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RESEARCH ARTICLE

Influences of plant type on bacterial and archaeal communities in constructed wetland treating polluted river water

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Abstract Both bacteria and archaeal communities can play important roles in biogeochemical processes in constructed wetland (CW) system. However, the influence of plant type on microbial community in surface water CW remains unclear. The present study investigated bacterial and archaeal communities in five surface water CW systems with different plant species. The abundance, richness, and diversity of both bacterial and archaeal communities considerably differed in these five CW systems. Compared with the other three CW systems, the CW systems planted with *Vetiveria zizanioides* or *Juncus effusus* L. showed much higher bacterial abundance but lower archaeal abundance. *Bacteria* outnumbered *archaea* in each CW system. Moreover, the CW systems planted with *V. zizanioides* or *J. effusus* L. had relatively lower archaeal but higher bacterial richness and diversity. In each CW system, bacterial community displayed much higher richness and diversity than archaeal community. In addition, a remarkable difference of both bacterial and archaeal community structures was observed in the five studied CW systems. *Proteobacteria* was the most abundant bacterial group (accounting for 33–60 %). *Thaumarchaeota* organisms (57 %) predominated in archaeal communities in CW systems planted with *V. zizanioides* or *J. effusus* L., while *Woesearchaeota* (23 or 24 %) and *Euryarchaeota* (23 or 15 %) were the major archaeal groups in CW systems planted with *Cyperus papyrus* or *Canna indica* L. Archaeal community in CW planted with *Typha orientalis* Presl was mainly composed of unclassified *archaea*. Therefore, plant type exerted a considerable influence on microbial community in surface water CW system.

Keywords *Archaea* · *Bacteria* · Constructed wetland · Microbial community · River water · Vegetation

Introduction

The improper management of industrial wastewater, urban sewage, and rural runoffs has led to the deterioration of the water quality of rivers, lakes, and ponds in China and many other nations. Due to their merits of simple operation and low cost, constructed wetland (CW) treatment systems have been widely applied to purify polluted surface water (Ge et al. 2015; Jia et al. 2014; Mohammadpour et al. 2015; Tournebize et al. 2015; Zheng et al. 2014). In CW system, the removal of pollutants is achieved via a variety of physical, chemical, and biological processes (Vymazal 2007). Bacterial community is involved in the biogeochemical cycles of CW treatment system and is widely accepted as the key player in dissipating both organic and inorganic pollutants (Bouali et al.

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2014; Chang et al. 2015; He et al. 2016). Hence, it is crucial to understand bacterial community and the associated influential parameters, which can improve the design and management of CW system and its water purification efficiency (Adrados et al. 2014; Bouali et al. 2014; He et al. 2016; Ligi et al. 2014; Zhong et al. 2015). So far, only a few previous studies have investigated bacterial community structure in surface water horizontal flow CW (HFCW) (Ligi et al. 2014; Tu et al. 2014; Yin et al. 2009; Zhi et al. 2015) and vertical flow CW (VFCW) (Guan et al. 2015; He et al. 2016). These previous studies revealed the variation of CW bacterial community diversity and structure with sampling site (or layer depth) and time; however, bacterial community abundance in surface water CW has received little attention. Only two studies reported the spatial change of bacterial abundance in full-scale CW systems treating river water (Ligi et al. 2014; Zhi et al. 2015). In addition, the links between bacterial community and environmental or operational parameters in CW treating surface water remains essentially unknown, although substrate type was found to be a key determinant to bacterial community diversity and structure in VFCW treating polluted river water (Guan et al. 2015).

Archaeal community is known to be an important player in biogeochemical processes (Liu et al. 2015a, Zhang et al. 2015a). However, information on CW archaeal community is still very limited. Several previous studies investigated archaeal community diversity and structure in CW system treating domestic wastewater (Bouali et al. 2012, 2013; Liu et al. 2015a), while only a recent study has characterized archaeal community diversity and structure in surface water CW treatment system (He et al. 2016). These previous studies reported the dynamics of archaeal community diversity and structure in various CW treatment systems, whereas CW archaeal community abundance has not been addressed. Moreover, information on the environmental or operational parameters influencing CW archaeal community is still lacking.

