

PLANKTON COMMUNITY AND FUNCTIONAL GROUPS IN FUHE RIVER, CHINA

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Abstract. Plankton are the foundation of the food chain in aquatic environments, and changes in phytoplankton community structure and function could pose risks to human health through their impacts on pollutant activity. We studied the correlation of plankton community and functional groups to the environmental factors in the Fuhe River, China. Water quality was evaluated based on Qr-index of phytoplankton diversity and functional group biomass. From September 2020 to August 2021, a total of 304 phytoplankton and 158 zooplankton species were collected. The phytoplankton were divided into 30 functional groups, whereas zooplankton were divided into nine functional groups. Phytoplankton functional groups were mainly composed of groups H1, MP, and W1. Among them, functional group MP had the greatest biomass, accounting for 34.37% of the phytoplankton biomass, followed by H1 (10.61%), and W1 (10.10%). The zooplankton functional groups mainly consisted of RF, RC, and SCF functional groups. The functional group RC accounted for 48.81% of the total zooplankton biomass, followed by RF (20.46%), and SCF (19.65%). The major environmental factors influencing phytoplankton functional groups were water temperature (WT), dissolved oxygen (DO), oxidation-reduction potential (ORP), and transparency (TS), whereas the major environmental factors influencing zooplankton functional groups were WT, pH, and DO. Overall, water quality of Fuhe River Basin was good, being slightly polluted or pollution-free.

Keywords: *density and biomass, species composition and diversity, water environment, Qr-index, relationship*

Introduction

Plankton, which involve phytoplankton and zooplankton, represents a group of tiny floating organisms found in water bodies and form the foundation of the food chain in aquatic environments (Zhao, 2016). Microscopic plants, commonly referred to as algae, are the main producers in the water column, and are the starting point of material cycling and energy flow in aquatic ecosystems (Nielsen et al., 2002). They are small individuals, have fast reproduction rates, short growth cycles, and are capable of photosynthesis. Protozoa, rotifers, branchiopods, and copepods, which are major consumers in the water column and also serve as open bait for fish, are examples of zooplankton (Zhang et al., 2010).

Shifts in plankton community structure or function could influence pollutant proliferation and action, and in turn, influence human health. Therefore, plankton community structure monitoring is an important water quality measurement tool and early warning system for water contamination in the wake of increased river pollution. Traditional methods of plankton community structure monitoring are usually based on systematic taxonomy, which divide aquatic organisms into taxonomic groups that are indicators of water quality, and enable biodiversity assessment. However, traditional

classification methods can hardly reflect the ecological functions of aquatic organisms (Hood et al., 2006). Consequently, ecologists have proposed the concept of functional groups, whose species characteristics reflect the ecological functions of aquatic organisms (Hood et al., 2006).

Phytoplankton functional groups represent well-defined groups of species with similar ecological (Reynolds et al., 2002; Padisak et al., 2006), morphological (Kruk et al., 2002, 2011), as well as functional characteristics (Naselli-Flores, 2000). Phytoplankton functional group classification is used in phytoplankton ecology research and water quality evaluation, and was first used to explore phytoplankton community succession patterns in still-water lakes and to monitor lake ecology (Padisak et al., 2006). Reynolds put forward a relatively comprehensive theory of phytoplankton functional groups based on the physiological, ecological, and morphological characteristics of phytoplankton (Reynolds et al., 2002). A major premise of the theory is that algae belonging to the same functional group usually grow in the same habitat type, and have similar sensitivity and tolerance to environmental factors. Compared with traditional classification methods, functional group classifications are more accurate in describing habitat characteristics and species distribution (Dong et al., 2013). It greatly simplifies the complex traditional biological classification system (Padisak et al., 2009) and provides a powerful tool for revealing algae community selection by habitat change and predicting algae community succession (Kruk et al., 2010).

In total, 39 functional groups of phytoplankton have been defined (Padisak et al., 2009). Compared with the study of phytoplankton functional groups, the study of zooplankton functional groups began later and was not comprehensive, with no unified classification basis. Most research on zooplankton functional groups have focused on ocean environments. The earliest such study (Quere et al., 2005) classified zooplankton into three functional groups, namely large (Doliolum, Euphausiacea, Pteropoda), medium (Copepods, Amphipoda and Caudates), and small (Ciliophora, Flagellate) zooplankton functional groups. However, there are few reports about functional groups of freshwater zooplankton. Recently, a study (An, 2016) divided zooplankton into 10 functional groups according to their size, feeding habits, and interactions with each other, including large copepods and cladocera carnivora (LCC), large copepods and cladocera filter feeders (LCF), middle copepods and cladocera carnivora (MCC), middle copepods and cladocera filter feeders (MCF), small copepods and cladocera carnivora (SCC), small copepods and cladocera filter feeders (SCF), rotifers carnivora (RC), rotifers filter feeders (RF), protozoa carnivora (PC), and protozoa filter feeders (PF). The division of marine zooplankton functional groups is more focused on the relationship between zooplankton and fish, whereas the division of freshwater zooplankton functional groups is more focused on the relationship between phytoplankton and zooplankton, as well as the relationships among zooplankton.

Phytoplankton are sensitive to environmental change, and will multiply in large quantities under suitable conditions. Numerous environmental factors, including water temperature (WT), pH, and nutrient concentrations, influence phytoplankton and zooplankton community structure. WT is one of the major environmental factors influencing the growth, reproduction, quantity, and distribution of zooplankton, and reportedly influences J, N, and Lo functional groups (Wang et al., 2019). In contrast, the MP functional group has been reported to be negatively correlated with nutrient concentrations and salinity, and the P and J functional groups are positively correlated

with nutrients and salinity (Hu et al., 2019a). With regard to zooplankton functional groups, the optimal temperatures for the growth of protozoa, rotifer, and branchiopoda and capuchin have been reported to be 20°C, 40°C, and 30°C, respectively, with their abundance peaking at the optimum temperature, and then gradually decreasing (Jin et al., 1991). Among them, RF, SCF, and MCC functional groups are positively correlated with temperature, RC and MCC functional groups are significantly positively correlated with electrical conductivity, and filter-feeding functional groups, RF and SCF, are positively correlated with ammonium-nitrogen (NH₄-N) and total nitrogen (N) concentrations, but negatively correlated with total phosphorus (P) concentration (Sun, 2019).

However, the responses of planktonic species and community composition to environmental factors do not accurately reflect the preferences of species. It has been demonstrated that planktons respond to combinations of environmental factors (Long et al., 2020). Therefore, planktonic functional groups are defined based on morphological, physiological, and habitat characteristics, in addition to dietary habits. Plankton functional groups exhibit similar levels of tolerance and sensitivity to environmental factors (Salmaso et al., 2015), so that functional groups are more appropriate for use in assessments of plankton responses to changes in environmental conditions (Kruk et al., 2002).

With increasing urbanization, the Fuhe River, the second largest river in Jiangxi Province, China, is increasingly affected by human activities, resulting in severe pollution. Plankton morphological characteristics can reflect the degree of river pollution; however, to the best of our knowledge, no study has previously explored plankton community structure and functional groups in the Fuhe River. The present study analyzed plankton community structure and functional groups in the Fuhe River, investigated the temporal and spatial trends of plankton in the Fuhe River and the relationship between functional groups of plankton and environmental factors in the Fuhe River, based on Pearson correlation analysis and redundancy analysis (RDA). Fuhe River water quality was evaluated based on physicochemical indexes and plankton indexes. The results of the present study could provide basic data that could facilitate effective resource management, environmental monitoring, and sustainable exploitation of the Fuhe River.

Materials and methods

Study area

Fuhe River is located in Jiangxi Province, China (116°17' E and 26°31' N), covers an area of 16,493 km², and is 348 km long (Hua, 2010). The entire Fuhe River basin has a subtropical humid monsoon climate, with a mild climate and abundant rainfall, with most of the precipitation concentrated in April–September (Yang et al., 2021), and considerable variation in time and space. The terrain of the basin slopes from southeast to northwest; in addition, it is surrounded by mountains on three sides, and is wide from north to south, and narrow from east to west. The upper reaches of Fuhe River are divided into two branches: the Xujiang River and the Litanhe River, which are 150 km and 65 km long, respectively. Downstream Fuhe River is located in Hongmen Town, Nancheng County, where the Hongmen Reservoir was built. The two rivers meet at the bottom of Nancheng, and are referred to as the Fuhe River after the confluence. The middle reaches are in a hilly region, from Nancheng to Fuhe River. The terrain of the basin is flat, wide and shallow, and there are two igneous dams in Shushan and

Liaofang. The following are gradually open plains or hills; Below Fuzhou is the lower reaches, it belongs to hilly plain area, the water flow is concentrated, past Chaibukou, into the Gan-Fu plain, and finally flows into Poyang Lake.

In the present study, plankton and environmental factor data were collected in November 2020, January 2021, April 2021, and July 2021. Based on the morphological characteristics at the habitat scale in the Fuhe River, the ecological habits of plankton, and to ensure representative distribution of sampling sites, nine sampling sites were set up in the Fuhe River from upstream to downstream (*Fig. 1*), namely Guangchang (S1, 116°19' E and 26°49' N), Nanfeng (S2, 116°32' E and 27°14' N), Lichuan (S3, 116°53' E and 27°19' N), Nancheng (S4, 116°38' E and 27°33' N), Yihuang (S5, 116°14' E and 27°33' N), Chongren (S6, 116°03' E and 27°46' N), Dongxiang (S7, 116°27' E and 28°07' N), Linchuan (S8, 116°21' E and 28°00' N), and Jinxian (S9, 116°10' E and 28°11' N). Each site was divided into three sampling points: left, middle, and right.

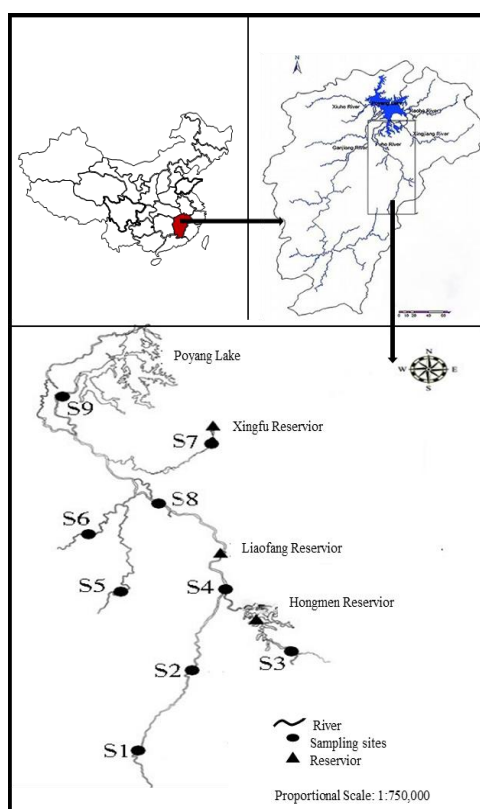


Figure 1. Sampling sites in the Fuhe River Basin, Jiangxi Province, China

Sample collection and processing

The collection of plankton samples entails two parts. First, a qualitative collection is used to analyze plankton species composition. Second, statistical analysis of the abundance, biomass, and diversity of plankton is carried out. The collection methods of plankton were according to ‘Research Methods for Freshwater Plankton (Zhang and Huang, 1991)’. The qualitative phytoplankton samples were collected using a No. 25 plankton net (0.064 mm). The net opening was placed 40–50 cm below the water surface in the direction of incoming water (in the case of still water, the net was dragged in the water column in a ‘∞’ shape) for 3–5 min. Each site was sampled at the left,

middle, and right sampling points. Afterward, the samples were put into specimen bottles, and 5 or 7% formalin added for fixation. The quantitative phytoplankton samples were collected using a water collector plexiglass water quality sampler, and samples were obtained at the left, middle and right sections. Subsequently, upper, middle, and lower water samples collected 50 cm, 100 cm, and 150 cm below the water surface, respectively, at the three points, were mixed, and 1 L was obtained at each point. After mixing with 5 mL Lugol's solution, the samples were fixed on the spot, and then transported to the laboratory for precipitation with a phytoplankton precipitant for 24~48 h. Afterward, 50 mL of bottom concentrated water samples were obtained again. The phytoplankton were classified according to the related academic literatures (Han, 1980; Hu and Wei, 2006; Weng and Xu, 2010; Anonymous, 2012).

