

# The Variation of Sediment Bacterial Community in Response to Anthropogenic Disturbances of Poyang Lake, China

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**Abstract** The impacts of different anthropogenic disturbances on the composition and metabolic function of sediment bacterial community in the largest freshwater lake- Poyang Lake of China were studied. A total of 12 surface sediment samples were collected from four sites, including an undisturbed central lake region (SMS) and three disturbed sites in fishery (NJS), industrial (RH) and tourism (BSZ) areas. Sediment physicochemical properties and heavy metal contents were combined with the results from Illumina Miseq and Biolog-Ecoplates to quantify the impact of environmental factors driving differences in sediment bacterial structure and microbial function. Our results showed that the bacterial community diversity (Shannon index) was higher in disturbed than in undisturbed areas, although the most predominant bacterial phyla in four studied sites were similar. However, the average well color development (AWCD) based on carbon source utilization pattern of the disturbed area was lower than undisturbed areas and the preference of carbon sources differed among the four studied areas. Site contaminants contributed to the distribution of distinct phyla which differentiated bacterial communities among sites. For example, the contents of

TN (1.80 g/kg) and TOC (12.34 g/kg) in NJS showed positive correlation with the abundance of *Deltaproteobacteria* and *Chloroflexi*; while the concentration of TP (0.43 g/kg), Cu (69.22 mg/kg) and Zn (134.89 mg/kg) in RH was positively correlated with the predominance of *Firmicutes* and *Verrucomicrobia*. These results indicated that microbial community carbon metabolic profiles changed with the shift of bacterial community structure, and disturbance-induced pollution enhanced the sediment bacterial diversity and reduced carbon metabolic activity.

**Keywords** Anthropogenic disturbance · Sediment · Bacterial community · Illumina Miseq sequencing · Metabolic function · Poyang Lake

## Introduction

Freshwater lakes are important source of domestic water and aquaculture, and also offer important habitat for global biodiversity (Dudgeon et al. 2006; Kumar et al. 2016). Rapid population growth and intensive human activities are contributing to an increase in heavy pollution in many freshwater lakes and making water supply and fish no longer safe (Azizullah et al. 2011). Most pollutants are deposited in lake sediment which often acts as a secondary pollution source (Kim 2003; Haddadchi et al. 2013; Heim and Schwarzbauer 2015). Microorganisms are ubiquitous and play key roles in decomposing, transforming organic matters and remineralizing nutrients (Burkhardt et al. 2014; Landa et al. 2014; Gad et al. 2015). Thus the composition and performance of the sediment microbial community has attracted much attention, and many studies have focused on the relationship between lake pollution and sediment microbes (Smorzewski and Schmidt 1991; Bennett and Metcalfe 1998; Konstantinidis et al. 2003;

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Xiao Jin and Yantian Ma contribute equally to this work.

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Devarajan et al. 2015). Previous studies on Dianchi Lake and 13 lakes in Yunnan Plateau suggested that the bacterial abundance was regulated by sediment total organic carbon (TOC) and total nitrogen (TN) (Bai et al. 2012; Zhang et al. 2015). Total phosphorus (TP), copper (Cu), and cadmium (Cd) in sediment were considered to be key factors driving spatial variation of bacterial community in Poyang Lake (Yu et al. 2015). A study demonstrated that the highest diversity of bacterial community appeared in moderately polluted samples, and the abundance of *Alphaproteobacteria* was increased with the level of heavy metals (Zhu et al. 2013a). These studies demonstrated the influence of sediment properties in shaping microbial community composition in freshwater lakes. However, most studies as mentioned above focused only on heavy metals or nutrient parameters, while contaminated aqueous environments are always complex in which multiple natural terrestrial sources (e.g. leaching, erosion) and anthropogenic origin (e.g. mining, sewage, smelting waste) lead to multi-source pollution (Yuan et al. 2014). Even though these results from previous studies focused on community structures rather than metabolic function, our knowledge about how the sediment bacterial community composition (BCC) respond to multiple source contamination is still far from comprehensive. Because these studies focused on community composition and not metabolic activity, we also have a poor understanding of how environmental factors drive sediment microbial function under different anthropogenic disturbances of lake ecosystems.

Modern biotechnology provides powerful tools for microbial study, making it is easier to conduct more comprehensive research on sediment-associated microorganisms. Molecular methods such as DGGE (Kowalchuk et al. 1998), PLFA (Macalady et al. 2000) and T-RFLP (Paissé et al. 2008), have increased the information availability for bacterial community composition comparing with cultural-dependent methods. However, these techniques have some notable disadvantages: limited amount of data and limited accuracy of species identification (Kircher and Kelso 2010). The latest sequencing method, Illumina Miseq high-throughput sequencing used in this study is more efficient for identifying the complicated profile of microbial community and providing greater throughput (Fang et al. 2015; Li et al. 2015). In addition, the Biolog-Ecoplates, which are suitable for microbial community level physiological profiling, have been widely used in assessing the microbial functional diversity of various environments (Tian et al. 2015).