Plants in CW treatment system can have profound influences on microbial community by providing microorganisms with habitats and plant media oxygen and carbon sources from root leakage (Caravaca et al. 2005; Wang et al. 2016; Zhao et al. 2012). The type of plant was found to have considerable effects on bacterial abundance, diversity, and community structure in CW system treating industrial or municipal wastewaters (Calheiros et al. 2010; Liu et al. 2016; Zhang et al. 2015b). However, there has been no report available on the influence of plant type on microbial community in CW system purifying surface water. Therefore, the main aim of this study was to investigate the influences of plant type on bacterial and archaeal communities in surface water CW system.

Materials and methods

Wetland description

Five VFCW systems (length 1.2 m, width 1 m, height 1.2 m) were established in 2012 to continuously treat the water of a polluted river located in Guangdong Province (southern China). Each CW system was filled with fine gravel (diameter 8–12 mm, height 90 cm). The top of the five CW systems was planted with *Cyperus papyrus* (wetland A), *Canna indica* L. (wetland B), *Vetiveria zizanioides* (wetland C), *Typha orientalis* Presl (wetland D), and *Juncus effusus* L. (wetland E), respectively. The retention time of water in each CW system was set to about 12 h. The average levels of ammonia nitrogen (NH_4^+-N) and total organic carbon (TOC) in the influent of each CW system were 2.5 and 25 mg/L, respectively, while the average removal rates of NH_4^+-N and TOC by each CW remained were 81–96 and 48–66 %, respectively (Table S1).

High-throughput sequencing analysis

In the current study, for each CW system, particle samples were collected from approximately 30 cm below the surface of gravel layer (in the CW central zone) in September in 2015. Samples A, B, C, D, and E denote the particle samples from wetlands A, B, C, D, and E, respectively. Total genomic DNA of particle sample was extracted using Powersoil DNA extraction kit (Mobio Laboratories, Carlsbad, CA) following the manufacturer's instructions. DNA quality was evaluated using 1.0 % agarose gel electrophoresis and then amplified using archaeal primer sets Arch519F (5′-CAGCCGCCGCGGTAA-3′)/Arch915R (5′-GTGCTCCCCCGC CAATTCCT-3′) and bacterial primer sets 515F (5′-GTGCCAGCMGCCGCGG-3′)/907R (5′-CCGTCAATTCMTTTRAGTTT-3′) (Dai et al. 2016; He et al. 2016; Wang et al. 2015; Yang et al. 2016), respectively. PCR products were checked by 1 % agarose gel electrophoresis and purified using QIAquick PCR purification kit (Qiagen Inc.), according to the manufacturer's instructions. Amplicons from triplicate samples were pooled in equal amounts and the mixture was submitted to Shanghai Majorbio Bio-pharm Technology Co., Ltd. to perform sequencing using the Illumina® HiSeq 2000 system. The obtained raw reads were deposited in the NCBI short-read archive under accession numbers SRP072797 (*bacteria*) and SRP072796 (*archaea*). The paired-end reads were assembled into composite reads using FLASH (Magoc and Salzberg 2011) and further processed using the Quantitative Insights into Microbial Ecology (QIIME) software pipeline according to the standard protocol (Caporaso et al. 2010). Putative chimeric sequences were screened and discarded using UCHIME (Edgar et al. 2011). Groups of related chimeric-free sequences were assigned to operational taxonomic units (OTUs) with a maximum genetic distance of 3 %, and α-diversities (Chao1 richness estimator and Shannon diversity index) were further calculated using the UPARSE pipeline (Edgar 2013). Taxonomic assignment of the representative sequences from each OTU was performed using the Silva 16S ribosomal RNA (rRNA) database (Quast et al. 2013). In addition, to compare the difference of microbial community composition among the five wetland samples, beta-diversity analysis was performed based on Bray–Curtis distance matrix of OTU composition for unweighted pair group method with arithmetic mean (UPGMA) clustering.

Quantitative PCR analysis

The number of bacterial and archaeal 16S rRNA genes was quantified by real-time quantitative PCR (qPCR) using the primer pairs 341F (5′-CCTACGGGAGGCAGCAG-3′)/534R (5′-ATTACCGCGGCTGCTGGCA-3′) and Arch349F (5′-GYGCASCAGKCGMGAAW-3′)/Arch806R (5′-GGACTACVSGGGTATCTAAT-3′), respectively, as previously described (Jung et al. 2011; Liu et al. 2014a; Yang et al. 2016). Standard curve was generated by tenfold serial dilution of standard plasmids, containing target bacterial or archaeal 16S rRNA genes. The average amplification efficiency and correlation coefficient (r^2) for bacterial and archaeal 16S rRNA genes were 97 % and 0.993 and 98 % and 0.998, respectively. Shapiro–Wilk test was used to test the data normality of microbial abundance, and Levene was used to test the homogeneity of variance. The results supported the usage of one-way analysis of variance (ANOVA), followed by Student–Newman–Keuls test to examine the significant difference ($P < 0.05$) in microbial abundance among wetland samples.

