winter was divided into five areas, in which the first area included the Qinlan Lake and Nanjishan area of Poyang Lake, the second area included the Yangtze River, the third area included the connected-river channel of Poyang Lake, the fourth area included the main lake area of Poyang Lake, and the fifth area included the Junshan Lake (Figure 3). The results of the NMDS plot were coincident with the Bray–Curtis resemblance matrix, indicating that the results were reliable (stress = 0.11; Figure 3).

3.4 Correlation between the community composition of zooplankton and environmental factors

Significant differences were detected in the water depth, turbidity, dissolved oxygen, chlorophyll-a, and salinity among the sampling areas (ANOVA, p < .05; Table 1). Additionally, significant differences were found in the water depth, temperature, total nitrogen, and velocity between the seasons (ANOVA, p < .05; Table 1). Redundancy analysis showed that Leptodoridae, Gastropidae, Centropagidae, Macrotrichidae, Daphniidae, Bosminidae, Lecanidae, Hexarthridae, and Diaptomidae in spring were correlated with water depth, velocity,
| Sampling areas                          | Time     | Code | Simpson | Chao1 | ACE   | Shannon | Total sequences | Total OTUs | Zooplankton sequences | Zooplankton OTUs |
|----------------------------------------|----------|------|---------|-------|-------|---------|-----------------|------------|-----------------------|-----------------|
| **Yangtze River**                      | Spring   | CJ1  | 0.82    | 143.56| 144.37| 3.65    | 16,565          | 171        | 5927                  | 108             |
|                                        | Summer   | CJ2  | 0.77    | 104.88| 108.52| 3.31    | 13,298          | 107        | 5694                  | 62              |
|                                        | Autumn   | CJ3  | 0.84    | 66.00  | 68.33  | 3.77    | 13,420          | 72         | 12,414                | 58              |
|                                        | Winter   | CJ4  | 0.63    | 63.40  | 67.03  | 2.34    | 16,348          | 76         | 13,671                | 45              |
|                                        | Mean     |      | 0.76    | 94.46  | 97.06  | 3.27    | 14,908          | 107        | 9427                  | 68              |
| **Main lake area of Poyang Lake**      | Spring   | PY1  | 0.88    | 231.57 | 243.69| 4.46    | 13,075          | 255        | 9451                  | 198             |
|                                        | Summer   | PY2  | 0.91    | 231.16 | 249.31| 4.49    | 17,320          | 300        | 14,724                | 262             |
|                                        | Autumn   | PY3  | 0.78    | 131.97 | 134.35| 3.29    | 16,649          | 166        | 10,546                | 133             |
|                                        | Winter   | PY4  | 0.81    | 128.61 | 134.77| 3.62    | 15,320          | 146        | 10,140                | 133             |
|                                        | Mean     |      | 0.84    | 180.83 | 190.53| 3.97    | 15,591          | 217        | 11,215                | 181             |
| **Nanjishan area of Poyang Lake**      | Spring   | NJ1  | 0.92    | 148.45 | 152.68| 4.69    | 17,046          | 181        | 16,535                | 160             |
|                                        | Summer   | NJ2  | 0.91    | 277.11 | 288.74| 4.89    | 17,234          | 211        | 16,892                | 193             |
|                                        | Autumn   | NJ3  | 0.89    | 178.13 | 179.02| 4.48    | 17,140          | 238        | 11,316                | 194             |
|                                        | Winter   | NJ4  | 0.83    | 91.00  | 93.14  | 3.78    | 16,840          | 101        | 16,755                | 90              |
|                                        | Mean     |      | 0.89    | 173.67 | 178.40| 4.46    | 17,065          | 183        | 15,375                | 159             |
| **Junshan Lake**                       | Spring   | JS1  | 0.22    | 65.00  | 74.27  | 0.96    | 17,374          | 90         | 1702                  | 63              |
|                                        | Summer   | JS2  | 0.85    | 167.69 | 175.65| 4.03    | 17,042          | 355        | 14,050                | 301             |
|                                        | Autumn   | JS3  | 0.86    | 95.87  | 100.46| 3.54    | 17,309          | 130        | 11,417                | 111             |
|                                        | Winter   | JS4  | 0.65    | 87.67  | 91.86  | 2.63    | 17,098          | 117        | 7304                  | 103             |
|                                        | Mean     |      | 0.65    | 104.06 | 110.56| 2.79    | 17,206          | 173        | 8618                  | 145             |
| **Qinglan Lake**                       | Spring   | QL1  | 0.58    | 120.88 | 122.94| 2.87    | 15,716          | 148        | 14,180                | 112             |