The qualitative zooplankton samples of protozoa, rotifers, cladocera, and copepods were collected in a manner similar to that of phytoplankton using the plankton net No. 25. After samples were collected, 10 mL of 7% formalin solution was added to fix the samples. The upper, middle, and lower water samples, at 50 cm, 100 cm, and 150 cm below the water surface, respectively, were mixed. Afterward, 1 L water samples were obtained with a water sampler, and 10 mL formalin added to fix it. The samples were left to stand for 48 h and concentrated to 50 mL. The zooplankton in the water samples were identified and classified with the related academic literature (Han, 1980).

In the course of collection, seven water quality indexes were measured, including WT, pH, oxidation-reduction potential (ORP), dissolved oxygen (DO), electrical conductivity (EC), and total dissolved solids (TDS), using an Aquaread AP-2000 portable multiparameter water quality meter (Bell Flow Systems Ltd., Buckingham, UK) at the investigation site, and transparency (TS) was measured using a Sechi disk. Data were recorded with markers and on printed forms, for subsequent processing.

Data processing

Plankton density

The number of phytoplankton and zooplankton cells in each liter of a water sample was calculated according to the visual field method. The formula is as follows:

(1) Calculation equation for phytoplankton density:

$$N = \frac{C}{F_s \times F_n} \times \frac{V}{U} \times P_n \quad (\text{Eq.1})$$

(2) Calculation equation for zooplankton density:

$$N = (V_s \times n)(V \times V_a) \quad (\text{Eq.2})$$

In *Equation 1*, “*N*” is the number of phytoplankton individuals in a 1 L water sample, “*C*” is the area of the counting frame (mm²), “*F_s*” is the area of each field of view (mm²), “*F_n*” is the number of fields, “*V*” is the volume of concentrated water sample per liter, “*U*” is the volume of the counting frame (mL), “*P_n*” is the number of phytoplankton cells counted in each frame.

In *Equation 2*, “*N*” is the number of zooplankton in 1 L of water (ind./L), which is the density, “*V*” is the sampling volume L, “*V_s*” is the sample concentration volume mL, and “*V_a*” is the counting volume mL.

The biomass of the plankton is its living weight. All biomass is the density multiplied by the average wet weight of the species.

Calculation of plankton diversity index

(1) Shannon-Wiener diversity index (H):

$$H = -\sum P_i \ln P_i \quad (\text{Eq.3})$$

(2) Margalef richness index (d):

$$d = (S - 1) / \ln N \quad (\text{Eq.4})$$

(3) Pielou homogeneity index (J):

$$J = H / \log(S) \quad (\text{Eq.5})$$

where “ N_i ” is the number of individuals of the “ i ” species, $P_i = n_i/N$, “ n_i ” is the number of individuals of the “ i ” species, “ N ” is the total number of individuals of all species (ind./L), and “ S ” is the number of plankton species (Soballe et al., 1987).

Calculation of plankton dominant species

$$Y = (n_i/N)f_i \quad (\text{Eq.6})$$

where “ f_i ” is the frequency of occurrence of the “ i ” species in each type, “ N ” is the total number of individuals of all species (ind./L), and “ N_i ” is the number of individuals of the “ i ” species. When “ Y ” is greater than or equal to 0.02, the dominant species is defined (Soballe et al., 1987).

The Qr-index

The trophic status of water bodies is evaluated based on phytoplankton functional groups and their biomass (Borics et al., 2007).

$$Q = \sum_{i=1}^S [p_i \cdot F_i] \quad (\text{Eq.7})$$

where “ S ” is the number of phytoplankton functional groups, “ p_i ” is the ratio of the biomass of the i -th functional group to the total biomass of the phytoplankton functional group, and “ F_i ” is the assigned value of the i -th functional group (Abonyi et al., 2012; Borics et al., 2007; Frau et al., 2019).

Because functional groups and environmental characteristics are all responsive to each other, phytoplankton data can be used and the environment can be evaluated more accurately. In the Qr-indexes, 0–1 is poor, 1–2 is tolerant, 2–3 is moderate, 3–4 is good, and 4–5 is very good (Abonyi et al., 2012).

Classification of plankton functional groups

Phytoplankton classification is based on habitat, and tolerance and sensitivity characteristics of each functional taxon, as identified in classifications of functional taxa

in previous studies (Padisak et al., 2006; Reynolds et al., 2002). For example, differences in phytoplankton species tolerance to different environmental factors (light, nutrients, etc.), differences in spatial distribution of individual phytoplankton with certain morphology, and differences in tolerance to other factors, such as P, carbon, and N in habitat, can be used to classify phytoplankton into functional groups. A total of 29 species of phytoplankton were collected in the present study (Table 1). The zooplankton were classified according to the division method (An, 2016), based on size, feeding habit, and trophic level (Shen et al., 1990). Zooplankton in freshwater ecosystems were divided into protozoan filter feeders (PF), protozoan predators (PC), rotifer filter feeders (RF), rotifer predators (RC), zooplankton filter feeders (SCF), SCC, MCF, MCC, LCC, and LCC (Table 2). The functional groups collected in this study did not include SCC and LCC, so that eight functional groups of zooplankton were defined in the present study.

Table 1. Classification of phytoplankton functional groups and the representative species

Functional groups	Representative species	Habitat template
A	<i>Diatoma vulgare</i>	Clear, deep, base poor lakes, with species sensitive to pH rise
B	<i>Cyclotella bodanica</i>	Mesotrophic small- and medium-sized lakes with species sensitive to the onset of stratification
C	<i>Cyclotella meneghiniana</i> , <i>Asterionella</i> sp.	Eutrophic small- and medium-sized lakes with species sensitive to the onset of stratification
D	<i>Synedra acus</i> , <i>Synedra ulna</i> , <i>Synedra actinastroides</i> , <i>Nitzschia levidensis</i>	Shallow turbid waters including rivers
E	<i>Dinobryon divergens</i>	Usually small, shallow, base poor lakes, or heterotrophic ponds
F	<i>Oocystis lacustris</i> , <i>Treubaria triappendiculata</i>	Clear, deeply mixed meso-eutrophic lakes
G	<i>Pandorina</i> sp.	Nutrient-rich conditions in stagnating water columns; small eutrophic lakes and very stable phases in larger river-fed basins, and storage reservoirs
H1	<i>Anabaena circinalis</i> , <i>Aphanizomenon</i> sp.	Eutrophic, both stratified and shallow lakes with low nitrogen content
J	<i>Selenastrum</i> sp., <i>Coelastrum microporum</i> , <i>Scenedesmus</i> sp., <i>Tetraedron</i> sp., <i>Crucigenia</i> sp., <i>Actinastrum hantzschii</i> , <i>Pediastrum</i> sp., <i>Golenkinia</i> sp., <i>Tetrastrum staurogeniaeforme</i>	Shallow, mixed, highly enriched systems (including many low-gradient rivers)
Lo	<i>Merismopedia minima</i> , <i>Merismopedia punctata</i> , <i>Chroococcus minor</i> , <i>Chroococcus limneticus</i> , <i>Peridinium</i> sp.	Deep and shallow, oligo to eutrophic, medium to large lakes
Lr	<i>Aulacoseira granulate</i>	Deep, eutrophic reservoirs with strong and persistent disturbances caused by water discharges
M	<i>Microcystis</i>	Eutrophic to hypertrophic, small- to medium-sized water bodies
MP	<i>Cymbella</i> sp., <i>Navicula</i> sp., <i>Gomphonema</i> sp., <i>Achnanthes breuipes</i> , <i>Cocconeis</i> sp., <i>Surirell</i> sp., <i>Eunoria</i> sp., <i>Pinnularia viridis</i> , <i>Oscillatoria</i> sp., <i>Oscillatoria subbrevis</i>	Frequently stirred up, inorganically turbid shallow lakes
N	<i>Cosmarium</i> sp., <i>Staurastrum</i> sp., <i>Euastrum</i> sp.	Continuous or semi-continuous mixed layer of 2–3 m in thickness. This association can be represented in shallow lakes where the mean depth is of this order or greater, as well as in the epilimnia of stratified lakes when the mixing criterion is satisfied
NA	<i>Staurodesmus</i> , <i>Staurastrum</i>	Oligo-mesotrophic, atelomictic environments at lower latitudes with species sensitive to destratification
P	<i>Melosira granulata</i> , <i>Melosira granulata</i> var. <i>angustissima</i> , <i>Fragilaria intermedia</i> , <i>Closterium</i> sp.	Similar to that of codon N but at higher trophic states
Q	<i>Gonyostomum semen</i>	Small acidic, humic lakes
S1	<i>Pseudoanabaena</i> sp., <i>Phormidium</i> sp., <i>Dactylococcopsis acicularis</i>	Turbid mixed environments. This codon includes only shade-adapted cyanoprokaryotes

S2	<i>Spirulina sp.</i>	Warm, shallow and often highly alkaline waters
SN	<i>Raphidiopsis sp.</i>	Warm mixed environments
TD	<i>Ulothrix sp.</i>	Mesotrophic standing waters, or slow-flowing rivers with emergent macrophytes
TB	<i>Melosira varians</i>	Highly lotic environments (streams and rivulets)
T	<i>Mougeotia sp.</i>	Persistently mixed layers, in which light is increasingly the limiting constraint and thus optically deep, mixed environments including clear epilimnia of deep lakes in summer
W1	<i>Phacus sp., Euglena geniculata</i>	Ponds, even temporary, rich in organic matter from husbandry or sewages
W2	<i>Trachelomonas spinubosa, Strombomonas sp.</i>	Meso-eutrophic ponds, even temporary, shallow lakes
WS	<i>Synura uvella, Synura pettersonii</i>	Ponds, even temporary, rich in organic matter from decomposition of vegetal matter (humic environments), but not acidic
X1	<i>Chlorella vulgaris, Ankistrodesmus sp.</i>	Shallow, eu-hypertrophic environments
X2	<i>Chlamydomonas sp., Chroomonas acuta</i>	Shallow, meso-eutrophic environments
X3	<i>Schroederia setigera</i>	Shallow, well mixed oligotrophic environments
Y	<i>Cryptomonas erosa, Cryptomonas ovata</i>	Mostly including large cryptomonads but also small dinoflagellates, refers to a wide range of habitats, which reflect the ability of its representative species to live in almost all lentic ecosystems when grazing pressure is low

Table 2. Classification of zooplankton functional groups

Functional groups	Functional groups	Length (mm)	Feeding habits
PF	Protozoa filter feeders		Feed on organic detritus, bacteria and algae
PC	Protozoa carnivore		Target small motile prey (other zooplanktons)
RF	Rotifer filter feeders		Feed on organic detritus, bacteria and algae
RC	Rotifer carnivore		Target small motile prey (including small protozoa, rotifer and crustaceans)
SCF	Small Copepods and Cladocerans filter feeders	≤0.7	Filter-feed on bacteria, algae, organic detritus and protozoa
MCF	Middle Copepods and Cladocerans filter feeders	0.7-1.5	Filter-feed on bacteria, algae, organic detritus, and protozoa
MCC	Middle Copepods and Cladocerans carnivore	0.7-1.5	Feed on rotifer, oligochaeta, chironomidae larvae, and other cladoceran
LCF	Large Copepods and Cladocerans filter feeders	≥ 1.5	Filter-feed on bacteria, algae, organic detritus, and protozoa

Data analysis

All data were compiled using MS Excel (Microsoft Corp., Redmond, WA, USA), and the Shannon-Wiener diversity index (H), Margalef index, and Pielou homogeneity index (J) were calculated and analyzed using Primer 5.0 (Premier Biosoft, Palo Alto, CA, USA). CANOCO 5.0 (Microcomputer Power, Ithaca, NY, USA) was used to conduct RDA on plankton and environmental factors, and the relationship between plankton and environmental factors is discussed.