Results

Wetland microbial community abundance

In this study, the number of bacterial 16S rRNA genes in the five studied wetland samples ranged between $2.47 \pm 0.03 \times 10^7$ and $9.84 \pm 0.05 \times 10^7$ copies per gram dry gravel (Fig. 1). Bacterial abundance in each wetland sample was significantly different from that in other samples ($P < 0.05$). The samples from wetlands C (planted with *V. zizanioides*) and E (planted with *J. effusus* L.) had much higher bacterial abundance than those from wetlands A (planted with *C. papyrus*), B (planted with *C. indica* L.), and D (planted with *T. orientalis* Presl) ($P < 0.05$). Moreover, the density of archaeal 16S rRNA genes in the five studied wetland samples varied from $1.26 \pm 0.08 \times 10^6$ to $8.78 \pm 0.09 \times 10^6$ copies per gram dry gravel (Fig. 2). The samples from wetlands C and E illustrated much lower archaeal abundance than the other three wetland samples ($P < 0.05$). Significant difference in archaeal abundance was also found among the samples from wetlands A, B, and D ($P < 0.05$). In addition, for each wetland sample, *bacteria* had much higher community size than *archaea* ($P < 0.05$).

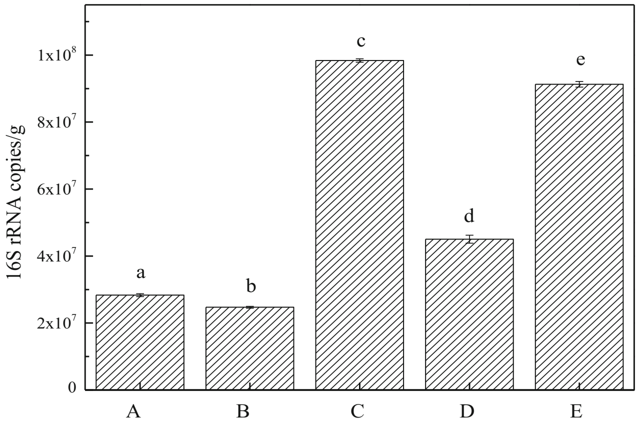

Fig. 1 Abundance of bacterial 16S rRNA gene in CW samples. *Different letters above the columns* indicate the significant differences ($P < 0.05$)

Wetland microbial community richness and diversity

In the present study, the number of bacterial sequences from each wetland sample was normalized to 21,016 for the comparison of bacterial community richness and diversity. The Good's coverage estimator revealed that 98.1–98.8 % of the bacterial OTUs were obtained in all wetland samples, which indicated that majority of the bacterial OTUs had been captured (Table 1). Each wetland bacterial library was composed of 993–1379 OTUs. Venn diagram demonstrated a large overlap in bacterial OTUs between the samples from wetlands C and E (Fig. 3). These two samples shared a total of 991 identical bacterial OTUs. A considerable overlap in bacterial OTUs was also observed among the three samples from

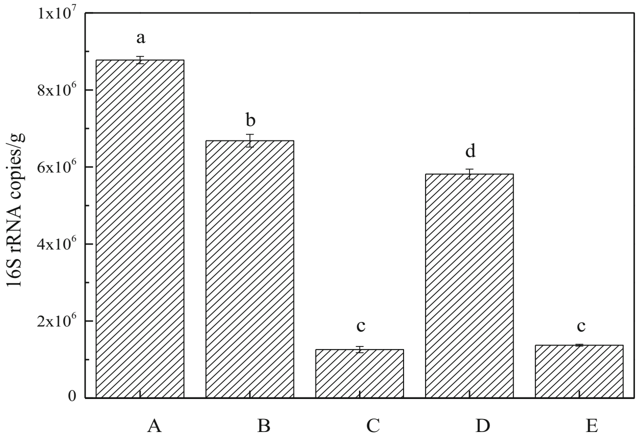

Fig. 2 Abundance of archaeal 16S rRNA gene in CW samples. *Different letters above the columns* indicate the significant differences ($P < 0.05$)