Poyang Lake, the biggest freshwater lake in China, is critical to maintain the aquatic biodiversity and drinking water resource, and also plays a vital role in flood regulation (Wang et al. 2014a). Due to development and excessive utilization of Poyang Lake, different types of pollution were frequently deposited in different regions. A large area of aquaculture activity is found in the Nanjishan (NJS) area, partly separated from the main lake basin in dry seasons. In this region, bait, dead

algae, and fish excreta lead to considerable organic pollution in sediment (Hu et al. 2005; Kou et al. 2016). The Raohe (RH) area has been polluted by heavy metals and TP which are attributed to industrial wastewater discharge from upper reaches of the Dexing copper and phosphate mines (He et al. 1998; Yuan et al. 2011; Gao et al. 2014). The Baishazhou (BSZ) region is located near a national wetland park and the contamination mainly comes from tourism. The Songmenshan (SMS) area is in the main water channel of Poyang Lake far away from the shore and less disturbed by anthropogenic activities. In this study, we investigated the variations of sediment bacterial community structure and function in response to different anthropogenic disturbances using Illumina Miseq sequencing and Biolog-Ecoplates. We hypothesized that: (1) different types of pollution associated with different anthropogenic disturbances caused variation in bacterial community structure; and (2) the microbial metabolic function changed and was correlated with the community structure variations.

