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ORIGINAL ARTICLE

Bacterial diversity and distribution in seven different estuarine sediments of Poyang Lake, China

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Abstract In this study, bacterial community compositions in seven different estuarine sediments of Poyang Lake were analyzed using 16S rRNA gene-targeted metagenomic approach. Remarkable differences in the bacterial diversity were observed in these different estuarine sediments. Le, Chang and Rao river samples exhibited the higher bacterial diversity; the Fu river sample showed the less diversity. Bacterial richness and diversity were positively regulated by sediment inorganic phosphorus, and nitrite nitrogen, total phosphorus and inorganic phosphorus were found to be important drivers for bacterial community compositions. Proteobacteria, Acidobacteria, Firmicutes, Chloroflexi, Bacteroidetes, Planctomycetes, Gemmatimonadetes, Actinobacteria, Nitrospirae, and Verrucomicrobia were the major components of sediment bacterial communities. Among them, Proteobacteria was the most dominant phylum, followed by Acidobacteria and Firmicutes. Our study gives a comprehensive insight into the structure of bacterial community of the different estuarine sediments of Poyang Lake, indicating that the environmental factors played a key role in influencing the bacterial community composition in the freshwater ecosystem.

Keywords Bacterial diversity · Bacterial community composition · Estuarine sediments · Poyang Lake

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Introduction

Microorganisms are crucial components in buried sediments and may account for more than 30 % of the biomass of the earth (Whitman et al. 1998). In freshwater lakes and other aquatic ecosystem sediments, microorganisms are important for decomposing, transforming organic matter (OM) and remineralizing nutrients, suggesting their crucial role in the earth's biogeochemical cycles (Zhao et al. 2012; Jurgens et al. 2000). Consequently, investigating the composition of the bacterial community is vital to understand the metabolic processes in freshwater and other aquatic ecosystems (Spring et al. 2000).

Previous studies indicated that environmental physicochemical factors, such as nutrient availability, sedimentation, salinity, OM, pH and temperature, could influence the microbial structures in aquatic ecosystems and were considered the major driving forces of microbial communities (Stepanauskas et al. 2003; Wu et al. 2008; Tijdens et al. 2008). Former studies showed that there are diverse, abundant, frequently exchanged and highly active microorganisms in sediment environments, and the environment presents varied environmental gradients (Huang et al. 2014). Therefore, sediments may provide a suitable natural environment for surveying the adaptations and shifts of microbial communities (Stepanauskas et al. 2003; Wu et al. 2008).

Currently, the excess use of nitrogen fertilizer, municipal wastewater and industrial effluent discharge has led to the eutrophication of aquatic ecosystems (McLaughlin et al. 2015; Haukka et al. 2006). In China, 50 % of the freshwater lakes investigated were eutrophic (Jin et al. 2005).

Poyang Lake is the largest fresh water lake in China, and it is located in the northern part of Jiangxi province, at the

southern bank of the Yangtze River. The Gan (GJ), Fu (FH), Xin (XJ), Rao (RH) and Xiu (UH) rivers flow into Poyang Lake, and it undergoes a great change in water level over the course of a year. The Le (LH) and Chang (CJ) rivers flow into the Rao River. The lake is the natural habitat of migratory birds, and it also offers important spawning grounds and food for many fishes (Wu et al. 2012). However, in recent years, the area of the lake fluctuates dramatically between the wet and dry seasons, the seasonal decline begins earlier and lasts longer (Zhang et al. 2011; Min and Zhan 2012), the size of the lake has been decreasing overall, the eutrophication degree is more and more serious because of industrialization and urbanization, and the water quality has deteriorated (Wu et al. 2011; Deng et al. 2011; Zhen et al. 2011).

Numerous studies have been conducted to investigate the water quality and the biodiversity of the fishes, birds, plants, and bacterioplankton communities of Poyang Lake (Wu et al. 2012; Liang et al. 2015; Yao et al. 2015; Fang et al. 2006; Guo et al. 2008). Most of these studies did not investigate the bacterial diversity and communities in the different estuarine sediments of Poyang Lake.

In this study, we aimed to determine the total bacterial diversities and community compositions in the different estuarine sediments of Poyang Lake by using 16S rRNA gene-targeted metagenomic approach. Furthermore, we analyzed the environmental physicochemical properties to investigate which factors have a significant impact on bacterial diversity, richness and community structures in those sediment samples.

Materials and methods

Ethics statement

The Jiangxi provincial water resources bureau concerned with protection of the Poyang Lake and Rivers. And it issued the permission for our sample collection. Our samples just contain many microorganisms, did not involve endangered or protected species.