Table 1 Bacterial community richness and diversity of CW samples

Sample	OTUs	Chao1 estimator	Shannon index	Good's coverage (%)
A	1002	1210	5.03	98.8
B	993	1222	4.91	98.6
C	1379	1704	5.7	98.2
D	1177	1491	5.11	98.4
E	1315	1749	5.28	98.1

Table 2 Archaeal community richness and diversity of CW samples

Sample	OTUs	Chao1 estimator	Shannon index	Good's coverage (%)
A	453	488	3.87	99.8
B	468	522	3.77	99.7
C	347	417	2.48	99.7
D	436	510	3.24	99.7
E	224	265	2.57	99.8

wetlands A, B, and D. They shared a total of 682 identical bacterial OTUs. However, only 459 bacterial OTUs were shared among all of the five studied wetland samples. The bacterial Chao1 richness estimator illustrated a remarkable variation in the five studied wetland samples, ranging from 1210 to 1749. The samples from wetlands C and E had much higher bacterial OTUs and Chao1 richness than those from other wetlands. Moreover, a remarkable change of bacterial Shannon diversity index was found in the five studied wetland samples, ranging from 4.91 to 5.7. The sample from wetland C had the highest bacterial community diversity followed by that from wetland E.

The number of archaeal sequences from each wetland sample was normalized to 28,372 to compare archaeal richness and diversity among wetland samples. The Good's coverage estimator ≥99.7 % suggested that archaeal OTUs in all wetland samples had been adequately captured (Table 2). Wetland archaeal libraries consisted of 224–468 OTUs. The samples from wetlands C and E had much less archaeal OTUs than those from wetlands A, B, and D. Venn diagram displayed a considerable overlap in archaeal OTUs between the samples from wetlands C and E (Fig. 4). They shared a total of 160 identical archaeal OTUs. The samples from wetlands A, B, and D shared 240 identical archaeal OTUs, showing a large overlap. However, only a total of 85 archaeal OTUs were shared among all wetland samples. In the five studied wetland samples, the archaeal Chao1 richness estimator ranged between 265 and 522. The samples from wetlands C and E also showed much lower archaeal Chao1 richness than other wetland samples. Moreover, in these wetland samples, archaeal community Shannon diversity index displayed a great variation. The samples from wetlands C and E (Shannon diversity index = 2.48 or 2.57) showed much lower archaeal community diversity than other wetland samples (3.24–3.87). In addition, for each wetland sample, compared with bacterial community, archaeal community had much lower OTUs, Chao1 richness, and Shannon diversity.

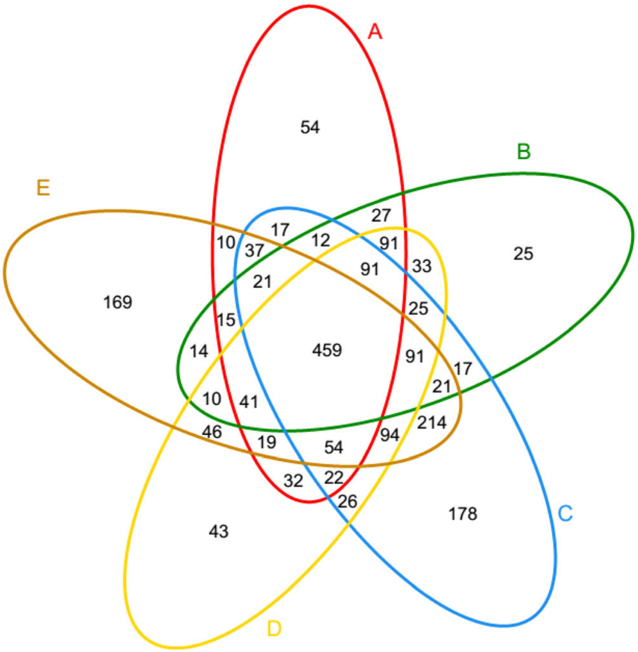

Fig. 3 Share bacterial OTUs among CW bacterial communities. The Venn diagram was plotted using program *R*