## Materials and Methods

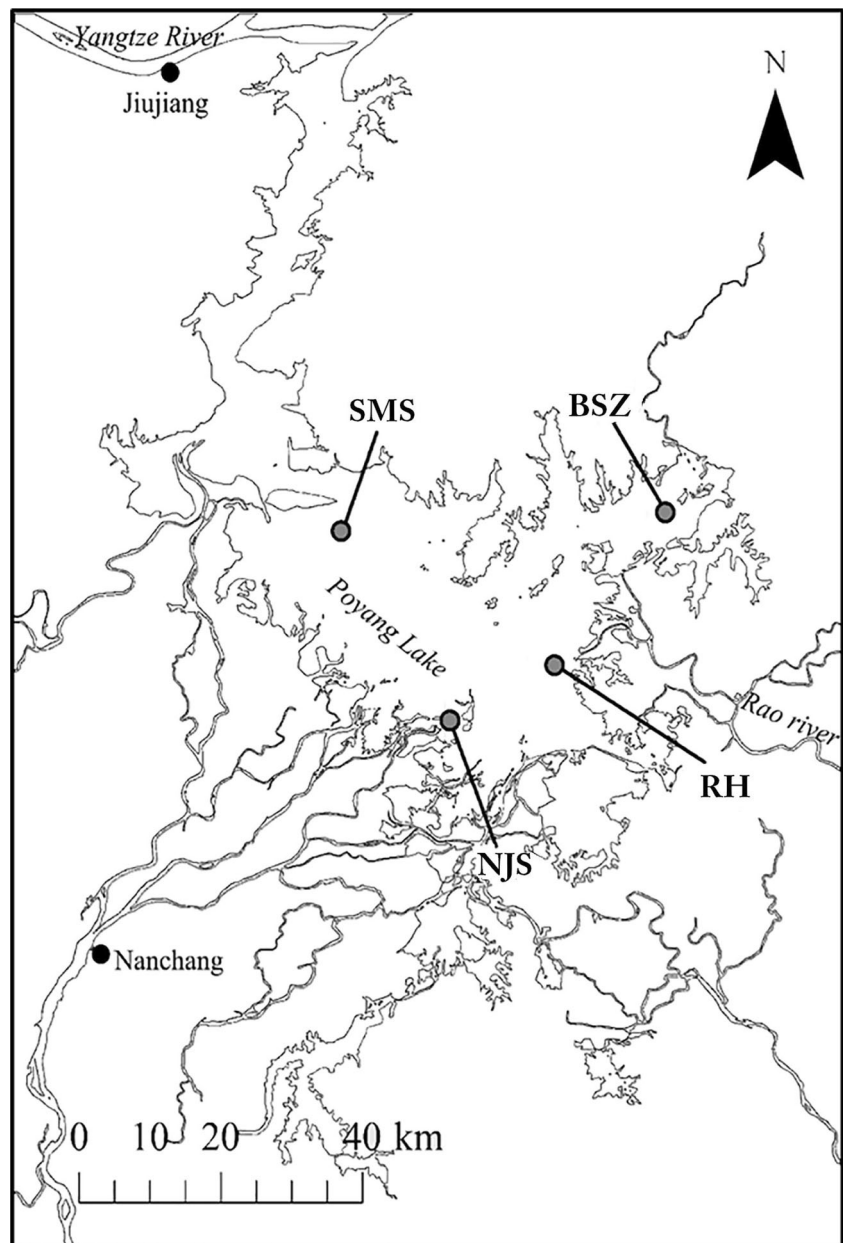
### Study Sites and Sample Collection

Surface sediment samples (0–5 cm) were collected in April, 2014 from four selected regions of Poyang Lake (Fig. 1): Songmenshan (SMS, 29°12'26.9"N, 116°11'28"E), Nanjishan (NJS, 28°55'0.1"N, 116°16'44.4"E), Raohe (RH, 29°0'39"N, 116°27'42"E) and Baishazhou (BSZ, 29°10'34"N, 116°37'14"E). Triplicate surface sediment samples were collected at each region using a grab sampler to obtain a total of 12 samples. Samples were temporarily stored in sterile polyethylene ziplock bags, and immediately put on ice and transported to the laboratory. Sediment samples were divided into two aliquots. One aliquot was stored at 4 °C for the measurement of sediment physicochemical parameters and Biolog-Ecoplates; the other aliquot was stored in sterile polypropylene tubes at –80 °C for molecular analysis.

### Measurement of Sediment Physicochemical Properties

Sediment pH was detected by testing the sediment paste containing 3 g sediment homogenized in 21 ml distilled waters and using a FE20K pH meter (Wang et al. 2014b). Sediment samples were dried in an oven at 100 °C overnight, homogenized and grounded to fine powder and sieved mechanically using a 0.25 mesh for the following analysis. Sediment ash-free-dry-mass (AFDM) was obtained through calcinations in a BF51800 muffle furnace (Thermal) at 550 °C for 4 h (Sponseller and Fisher 2008). Total nitrogen (TN), total organic carbon (TOC) and total phosphorus (TP) were analyzed using the microkjeldahl method (Lemon et al. 1992), the Walkley-Black wet oxidation procedure (Schumacher 2002)

**Fig. 1** Locations of the four selected sampling sites in Poyang Lake



and vanadium-molybdenum-yellow photometric method (Yang et al. 2012), respectively. The concentrations of heavy metals including copper (Cu), zinc (Zn), lead (Pb) and cadmium (Cd) were quantified with the digested samples using AA800 atomic absorption spectrophotometer (Zhao et al. 2010).

#### DNA Extraction and High-Throughput Sequencing

Microbial genomic DNA was extracted from 0.3 g sediment (wet-weight) using a Power Soil DNA Isolation kit (MoBio) following the manufacturer's instructions. The quality of extracted DNA was checked in a NanoDrop 2000. Afterwards, extracted DNA samples were sent to BGI Co. Ltd. for

Illumina Miseq sequencing of bacterial community. PCR amplicon libraries were constructed with the primers 515F and 806R (Bergmann et al. 2011) that targeted the V4 hyper-variable regions of bacterial 16S rRNA genes. Obtained raw sequence reads were processed using the Usearch 3.0 and Python software package for quality control and species annotation. Singleton and chimeric sequences were removed in this step. The remaining sequence reads were clustered into operational taxonomic units (OTUs) at 3% difference, some archaea sequences were abandoned in further analyses. The sequence data generated in this study was deposited in the NCBI Sequence Read Archive and are available under the project number *SPR068335*.

## Biolog-EcoPlates Analysis

The Biolog-EcoPlate method (Christian and Lind 2007) was carried out in this study to measure the carbon source utilization. Specifically, approximate 10 g (dry weight equivalent) of fresh sediment was suspended in 90 ml saline solution (0.85% NaCl, w/v), shaken for 30 min on a rotary shaker, and diluted 100-fold. 150  $\mu$ l of the diluted samples were added directly into EcoPlates (BIOLOG, Hayward, CA, USA), and then incubated in dark condition at 25 °C for 10 days and measured at 590 nm every 12 h with an EMax Precision Microplate Reader (BIOLOG, Hayward, CA, USA). The first reading was performed immediately after inoculation. The rate of carbon metabolism on Biolog plates over time was determined by calculating the average well color development (AWCD, Average Well Color Development) using the method of Garland (Gomez et al. 2006).

## Statistical Analysis

Based on taxonomic annotation, obtained sequences were grouped at phylum level to construct rarefaction curves and diversity indices of Chao1, Simpson and Shannon. NMDS was processed using the Mothur program. The diversity indices of carbon utilization and ANOSIM analysis were calculated using the PRIMER5 program. To investigate the relationship between microbial community and environmental parameters, Monte Carlo tests and Redundancy analysis (RDA) were performed in CANOCO5.0. Differences of sediment parameters among sampling sites was assessed by one-way ANOVA using SPSS 20.0. Pearson coefficient correlations between series of parameters and microbial community datasets were also conducted using SPSS 20.0.  $P < 0.05$  was considered to be statistically significant.