Results

Physicochemical factors

See Table 3 for WT, pH, ORP, DO, EC, TDS, and TS trends in the Fuhe River Basin. The highest and lowest mean temperatures were 20.88°C at S2 and 18.73°C at S7. The

highest temperature change in S2 was 32.96°C, while the lowest temperature was 8.8°C. The Fuhe River water had a neutral to weak alkaline pH. The average pH value at S9 was the highest, at 8.30, and that at S7 was the lowest, at 7.60. The pH value of S5 changed the most, with a maximum value of 8.56, and a minimum value of 7.24. The mean ORP at S8 was the highest, at 149.58 mv, and the lowest at S3, at 89.21 mv. S8 has the largest ORP change, and the maximum ORP was 217.60 mv, and the minimum was 81.56 mv. The highest average DO value was 10.11 mg/L at S8, and the lowest was 7.61 mg/L, at S7, whereas the greatest change in DO value was 11.98 mg/L, and the lowest change in DO value was 6.76 mg/L, at S5. The highest and lowest average EC values were 263.83 µs/cm at S7 and 96.75 µs/cm at S5, and the highest and lowest EC values were 434.97 µs/cm, and 92.69 µs/cm, respectively. The highest and lowest average TDS values were 187.25 mg/L at S7 and 62.38 mg/L at S1, respectively. In addition, the highest and lowest TDS values were 282.00 mg/L at S7 and 92.5 mg/L, respectively. The highest and lowest average TS values were 81.00 cm, at S1, and 36.75 cm, at S7. The highest TS value was 180.00 cm, at S2, and the lowest TS value was 33.5 cm.

Table 3. Changes in environmental factors at each point of the Fuhe River (standard deviation of the mean)

Sampling sites	WT (°C)	pH	ORP (mv)	DO (mg/L)	EC (µs/cm)	TDS (mg/L)	TS (cm)
S1	19.48±11.98	7.99±0.33	99.20±53.20	10.05±2.17	96.88±18.12	62.38±11.62	81.00±35.00
S2	20.88±12.08	8.18±0.42	106.34±42.56	9.83±2.14	136.13±30.87	87.50±19.50	73.25±106.75
S3	19.34±11.04	7.91±0.40	89.21±112.94	9.14±2.47	109.00±17.00	71.00±12.00	56.75±18.25
S4	20.44±9.09	8.27±0.25	120.01±52.09	9.98±1.52	141.50±15.50	94.00±8.00	50.00±10.00
S5	19.12±11.32	7.90±0.66	108.72±55.28	9.37±2.61	96.75±26.25	66.25±31.25	56.00±34.00
S6	19.87±10.66	8.04±0.29	142.83±39.32	9.66±2.02	117.75±25.50	77.50±20.50	75.50±44.50
S7	18.73±10.13	7.60±0.38	118.4±19.80	7.61±1.95	263.83±171.14	187.25±94.75	36.75±13.25
S8	19.52±11.42	7.75±0.32	149.58±68.02	10.11±2.23	120.25±35.75	83.00±24.00	68.50±44.50
S9	19.15±10.70	8.30±0.26	113.79±18.01	9.53±2.39	147.58±29.42	95.67±19.33	51.00±37.00

Plankton species composition and distribution

In the present study, 304 species (including varieties and forms) of phytoplankton were found in Fuhe River, belonging to 8 phyla, 11 classes, 24 orders, 45 families, and 99 genera (Table A1). Among them, the diatom was the most abundant, accounting for 37% of the total species identified, followed by the green algae phylum, accounting for 35% of the total number of species. Gymnospora, cyanophyta, methanogens, Chrysophyta, Cryptophyta, and Xanthophyta accounted for 13%, 9%, 2%, 2%, 1%, and 1% of the total species, respectively. The order of species from high to low abundance across the sampling sites was as follows: S4(176) > S7(165) > S6(152) > S2(128) > S9(113) > S8(109) > S3(104) > S1(100) = S5(100) (Fig. 2).

There were 158 species of zooplankton that could be identified to the species level, including 4 phyla, 6 classes, 14 orders, 31 families, and 62 genera (Table A2). Among them, rotifer species were the most abundant, accounting for 42% of the total species, followed by Protozoa, branchipoda, and hornpods, which accounted for 32% 15%, and 11% of the total species, respectively. The order of species from high to low abundance across the sampling sites was as follows: S4 (89) > S6 (66) > S3 (59) > S7 (52) > S1 (51) = S8 (51) > S2 (49) = S9 (49) > S5 (42) (Fig. 2).

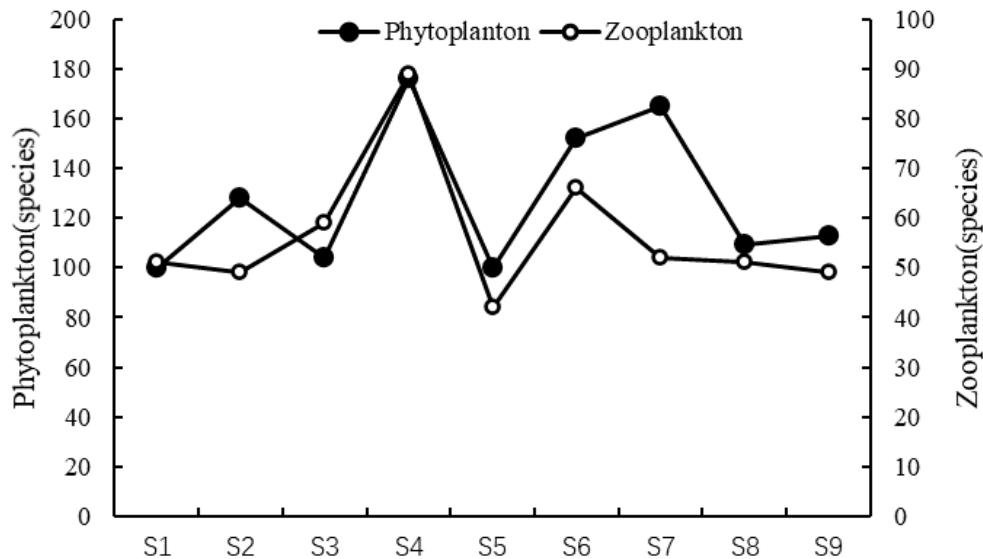


Figure 2. Phytoplankton and zooplankton trends in the Fuhe River

Plankton density and biomass

Phytoplankton cell densities in Fuhe River ranged from 1.29 to 49.86 cells/L, with a mean of 13.89 cells/L. Average phytoplankton density was the highest at S2 (29.40 cells/L) and the lowest at S5 (3.51 cells/L) (Fig. 3A). In addition, phytoplankton biomass varied from 2.05 to 131.71 mg/L, with a mean of 41.37 mg/L (Fig. 3B). Similarly, the average value of S2 was the highest (61.85 mg/L) and that of S5 was (17.80 mg/L) the lowest. There were significant seasonal differences in phytoplankton density and biomass, with higher density and biomass in summer, followed by in spring and autumn, and the least in winter (Fig. 3).

Zooplankton in the Fuhe River Basin ranged from 50.00 to 4950.00 ind/L, with an average of 638.19 ind/L (Fig. 3C), and the average zooplankton density was the highest at S3 (1920.83 ind/L) and the lowest at S7 (195.83 ind/L). The variation of zooplankton density mean values was more obvious, with the highest density in summer, followed by in spring, winter, and autumn. Zooplankton biomass ranged from 0.0013 to 6.39 mg/L, with an average of 0.67 mg/L (Fig. 3D). The mean value of zooplankton biomass in S3 was the highest (2.48 mg/L) and the lowest in S9 (0.22 mg/L). The average zooplankton biomass changed little, with the highest biomass in spring, followed by that in summer, the lowest in autumn and the lowest in winter.

Diversity characteristics

The Margalef richness index (d) of phytoplankton was in the 16.02–22.78 range, with an average of 18.61. The Pielou evenness index (J) was between 0.75 and 0.88, with an average of 0.84. In addition, Shannon-Wiener diversity index (H) ranged from 3.20 to 3.66, with a mean of 3.50 (Table 4). Zooplankton richness was in the 4.18–13.84 range, with a mean of 8.96. Evenness index was in the 0.79–0.89 range, with a mean of 0.86. Diversity index was in the 0.79–2.35 range, with a mean of 1.32 (Table 4). The Shannon-Wiener diversity indices (H) of phytoplankton were all > 3, which indicates that Fuhe River is in a slightly polluted or an unpolluted state.

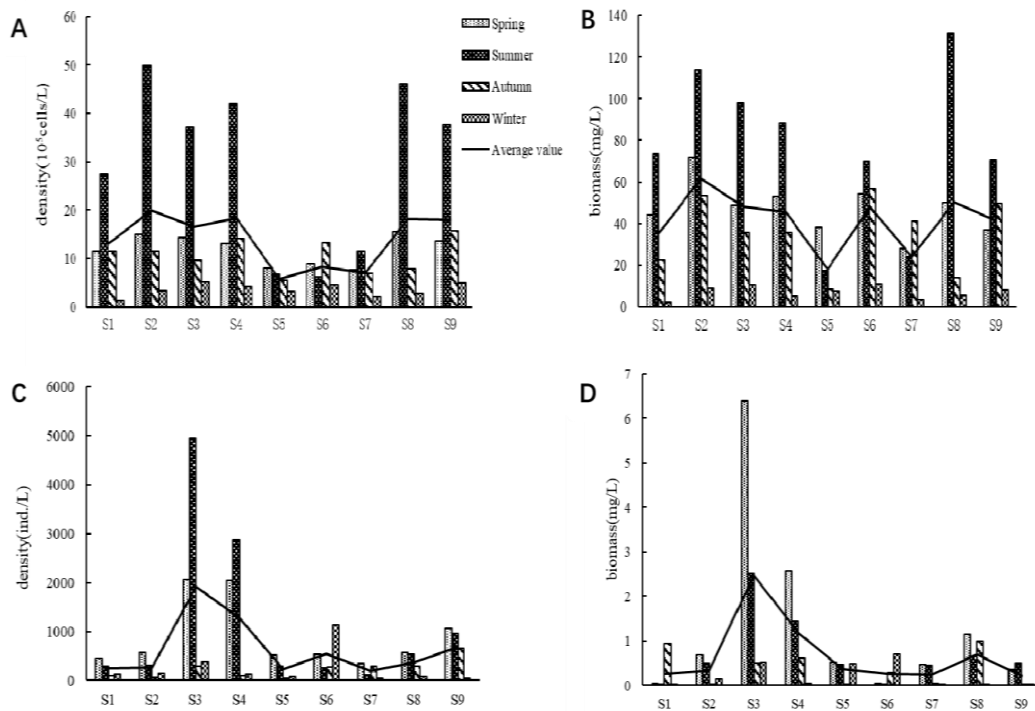


Figure 3. Density and biomass of phytoplankton and zooplankton in the Fuhe River (A and B illustrate the number of cells and biomass of phytoplankton, respectively; C and D illustrate the number of individuals and biomass of zooplankton, respectively)

Table 4. Characteristics of the sampling sites in the Fuhe River

Sampling sites	Phytoplankton			Zooplankton			Water pollution types
	D	J	H	D	J	H	
S1	19.28	0.84	3.56	5.08	0.79	0.82	Pollution is light or no
S2	19.88	0.89	3.85	13.57	0.84	0.96	Pollution is light or no
S3	17.89	0.82	3.52	13.16	0.84	2.35	Pollution is light or no
S4	18.10	0.83	3.59	11.18	0.84	1.88	Pollution is light or no
S5	17.23	0.86	3.26	7.79	0.91	0.96	Pollution is light or no
S6	19.10	0.86	3.50	4.18	0.83	1.24	Pollution is light or no
S7	22.78	0.88	3.56	10.25	0.87	0.79	Pollution is light or no
S8	17.20	0.75	3.20	7.79	0.92	1.22	Pollution is light or no
S9	16.02	0.82	3.44	7.61	0.86	1.65	Pollution is light or no

Dominant plankton species

Dominant plankton species in the Fuhe River were determined based on a dominance index $Y \geq 0.02$. There were 27 dominant phytoplankton species, belonging to six families (Table 5), including *Aphanizomenon. sp* (14.04) of Cyanophyta; *Chroomonas acuta* (0.94), *Cryptomonas ovata* (1.84) of Cryptophyta; *Chromulina sp.* (1.83) of Chrysophyta; *Cyclotella sp.* (5.19) of Bacillariophyta; and *Chlamydomonas sp.* (18.54), *Chlorella vulgaris* (7.12), *Dictyosphaerium ehrenbergianum* (0.60), *Actinastrum sp.* (0.79) of Chlorophyta. Bacillariophyta and Chlorophyta were the dominant families. There were eight dominant zooplankton species, belonging to two phyla (Table 5), namely *Diffugia oblonga* (0.46) of Protozoa and *Trichocerca bicristata* (0.73) of Trochelminthes.