Site description, sample collection

Sediment samples were collected from seven typical estuaries of Poyang Lake (Fig. 1). The longitude and latitude of these estuaries are shown in Table 1. The up to 5 cm sediments were collected in these different estuaries in October 2014. At the same site, five samples were collected and mixed together for homogenization. All samples were divided into two parts: one for immediate chemical analysis and another stored at −80 °C for DNA extraction.

Chemical analysis

Air-dried sediment/soil samples that had been sieved using a 2.0-mm sieve were used for analysis. At each station, in situ measurements of sediment temperature were recorded with a portable electronic thermometer. Sediment pH was determined by a multi-parameter pH meter (Sartorius PB-10, Germany) with a soil to water ratio of 1:10. Sediment total nitrogen (TN) was determined by the semi-micro Kjeldahl method (Fawcett 1954). Sediment inorganic nitrogen, including Ammonia–Nitrogen (NH_4^+-N), Nitrite-Nitrogen (NO_2^--N) and Nitrate-Nitrogen (NO_3^--N), were extracted in a 1 mol L^{-1} KCl solution. The concentrations of ammonia and nitrite in the soil extract were measured using colorimetric methods (Schütz and Nuñer 2007), and nitrate was measured using the UV spectrometric method (Ding et al. 2014). Total phosphorus (TP) was analyzed by the ammonium molybdate method (Ebina et al. 1983), and inorganic phosphorus (IP) was measured according to Aspila et al. (1976). Chemical analyses were performed in triplicate.

DNA extraction from sediment samples

DNA extraction from 0.5 g of each sediment sample was performed by using a MoBio UltraClean™Soil DNA isolation kit (SanDiego, CA, USA) following the manufacturer's instructions. Finally, the DNA was eluted with TE buffer. The amount and purity of DNA were determined by using a NanoDrop® Spectrophotometer ND-1000 (Thermo Fisher Scientific, USA) based on the absorbency of A260 and the ratio of A260/A280, respectively. The extracted total microbial DNA was stored at −80 °C prior to analysis.

Amplicon generation

The variable V4 region of the bacterial 16S rRNA gene was amplified with the general 16S rRNA gene primers 515F and 806R containing the specific barcode sequence. The forward primer (515F) was 5′-*GTTTCG*GTGCCAGC MGCCGCGGTAA-3′, where the sequence of the barcode is shown in italics. The reverse primer (806R) was 5′-*GTG AAA*GGACTACHVGGGTWTCTAAT -3′, where the sequence of the barcode is shown in italics. All PCR reactions were carried out in 30 μLs with 15μL of Phusion® High-Fidelity PCR Master Mix (New England Biolabs), 0.2 μM of forward and reverse primers and approximately 10 ng template DNA. Thermal cycling consisted of initial denaturation at 98 °C for 1 min, followed by 30 cycles of denaturation at 98 °C for 10 s, annealing at 50 °C for 30 s, and elongation at 72 °C for 60 s. Finally, extension occurred for 10 min at 72 °C.