## Results

### Characterization of Sediment Physicochemical Properties

The detected physicochemical parameters and heavy metal contents from sediment samples were shown in Table 1.

Most of the parameters differed significantly among the four sites. All samples showed weak acidity, pH values ranging from 5.67 (NJS) to 6.63 (SMS). NJS samples had the highest contents of AFDM and TN among these four sampling sites, while SMS samples had the lowest content. The contents of TP, Cu and Zn from RH were significantly higher than other three sites, while BSZ was the second highest. The contents of TOC and Pb had no obvious difference among the four sites.

### BCCs Revealed by Illumina Miseq Sequencing

A total of 259,216 partial sequences of bacterial 16S rRNA genes with an average length of 252 bp passed the quality control procedures. The OTU numbers of sediment samples ranged between 2350 and 2779, and obvious difference was observed among four sites ( $P < 0.05$ ). The Shannon-Wiener and Simpson indexes were significantly lower in undisturbed SMS than other disturbed area (RH, BSZ and NJS) (Table 2). We performed rarefaction analysis on 12 samples and none of our samples showed a full saturation in rarefaction curves (Fig. S1).

We obtained a distinct pattern of taxonomic composition among the four sampling sites (Fig. 2). A total of 31 phyla were found in all sediment samples, and the most dominant bacterial lineages present were *Proteobacteria* (58.60%), *Firmicutes* (12.62%), *Bacteroidetes* (5.28%), *Chloroflexi* (4.62%), *Nitrospira* (4.21%) and *Verrucomicrobia* (3.76%) which on behalf of 89% of sequences in total. *Proteobacteria* was dominated by *Deltaproteobacteria* (22.50%), *Betaproteobacteria* (12.98%), *Gammaproteobacteria* (16.06%) and *Alphaproteobacteria* (7.02%). NMDS ordination analysis displayed a clear separation of BCCs among the four regions (Fig. 3). ANOSIM ( $r = 0.867$ ;  $P < 0.05$ ) analyses further confirmed the robustness of this separation. The distribution of BCCs in NMDS ordination could be divided into three parts. The taxonomic composition of SMS was represented by *Gammaproteobacteria* (24%), *Deltaproteobacteria* (18%), and *Bacteroidetes* (7%) which differentiated SMS with the other three sites. The taxonomic composition of RH and NJS could be represented by *Verrucomicrobia*, *Firmicutes* and *Delproteotabacteria*, *Chloroflexi*, respectively, and the distribution of BSZ was located between NJS and RH.

**Table 1** The physicochemical parameters and heavy metal contents from sediment samples of Poyang Lake

	pH	AFDM (%)	TP (g/kg)	TN (g/kg)	TOC (g/kg)	Cd (mg/kg)	Cu (mg/kg)	Pb (mg/kg)	Zn (mg/kg)
SMS	6.63 $\pm$ 0.02 <sup>a</sup>	5.18 $\pm$ 0.16 <sup>c</sup>	0.18 $\pm$ 0.02 <sup>c</sup>	0.56 $\pm$ 0.10 <sup>c</sup>	7.89 $\pm$ 0.58 <sup>a</sup>	NS <sup>b</sup>	13.96 $\pm$ 1.15 <sup>c</sup>	2.77 $\pm$ 0.46 <sup>a</sup>	46.47 $\pm$ 1.80 <sup>c</sup>
NJS	5.67 $\pm$ 0.10 <sup>c</sup>	7.74 $\pm$ 0.70 <sup>a</sup>	0.27 $\pm$ 0.03 <sup>b</sup> <sup>c</sup>	1.80 $\pm$ 0.08 <sup>a</sup>	12.34 $\pm$ 2.06 <sup>a</sup>	NS <sup>b</sup>	16.68 $\pm$ 2.61 <sup>c</sup>	3.33 $\pm$ 0.44 <sup>a</sup>	45.92 $\pm$ 7.40 <sup>c</sup>
RH	5.82 $\pm$ 0.10 <sup>bc</sup>	5.21 $\pm$ 0.58 <sup>c</sup>	0.43 $\pm$ 0.01 <sup>a</sup>	0.58 $\pm$ 0.08 <sup>c</sup>	8.98 $\pm$ 0.61 <sup>a</sup>	2.08 $\pm$ 0.81 <sup>a</sup>	69.22 $\pm$ 7.19 <sup>a</sup>	4.27 $\pm$ 0.56 <sup>a</sup>	134.89 $\pm$ 7.81 <sup>a</sup>
BSZ	6.42 $\pm$ 0.28 <sup>ab</sup>	5.92 $\pm$ 0.29 <sup>ab</sup>	0.37 $\pm$ 0.07 <sup>ab</sup>	1.24 $\pm$ 0.18 <sup>b</sup>	10.83 $\pm$ 0.62 <sup>a</sup>	0.59 $\pm$ 0.38 <sup>ab</sup>	39.34 $\pm$ 5.42 <sup>b</sup>	3.98 $\pm$ 0.67 <sup>a</sup>	81.40 $\pm$ 10.57 <sup>b</sup>