Table 5. Dominant plankton species in the Fuhe River

Species and dominance values (in parenthesis)				
Phytoplankton				
Cyanophyta				
<i>M. tenuissima</i> (0.07)	<i>Microcystis sp.</i> (0.02)	<i>Aphanizomenon sp.</i> (14.04)		
Cryptophyta				
<i>C. acuta</i> (0.94)	<i>C. ovata</i> (1.84)	<i>C. erosa</i> (0.12)		
Chrysophyta				
<i>Chromulina sp.</i> (1.83)				
Xanthopyta				
<i>Tribonema sp.</i> (0.03)				
Bacillariophyta				
<i>M. granulata</i> (0.14)	<i>C. meneghiniana</i> (0.09)	<i>Cyclotella sp.</i> (5.19)	<i>S. acus</i> (0.03)	<i>S. ulna</i> (0.11)
<i>Synedra sp.</i> (0.03)	<i>N. capitatoradiata</i> (0.23)	<i>N. paradoxa</i> (0.07)	<i>N. wullerstorffii</i> (0.38)	<i>N. palea</i> (0.15)
Chlorophyta				
<i>Chlamydomonas sp.</i> (18.54)	<i>C. vulgaris</i> (7.12)	<i>S. bibrainum</i> (0.08)	<i>S. setigera</i> (0.10)	<i>Ankistrodesmus sp.</i> (0.03)
<i>D. ehrenbergianum</i> (0.60)	<i>Actinastrum sp.</i> (0.79)	<i>S. quadricauda</i> (0.22)	<i>M. pusillum</i> (0.32)	
Zooplankton				
Protozoa				
<i>D. oblonga</i> (0.46)	<i>D. balbianii</i> (0.27)	<i>D. balbianii nanum</i> (0.04)	<i>Paramecium sp.</i> (0.03)	<i>S. gyrans</i> (0.05)
Trochelminthes				
<i>B. calyciflorus</i> (0.19)	<i>P. dolichoptera</i> (0.07)	<i>T. bicristata</i> (0.73)		

Functional groups of plankton

The phytoplankton species in the Fuhe River were divided into 30 functional groups (Padisak et al., 2009; Reynolds et al., 2002) according to the relationships between phytoplankton and various water qualities (Table 1). The main phytoplankton functional groups were C, D, G, H1, M, MP, W1, X2 and Y, which accounted for 95.63% of the total phytoplankton biomass. Among them, MP had the greatest biomass, accounting for 34.37% of the phytoplankton biomass, and the change value at each site was 2.49%~6.90%, followed by H1, which accounted for 10.61% of the phytoplankton biomass, and the change value at each site was 0.29%~3.58%. In addition, W1 accounted for 10.10% of the phytoplankton biomass, and the change value at each site was 0.45%~2.39%. Functional group D accounted for 9.29% of the phytoplankton biomass, and the change value at each site was 0.31%~1.70%. Functional group X2 accounted for 8.13% of the phytoplankton biomass, and the change value at each site was 0.20%~2.34%. Functional group M accounted for 6.42% of the phytoplankton biomass, and the change value at each site was 0.05%~1.42%. Functional group G accounted for 6.24% of the phytoplankton biomass, and the change value at each site was 0.01%~0.22%. Functional group C accounted for 5.85% of the phytoplankton biomass, and the change value at each site was 0.13%~1.21%. Functional group Y accounted for 4.63% of the phytoplankton biomass, and the change value at each point was 0.43%~1.97%. Among the above functional groups, MP, H1, and W1 play important roles in the composition of phytoplankton in Fuhe River. Functional groups MP, H1, and W1 had the highest biomass at sites S6; S8, and S6, respectively (Fig. 4).

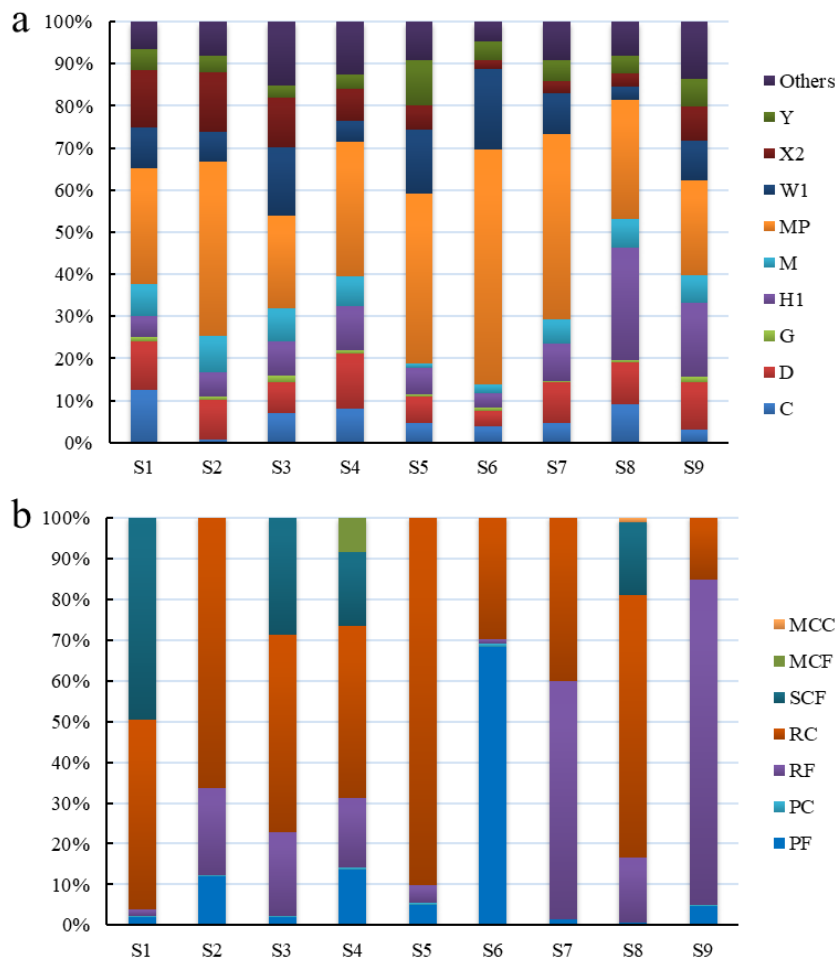


Figure 4. Biomass trends of functional groups of zooplankton in the Fuhe River (“a” is the functional group of phytoplankton, “b” is the functional group of zooplankton)

Based on their feeding habits, the zooplankton in the Fuhe River can be divided into eight functional groups, including PF, PC, RF, RC, SCF, MCF, and MCC, with RC having the greatest biomass, and accounting for 48.81% of the total zooplankton biomass (Fig. 4). Functional groups PF, RF, RC, SCF, MCF, and MCC were mostly distributed in S6, S9, S6, S1, S4, and S8, respectively.

Water quality evaluation based on the Qr-index

The Qr-index is a water quality evaluation index based on the adaptability of phytoplankton functional groups to environmental change. The method reflects the water quality status more accurately. The Qr-index at each site in the Fuhe River basin ranged from 2.11 to 4.63. The order of the magnitudes of Qr-value at the various sites was as follows: S6 > S1 > S5 > S2 = S7 > S4 > S9 > S8 > S3 (Table 6). The lower the Qr-value, the higher the nutrient levels in the water body, and the larger the Qr-value, the lower the water nutrient levels (Yin et al., 2016). According to the Qr-values observed, water quality at S1 and S6 was excellent, water quality at S2, S4, S5, and S7 was good, and water quality at S3, S8, and S9 was moderate. Therefore, the overall water quality in the Fuhe River basin was good, and the degree of pollution was light. The results above are consistent with the results of biodiversity out.

Table 6. *Qr-index and water quality evaluation of phytoplankton at each site in the Fuhe River*

	S1	S2	S3	S4	S5	S6	S7	S8	S9
Qr-value	4.18	3.41	2.11	3.06	3.65	4.63	3.41	2.71	2.91
Water quality assessment	Very good	Good	Medium	Good	Good	Very good	Good	Medium	Medium

Relationship between plankton and environmental factors

The results of the RDA analysis between the number of phytoplankton species and environmental factors in the Fuhe River are shown in *Figure 5A*. The relationships between phytoplankton and environmental factors were mainly concentrated in the first quadrant and fourth quadrant. The eigenvalues of axis 1 and axis 2 were 0.7508 and 0.0928, respectively, which explained a total of 92.5% of the species variation in each phytoplankton phylum. Most species were distributed in the first quadrant and were mainly influenced by WT, TS, ORP, TDS, and EC. Among them, Bacillariophyta and Pyrrophyta species were positively correlated with TS and ORP, and negatively correlated with DO. Cryptophyta species had a negative correlation with WT. Conversely, Xanthophyta were positively correlated with WT, and Cyanophyta, Euglenophyta, Chrysophyta, and Chlorophyta species were positively correlated with TDS and EC.

The relationships between zooplankton and environmental factors, with eigenvalues of 0.563 and 0.285 for axis 1 and 2, respectively, together explained 93.1% of the species variation in each zooplankton phylum. The relationships were mainly concentrated in the first and second quadrants, and WT, pH, ORP, and DO, were the major influencing factors. Trochelminthes and Copepoda species were positively correlated with DO and ORP, and negatively correlated with TS. Protozoa and Cladocera were positively correlated with WT and pH, whereas EC and TDS did not significantly influence zooplankton.

The RDA analysis results for dominant phytoplankton species based on their relationships with environmental factors are illustrated in *Figure 5B*. The eigenvalues of axis 1 and axis 2 were 0.5767 and 0.2845, respectively, which together explained 95.4% variation in the dominant phytoplankton species. Most species were distributed in the first quadrant and were mainly influenced by WT, EC, and TDS. Among them, *Merismopedia tenuissima*, *Microcystis sp.*, *Aphanizomenon sp.*, *Chroomonas acuta*, *Cryptomonas ovata*, *Cryptomonas erosa*, *Chromulina sp.*, *Tribonema sp.*, *Melosira granulata*, *Cyclotella sp.*, *Synedra acus*, *Synedra sp.*, *Navicula capitatoradiata*, *Nitzschia palea*, *Chlorella vulgaris*, *Selenastrum bibraianum*, *Schroederia setigera*, *Ankistrodesmus sp.*, *Dictyosphaerium ehrenbergianum*, *Actinastrum sp.*, *Scenedesmus quadricauda*, and *Micractinium pusillum* were positively correlated with WT, EC, and TDS. *Synedra ulna*, *Nitzschia paradoxa*, and *Chlamydomonas sp.* were positively correlated with ORP, and negatively correlated with pH and TS. In contrast, *Cyclotella meneghiniana* was mainly positively correlated with WT, while *Nitzschia wullerstorffii* was not significantly influenced. The eigenvalues of axis 1 and 2 were 0.669 and 0.1805, which together explained 96.1% of the variation in the dominant species. Similarly, the dominant zooplankton were mainly distributed in the first quadrant, which was most affected by TS and ORP. Among them, *Diffugia oblonga*, *Didinium balbianii*, *Didinium balbianii nanum*, *Polyarthra dolichoptera*, and *Trichocerca bicristata* were more negatively correlated with TS and ORP. *Stribilidium gyrans* was

positively correlated with DO and pH, and negatively correlated with EC and TDS. In contrast, *Brachionus calyciflorus* was positively correlated with EC and TDS, and negatively correlated with DO and pH.