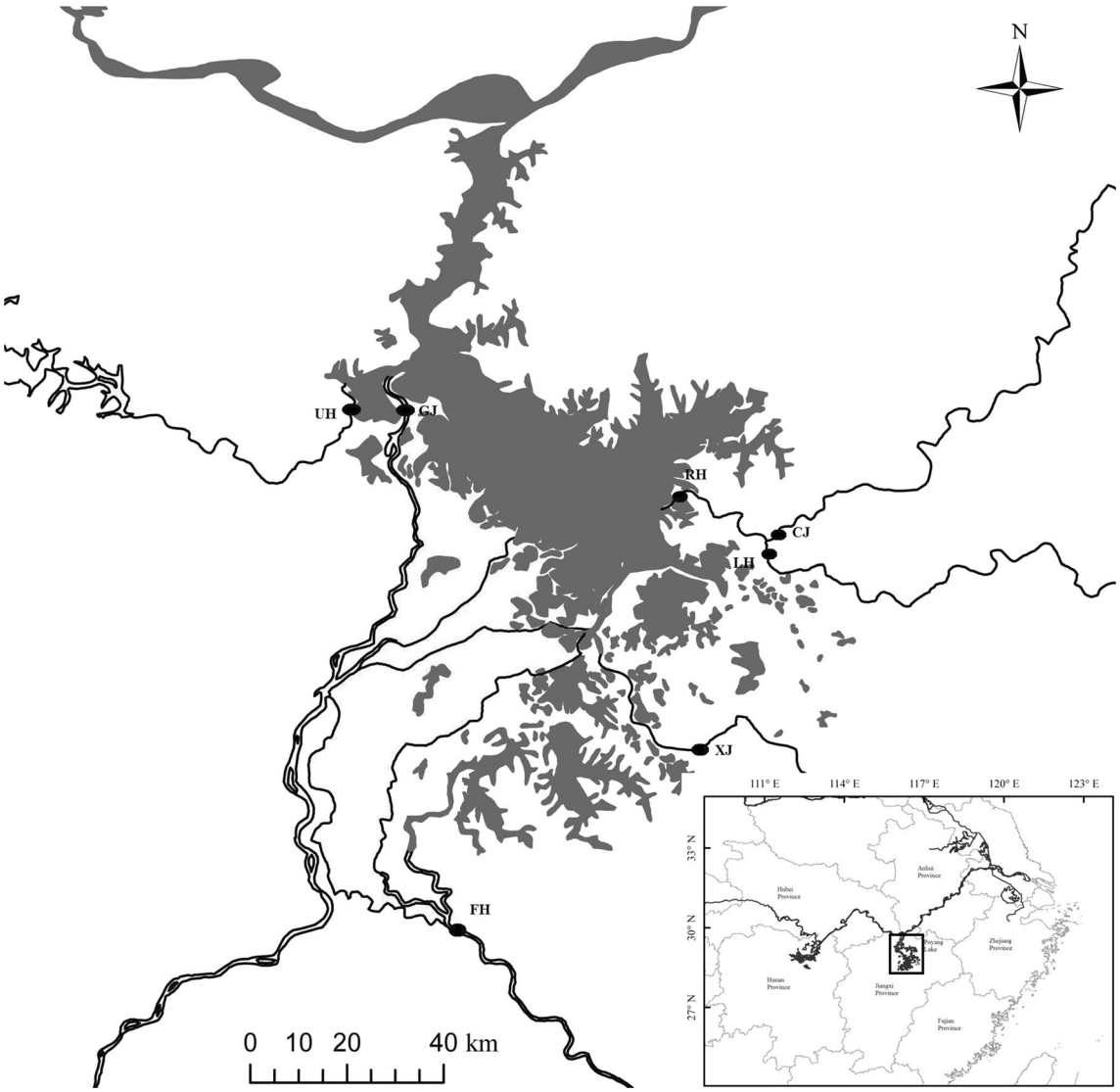

Fig. 1 Collection sites of all samples. (The abbreviations of all samples are as follows: *UH* Xiu River, *GJ* Gan River, *FH* Fu River, *XJ* Xin River, *RH* Rao River, *CJ* Chang River, *LH* Le River)

Table 1 Physicochemical properties of the different estuarine sediments of Poyang Lake and local meteorological conditions at their sampling sites

Sediment sample	Longitude and latitude	T °C	pH	TN (g/kg)	NH_4^+-N (mg/kg)	NO_2^-N (mg/kg)	NO_3^-N (mg/kg)	TP (g/kg)	IP (g/kg)
LH	116°69′E,28°97′N	17.4	6.09	1.31 ± 0.04	79.39 ± 1.01	0.18 ± 0.02	4.31 ± 0.04	0.41 ± 0.03	0.34 ± 0.01
CJ	116°69′E,28°97′N	19.9	6.76	0.75 ± 0.05	40.31 ± 0.62	0.18 ± 0.02	0.43 ± 0.09	0.24 ± 0.03	0.17 ± 0.02
RH	116°46′E,29°01′N	20.1	6.50	1.13 ± 0.04	53.75 ± 0.55	0.29 ± 0.07	0.95 ± 0.08	0.33 ± 0.04	0.25 ± 0.02
XJ	116°42′E,28°72′N	19.5	6.69	0.73 ± 0.03	47.54 ± 0.81	0.23 ± 0.02	0.53 ± 0.03	0.40 ± 0.02	0.32 ± 0.03
FH	116°08′E,28°46′N	19.1	6.52	0.71 ± 0.03	52.05 ± 0.49	0.05 ± 0.01	0.61 ± 0.04	0.25 ± 0.04	0.17 ± 0.01
GJ	116°01′E,29°18′N	20.4	6.72	0.86 ± 0.03	50.31 ± 0.76	0.23 ± 0.05	0.61 ± 0.03	0.24 ± 0.02	0.17 ± 0.02
UH	116°01′E,29°19′N	20.7	6.39	0.89 ± 0.03	41.06 ± 0.66	0.11 ± 0.02	0.81 ± 0.05	0.23 ± 0.03	0.15 ± 0.02

UH Xiu River, *GJ* Gan River, *FH* Fu River, *XJ* Xin River, *RH* Rao River, *CJ* Chang River, *LH* Le River, *T* temperature, *TN* total nitrogen, NH_4^+-*N* ammonia nitrogen, NO_2^--*N* nitrite nitrogen, NO_3^--*N* nitrate nitrogen, *TP* total phosphorus, *IP* inorganic phosphorus

PCR product quantification, qualification and purification

We mixed the same volume of 1X loading buffer (containing SYB green) with PCR products and ran electrophoresis on a 2 % agarose gel for detection. PCR products were mixed in equidensity ratios. Then, mixture PCR products were purified with a GeneJET Gel Extraction Kit (Thermo Scientific).