|                                        | Summer   | QL2  | 0.92    | 256.52 | 271.14| 4.91    | 11,893          | 271        | 8710                  | 221             |
|                                        | Autumn   | QL3  | 0.70    | 139.05 | 139.37| 3.16    | 10,973          | 142        | 10,170                | 123             |
|                                        | Winter   | QL4  | 0.93    | 134.08 | 134.58| 4.94    | 7814           | 152        | 7317                  | 138             |
|                                        | Mean     |      | 0.78    | 162.63 | 167.01| 3.97    | 11,599          | 178        | 10,094                | 149             |
| **Connected river channel of Poyang Lake** | Autumn | TJ3  | 0.77    | 125.69 | 131.55| 3.24    | 17,091          | 188        | 16,252                | 164             |
|                                        | Winter   | TJ4  | 0.54    | 93.88  | 95.08  | 2.24    | 16,381          | 118        | 4886                  | 86              |
|                                        | Mean     |      | 0.66    | 109.79 | 113.32| 2.74    | 16,736          | 153        | 10,569                | 125             |
salinity, dissolved oxygen, and total nitrogen (Figure 4a). Sididae, Asplanchnidae, Cyclopidae, Filinidae, Brachionidae, Synchaetidae, Philodinidae, and Chydoridae in spring were correlated with water velocity and chlorophyll-a (Figure 4a). Lepadellidae, Trichocercidae, and Testudinellidae in spring were correlated with turbidity, pH, and chlorophyll-a (Figure 4a). Diaptomidae, Sididae, Moinidae, Synchaetidae, Flosculariidae, Filinidae, and Testudinellidae in summer were correlated with dissolved oxygen, salinity, total phosphorus, and total nitrogen (Figure 4b). Asplanchnidae, Hexarthridae, Trichocercidae, Brachionidae, Calanidae, Daphniidae, Lepadellidae, and Cyclopidae in summer were correlated with turbidity, water temperature, pH, and chlorophyll-a (Figure 4b). Leptodoridae, Lecanidae, and Macrotrichidae in summer were correlated with turbidity and chlorophyll-a (Figure 4b). Gastropidae and Bosminidae in summer were correlated with dissolved oxygen, water depth, water velocity, and total nitrogen (Figure 4b). Macrotrichidae, Synchaetidae, Cyclopidae, Brachionidae, Lecanidae, Asplanchnidae, Moinidae, Chydoridae, Sididae, Bosminidae, Adinetidae, and Filinidae in autumn were correlated with turbidity, total phosphorus, total nitrogen, pH, and chlorophyll-a (Figure 4c). Diaptomidae, Testudinellidae, Hexarthridae, Leptodoridae, and Gastropidae in autumn were correlated with water temperature, total phosphorus,
and dissolved oxygen (Figure 4c). Diaptomidae, Testudinellidae, Hexarthridae, Leptodoridae, and Gastropidae in autumn were correlated with water temperature, total phosphorus, and dissolved oxygen (Figure 4c). Centropagidae, Daphniidae, and Trichocercidae in autumn were correlated with salinity, water depth, water velocity, water temperature, and dissolved oxygen (Figure 4c). Leptodoridae, Gastropidae, Centropagidae, Macrotrichidae, Daphniidae, Bosminidae, Lecanidae, Hexarthridae Sididae, Asplanchnidae, Filinidae, Brachionidae, Synchaetidae, Philodinidae, Chyadoridae, Lepadellidae, Trichocercidae, and Testudinellidae in winter were correlated with water temperature, pH, and chlorophyll-a (Figure 4d). Cyclopidae and Diaptomidae in winter were correlated with total phosphorus, water depth, water velocity, total nitrogen, and dissolved oxygen (Figure 4d). Hexarthridae and Adinetidae in winter were correlated with water depth, water velocity, salinity, and turbidity (Figure 4d).
Knowledge of accurate biodiversity estimates is important for effective conservation and management of natural resources (Dudgeon et al., 2006). Improved biodiversity monitoring programs are important for maintaining the integrity of freshwater ecosystems (Dudgeon et al., 2006). DNA metabarcoding has been widely used for the detection of many taxa in freshwater ecosystems (Lopes et al., 2017; Valentini et al., 2016). Understanding the potential of DNA metabarcoding to identify aquatic biodiversity and the distribution dynamics in freshwater ecosystems is important for improving biodiversity monitoring (Thomsen & Willerslev, 2015). In this study, to determine the seasonal and spatial zooplankton variations and association of water quality, the diversity of zooplankton was analyzed using DNA metabarcoding in the Poyang Lake Basin. The results showed that the combined OTU-table of the same zooplankton species from the Poyang Lake Basin was categorized into...
92 species, 45 genera, 26 families, eight orders, four classes, and two phyla using DNA metabarcoding, which was similar to a recent study using traditional biomonitoring methods (Chen et al., 2020; Lu et al., 2021; Lv, 2019). In addition, rotifers constitute the most diverse group within the zooplankton community using traditional biomonitoring methods (Chen et al., 2020; Hu et al., 2019; Lu et al., 2021; Lv, 2019; Qin et al., 2020). DNA metabarcoding in this study also revealed rotifers as the most diverse group.