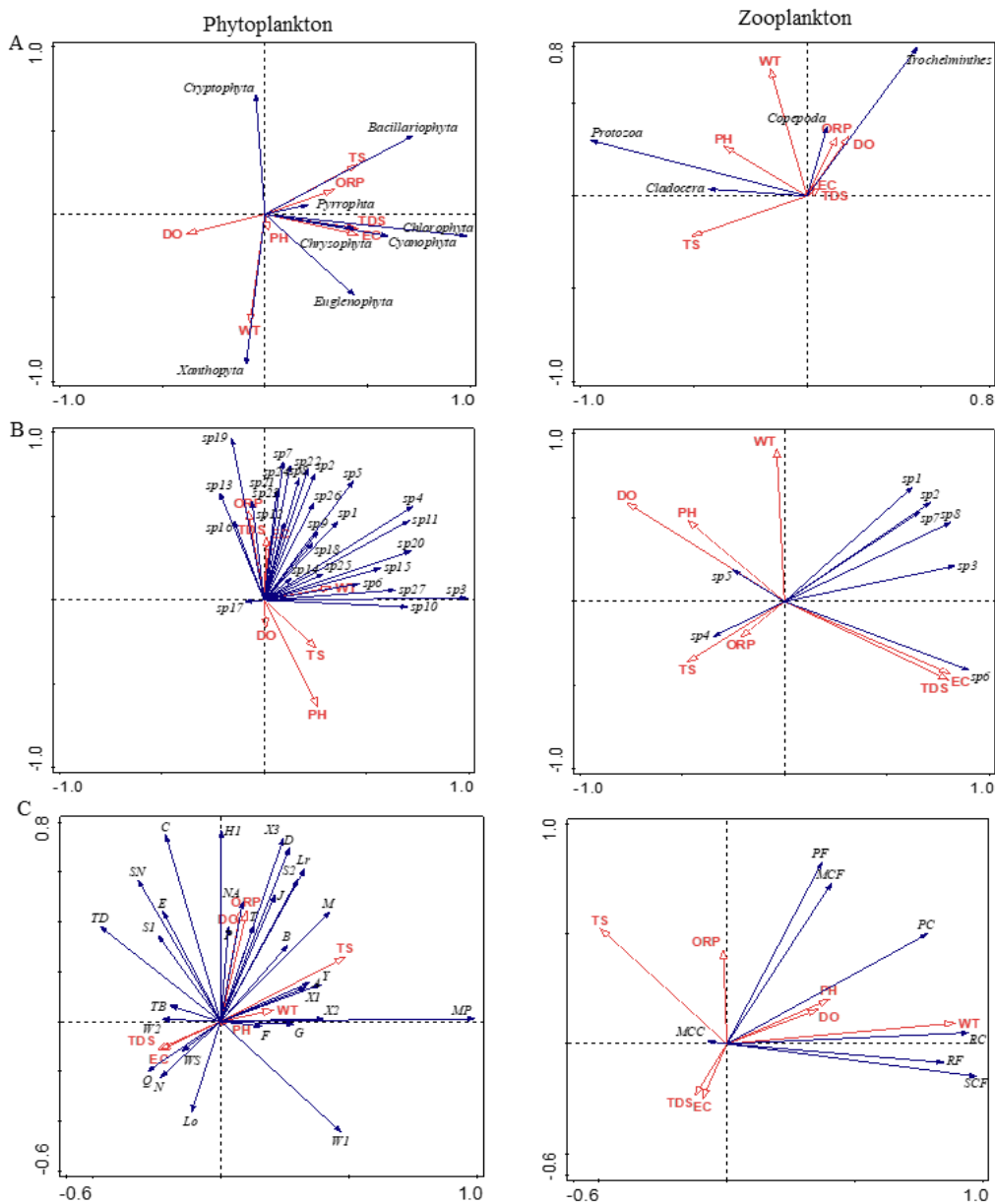


Figure 5. Relationship between plankton and environmental factors in the Fuhe River (A illustrates the RDA analysis between the number of plankton species and environmental factors in the Fuhe River; B illustrates the RDA analysis results for dominant plankton species based on their relationships with environmental factors; C illustrates correlation of biomass of plankton functional groups and environmental factors)

The RDA results of the biomass of 30 phytoplankton functional groups varied with environmental factors, and the eigenvalues of axis 1 and axis 2 were 0.5796 and 0.1595, respectively (Fig. 5C), which explained 91.5% of the variation in phytoplankton functional groups. Most phytoplankton functional groups were distributed in the first

quadrant and second quadrant, and the major environmental factors influencing each functional group were DO, ORP, TS, and WT. Among them, functional groups A, B, M, X1, X2, and Y were mainly positively correlated with WT and TS, while negatively related to TDS and EC. Functional groups D, X3, S2, J, Lr, T, NA, H1 and P were positively correlated with ORP and DO. Functional groups C, E, SN, S1, TD, and TB were also positively correlated with ORP and DO. Functional groups W2, WS, Q, N and Lo were positively correlated with TDS and EC, and negatively correlated with WT and TS. Conversely, functional groups W1, F, and G were mainly positively correlated with pH.

The results of RDA analysis between the nine zooplankton functional groups and environmental factors indicated that the eigenvalues of axis 1 and axis 2 were 0.5362 and 0.2365, respectively, which together explained 91.4% of the variation in zooplankton functional groups. The relationships between biomass and environmental factors for the seven major zooplankton functional groups are indicated by the eigenvalues of axis 1 and axis 2 of 0.85822 and 0.0338, respectively, which together explained 91.9% of the changes in zooplankton functional groups. The functional groups of zooplankton are mainly concentrated in the first quadrant, which are mainly affected by WT, pH, and DO. Among them, functional groups PF, PC, RC and MCF were positively correlated with pH, DO, and ORP, but negatively correlated with TDS and EC. Functional groups RF and SCF were positively correlated with WT. However, there was no significant correlation between MCC and environmental factors.

Discussion

The present study identified 304 phytoplankton species (including varieties and variants) in the Fuhe River basin, mainly in the diatom and green algae phyla, and the number of species in the midstream section of the river was higher than that those upstream and downstream. The results are largely consistent with phytoplankton species composition (Du, 2020; Liu et al., 2012). In addition, in the present study, 158 zooplankton species, mainly concentrated in Protozoa and Rotifer, were observed, which is inconsistent with the findings of Ji et al. for zooplankton in the mainstream of the Fuhe River. In a previous study, 41 zooplankton species were collected in the mainstream of the Fuhe River (Ji et al., 2013), mainly including rotifer, with only 5 protozoan species. In both zooplankton and phytoplankton, the numbers in the middle reaches were more than those in the upper and lower reaches. In addition, phytoplankton and zooplankton abundances were the highest in Cheng Nan and the least in Yihuang (Fig. 2). Furthermore, phytoplankton density and biomass were the highest in Nanfeng and the lowest in Xiangyi, and zooplankton density and biomass were the highest in Lichuan.

The aquatic environment influences the distribution of phytoplankton functional groups, and the presence of different phytoplankton functional groups reflects distinct water environments (Yin et al., 2016). The dominant functional groups derived based on phytoplankton functional group biomass proportions at each site in the Fuhe River were mainly D, J, MP, P, and W1, with more than 50 species, which exhibit capacity to exploit eutrophic aquatic conditions, which also indicates the eutrophic status of the Fuhe River to some extent. In addition, the main functional groups with high biomass were phytoplankton functional groups MP, H1, and W1, among which, MP, H1, and W1, which inhabit inorganic turbid water bodies, eutrophic low-N water bodies, and

small inorganic and shallow water bodies, respectively, mainly dominated the Fuhe River. The bioinorganic turbid water bodies were mainly dominated by *Cymbella sp.*, *Navicula sp.*, and *Gomphonema sp.* of Bacillariophyta; *Anabaena circinalis* and *Aphanizomenon sp.* living in eutrophic, low N-containing water bodies and small organic water bodies, shallow water species mainly include species such as *Phacus Sp.* and *Euglena geniculata* were dominant. Hongmen Reservoir and Liaofang Reservoir, two major reservoirs in the upper tributaries and the main channel of the Fuhe River, can frequently disturb the water bodies. In addition, the water bodies collected by the reservoirs can become eutrophic after extended periods of storage. Furthermore, water levels in the lower reaches of the reservoirs are relatively shallow, so that the aquatic environment of the Fuhe River is conducive for the growth and development of a large number of functional groups, including MP, H1, and W1 (Padisak et al., 2006).

Twenty-one functional groups had relatively low biomass, including A, B, E, F, J, Q, and N. The water bodies that mainly hosted the functional groups above had low, moderate, or high nutrient concentrations, low acidity, high humus, low TS, warm temperatures, high alkalinity, and fast water flows. The average pH value of Fuhe River ranges from 7.77 to 8.12, and it is mainly a neutral or weak alkaline water body, with obvious temperature differences in the four seasons. Therefore, the results are consistent with the environmental variability in the Fuhe River.

The Fuhe River has been reported to be dominated by functional groups PF, RF, RC, and SCF, which are mainly algae, bacteria, detritus-feeding, and small protozoan-feeding species, which is consistent with the findings that rotifers, protozoan, and other small zooplankton species are dominant in the Fuhe River. The functional group PF is composed of species such as *Arcella vulgaris*, *Arcella arenaria*, and *Strombidium viride*, which live mainly in eutrophic water bodies, and some studies have shown that protozoa mainly feed on single-celled microalgae, and the phytoplanktons with higher densities in spring and winter are *Cyclotella meneghiniana*, *Aulacoseira granulate*, *Synedra acus*, and other large phytoplankton (Hu et al., 2019b). The results also show that aquatic environments with high water flow and high sediment content are conducive for protozoa than for other zooplankton (Dai et al., 2019). The RF functional group is mainly composed of rotifers with low temperature tolerance and wide distribution, such as *Brachionus angularis*, *Asplanchnopus multiceps*, and *Synchaeta pectinata*, which constitute the major filter-feeding phytoplankton. This functional group is able to control phytoplankton in spring and winter (Du, 2020). The total biomass of the RC group, which mainly feeds on rotifers, protozoa, other rotifers and small crustaceans, was the highest. The functional group SCF consists of small zooplankton, which feed on algae, bacteria, debris, and protozoa, such as *Bosmina longirostris* and nauplii. The biomass of zooplankton at S3, which represents the dam of the Hongmen Reservoir, was the greatest. Some tetrads have farmers in the sampling area; therefore, feed and fertilizer applied in the farms could promote zooplankton growth at such sites. The S4 site harbored the highest number of zooplankton species, which may be attributed the location of S4 at the intersection of two upstream tributaries, so that it is the gathering point of zooplankton from two tributaries on the dam of Liaofang Reservoir.