Library preparation and sequencing

Sequencing libraries were generated using the NEB Next® Ultra™ DNA Library Prep Kit for Illumina (NEB, USA) following the manufacturer's recommendations, and index codes were added. The library quality was assessed on the Qubit@ 2.0 Fluorometer (Thermo Scientific) and Agilent Bioanalyzer 2100 system. Finally, the library was sequenced on an Illumina MiSeq platform.

Data analysis

Paired-end reads from the original DNA fragments were merged using FLASH (Magoč and Salzberg 2011), a very fast and accurate analysis tool that was designed to merge paired-end reads when at least some of the reads overlap the read generated from the opposite end of the same DNA fragment. Paired-end reads were assigned to each sample according to the unique barcodes.

Sequences analyses were performed by the UPARSE software package (Uparse v7.0.1001, http://drive5.com/uparse/) (Edgar 2013) using the UPARSE-OTU and UPARSE-OTUref algorithms. In-house Perl scripts were used to analyze alpha (within samples) and beta (among samples) diversity. Sequences with ≥97 % similarity were assigned to the same OTUs. We picked representative sequences for each OTU and used the RDP classifier (Version 2.2, http://sourceforge.net/projects/rdp-classifier/) (Wang et al. 2007) to annotate taxonomic information for each representative sequence. To compute Alpha Diversity, we rarified the OTU table and calculated three metrics: Chao1 (estimates the species abundance), Observed Species (estimates the number of unique OTUs found in each sample), and the Shannon index. Rarefaction curves were generated based on these three metrics.

A graphical representation of the relative abundance of bacterial diversity from phylum to species can be visualized using a Krona chart (Ondov et al. 2011).

Statistical analysis

A Kendall's correlation between environment factors and bacterial richness, diversity and composition were conducted using SPSS 16.0 software.

Nucleotide sequence accession numbers

The nucleotide sequences of bacterial 16S ribosome DNA gene fragments have been deposited at the NCBI Sequence Read Archive under accession numbers SRR2837836 (LS sample), SRR2854158 (CS sample), SRR2854159 (RS sample), SRR2854634 (XS sample), SRR2886900 (FS sample), SRR2886926 (GS sample), and SRR2886938 (US sample).

Results

Sediment chemical properties

Physicochemical characteristics of sediment samples collected from seven sites varied differently depending on the parameters measured (Table 1). The temperature of the different sites ranged from 17.4 to 20.7 °C, and the pH values ranged from 6.09 to 6.76. Among them, temperature and pH values of Le river were lower than that of other sites (Table 1). The average concentrations of the TN in these estuarine sediments ranged from 0.71 to 1.31 g kg^{-1}, but the differences were not significant different. The concentration of NH_4^+-N ranged from 40.31 to 79.39 mg kg^{-1}, of which Le river sample showed the highest one. However, the concentration of NO_2^--N and NO_3^--N were extremely low, they ranged from 0.05 to 0.29 mg kg^{-1} and 0.53 to 4.31 mg kg^{-1}, respectively (Table 1). TP and IP concentrations were additional evaluation indexes of the sediment. In our study, the concentrations of TP and IP ranged from 0.23 to 0.41 g/kg and 0.17 to 0.34 g/kg, respectively (Table 1).

Diversities of bacterial communities

To determine the bacterial community of these different estuarine sediments of Poyang Lake, metagenomic technology was adopted targeting the V4 region of the bacterial 16S rDNA gene with the Illumina Miseq platform. A total of 301,415 effective tags were obtained from the seven sediment samples, with an average length of 291 nucleotides. Each of the 7 libraries contained between 24,751 and 66,133 tags. The efficient percentage ranged from 71.80 to 75.47 % (Table 2). And Q20 and Q30 values were above

Table 2 Statistics and alpha diversity of all samples

Sample name	PE reads	Effective tags	Effective (%)	Q20	Q30	OTU (97 %)	Chao1 (97 %)	Shannon (97 %)	Simpson (97 %)
LS	47,239	35,245	74.61	99.55	98.19	2261	2557.32	9.06	0.993
CS	72,077	51,751	71.80	99.57	98.28	2020	2358.95	9.03	0.994
RS	32,796	24,751	75.47	99.56	98.21	1990	2229.70	8.76	0.992
XS	88,769	66,133	74.50	99.56	98.20	2413	3174.54	8.81	0.987
FS	75,969	56,802	74.77	99.58	98.28	1499	1964.46	7.17	0.960
GS	53,261	39,504	74.17	99.55	98.20	1829	2490.00	7.39	0.974
US	36,209	27,229	75.20	99.57	98.29	1594	1831.11	7.60	0.971