Significant differences in the diversity of zooplankton were found among the different seasons. The diversity of zooplankton in spring and summer was greater than those in autumn and winter, which was similar to those in studies based on traditional biomonitoring methods (Chen et al., 2020; Lu et al., 2021; Lv, 2019). Such temporal distribution patterns of zooplankton in the Poyang Lake Basin have also been reported by previous microscopy-based studies (Chen et al., 2020; Lu et al., 2021; Lv, 2019). The temporal distribution in the relative abundance of zooplankton major groups was also consistent with the plankton ecology group model (PEG model emphasized the role of physical factors, grazing and nutrient limitation for phytoplankton, and the role of food limitation and fish predation for zooplankton; Sommer et al., 2012). It may be related to the seasonality in most subtropical lakes and rivers (Scarabotti et al., 2017; Srifa et al., 2016). The synergistic coupling between the change in season and water level led to seasonal variation in the zooplankton community in the Poyang Lake Basin.

Significant differences in the diversity of zooplankton were found among the sampling areas. The diversity of the zooplankton in the main lake area of Poyang Lake and the Nanjishan area of Poyang Lake (southern district in Poyang Lake) were greater than those in the other sampling areas. Spatial changes in the zooplankton in our study were similar to those in studies based on traditional biomonitoring methods (Chen et al., 2020; Lu et al., 2021; Lv, 2019). Some studies have shown that habitat variability of the Poyang Lake Basin could affect the community structure of zooplankton based on traditional biomonitoring methods (Lu et al., 2021; Lv, 2019; Qin et al., 2020). Indeed, the habitat diversity of the lake area is higher than that of the other sampling areas. The lake area has abundant nutrients and a stable water body, which provides a good habitat for the growth of zooplankton (Liu et al., 2020). The relatively rapid water flow in the connected river channel of Poyang Lake and the Yangtze River is not conducive to the growth and survival of zooplankton (Li et al., 2019; Liu et al., 2020). Uncovering the environmental factors affecting the observed deterministic community dynamics of zooplankton is a key challenge. In this study, the community composition of zooplankton was correlated with turbidity, water temperature, pH, total phosphorus, and chlorophyll-a, which was similar to studies based on traditional biomonitoring methods (Lu et al., 2021; Lv, 2019; Qin et al., 2020). Indeed, some studies have shown that environmental factors affected the community composition of zooplankton (Hu et al., 2014, 2019; Hussain et al., 2016; Trevisan & Forsberg, 2007). Water temperature is an important environmental factor that affects the composition of zooplankton community (Kagalou et al., 2010). For example, water temperature could affect the growth and reproduction of zooplankton (Hu et al., 2008, 2019). Hu et al. (2019) found that pH had a significant effect on the seasonal variation of the zooplankton community. This study also showed that pH negatively affected the community composition of zooplankton. Total phosphorus was strongly correlated with the biomass of algae, resulting in an increase in zooplankton production (Qin et al., 2020; Trevisan & Forsberg, 2007). Chlorophyll-a and total phosphorus in spring and summer were the main environmental factors affecting the community composition of zooplankton in this study.