Superscript letters that differ within column indicate significant differences among the observed sites ( $P < 0.05$ )



**Table 2** The bacterial community indices revealed by Illumina MiSeq sequencing from sediment samples of Poyang Lake

	Quality filter reads	OTUs	Chao1	Shannon	Simpson
SMS	22,172 ± 1046 <sup>a</sup>	2350 ± 157 <sup>b</sup>	3269.28 ± 297.90 <sup>b</sup>	5.99 ± 0.03 <sup>b</sup>	0.02 ± 0.003 <sup>a</sup>
NJS	25,538 ± 122 <sup>a</sup>	2362 ± 109 <sup>b</sup>	3285.70 ± 124.66 <sup>b</sup>	6.29 ± 0.16 <sup>a</sup>	0.01 ± 0.001 <sup>b</sup>
RH	22,628 ± 1286 <sup>a</sup>	2779 ± 59 <sup>a</sup>	3987.98 ± 36.38 <sup>a</sup>	6.39 ± 0.06 <sup>a</sup>	0.01 ± 0.001 <sup>b</sup>
BSZ	24,580 ± 1265 <sup>a</sup>	2689 ± 80 <sup>ab</sup>	3937.55 ± 88.52 <sup>a</sup>	6.32 ± 0.10 <sup>a</sup>	0.01 ± 0.002 <sup>b</sup>

Superscript letters that differ within column indicate significant differences among the observed sites ( $P < 0.05$ )

### Microbial Metabolic Activity Revealed by Biolog-EcoPlate Analysis

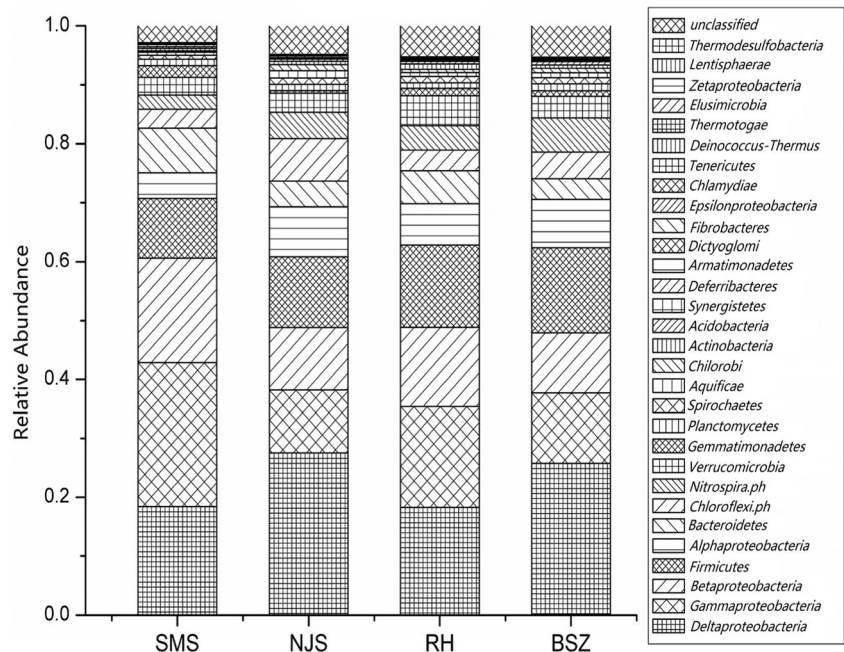
Biolog-Ecoplate analysis was used to qualitatively and quantitatively evaluate physiological profile of microbes in community level from different sample sites. The metabolic curves exhibited similar patterns after logarithmic increase state (40–90 h) (Fig. S2). We selected the timing point of 60-h for further analysis on diverse utilize types of carbon source because it showed the highest slope of the logarithmic phase which indicated the rate of carbon source utilization. The AWCD presented a gradient orders as follows: SMS (0.4968) > BSZ (0.3612) > RH (0.2436) > NJS (0.1989) ( $p < 0.05$ ) at 60-h point. Therefore, the rate of carbon source utilization in disturbed area was lower than undisturbed areas.