LS, CS, GS, XS, RS, US and FS indicate the sediments of LH, CJ, CJ, XJ, RH, UH and FH

99.55 and 98.19 %, respectively. All further analyses were performed on these effective tags. At a >97 % sequence identity threshold, 2261, 2020, 1990, 2413, 1499, 1829 and 1594 OTUs were identified in LS (sediment of Le river), CS (sediment of Chang river), RS (sediment of Rao river), XS (sediment of Xin river), FS (sediment of Fu river), GS (sediment of Gan river) and US (sediment of Xiu river), respectively (Table 2), of which the XS sample possessed the highest OTUs, followed by the LS sample. OTUs were determined to calculate the richness, diversity and rarefaction curves of the microbial communities. The rarefaction curves showed a similar pattern for all the samples, and suggested that the bacterial community was well represented since they became gentle while the number of sequences analyzed increased (Fig. 2).

Richness indexes of Chao1, evaluated at 97 % similarity, showed a similar comparative trend in predicting number of OTUs. Sample from LS had the highest richness (Chao1 = 2557.32), while sample from FS had the lowest one (Chao1 = 1964.46). The highest sediment bacterial diversity (Shannon index = 9.06) was found at LS sample, while the lowest one was at FS (Shannon index = 7.17) (Table 2). A similar tendency was observed for Simpson index, we found that LS and CS samples showed higher bacterial diversity (Simpson index = 0.993, 0.994), and FS sample was the lowest one (Simpson index = 0.960).

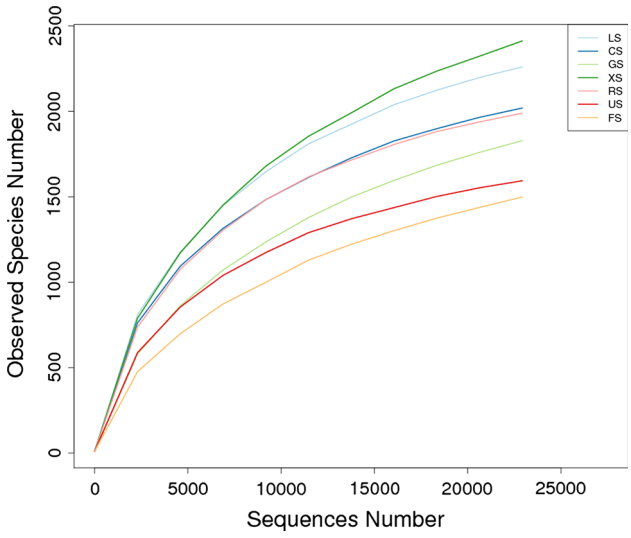

Fig. 2 Rarefaction curves of all samples

Bacterial community structure

In this study, the use of the 16S rRNA gene analyses resulted in the identification of 10 different phyla in all samples (the proportion ranged from 94.11 % to 98.19 %), including Proteobacteria, Acidobacteria, Firmicutes, Chloroflexi, Bacteroidetes, Planctomycetes, Gemmatimonadetes, Actinobacteria, Nitrospirae, and Verrucomicrobia. The majority of bacterial sequences in all samples belonged to these phyla Proteobacteria, Acidobacteria and Firmicutes, which represented 38.28 to 69.81 %, 2.83 to 21.09 %, and 7.68 to 18.20 % of each total sequences, respectively (Fig. 3).

At the class level, the bacterial taxa were distributed in Betaproteobacteria, Alphaproteobacteria, Acidobacteria, Gammaproteobacteria, Clostridia, Deltaproteobacteria, Anaerolineae, Bacilli, Sphingobacteria and Planctomycetia (the proportion ranged from 68.70 to 90.49 %). Among them, Betaproteobacteria (15.65–40.66 %) was the most dominant bacterial class in all samples except XS sample (Fig. 4). Acidobacteria (17.33 %) proved to be predominant in XS library, followed by Betaproteobacteria (13.90 %).

At the genus level (the lowest level assigned), *Janthinobacterium*, *Pseudomonas*, *Acinetobacter*, *Brevundimonas*, *Clostridium*, *Geobacter*, *Kaistobacter*, *Exiguobacterium*, *Rhodoplanes*, and *Polaromonas* were the top 10 dominant genera in all samples. *Janthinobacterium* exhibited more proportional representation in GS (23.81 %), US (24.85 %) and FS (16.19 %) samples, *Pseudomonas* was more abundant in GS (9.50 %) and FS (8.16 %) samples, *Acinetobacter* showed more abundant in XS (7.93 %) sample, *Brevundimonas* showed more abundant in FS sample (6.47 %), and *Clostridium* exhibited more proportional representation in GS sample (5.07 %) (Fig. 5).