4.2 | Effect of human activity on the seasonal and spatial variability of zooplankton diversity

The Poyang Lake Basin is one of the most human disturbance basins in China, and biodiversity conservation faces great challenges (Li et al., 2019; Liu, Liu, et al., 2019; Liu, Qin, et al., 2019; Zhang et al., 2020). Human activities have affected the Poyang Lake Basin’s freshwater organisms and their habitats with continual socioeconomic development (Zhang et al., 2020). The degraded habitat in Poyang Lake Basin has seriously affected freshwater biodiversity (Li et al., 2019). The degradation process is driven by human activities, such as sand mining, dam construction, water pollution, and overfishing in the basin (Li et al., 2019; Liu, Liu, et al., 2019; Liu, Qin, et al., 2019). For example, the increasing concentrations of nutrients and heavy metals have resulted in water quality deterioration, which indirectly affected zooplankton diversity (Liu et al., 2020; Lu et al., 2021). Sand mining has changed the physicochemical factors of water, affecting the zooplankton community (Johnson et al., 2012; Narin & Michel, 2009). Dam constructions led to significant change in hydrological conditions, affecting the zooplankton community (Liu et al., 2017; Liu, Liu, et al., 2019; Liu, Qin, et al., 2019). This study using DNA metabarcoding proved the seasonal and spatial differences in the community structure of zooplankton response to changes in environmental factors in the Poyang Lake Basin. Habitat variations affected by human activities and seasonal change could be the main driving factors for the variations of zooplankton community. Therefore, anthropogenic pressures need more attention in the Poyang Lake Basin.

AUTHOR CONTRIBUTIONS

Xuemei Xue Qiu: Data curation (equal); formal analysis (equal); investigation (equal); methodology (equal); resources (equal); software (equal); writing – original draft (equal); writing – review and editing (equal). Xiongjun Liu: Data curation (equal); formal analysis (equal); funding acquisition (equal); investigation (equal); methodology (equal); resources (equal); software (equal); writing – original draft (equal); writing – review and editing (equal). Quanfeng Lu: Investigation (equal); resources (equal); Jinping Chen: Investigation (equal); resources (equal); Tao Liang: Investigation (equal); resources (equal). Weikai Wang: Investigation (equal); resources (equal). Shan Ouyang: Writing – original draft (equal); writing – review and editing (equal).
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CONFLICT OF INTEREST
None declared.

DATA AVAILABILITY STATEMENT
All raw sequences were deposited in the NCBI Sequence Read Archive under accession number SRA Accession no. PRJNA661399.

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REFERENCES
Aguilar, R., Quesada, M., Ashworth, L., Herreries-Diego, Y., & Lobo, J. (2008). Genetic consequences of habitat fragmentation in plant populations: Susceptible signals in plant traits and methodological approaches. Molecular Ecology, 17, 5177–5188. https://doi.org/10.1111/j.1365-294X.2008.03971.x

Arroyo-Rodriguez, V., Melo, F. P. L., Martinez-Ramos, M., Bongers, F., Chazdon, R. L., Meave, J. A., Norden, N., Santos, B. A., Leal, I. R., & Tabarelli, M. (2017). Multiple successional pathways in human-modified tropical landscapes: new insights from forest succession, forest fragmentation and landscape ecology research. Biological Reviews, 92, 326–340. https://doi.org/10.1111/brv.12231

Belle, C. C., Stoeckle, B. C., & Geist, J. (2019). Taxonomic and geographical representation of freshwater environmental DNA research in aquatic conservation. Aquatic Conservation: Marine and Freshwater Ecosystems, 29, 1996–2009. https://doi.org/10.1002/aqc.3208

Bolyen, E., Rideout, J. R., Dillon, M. R., Bokulich, N. A., Abnet, C. C., Al-Ghalith, G. A., Alexander, H., Alm, E. J., Arumugam, M., Asnicar, F., Bai, Y., Bisanz, J. E., Bittinger, K., Brejnrod, A., Brislawn, C. J., Brown, C. T., Callahan, B. J., Caraballo-Rodriguez, A. M., Chase, J., ... Caporaso, J. G. (2019). Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. Nature Biotechnology, 37, 852–857. https://doi.org/10.1038/s41587-019-0209-9

Borcard, D., Gillet, F., & Legendre, L. (2011). Numerical ecology with R. Springer.