Since a large number of water conservancy projects have been undertaken and cascade dams built in the mainstream of the Fuhe River, the water quantity in each reach has changed considerably, and the subsequent changes in the aquatic ecosystems influence plankton growth. Numerous researchers have studied the influence of

environmental factors on plankton community structure; for example, in a study of plankton and environmental factors in the Yangtze River (Yang, 2016), WT, DO, and TDS were the major environmental factors influencing phytoplankton community structure, whereas TS, NH₄-N, etc. were the major factors influencing zooplankton community structure. In a study on phytoplankton composition of Shuifeng Reservoir, within a certain range, the higher the WT, the stronger the light, the longer the light period, the higher the nutrient content, and the slower the water flow, the greater the phytoplankton growth and reproduction (Wei, 2021). Phytoplankton is also a factor influencing zooplankton (Wang et al., 2007). Furthermore, WT plays an important role in the distribution of phytoplankton communities (Becker et al., 2009). WT can control the respiration intensity and the photosynthesis enzymatic reactions of phytoplankton, which directly affects their growth and reproduction (Blinn, 1993). According to the RDA analysis results, the main TS of functional groups A, B, M, X1, X2 and Y were positively correlated with WT, and the functional groups were mainly dominated by Bacillariophyta and Cryptophyta species. TS represents the clarity of the water body, which corresponds to the distribution of phytoplankton, sediment and suspended matter (Li et al., 2015; Nielsen et al., 2002; Zhang et al., 2003). TS is mainly caused by the existence of phytoplankton. An increase in algae, leads to a decrease in TS. Some studies have shown that the optimal growth temperature range for most diatoms is 15°C–25°C (Du, 2020). The average WT of Fuhe River was 8.8°C~32.96°C, which is relatively high, so that winter and spring are more conducive periods for diatom growth than summer and autumn. Conversely, C, D, E, S_N, S1, T_D, T_B and other functional groups exhibit better growth in water with high DO, which is positively correlated with ORP. Functional groups W2, W_S, Q, N, and Lo exhibit positive correlations with TDS and EC, and prefer to be in environments with solid particles, such as water with gravel as the bottom.

WT also influences zooplankton abundance, distribution, and community structure (Chen et al., 2010; Devreker et al., 2004). In the present study, the major factors influencing zooplankton community structure were WT, pH and DO, and the PF, PC, RF, RC, and SCF functional groups were positively correlated with WT. TS is also a key environmental factor influencing zooplankton community structure (Wang et al., 2017). In the present study, RF, RC, and SCF functional groups were negatively correlated with TS, while Fuhe River TS was low, which is consistent with the analysis results.

Phytoplankton are widely used to evaluate water quality, and the most extensively used tools are diversity index evaluation and Qr-index. The difference between the two methods is that the diversity index evaluation method reflects water quality based on the composition of various biological species in the water body, and is a function of species and abundance distribution. Studying the diversity and dynamic characteristics of phytoplankton in water facilitates the evaluation of water quality (Li et al., 2012). The Qr-index is the weighted average of the total value of all co-occurring functional groups. The Qr-index, which is primarily based on the abundance of the functional group F, has been used extensively in phytoplankton ecology research and water quality evaluation (Padisak et al., 2006). However, it still needs to be improved; for example, Padisa et al.'s classification index when assigning the impact factor F. It is not accurate enough, and the results are easily influenced by subjective factors.

The Shannon-Wiener diversity index (H) of phytoplankton at all sites was > 3, and the order was as follows: S2 > S4 > S1 = S7 > S3 > S6 > S9 > S5 > S8. According to

the results, river water quality was generally pollution-free or had low pollution. The Q_r index at all sites in the Fuhe River Basin was 2.71–4.63. The smaller the Q_r value, the higher the nutrient levels in the water body (Yin et al., 2016). The order of the magnitudes of Q_r -values in all the sites was as follows: $S_6 > S_1 > S_5 > S_2 = S_7 > S_4 > S_9 > S_8 > S_3$. Based on the Q_r -values, the water quality at S_1 and S_6 sites were excellent, those at S_2 , S_4 , S_5 , and S_7 sites showed good quality, whereas those at S_3 , S_8 , and S_9 sites showed moderate water quality. Therefore, the overall water quality of Fuhe River Basin is good, and the degree of pollution is low. Overall, there was no considerable difference between the Q_r -value results and the Shannon-Wiener diversity index results.

Conclusion

We identified 30 phytoplankton functional groups and 9 zooplankton functional groups by the living environment and ecological type of plankton. The functional groups were mainly composed of groups H1, MP, and W1 of phytoplankton and RF, RC, and SCF of zooplankton. WT, DO, ORP, and TS were likely the critical factors affecting phytoplankton communities, whereas the major environmental factors influencing zooplankton communities were WT, pH, and DO. This study confirmed the potential utility of the phytoplankton functional groups method in the Fuhe River water quality assessment, which was based on Q_r -index of phytoplankton diversity and functional group biomass. The results show that Shannon-Wiener diversity index (H) of phytoplankton at all sites was >3 . And the Q_r index at all sites in the Fuhe River Basin was 2.71–4.63. The two evaluation methods can be combined to conclude that the water quality of the Fuhe River is lightly polluted or non-polluted state, and the water quality condition is good. This study further complements the relevant data of the Fuhe River basin, and more fully demonstrates the plankton community structure and water quality in the basin, providing basic information for the future management and protection of the Fuhe River.

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Conflict of interests. The authors declare that they have no conflict of interest.

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APPENDIX

Table A1. List of phytoplankton

Species	S1	S2	S3	S4	S5	S6	S7	S8	S9	Functional groups
Cyanophyta										
<i>Chroococcus</i> sp.		√					√			LO
<i>Merismopedia punciata</i>	√	√		√		√				LO
<i>Merismopedia</i> sp.	√	√	√				√	√	√	LO
<i>Merismopedia elegans</i>			√	√						LO
<i>Merismopedia tenuissima</i>	√	√		√	√	√		√		LO
<i>Microcystis incerta</i>	√	√		√	√		√	√		M
<i>Microcystis</i> sp.	√	√	√	√		√	√	√	√	M
<i>Coelosphaerium</i> sp.	√		√			√	√			LO
<i>Oscillatoria</i> sp.		√		√		√	√	√		MP
<i>Oscillatoria tenuis</i>	√	√		√	√	√	√	√	√	MP
<i>Oscillatoria limosa</i>	√	√		√	√	√	√	√	√	MP
<i>Oscillatoria princeps</i>	√	√	√	√	√	√	√		√	MP
<i>Oscillatoria tenuis</i>	√	√	√	√	√	√	√	√		MP
<i>Oscillatoria okni</i>	√	√		√			√	√	√	MP
<i>Oscillatoria chalybea</i>		√		√			√			MP
<i>Oscillatoria borneti</i>		√		√	√	√	√	√	√	MP
<i>Spirulina</i> sp.	√	√	√	√	√	√	√	√	√	S2
<i>Phormidium</i> sp.	√	√		√		√	√	√	√	S1
<i>Lyngbya</i> sp.					√				√	S1
<i>Nostoc commune</i>		√	√					√		H1
<i>Nostoc paludosum</i>		√		√				√		H1
<i>Anabaena fortissima</i>	√	√		√	√	√	√			H1
<i>Anabaena azotica</i>	√			√		√				H1

<i>Anabaena circinalis</i>	√		√	√						H1
<i>Anabaena sp.</i>	√	√	√	√	√	√	√	√		H1
<i>Raphidiopsis sp.</i>			√	√		√				SN
<i>Aphanizomenon sp.</i>	√	√	√	√	√	√	√	√	√	H1
Cryptophyta										
<i>Chroomonas acuta</i>	√	√		√	√	√	√	√	√	X2
<i>Cryptomonas ovata</i>	√	√		√	√	√	√	√	√	Y
<i>Cryptomonas erosa</i>	√	√			√	√			√	Y
Pyrrophyta										
<i>Gymnodinium aeruginosum</i>								√		Y
<i>Peridinium umbonatum</i>		√				√	√			LO
<i>Peridinium willei</i>			√	√		√	√			LO
<i>Peridinium cunningtomii</i>						√				LO
<i>Peridinium inconspicuum</i>					√					LO
<i>Peridinium sp.</i>						√	√			LO
<i>Ceratium hirundinella</i>	√		√	√	√	√	√	√	√	LO
Chrysophyta										
<i>Chromulina sp.</i>	√		√	√	√	√	√	√	√	E
<i>Mallomonas sp.</i>	√			√		√	√	√	√	E
<i>Synura sp.</i>		√		√	√		√			WS
<i>Dinobryon divergens</i>			√	√	√	√				E
<i>Dinobryon sp.</i>			√							E
<i>Dinobryon bavaricum</i>			√	√						E
Xanthophyta										
<i>Tribonema affine</i>		√	√	√		√		√		T
<i>Tribonema viride</i>			√						√	T
<i>Tribonema sp.</i>	√	√	√	√	√	√	√	√	√	T
<i>Gonyostomum depressum</i>	√		√					√		Q
Bacillariophyta										
<i>Melosira granulata</i>	√	√	√	√	√	√	√		√	Lr
<i>Melosira granulata var. angustissima</i>					√					P
<i>Melosira granulata var sp.iralis</i>	√	√		√	√	√	√	√	√	P
<i>Melosira varians</i>	√			√	√	√		√		TB
<i>Melosira sp.</i>	√			√		√	√	√	√	Lr
<i>Coscinodiscus sp.</i>				√				√		C
<i>Cyclotella meneghiniana</i>	√		√	√	√		√	√	√	C
<i>Cyclotella bodanica</i>	√									B
<i>Cyclotella sp.</i>	√	√	√	√	√	√	√	√	√	B
<i>Attheya zachariasi</i>	√								√	F
<i>Asterionella sp.</i>	√	√	√	√		√	√	√	√	C
<i>Synedra acus</i>	√	√	√	√	√	√	√	√	√	D
<i>Synedra ulna var. amphirhynchus</i>						√				D
<i>Synedra ulna</i>	√	√	√	√	√	√	√	√	√	D
<i>Synedra capitata</i>				√						D
<i>Synedra sp.</i>	√		√	√	√	√	√	√	√	D
<i>Fragilaria crotonensis</i>				√	√				√	P
<i>Fragilaria biceps</i>	√		√	√	√	√	√	√	√	P
<i>Fragilaria intermedia</i>	√	√	√	√	√	√	√	√	√	MP
<i>Fragilaria capucina</i>	√			√					√	P
<i>Fragilaria sp.</i>	√	√	√	√	√	√	√	√	√	P
<i>Diatoma vulgare</i>	√			√	√		√			A
<i>Diatoma tenue</i>						√				A
<i>Diatoma sp.</i>	√	√		√		√	√	√	√	A