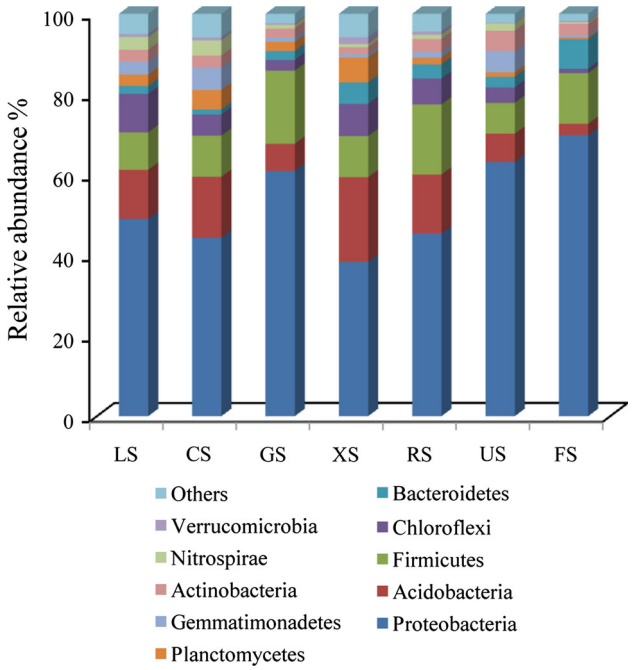

Fig. 3 Bacterial composition of the communities in all samples (Phylum level)

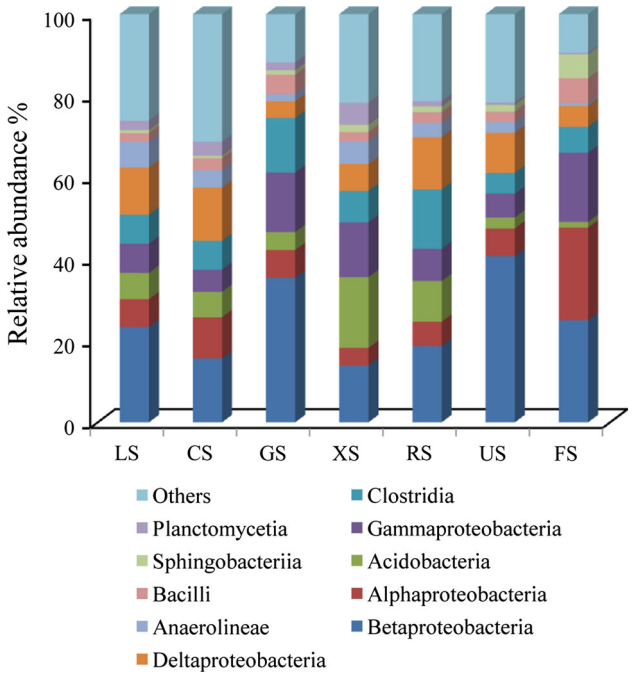

Fig. 4 Bacterial composition of the communities in all samples (Class level)

Influential factors on bacterial communities

Kendall's correlation analysis indicated that the bacterial OTU number and Chao1 estimator were positively correlated to the levels of sediment inorganic phosphorus

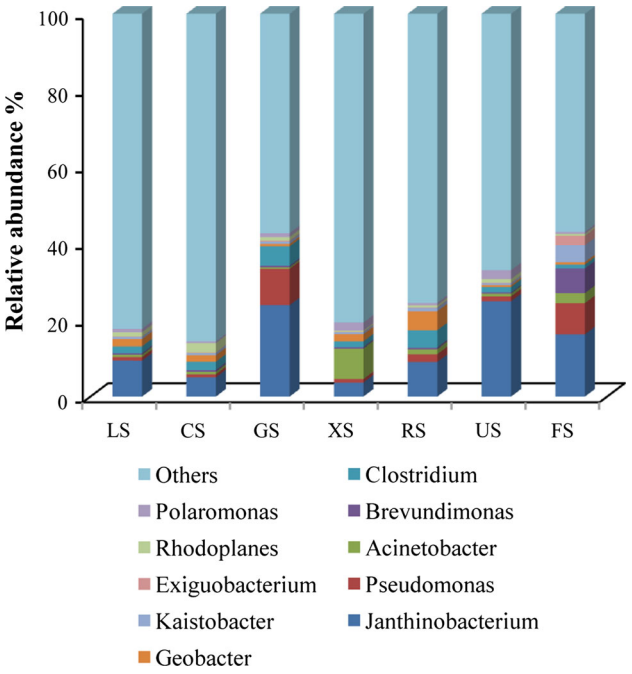

Fig. 5 Bacterial composition of the communities in all samples (Genus level)

($P < 0.05$). However, bacterial Shannon diversity illustrated no significant correlation with the determined parameters ($P > 0.05$) (Table 3).