Bucklin, A., Lindeque, P. K., Rodriguez-Ezepeleta, N., Albaina, A., & Lehtiniemi, M. (2016). Metabarcoding of marine zooplankton: Prospects, progress and pitfalls. Journal of Plankton Research, 38(3), 393–400. https://doi.org/10.1093/plankt/fbw023

Celik, K., Bokzurt, A., & Sevindik, T. O. (2019). Seasonal dynamics of the zooplankton community in the temperate eutrophic aygören reservoir (balıkesir), turkey related to certain physicochemical parameters of water. Turkish Journal of Fisheries and Aquatic Sciences, 19, 503–512.

Chen, J. Q., Zhao, K., Cao, Y., Wu, B., Pang, W. T., You, Q. M., & Wang, Q. X. (2020). Zooplankton community structure and its relationship with environmental factors in Poyang Lake. Acta Ecological Sinica, 40, 1–15.

Choquet, M., Kosobokova, K., Kwaśniewski, S., Hatlebakk, M., Dhanasiri, A. K. S., Melle, W., Daase, M., Svensen, C., Sereide, J. E., & Hoarau, G. (2018). Can morphology reliably distinguish between the Copepods calanus finmarchicus and C. glacialis, or is DNA the only way? Limnology and Oceanography - Methods, 16, 237–252.

Cole, J. R., Wang, Q., Cardenas, E., Fish, J., Chai, B., Farris, R. J., Kulam-Syed-Mohideen, A. S., McGarrell, D. M., Marsh, T., Garrity, G. M., & Tiedje, J. M. (2009). The Ribosomal Database Project: Improved alignments and new tools for rRNA analysis. Nucleic Acids Research, 37, D141–D145. https://doi.org/10.1093/nar/gkn879

Degnan, P. H., & ochman, H. (2012). Illumina-based analysis of microbial community diversity. The ISME Journal, 6, 183–194. https://doi.org/10.1038/ismej.2011.74

Deiner, K., Walser, J.-C., Mächler, E., & Altermatt, F. (2015). Choice of capture and extraction methods affect detection of freshwater biodiversity from environmental DNA. Biological Conservation, 183, 53–63. https://doi.org/10.1016/j.biocon.2014.11.018

Dejean, T., Valentini, A., Miquel, C., Taberlet, P., Bellemain, E., & Miaud, C. (2012). Improved detection of an alien invasive species through environmental DNA barcoding: The example of the American bullfrog Lithobates catesbeianus. Journal of Applied Ecology, 49, 953–959.

DeSantis, T. Z., Hugenholtz, P., Larsen, N., Rojas, M., Brodie, E. L., Keller, K., Huber, T., Dalevi, D., Hu, P., & Andersen, G. L. (2006). Greengenes, a chimera-checked 16S rRNA gene database and workbench compatible with ARB. Applied and Environmental Microbiology, 72, 5069–5072. https://doi.org/10.1128/AEM.03006-05

Djurhuus, A., Pitz, K., Sawaya, N. A., Rojas-Márquez, J., Michaud, B., Montes, E., Muller-Karger, F., & Breitbart, M. (2018). Evaluation of marine zooplankton community structure through environmental DNA metabarcoding. Limnology and Oceanography: Methods, 16, 209–221. https://doi.org/10.1002/lom3.10237

Dudgeon, D., Arthington, A. H., Gessner, M. O., Kawabata, Z.-I., Knowler, D. J., Lévêque, C., Naiman, R. J., Prieur-Richard, A.-H., Soto, D., Stiassny, M. L. J., & Sullivan, C. A. (2006). Freshwater biodiversity: Importance, threats, status and conservation challenges. Biological Reviews, 81, 163–182. https://doi.org/10.1111/j.1464-7931.2006.006950

Edgar, R. C. (2010). Search and clustering orders of magnitude faster than BLAST. Bioinformatics, 26, 2460–2461. https://doi.org/10.1093/bioinformatics/btp461

Elbrecht, V., Vamos, E. E., Steinke, D., & Leese, F. (2018). Estimating intraspecific genetic diversity from community DNA metabarcoding data. PeerJ, 6, e4644. https://doi.org/10.7717/peerj.4644

Feng, L., Han, X. X., Hu, C. M., & Chen, X. L. (2016). Four decades of wetland changes of the largest freshwater lake in China: Possible linkage to the Three Gorges Dam? Remote Sensing of Environment, 176, 43–55. https://doi.org/10.1016/j.rse.2016.01.011

Goldberg, C. S., Turner, C. R., Deiner, K., Klymus, K. E., Thomsen, P. F., Murphy, M. A., Spear, S. F., McKee, A., Oyler-McCance, S. J., Cormon, R. S., Laramie, M. B., Mahon, A. R., Lance, R. F., Pilling, D. S., Strickler, K. M., Waits, L. P., Fremier, A. K., Takahara, T., Herder, J. E., ... Taberlet, P. (2016). Critical considerations for the application of environmental DNA methods to detect aquatic species. Methods in Ecology and Evolution, 7, 1299–1307.