<i>Tabellaria fenestrata</i>								√		N
<i>Tabellaria sp.</i>				√		√		√	√	N
<i>Eunotia arcus</i>				√						MP
<i>Eunotia sp.</i>						√		√	√	MP
<i>Cocconeis placentula</i>	√	√	√	√				√		MP
<i>Achnanthes affinis</i>					√					MP
<i>Achnanthes lanceolata</i>	√			√						MP
<i>Achnanthes inflata</i>						√		√		MP
<i>Achnanthes sp.</i>	√	√	√	√	√	√	√	√	√	MP
<i>Mastogloia sp.</i>			√	√		√			√	MP
<i>Stauroneis acuta</i>			√	√						MP
<i>Stauroneis sp.</i>	√	√	√	√	√	√	√	√	√	MP
<i>Navicula capitatoradiata</i>	√	√	√	√		√	√	√		MP
<i>Navicula rhynchocephala</i>				√						MP
<i>Navicula reichardtiana</i>					√				√	MP
<i>Navicula radiosa</i>				√						MP
<i>Navicula avenacea</i>								√		MP
<i>Navicula amphibola</i>					√					MP
<i>Navicula sp.</i>				√	√				√	MP
<i>Pinnularia viridis</i>					√	√	√			MP
<i>Pinnularia subcapitata</i> var. <i>stauroneiformis</i>		√				√	√			MP
<i>Pinnularia acrosphaeria</i>			√			√	√			MP
<i>Pinnularia microstauron</i>				√		√	√			MP
<i>Pinnularia platycephala</i>		√					√	√	√	MP
<i>Pinnularia nobilis</i>						√				MP
<i>Pinnularia rangoonensis</i>	√			√	√	√	√			MP
<i>Pinnularia sp.</i>			√			√				MP
<i>Gyrosigma acuminatum</i>		√	√	√	√	√	√		√	MP
<i>Gyrosigma kuetzingii</i>						√				MP
<i>Gyrosigma spencerii</i>		√		√	√	√	√			MP
<i>Gyrosigma scalproides</i>	√				√	√	√			MP
<i>Gyrosigma parkerii</i>					√	√				MP
<i>Gyrosigma sp.</i>			√		√		√			MP
<i>Diploneis oblongella</i>				√			√		√	MP
<i>Diploneis elliptica</i>	√		√		√		√			MP
<i>Cymbella perpusilla</i>							√	√		MP
<i>Cymbella excisa</i>	√									MP
<i>Cymbella prostrate</i>		√								MP
<i>Cymbella cistula</i> var. <i>hebetata</i>					√					MP
<i>Cymbella subcistula</i>	√		√	√	√	√	√			MP
<i>Cymbella affinis</i>				√						MP
<i>Cymbella turgidula</i>				√		√				MP
<i>Cymbella tumida</i>	√	√			√	√	√		√	MP
<i>Cymbella parva</i>		√				√	√			MP
<i>Cymbella sinensis</i>		√			√	√				MP
<i>Cymbella hantzschiana</i>						√				MP
<i>Cymbella schweicberdtii</i>								√		MP
<i>Cymbella sp.</i>	√				√	√		√		MP
<i>Gomphonema parvulum</i>				√	√				√	TB
<i>Gomphonema kaznakowii</i>							√			MP
<i>Gomphonema gracile</i>							√			MP
<i>Gomphonema constrictum</i>	√	√		√		√				MP
<i>Gomphonema constrictum</i> var. <i>turgidum</i>		√								MP

<i>Gomphonema constrictum</i> var. <i>ventricosum</i>							√	√	MP
<i>Gomphonema intricatum</i>			√				√		MP
<i>Gomphonema hedinii</i>						√			MP
<i>Gomphonema</i> sp.		√	√	√	√	√	√	√	MP
<i>Didymosphenia geminata</i>	√	√					√		MP
<i>Nitzschia longissima</i>		√					√		D
<i>Nitzschia lorenziana</i>								√	D
<i>Nitzschia paradoxa</i>	√	√		√	√	√	√	√	D
<i>Nitzschia sigmoidea</i>				√	√	√			D
<i>Nitzschia wullerstorffii</i>		√		√	√	√	√	√	D
<i>Nitzschia nana</i>		√				√	√	√	D
<i>Nitzschia acicularis</i>	√	√		√			√	√	D
<i>Nitzschia constricta</i>								√	D
<i>Nitzschia calida</i>	√								D
<i>Nitzschia acula</i>		√			√		√		D
<i>Nitzschia palea</i>	√	√	√	√	√	√	√	√	D
<i>Nitzschia subcohaerens</i>						√			D
<i>Nitzschia obtusa</i>	√	√		√			√		D
<i>Nitzschia levidensis</i>		√				√	√	√	D
<i>Nitzschia</i> sp.			√	√	√				D
<i>Rhopalodia</i> sp.				√					MP
<i>Cymatopleura solea</i>					√	√	√		MP
<i>Cymatopleura solea</i> var. <i>apiculata</i>							√		MP
<i>Cymatopleura</i> sp.						√			MP
<i>Surirella bifrons</i>				√	√	√			MP
<i>Surirella biseriata</i>		√		√		√	√	√	MP
<i>Surirella linearis</i>	√								MP
<i>Surirella angustata</i>			√	√			√	√	MP
<i>Surirella capronii</i>				√	√				MP
<i>Surirella brebissonii</i>							√		MP
<i>Surirella brebissonii</i>								√	MP
<i>Surirella tenera</i>	√	√	√	√	√	√	√	√	MP
<i>Surirella splendida</i>				√					MP
<i>Surirella robusta</i>	√	√	√	√	√	√	√	√	MP
<i>Surirella nervosa</i>				√			√	√	MP
<i>Surirella</i> sp.								√	MP
Euglenophyta									
<i>Euglena spirogyra</i>				√					W1
<i>Euglena viridis</i>	√		√		√	√	√	√	W1
<i>Euglena geniculata</i>		√				√	√	√	W1
<i>Euglena pisciformis</i>	√	√	√	√	√	√	√		W1
<i>Euglena thinophila</i>			√		√		√	√	W1
<i>Euglena acus</i>			√				√	√	W1
<i>Euglena oxyuropsis</i>							√		W1
<i>Euglena brevicaudata</i>		√							W1
<i>Euglena oxyuris</i>						√			W1
<i>Euglena ehrenbergii</i>		√						√	W1
<i>Euglena deses</i>				√		√			W1
<i>Euglena</i> sp.			√			√			W1
<i>Phacus anomalus</i>				√		√	√		W1
<i>Phacus circulatus</i>								√	W1
<i>Phacus triqueter</i>	√								W1
<i>Phacus lemmermannii</i>			√	√		√			W1

<i>Phacus ovalis</i>							√			W1
<i>Phacus longicauda</i>			√							W1
<i>Phacus sp.</i>			√				√			W1
<i>Lepocinclis reeuwykiana</i>							√			W1
<i>Lepocinclis sp.</i>		√	√			√	√			W1
<i>Trachelomonas planctonica</i>						√				W2
<i>Trachelomonas australica</i>			√				√			W2
<i>Trachelomonas mirabilis</i>			√							W2
<i>Trachelomonas armata</i>			√							W2
<i>Trachelomonas felix</i>			√				√	√		W2
<i>Trachelomonas oblonga</i>			√	√		√		√		W2
<i>Trachelomonas volvocina</i>				√			√			W2
<i>Trachelomonas curta</i>							√			W2
<i>Trachelomonas lacustris</i>					√					W2
<i>Trachelomonas pulcherrima</i>	√									W2
<i>Trachelomonas sp.</i>		√	√				√			W2
<i>Strombomonas borystheniensis</i>						√				W2
<i>Strombomonas acuminata</i>		√					√			W2
<i>Strombomonas fusiformis var. lonicauda</i>									√	W2
<i>Strombomonas sp.</i>				√		√		√		W2
<i>Peranema sp.</i>		√			√	√	√			W1
<i>Khawkinia acutecouato</i>		√	√	√			√	√		W1
<i>Khawkinia variabilis</i>	√	√	√	√	√	√	√	√	√	W1
Chlorophyta										
<i>Chlamydomonas sp.</i>	√	√	√	√		√	√	√		X2
<i>Carteria sp.</i>								√	√	G
<i>Lobomonas sp.</i>			√	√		√				X2
<i>Gonium sp.</i>	√	√	√	√		√	√	√		W1
<i>Pandorina morum</i>	√	√	√	√	√	√	√	√	√	G
<i>Eudorina elegans</i>	√	√	√	√	√		√	√	√	G
<i>Eudorina echidna</i>									√	G
<i>Pleodorina californica</i>				√						G
<i>Volvox africanus</i>	√	√	√	√	√	√	√	√	√	G
<i>Volvox globator</i>			√							G
<i>Tetraspora lacustris</i>				√			√			TD
<i>Chlorella vulgaris</i>	√	√	√	√	√	√	√	√	√	X1
<i>Tetraedron trigonum</i>		√		√		√	√		√	J
<i>Tetraedron planktonicum</i>							√			J
<i>Tetraedron tumidulum</i>						√				J
<i>Tetraedron sp.</i>						√			√	J
<i>Treubaria triappendiculata</i>		√		√					√	F
<i>Kirchneriella sp.</i>		√	√	√		√	√	√	√	F
<i>Selenastrum bibraianum</i>	√	√		√		√	√	√		F
<i>Golenkinia sp.</i>				√	√		√		√	J
<i>Chodatella ciliata</i>				√						J
<i>Chodatella longiseta</i>				√				√		J
<i>Chodatella sp.</i>			√	√		√	√			J
<i>Polyedriopsis sp.</i>										J
<i>Schroederia setigera</i>				√		√				X3
<i>Schroederia spiralis</i>			√	√		√	√		√	X3
<i>Schroederia robusta</i>								√		X3
<i>Schroederia sp.</i>		√	√				√		√	X3
<i>Oocystis sp.</i>		√	√	√	√	√	√	√	√	F

<i>Ankistrodesmus sp.</i>	√	√		√	√	√	√	√	√	X1
<i>Ankistrodesmus acicularis</i>							√			X1
<i>Ankistrodesmus spiralis</i>	√	√		√	√	√	√	√	√	X1
<i>Ankistrodesmus spiralis var. fasciculatus</i>					√	√		√	√	X1
<i>Ankistrodesmus falcatus</i>		√		√		√	√			X1
<i>Dictyosphaerium ehrenbergianum</i>	√	√	√	√		√	√	√	√	F
<i>Actinastrum sp.</i>	√	√	√	√	√	√	√	√	√	J
<i>Hydrodictyon reticulatum</i>		√								J
<i>Pediastrum simplex</i>	√	√	√	√	√		√		√	J
<i>Pediastrum sturmii</i>										J
<i>Pediastrum biradiatum</i>	√	√		√		√	√		√	J
<i>Pediastrum duplex</i>	√	√	√	√	√	√	√	√	√	J
<i>Pediastrum boryanum</i>				√						J
<i>Stauridium tetras</i>	√							√	√	J
<i>Scenedesmus dimorphus</i>	√	√	√	√	√	√	√			J
<i>Scenedesmus javaensis</i>		√		√					√	J
<i>Scenedesmus bicaudatus</i>		√	√	√		√	√	√	√	J
<i>Scenedesmus bijuba</i>				√		√				J
<i>Scenedesmus granulatus</i>	√		√	√		√	√	√		J
<i>Scenedesmus denticulatus</i>							√			J
<i>Scenedesmus furcatus</i>							√		√	J
<i>Scenedesmus armatus</i>	√	√	√	√	√		√	√	√	J
<i>Scenedesmus protuberans</i>		√		√			√			J
<i>Scenedesmus quadricauda</i>	√	√	√	√	√	√	√	√	√	J
<i>Scenedesmus sp.</i>		√		√	√	√	√	√		J
<i>Crucigenia rectangularis</i>			√	√		√				J
<i>Crucigenia tetrapedia</i>			√	√				√	√	J
<i>Crucigenia apiculata</i>		√	√			√	√			J
<i>Crucigenia lauterbornii</i>				√						J
<i>Crucigenia quadrata</i>				√			√			J
<i>Westella sp.</i>	√	√	√	√	√		√		√	F
<i>Tetrastrum heterocanthum</i>				√				√	√	J
<i>Tetrastrum hastiferum</i>							√			J
<i>Acanthosphaera zachariasi</i>		√		√						J
<i>Micractinium bornhemiensis</i>		√		√			√			J
<i>Micractinium pusillum</i>		√	√	√		√	√	√	√	J
<i>Coelastrum sphaericum</i>		√		√		√	√			J
<i>Coelastrum microporum</i>								√	√	J
<i>Coelastrum reticulatum</i>				√						J
<i>Cladophora glomerata</i>		√		√			√		√	TD
<i>Oedogonium sp.</i>	√	√	√	√	√	√	√	√		TD
<i>Stigeoclonium sp.</i>	√	√	√	√	√	√	√	√	√	TD
<i>Ulothrix zonata</i>					√	√	√	√		MP
<i>Ulothrix sp.</i>	√		√	√	√	√	√	√	√	MP
<i>Closterium lanceolatum</i>					√		√	√		P
<i>Closterium ehrenbergii</i>						√				P
<i>Closterium pritchardianum</i>			√	√	√				√	P
<i>Closterium lunula</i>		√		√			√			P
<i>Closterium acerosum</i>	√	√		√	√	√	√	√	√	P
<i>Closterium eboracense</i>						√				P
<i>Closterium pseudonasutum</i>		√		√			√			P
<i>Closterium gracile</i>		√	√	√			√			P
<i>Closterium toxon</i>			√		√					P