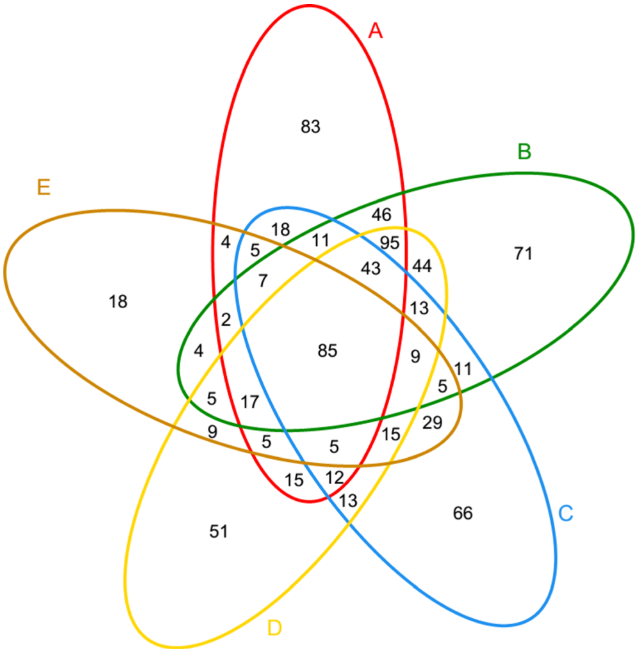

Fig. 4 Share archaeal OTUs among CW archaeal communities. The Venn diagram was plotted using program *R*

UPGMA clustering analysis of wetland microbial communities

The result of UPGMA clustering indicated that bacterial communities in the five studied wetland samples could be divided into two distinct clades (Fig. 5). The samples from wetlands C and E were grouped together, while they were clearly separated from other wetland samples. In addition, UPGMA clustering of archaeal communities also illustrated that the five studied wetland samples could be assigned into two distinct groups (Fig. 6). The samples from wetlands C and E formed a group, while the samples from wetlands A, B, and D were clustered into another group.

Wetland microbial community composition

In the current study, a total of 11 bacterial phyla were ubiquitously identified among the five studied CW samples, including *Proteobacteria*, *Cyanobacteria*, *Bacteroidetes*, *Acidobacteria*, *Chloroflexi*, *Chlorobi*, *Firmicutes*, *Nitrospirae*, *Planctomycetes*, *Gemmatimonadetes*, and *Actinobacteria* (Fig. 7). *Proteobacteria* was the largest phylum group in wetland samples A, B, C, and D (accounting for 49–60 %) and the second most abundant phylum group in wetland sample E (33 %). A considerable difference in the proteobacterial proportion was found in these five wetland samples. *Cyanobacteria* organisms illustrated a high proportion in wetland sample E (34 %) but became much less abundant in other wetland samples (1–10 %). In contrast, *Bacteroidetes* organisms showed lower proportion in wetland sample E (4 %) than in other four wetland samples (8 or 12 %). Moreover, the proportion of *Acidobacteria* (5–10 %), *Chloroflexi* (4–8 %), *Chlorobi* (1–5 %), and *Firmicutes* (1–8 %) also showed evident variation in the studied five wetland samples.