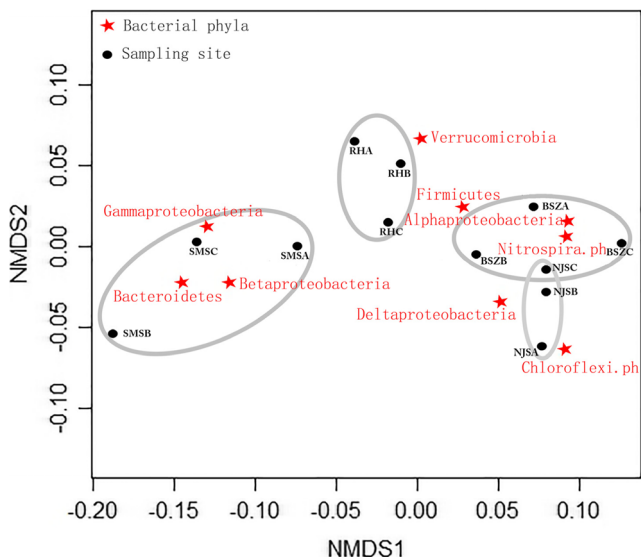
Significant differences were detected on the utilization preference of six classes of carbon source from the four sampling sites at 60-h point (Fig. 4). Except for phenolic acids, the utilization efficiency of all carbon sources peaked in SMS. The utilization efficiency of polymer and carbohydrate was lower than other carbon classes, and the lowest efficiency occurred in RH ( $P < 0.05$ ). The utilization of phenolic acids,

carboxylic acids, amino acids and amine showed the lowest efficiency in NJS area ( $P < 0.05$ ).

### The Influence of Sediment Properties on Bacterial Community Structures

Sediment properties had a significant impact on the structure of bacterial communities, and the RDA ordination results displayed their relationship (Fig. 5). It was revealed that the distribution of BCCs was significantly correlated to TP, TOC, pH and TN ( $p < 0.05$ ). Pearson correlation analysis also revealed that the abundance of dominant phyla was influenced by sediment properties. *Alphaproteobacteria*, *Chloroflexi*, *Deltaproteobacteria* were mainly positively correlated with TN and TOC, while *Gammaproteobacteria* was negatively correlated with TN and TOC. *Nitrospira* was mainly positively affected by TP, while *Firmicutes* and *Verrucomicrobia* were mainly positively affected by TP and heavy metals (Fig. 6). Nevertheless, the distribution of bacterial phyla was mainly affected by different factors in different sampling sites (Table S1).

**Fig. 2** Sediment bacterial community composition in different areas of Poyang Lake revealed by Illumina MiSeq sequencing

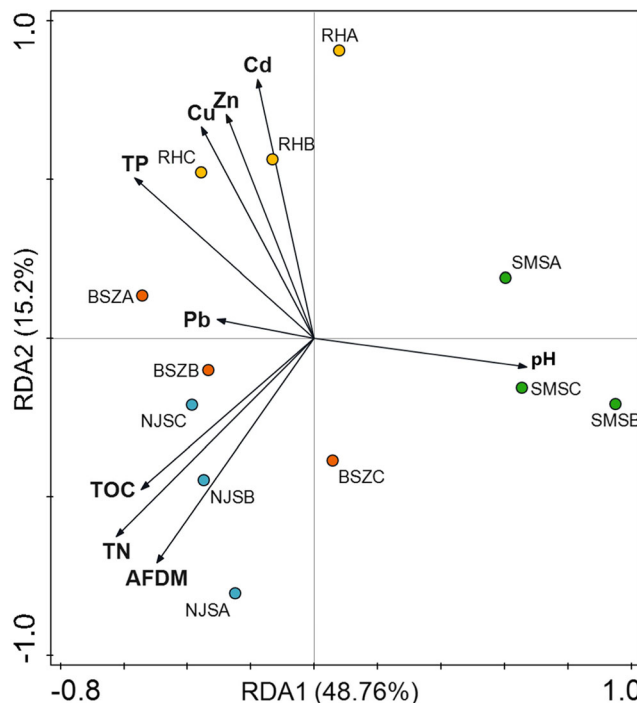
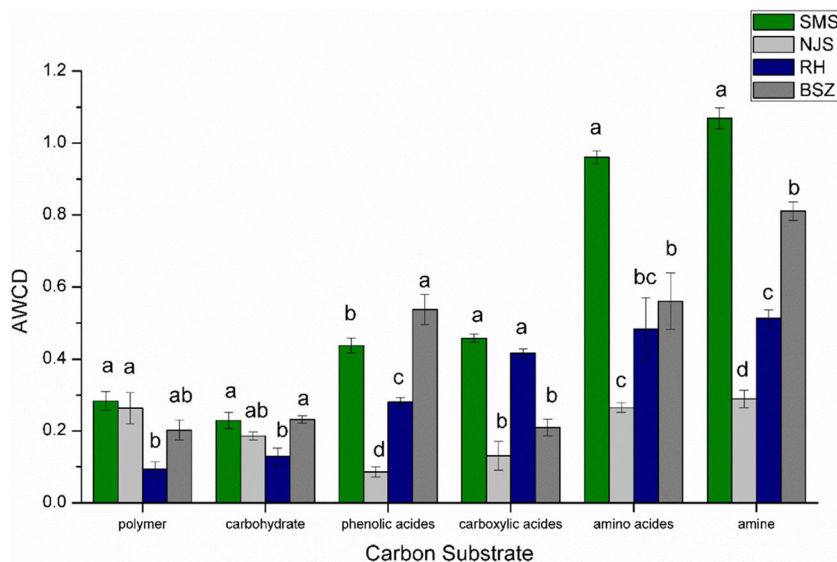