Gomes, L. F., Pereira, H. R., Gomes, A. C., Vieira, M. C., Martins, P. R., Roitman, I., & Vieira, L. C. G. (2019). Zooplankton functional-approach studies in continental aquatic environments: A systematic
Narin, R., & Michel, J. (2009). A biological and physical monitoring program to evaluate long-term impacts from sand dredging operations in the United States outer continental shelf. *Journal of Coastal Research*, 20, 126–137.

Oksanen, J., Blanchet, F. G., Kindt, R., Legendre, P., Minchin, P. R., O’Hara, R. B., Simpson, G. L., Solymos, P., Stevens, M. H. H., & Wagner, H. (2015). vegan: Community ecology package. R package version 2.3-2. Retrieved from http://cran.r-project.org

Pawlowski, J., Laure, A. P. G., & Florian, A. (2020). Environmental DNA. *Molecular Ecology*, 29, 4258–4264. https://doi.org/10.1111/1365-294X.13643

Qin, H., Cao, X., Cui, L., Lv, Q., & Chen, T. (2020). The influence of human interference on zooplankton and fungal diversity in Poyang lake watershed in China. *Diversity*, 12, 296–312. https://doi.org/10.3390/d12080296

Qi, H., Cao, X., Liu, Q., & Chen, T. (2020). The influence of human interference on zooplankton and fungal diversity in Poyang lake watershed in China. *Diversity*, 12, 296–312. https://doi.org/10.3390/d12080296

Quast, C., Pruesse, E., Yilmaz, P., Gerken, J., Schweer, T., Yarza, P., Peplies, J., & Glöckner, F. O. (2013). The SILVA ribosomal RNA gene database project: Improved data processing and web-based tools. *Nucleic Acids Research*, 41, 590–596. https://doi.org/10.1093/nar/gks1219

R Development Core Team (2011). R: A language and environment for statistical computing. R Foundation for Statistical Computing.

Ren, Z., Qu, X., Zhang, M., Yu, Y., & Peng, W. (2019). Distinct bacterial communities in wet and dry seasons during a seasonal water level fluctuation in the largest freshwater lake (Poyang Lake) in China. *Frontiers in Microbiology*, 10, 1167. https://doi.org/10.3389/fmicb.2019.01167

Rey, A., Corell, J., & Rodríguez-Ezepeleta, N. (2020). Metabarcoding to study zooplankton diversity. *Zooplankton Ecology*, 231, 1–12.

Scarabotti, P. A., Demonte, L. D., & Pouilly, M. (2017). Climatic seasonality, hydrological variability, and geomorphology shape fish assemblage structure in a subtropical floodplain. *Freshwater Science*, 36, 653–668. https://doi.org/10.1086/693441

Sigsgaard, E. E., Carl, H., Møller, P. R., & Thomsen, P. F. (2015). Monitoring the near-extinct European weather loach in Denmark based on environmental DNA from water samples. *Biological Conservation*, 183, 46–52. https://doi.org/10.1016/j.biocon.2014.11.023

Sigsgaard, E. E., Nielsen, I. B., Bach, S. S., Lorenzen, E. D., Robinson, D. P., Knudsen, S. W., Pedersen, M. W., Jaidah, M. A., Orlando, L., Willerslev, E., Møller, P. R., & Thomsen, P. F. (2016). Population characteristics of a large whale shark aggregation inferred from seawater environmental DNA. *Nature Ecology & Evolution*, 1, 0004.