<i>Closterium kuetzingii</i>				√				√		P
<i>Closterium sp.</i>				√		√	√			P
<i>Penium cylindrus</i>				√				√		P
<i>Penium margaritaceum</i>		√				√				N
<i>Euastrum ansutum</i>	√			√						N
<i>Euastrum dubium</i>				√						N
<i>Staurodesmus alternans</i>		√					√			NA
<i>Staurastrum manfeldtii</i>									√	NA
<i>Staurastrum planctonicum</i>			√	√			√			NA
<i>Staurastrum willsii</i>	√						√	√		NA
<i>Staurastrum sp.</i>		√				√	√	√	√	NA
<i>Cosmarium laeve</i>		√		√		√	√	√		N
<i>Cosmarium vexatum</i>				√		√				N
<i>Cosmarium impressulum</i>		√		√		√				N
<i>Cosmarium obtusatum</i>	√	√		√		√		√		N
<i>Cosmarium binum</i>		√		√		√				N
<i>Cosmarium sp.</i>		√		√				√		N
<i>Spondylosium planum</i>				√				√	√	N
<i>Spondylosium moniliforme</i>					√	√				N
<i>Spondylosium papiuosum</i>			√	√	√		√		√	N
<i>Spirogyra sp.</i>	√	√	√	√	√	√	√	√	√	TD
<i>Mougeotia sp.</i>		√	√	√	√	√	√	√	√	T
<i>Mougeotia parvula</i>	√		√	√						T

“√” indicates the presence of the species at that point

Table A2. List of zooplankton

Species	S1	S2	S3	S4	S5	S6	S7	S8	S9	Functional groups
Protozoa										
<i>Amoeba gorgonia</i>		√	√							PF
<i>Amoeba striata</i>		√			√	√				PF
<i>Amoeba proteus</i>		√						√		PF
<i>Vahlkampfia guttula</i>		√	√	√	√	√				PF
<i>Arcella vulgaris</i>		√			√					PF
<i>Arcella discoides</i>	√		√	√	√					PF
<i>Arcella arenaria</i>	√	√	√	√	√	√	√			PF
<i>Arcella mitrata</i>		√		√		√	√	√		PF
<i>Heleopera sylvatica</i>	√		√		√	√				PF
<i>Cucurbitella mespiliformis</i>				√					√	PF
<i>Cucurbitella hemisphaerica</i>	√	√			√					PF
<i>Cucurbitella nidulus</i>		√	√			√	√	√	√	PF
<i>Centropyxis aerophides</i>				√	√	√				PF
<i>Centropyxis discoides</i>		√						√		PF
<i>Diffflugia acuminata</i>			√	√		√				PF
<i>Diffflugia oblonga</i>		√		√		√	√			PF
<i>Diffflugia corona</i>		√	√	√	√	√	√	√	√	PF
<i>Diffflugia lobostoma</i>			√	√		√	√	√		PF
<i>Diffflugia lebes</i>				√						PF
<i>Diffflugia globulosa</i>		√		√	√		√		√	PF
<i>Diffflugia limnetica</i>						√				PF
<i>Diffflugia urceolata</i>		√		√		√			√	PF

<i>Diffugia sp.</i>				√				√	√	PF
<i>Euglypha tuberculata</i>							√			PF
<i>Trinema enchelys</i>									√	PF
<i>Actinophrys sol</i>		√	√							PF
<i>Acanthocystis brevicirrhis</i>	√									PF
<i>Acanthocystis erinaceus</i>	√			√						PF
<i>Didinium balbianii</i>	√		√	√		√			√	PC
<i>Didinium balbianii nanum</i>	√	√	√	√					√	PC
<i>Didinium nasutum</i>		√	√	√	√				√	PC
<i>Paramecium sp.</i>			√	√						PF
<i>Chilodonella algivora</i>		√		√						PF
<i>Glaucoma frontata</i>		√	√	√	√				√	PF
<i>Frontonia sp.</i>	√		√			√	√	√		PF
<i>Vorticella similis</i>				√			√			PF
<i>Vorticella convallaria</i>										PF
<i>Vorticella campanula</i>				√					√	PF
<i>Vorticella picta</i>						√			√	PF
<i>Vorticella kahli</i>					√	√	√			PF
<i>Vorticella sp.</i>			√	√		√				PF
<i>Epistylis lacustris</i>				√			√			PF
<i>Epistylis anastatica</i>		√		√			√			PF
<i>Epistylis urceolata</i>						√				PF
<i>Spirostomum minus</i>		√			√		√	√	√	PF
<i>Stentor amethystinus</i>		√		√		√	√			PF
<i>Stribilidium gyrans</i>	√	√	√	√	√	√	√	√	√	PF
<i>Strombidium viride</i>		√	√	√		√			√	PF
<i>Tintinnidium fluviatile</i>		√	√	√					√	PF
<i>Euplotes terricola</i>							√			PF
<i>Acineta sp.</i>						√				PF
Trochelminthes										
<i>Rotaria tardigrada</i>	√	√	√	√	√	√	√	√	√	RF
<i>Macrotrachela nana</i>		√			√		√			RF
<i>Dicraniphorus lvtkeni</i>		√								RF
<i>Dicraniphorus uncinatus</i>	√									RF
<i>Brachionus plicatilis</i>				√						RF
<i>Brachionus calyciflorus</i>	√	√	√	√	√	√	√	√	√	RF
<i>Brachionus urceus</i>	√	√		√		√		√	√	RF
<i>Brachionus quadridentatus</i>							√			RF
<i>Brachionus angularis</i>								√	√	RF
<i>Brachionus forficula</i>	√			√		√		√		RF
<i>Brachionus falcatus</i>	√	√	√	√		√	√	√	√	RF
<i>Brachionus budapestiensis</i>									√	RF
<i>Brachionus leydigi</i>		√		√						RF
<i>Brachionus diversicornis</i>			√					√	√	RF
<i>Platylabus quadricornis</i>				√			√			RF
<i>Platylabus militaris</i>			√	√		√		√	√	RF
<i>Lepadella ovalis</i>	√							√		RF
<i>Lepadella venefica</i>		√								RF
<i>Colurella uncinata</i>		√		√						RF
<i>Keratella quadrata</i>							√	√		RF
<i>Keratella cochlearis</i>	√		√	√				√		RF
<i>Keratella valga</i>	√		√	√			√	√		RF
<i>Anuraeopsis fissa</i>				√	√					RF

<i>Proales decipiens</i>							√			RF
<i>Epiphanes senta</i>	√			√	√			√	√	RF
<i>Notholon acuminata cincta</i>				√		√				RF
<i>Notholon acuminata</i>	√	√	√		√	√	√	√	√	RF
<i>Euchlanis parva</i>	√				√					RF
<i>Euchlanis pellucida</i>			√	√			√			RF
<i>Euchlanis dilalata</i>	√			√	√	√			√	RF
<i>Cephalodella exigua</i>	√									RF
<i>Cephalodella sterea</i>	√									RF
<i>Cephalodella gibba</i>	√		√	√						RF
<i>Cephalodella catellina</i>				√	√					RF
<i>Proales minima</i>			√							RF
<i>Asplanchna priodonta</i>	√	√	√	√	√	√	√	√		RC
<i>Asplanchna girodi</i>		√	√				√	√	√	RC
<i>Asplanchna brightwelli</i>	√	√	√	√	√		√	√	√	RC
<i>Ascomorpha saltans</i>		√	√	√	√		√	√		RF
<i>Ascomorpha ecaudis</i>	√		√	√	√	√		√		RF
<i>Asplanchnopus multiceps</i>	√		√	√						RF
<i>Synchaete longipes</i>	√		√							RF
<i>Synchaete pectinata</i>	√	√	√	√			√	√	√	RF
<i>Testudinella sp.</i>	√									RF
<i>Testudinella mucronata</i>	√		√	√	√					RF
<i>Polyarthra trigla</i>	√		√	√		√	√	√	√	RC
<i>Polyarthra vulgaris</i>	√		√			√	√	√		RC
<i>Polyarthra dolichoptera</i>	√		√	√		√	√	√	√	RC
<i>Trichocerca bicristata</i>						√	√			RF
<i>Trichocerca elongata</i>					√					RF
<i>Trichocerca longiseta</i>										RF
<i>Diurella weberi</i>								√		RF
<i>Lecane ungulata</i>			√		√	√			√	RF
<i>Lecane niothis</i>			√					√		RF
<i>Monostyla bulla</i>		√	√	√		√	√			RF
<i>Monostyla lunaris</i>						√				RF
<i>Monostyla elachis</i>	√		√			√	√			RF
<i>Monostyla closterocerca</i>								√		RF
<i>Harringia eupoda</i>	√						√		√	RF
<i>Filinia minuta</i>	√		√		√		√	√	√	RF
<i>Pompholyx sulcata</i>								√		RF
<i>Pompholyx complanata</i>			√			√	√	√		RF
<i>Notommata cyrtopus</i>	√									RF
<i>Notommata pachyura</i>						√				RF
<i>Resticula melandocus</i>				√		√				RF
<i>Eosphora najas</i>					√					RF
Cladocera										
<i>Diaphanosoma brachyurum</i>	√								√	MCF
<i>Diaphanosoma leuchtenbergianum</i>	√			√		√				MCF
<i>Diaphanosoma sarsi</i>		√	√	√	√	√	√		√	MCF
<i>Ceriodaphnia setosa</i>								√	√	MCF
<i>Ceriodaphnia laticaudata</i>					√					MCF
<i>Scapholeberis aurita</i>						√				MCF
<i>Scapholeberis mucronata</i>							√			MCF
<i>Daphnia carinata</i>						√				LCF
<i>Daphnia cucullata</i>				√						MCF

<i>Simocephalus exspinosu</i>				√	√					SCF
<i>Moina rectirostris</i>		√					√	√	√	MCF
<i>Moina macrocopa</i>				√						MCF
<i>Bosmina longirostris</i>	√	√	√	√	√	√	√	√	√	SCF
<i>Bosmina coregoni</i>									√	SCF
<i>Bosmina fatalis</i>		√		√		√		√		SCF
<i>Bosminopsis deitersi</i>	√		√	√		√		√	√	SCF
<i>Chydorus ventricosus</i>						√				MCF
<i>Chydorus sphaericus</i>						√				MCF
<i>Alona rectangulara</i>						√				MCF
<i>Alona diaphana</i>						√				MCF
<i>Alona quadrangularis</i>										MCF
<i>Pleuroxus hamulatus</i>						√				SCF
<i>Pleuroxus laevis</i>			√							SCF
<i>Camptocercus rectirostris</i>	√					√				MCF
Copepoda										
<i>Nauplii</i>		√	√	√		√	√	√	√	SCF
<i>Cyclops vicinus</i>			√			√	√	√		MCF
<i>Macrocylops albidus</i>	√				√	√				MCF
<i>Eucyclops serrulatus</i>			√	√			√	√	√	MCF
<i>Eucyclops speratus</i>	√	√	√	√	√	√		√	√	MCF
<i>Eucyclops macruruides</i>										MCF
<i>Tropocyclops prasinus</i>			√	√					√	SCF
<i>Mesocyclops leuckarti</i>	√	√	√	√	√	√	√	√	√	MCC
<i>Paracyclops affinis</i>	√				√					MCF
<i>Acanthocyclops bicuspidatus</i>	√				√					MCF
<i>Microcyclops varicans</i>						√				SCF
<i>Thermocyclops brevifurcatus</i>										MCC
<i>Mogolodiptomus schmackeri</i>				√		√			√	MCF
<i>Phyllodiptomus tunguidus</i>						√	√	√		MCF
<i>Neurodiaptomus mariadivigae</i>							√	√		MCF
<i>Microarthridion litospinatus</i>							√			SCF
<i>Schmackeria inopinus</i>		√								LCF

“√” indicates the presence of the species at that point