**Fig. 3** Non-metric multidimensional scaling (NMDS) analysis based on Bray-Curtis distances of microbial communities. Constrained phyla were shown in cycles. Letters A, B and C mean the triplicate samples of the four sampling sites

**The Correlation of Bacterial Composition and Metabolic Activity**

As shown in Fig. 6, most abundant phyla had significant correlations with carbon substrates (Table S2). *Gammaproteobacteria* and *Betaproteobacteria* were positively associated with carboxylic acids, amino acids or amine ( $P < 0.05$ ), while *Alphaproteobacteria*, *Chloroflexi* and *Nitrospira* showed negative correlation ( $P < 0.05$ ). *Deltaproteobacteria* was negatively correlated with carboxylic acids, and *Verrucomicrobia* was negatively correlated with polymer ( $P < 0.05$ ). Furthermore, RDA ordination was performed to explore the relationship between carbon metabolic profile and major bacterial phyla (Fig. 7). *Verrucomicrobia* and

**Fig. 4** The utilization difference of various carbon substrates in four areas of Poyang Lake (60-h point). Letters that differ within columns indicate significant differences among the sampling sites ( $P < 0.05$ )



**Fig. 5** Redundancy analysis (RDA) ordination between bacterial community composition and environmental parameters. Letters A, B and C mean the triplicate samples from the four sampling sites

*Firmicutes* mainly contributed to the carbon metabolic pattern of RH area, *Deltaproteobacteria* and *Chloroflexi* mainly functioned in NJS samples. *Gammaproteobacteria*, *Bacteroidetes* and *Betaproteobacteria* collectively functioned in both SMS and BSZ samples, while *Nitrospira* and *Alphaproteobacteria* showed negative effects in SMS and BSZ.

As the regression estimate shown in Fig. 8, changes in the sediment bacterial community were significantly correlated with metabolism: the greater community phylogenetic



RH sites was found to be at moderate to high levels through calculating the geo-accumulation index of heavy metals (Praveena et al. 2008). High levels of TP, TN, and TOC from aquaculture and human activity were previously documented as sources for organic pollution and eutrophication in the lake ecosystem (Wang et al. 2003; Zhao et al. 2007; Zhu et al. 2013b). Here, the aquaculture activity in NJS area also resulted in the extensive accumulation of TN and TOC.

The observed Poyang Lake sediment bacterial community Shannon index ranged from 5.99 to 6.39 (Fig. 2), which was lower than the results from severe eutrophic water-Dianchi Lake (Bai et al. 2012), but higher than the results from moderate eutrophic water of Vidy Bay (Thevenon et al. 2012; Sauvain et al. 2014). Among the four regions investigated in this work, anthropogenic disturbed area (NJS, RH and BSZ) had higher Shannon index than the uncontaminated area (SMS), and the heavy metal polluted area RH had the highest bacterial Shannon index. Similar results were confirmed in another study where heavy metal pollution could enhance the bacterial Shannon index (Ni et al. 2015). In a word, sediment bacterial diversity could be increased by many pollutants.

In this study, the most dominant bacterial lineages of Poyang Lake sediment were *Proteobacteria*, *Firmicutes*, *Bacteroidetes*, *Chloroflexi*, *Nitrospira* and *Verrucomicrobia*. Similar results were also reported in previous investigations in which the benthic bacterial community of Poyang Lake was dominated by *Deltaproteobacteria*, *Betaproteobacteria* and *Verrucomicrobia* (Kou et al. 2015; Ding et al. 2015).