Sommer, U., Adrian, R., De Senerpont Domis, L., Elser, J. J., Gaedke, U., Ibelings, B., Jeppesen, E., Lürling, M., Molinero, J. C., Mooij, W. M., van Donk, E., & Winder, M. (2012). Beyond the Plankton Ecology Group (PEG) model: Mechanisms driving plankton succession. *Annual Review of Ecology Evolution and Systematics*, 43, 429–448. https://doi.org/10.1146/annurev-ecolsys-110411-160251

Srifa, A., Philps, E. J., Cichra, M. F., & Hendrickson, J. C. (2016). Phytoplankton dynamics in a subtropical lake dominated by cyanobacteria: Cyanobacteria ‘Like it Hot’ and sometimes dry. *Aquat. Ecol.*, 50, 163–174. https://doi.org/10.1007/s10452-015-9565-4

Stefanni, S., Stankovic, D., Borme, D., De Olazabal, A., Juretic, T., Pallavicini, A., & Tirelli, V. (2018). Multi-marker metabarcoding approach to study mesozooplankton at basin scale. *Scientific Reports*, 8, 12085. https://doi.org/10.1038/s41598-018-30157-7

Stoeckle, B. C., Ralph, K., & Geist, J. (2016). Environmental DNA as a monitoring tool for the endangered freshwater pearl mussel (*Margaritifera margaritifera* L.): A substitute for classical monitoring approaches? *Aquatic Conservation: Marine and Freshwater Ecosystems*, 26, 1120–1129.

Taberlet, P., Coissac, E., Hajibabaei, M., & Rieseberg, L. H. (2012). Environmental DNA. *Molecular Ecology*, 21, 1789–1793. https://doi.org/10.1111/j.1365-294X.2012.05542.x

Teten Braak, C. J. F., & Verdonchot, P. F. M. (1995). Canonical correspondence analysis and related multivariate methods in aquatic ecology. *Aquatic Science*, 57, 255–289. https://doi.org/10.1007/BF00877430

Thomsen, P. F., Kielgast, J., Iversen, L. L., Wuif, C., Rasmussen, M., Gilbert, M. T. P., Orlando, L., & Willerslev, E. (2012). Monitoring endangered freshwater biodiversity using environmental DNA. *Molecular Ecology*, 21, 2565–2573. https://doi.org/10.1111/j.1365-294X.2011.05418.x

Thomsen, P. F., & Willerslev, E. (2015). Environmental DNA – An emerging tool in conservation for monitoring past and present biodiversity. *Biological Conservation*, 183, 4–18. https://doi.org/10.1016/j.bioc.2014.11.019

Trevisan, G. V., & Forsberg, B. R. (2007). Relationships among nitrogen and total phosphorus, algal biomass and zooplankton density in the central Amazonia lakes. *Hydrobiologia*, 586, 357–365. https://doi.org/10.1007/s10750-007-0705-7

Valentini, A., Taberlet, P., Maud, C., Civade, R., Herder, J., Thomsen, P. F., Bellemain, E., Besnard, A., Coissac, E., Boyer, F., Gaboriaud, C., Jean, P., Poulet, N., Roset, N., Copp, G. H., Geniez, P., Pont, D., Argillier, C., Baudoin, J.-M., … Dejean, T. (2016). Next-generation monitoring of aquatic biodiversity using environmental DNA metabarcoding. *Molecular Ecology*, 25, 929–942. https://doi.org/10.1111/mec.13428

Walczyńska, K. S., Sareide, J. E., Weydmann-Zwolicka, A., Ronowicz, M., & Gabrielsen, T. M. (2019). DNA barcoding of cirripedia larvae reveals new knowledge on their biology in arctic coastal ecosystems. *Hydrobiologia*, 837, 149–159. https://doi.org/10.1007/s10750-019-3967-y

Walsh, J. R., Spear, M. J., Shannon, T. P., Krysan, P. J., & Vander Zanden, M. J. (2018). Using edna, sediment subfossils, and zooplankton nets to detect invasive spiny water flea (*Bythotrephes longimanus*). *Biological Invasions*, 21, 377–389. https://doi.org/10.1007/s10530-018-1862-5

Wei, F. S., Kou, H. R., & Hong, S. J. (1989). *Methods for the examination of water and wastewater*. China Environmental Science Press.

WWF (2014). *Living Planet Report 2014*: Summary. (eds McLellan R, Iyengar L, Jefferies B, Oerlemans N), WWF, Gland, Switzerland.

Zhang, H., Kang, M., Shen, J., Wu, J. M., Li, J. Y., Du, H., Wang, C. Y., Yang, H. L., Zhou, Q., Liu, Z. G., Gorfine, H., & Wei, Q. W. (2020). Rapid change in Yangtze fisheries and its implications for global freshwater ecosystem management. *Fish and Fisheries*, 21, 601–620.

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