Sediment nitrite nitrogen was negatively correlated with relative abundance of Proteobacteria ($P < 0.05$). Chloroflexi showed a significant positive correlation with both sediment total phosphorus and inorganic phosphorus ($P < 0.05$). Nitrospirae was positively affected by sediment total nitrogen, and Verrucomicrobia showed positive correlation with sediment nitrite nitrogen, total phosphorus and inorganic phosphorus ($P < 0.05$) (Table 3).

Discussion

Bacterial community diversity and composition in the Poyang Lake has been well documented (Wu et al. 2012). However, the bacterial communities in different estuarine sediments of Poyang Lake were overlooked for a long time, and which bacteria take part in the important nutrient cyclings in these sediments were still unknown. This is the first comprehensive study on the overall composition of bacterial community in these estuarine sediments of Poyang Lake.

Chemical properties of these seven different estuarine sediments of Poyang Lake

Poyang Lake, the largest freshwater lake in China, is the most important mainstream connected with the Yangtze

Table 3 Statistical analysis of microbial communities with sediment chemical properties

	Parameter	T	pH	TN	NH_4^+-N	NO_2^--N	NO_3^-N	TP	IP
Microbial diversity	OTU number	−0.429	0.048	0.143	0.451	0.048	0.000	0.488	0.617* (0.030)
	Chao1 estimator	−0.333	0.143	0.048	0.143	0.350	−0.098	0.488	0.617* (0.030)
	Shannon diversity	−0.333	−0.048	0.429	−0.048	0.150	0.098	0.390	0.514
Bacterial composition	Proteobacteria	0.238	−0.238	0.048	0.143	−0.551* (0.045)	0.195	−0.293	−0.411
	Acidobacteria	−0.143	0.143	0.048	−0.238	0.451	−0.098	0.195	0.309
	Firmicutes	0.143	0.238	−0.238	0.238	0.451	0.000	0.000	0.000
	Chloroflexi	−0.333	−0.238	0.429	0.143	0.350	0.293	0.586* (0.034)	0.720* (0.014)
	Bacteroidetes	−0.143	−0.048	−0.333	0.143	−0.050	0.000	0.098	0.000
	Planctomycetes	−0.238	0.238	−0.048	−0.143	0.350	−0.195	0.293	0.411
	Gemmatimonadetes	0.238	−0.048	0.429	−0.238	−0.050	0.098	−0.195	−0.103
	Actinobacteria	0.333	−0.333	0.333	0.048	−0.150	0.293	−0.293	−0.309
	Nitrospirae	0.143	−0.143	0.524* (0.049)	−0.143	0.050	0.195	−0.098	0.000
	Verrucomicrobia	−0.333	0.143	0.048	0.143	0.551* (0.045)	−0.098	0.586* (0.034)	0.720* (0.014)

* Correlation between two parameters is significant at the level of 0.05 (two tailed)

River. It plays a crucial role in the maintenance of the aquatic biota of the Yangtze Basin (Wang et al. 2007), and it is located in a globally important ecological area (Liang et al. 2015). The Gan, Fu, Xin, Rao and Xiu rivers flow into Poyang Lake. The water regime of Poyang Lake is controlled by the five tributaries (Shankman et al. 2006). Determining the environmental physicochemical properties and bacterial community compositions of these different estuaries of Poyang Lake may be helpful in assessing, understanding and maintaining the water quality of Poyang Lake.

From our study, we found that the Le River showed the highest total nitrogen and ammonia nitrogen concentration. The high total nitrogen and ammonia nitrogen content of this river may be caused by the number of fisheries in Poyang County. As we know, protein-rich wastes from aquaculture systems could increase total nitrogen, ammonia nitrogen and total organic carbon (Mook et al. 2012). Additionally, we found that the total phosphorus and inorganic phosphorus content of the Xin and Le rivers were higher than the other estuaries. This may be due to the mining of the phosphate rock mountain in Shangrao City, which is located upstream of the Xin river.

Bacterial diversities in estuarine sediments

In this study, the bacterial diversities in estuarine sediments of Poyang Lake were obtained using Illumina Miseq sequencing. Our analysis revealed a high biodiversity in these estuarine ecosystems, reflecting the rich chemical features of these environments (Qu et al. 2008). Among them, LS and XS showed higher bacterial richness and diversity, this maybe due to the higher concentrations of nitrogen and phosphorus in these two samples. Beside that, Kendall's correlation analysis also indicated that bacterial diversity and richness were found to be likely positively affected by sediment inorganic phosphorus. Previous studies have indicated that in freshwater lacustrine sediment ecosystems, greater amounts of nutrients are thought to support richer and more diverse bacterial communities through increased niche partitioning (Dykhuizen 1998). And, phosphorus, as a major nutrient for aquatic ecology, has been recognized as the most critical nutrient limiting lake productivity, it has significant impacted on the bacteria community structure in lake sediment (Doricha et al. 1984; Jin et al. 2005; Song et al. 2012). Our results suggested that abundant nitrogen and phosphorus might cause high bacterial richness and diversity. Other chemical factors, such as total organic carbon, metal ion, etc., might also regulate the distribution of sediment bacteria in these estuaries. This still need further research.