In SMS area, *Gammaproteobacteria*, *Bacteroidetes* and *Betaproteobacteria* were the phyla which differentiated the BCCs of SMS from other regions (Fig. 3). In a previous study, *Gammaproteobacteria* showed higher abundance in undisturbed area than disturbed area (Haller et al. 2011). *Betaproteobacteria* and *Bacteroidetes* were most frequently detected in sediment samples from the lake without intermittent disturbances (Leon et al. 2012), and *Bacteroidetes* was also abundantly detected in a pond without mariculture (Li et al. 2015). Therefore, the abundance of *Gammaproteobacteria*, *Betaproteobacteria* and *Bacteroidetes* in SMS sediment may represent an undisturbed or unpolluted environment. Furthermore, pH played an important role in determining the SMS bacterial community according to the redundancy analysis (RDA) (Fig. 5), and this point was frequently reported in other studies (Lauber et al. 2009). The highest carbon source metabolic efficiency (AWCD) was detected in SMS area, which may indicate that less anthropogenic disturbances help to maintain metabolic capacity (Gryta et al. 2014). The typical SMS groups (*Gammaproteobacteria*, *Bacteroidetes* and *Betaproteobacteria*) showed significantly positive correlation with carboxylic acids, amino acids, and amines. Therefore, these results may indicate that the three phyla have potential to utilize the three types of carbon sources, but the direct relation between these phyla and carbon source was still unclear.

In NJS area, only *Deltaproteobacteria* and *Chloroflexi* contributed to the community specificity as contrasted with other sites. RDA analysis (Fig. 5) demonstrated that TN and TOC were the main factors influencing bacterial community structure of NJS (Shao et al. 2011; Zhang et al. 2015). *Chloroflexi* was widely distributed in surface sediment of various freshwater lakes (Kadnikov et al. 2012), especially in eutrophic conditions (Niu et al. 2011). *Deltaproteobacteria* was found in water and soil environments rich in organic carbon and played a significant role in the global carbon cycles (Rodionov et al. 2004). Thus, *Deltaproteobacteria* and *Chloroflexi* were expected to involve in the metabolic process of high organic nutrients. Furthermore, *Deltaproteobacteria* and *Chloroflexi* showed negative correlations with carboxylic acids and amino acids. Amino acids and carboxylic acids can be considered as part of the major pool of immobilized N (Liu et al. 2014) and labile pool of organic matter (Pullin et al. 2004) respectively, and they played an important role in metabolism process. The negative correlation may suggest that *Deltaproteobacteria* and *Chloroflexi* are unable to utilize these two types of carbon sources or the sources inhibit the utilization process. In terms of the integral metabolic activities, a recent study (Wang et al. 2016) found that soils with organic contamination lead to lower AWCD, which was in consistent with the findings of this study.

The distribution of *Verrucomicrobia* and *Firmicutes* was representative for RH area, as the presences of heavy metals (Cu, Zn, Cd) and TP may provide selected pressures for these two phyla. Sauvain et al. (2014) had claimed that the predominance of endospore-forming *Firmicutes* often occurred in the wastewater polluted by trace metals, and strong correlation between *Firmicutes* and heavy metals was distinct. *Verrucomicrobia* was a bacteria phylum often detected in water and soil environments such as Kasumigaura Lake and Taihu Lake (Tamaki et al. 2005; Xi et al. 2007), and appeared to be positively associated with Hg and TN (Zeng et al. 2008; Vishnivetskaya et al. 2011). Furthermore, *Verrucomicrobia* and *Firmicutes* also showed apparent influence on metabolic function of sediment bacteria in RH area, and the significant negative correlation with polymers might indicate that these two phyla could not utilize polymers or even were inhibited by high concentration of polymers. This phenomenon could be explained by previous studies, which suggested that Cu could improve the capacity of communities to utilize polymers in low content and inhibit the capacity in high content (Guo et al. 2012). Moreover, our results verified that increasing the contents of heavy metals and TP would reduce the metabolic level (AWCD) of sediment microbial community in freshwater lakes (Wang et al. 2004).

The distribution of *Alphaproteobacteria* and *Nitrospira* in BSZ area could discriminate BSZ from other sites. The sediment physicochemical data of BSZ documented the presence of both nutrient and heavy metal pollutants, but no parameter



passed the Monte Carlo tests, suggesting BCCs in the BSZ may be synergistically regulated by multiple factors, including heavy metals and nutrients.

To sum up, both bacterial community structure and metabolic function of sediment in Poyang Lake were sensitive to various anthropogenic disturbance-induced contaminations; different types of anthropogenic disturbance consistently increased bacterial diversity but decreased the metabolic activity (AWCD). In addition, different bacterial groups were found to specifically respond to the presence of certain pollutants and these groups are candidates of bio-indicators for lake sediment pollution. For this purpose, further studies should be carried out to quantify the typical proportions of these candidates in sediment bacterial community, and verify the effectiveness in different freshwater lake ecosystems.

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#### Compliance with Ethical Standards

**Conflict of Interest** The authors declare that there is no conflict of interests regarding the publication of this paper.

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