Bacterial community structure in estuarine sediments

As we know, "Global Dispersal" is the major conflicting hypothesis in microbial biodiversity studies (Martiny et al. 2006). It suggests that microorganisms are ubiquitous and have few barriers to gene flow resulting in similar microbial communities across different spatial scales and habitats. Since this study showed the similar bacterial communities in seven different estuarine sediments that have been described in other soil/sediment environmental, this finding further supports the hypothesis. Previous studies indicated that the soil/sediment bacterial communities were normally comprised of the 9 major bacterial phyla: Proteobacteria, Actinobacteria, Acidobacteria, Chloroflexi, Bacteroidetes, Firmicutes, Planctomycetes, Verrucomicrobia and Gemmatimonadetes (Janssen

2006). In our study, the bacterial communities of all estuarine sediment samples were also found to belong to those 9 bacterial phyla, and among them, bacterial communities in all samples were predominated by Proteobacteria, a metabolically diverse group of Gram-negative bacteria frequently found in freshwater sediment (Zhang et al. 2015; Fierer et al. 2007). Acidobacteria and Firmicutes were the secondary and tertiary phyla in these estuarine sediment samples. Acidobacteria and Firmicutes are ubiquitous in freshwater lake sediment and are known to degrade a variety of organic compounds (Tamaki et al. 2005; Kirchman 2002). So, their dominance of the sediment of this eutrophic estuary is not surprising. Our findings may indicate that members of the predominant taxa are well adapted to the surficial layer of freshwater sediments regardless of geographical location, and the predominance of Proteobacteria, Acidobacteria and Firmicutes in all samples suggested that they may be actively involved in the functioning and processes of estuarine sediment of Poyang Lake.

At the genus level, *Acinetobacter* was richer in XS sample. *Acinetobacter* was reported as one of commonly detected phosphorus-accumulating microorganisms in sediment (Martins et al. 2011), which may explain their concentration in phosphorus enriched sediment sample of Xin river. Besides, we also found that *Janthinobacterium* was abundant in GS, US and FS samples, previous studies have showed that *Janthinobacterium* may be included in anaerobic metabolism linked to denitrification cycling (McTaggart et al. 2014). The presence of *Janthinobacterium* species may be valuable for the denitrification cycling in GS, US, and FS samples.

Influential factors on bacterial communities

Generally, many studies have reported that environmental factors, such as total nitrogen, phosphorus and other nutrient elements, have impacts on bacterial colonization in sediment samples (Stepanauskas et al. 2003; Wu et al. 2008; Tijdens et al. 2008; Angeloni et al. 2006; Zeng et al. 2009). When the nutrient elements increased, the biomass of phytoplankton, algae and bacteria also increased, as there is a mutualistic relationship among these organisms (Hietala et al. 2004; Wetzel 1983). Similar results were found in our study. Nitrite nitrogen, total phosphorus and inorganic phosphorus were found to be important drivers for the distribution of sediment Proteobacteria, Chloroflexi, Nitrospirae and Verrucomicrobia communities in estuarine sediments of Poyang Lake. The results of the present study support the idea that environmental changes could be evaluated using the composition variation of bacterial communities. Although other environmental variables were not statistically significant, an influence of synergistic reaction of these nutrients on the distribution of bacterial community structures still cannot be excluded. More information is needed in this area.

In conclusion, as the first study of the bacterial diversity and community of the different estuarine sediments of Poyang Lake, our study demonstrated that the bacterial diversities varied among the different samples. LS and XS samples exhibited the higher bacterial richness and diversity, and the FS sample showed the least diversity, which was in accordance with the environmental nutrient content. Bacterial diversity was affected by sediment inorganic phosphorus. Nitrite nitrogen, total phosphorus and inorganic phosphorus were also found to be important drivers for bacterial community compositions. Proteobacteria predominated in all sediment bacterial communities, followed by Acidobacteria and Firmicutes, they might be involved in various biogeochemical processes in sediment. Our study points to the interactions between bacterial community composition and sediment environmental physicochemical factors, which could shed light on the functional roles of microorganisms involved in the earth's biogeochemical cycles in the freshwater lake ecosystem.

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