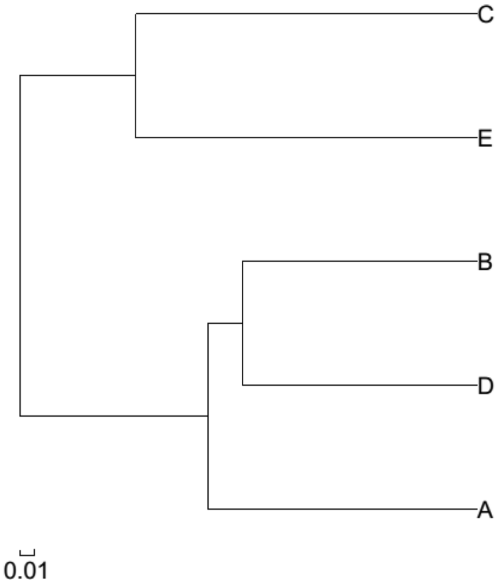

Fig. 5 UPGMA clustering of CW bacterial communities

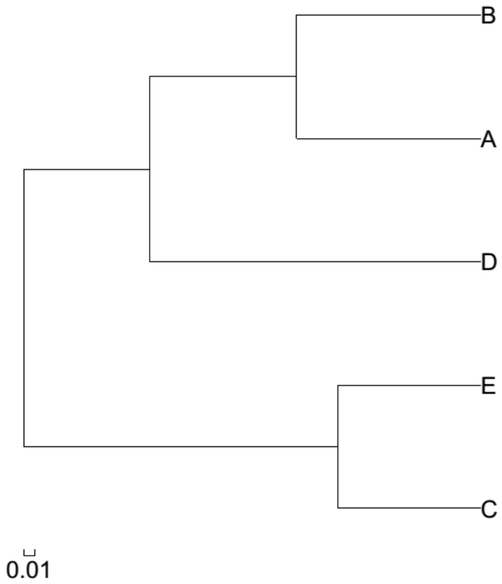

Fig. 6 UPGMA clustering of CW archaeal communities

In each wetland sample, a considerable proportion of archaeal sequences could not be affiliated with any known archaeal phylum (accounting for 41–85 %) (Fig. 8). *Thaumarchaeota* organisms predominated in wetland samples C and E (57 %) but became a minor archaeal group in other three wetland samples (1 %). *Woesearchaeota* (formerly known as Deep Sea Hydrothermal Vent Group 6 (DHVEG-6)) organisms displayed high proportion in wetland samples A (23 %) and B (24 %), but illustrated much lower proportion in other wetland samples (1 or 8 %). The proportion of *Euryarchaeota* organisms was also much higher in wetland samples A (23 %) and B (15 %) than in other wetland samples (1 or 2 %). In addition, the proportion of *Bathyarchaeota* organisms also showed a remarkable shift in the five studied wetland samples (0–8 %).

Discussion

Influence of plant type on wetland microbial abundance

Several previous studies indicated the considerable influence of plant type on bacterial community abundance in CW systems treating industrial or municipal wastewaters (Calheiros et al. 2010; Liu et al. 2016; Vymazal et al. 2001; Zhang et al. 2015b), whereas Calheiros et al. (2009) suggested no significant influence of plant type on bacterial community abundance in CW system for tannery industrial wastewater treatment. So far, there has been no report available on the influence of plant type on bacterial abundance in surface water CW system. In this study, qPCR targeting bacterial 16S rRNA

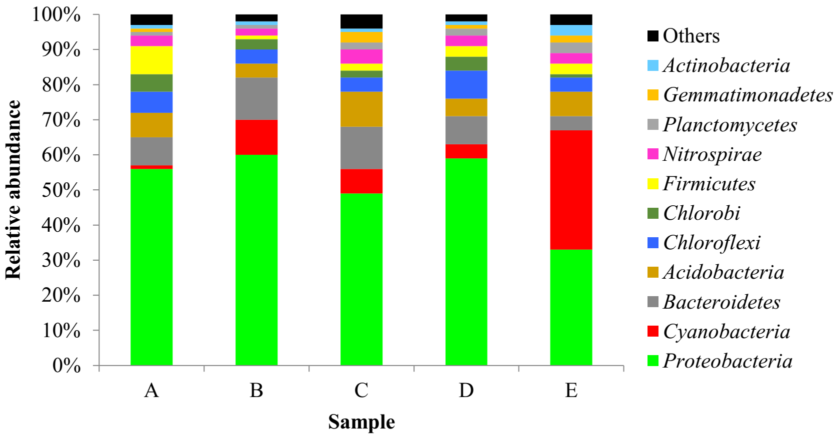

Fig. 7 Comparison of the quantitative contribution of the sequences affiliated with different bacterial phyla to the total number of bacterial sequences from wetland samples. Others include unclassified bacteria and the bacterial phyla with the relative abundance less than 1 % in each sample

genes was used to quantify the bacterial abundance in five surface water CW systems with different plant species (*C. papyrus*, *C. indica* L., *V. zizanioides*, *T. orientalis* Presl, or *J. effusus* L.). A remarkable difference in bacterial abundance was found among these CW systems. Wetlands planted with *V. zizanioides* or *J. effusus* L. had much higher bacterial abundance than other wetlands. Therefore, the present study provided the evidence for the first time that plant species could have a considerable effect on bacterial abundance in surface water CW system. Moreover, there is a paucity of knowledge on the influence of plant type on archaeal abundance in CW system. In this study, the remarkable difference in archaeal abundance was also observed among five surface water CW systems with different plant species, using PCR targeting archaeal 16S rRNA gene, which illustrated the profound influence of plant type on archaeal abundance. In addition, the present study further compared the community size of *archaea* and *bacteria* in surface water CW systems. In each CW, *archaea* was much less abundant than *bacteria*. However, wetlands planted with *V. zizanioides* or *J. effusus* L. had highest bacterial abundance but lowest archaeal abundance. This suggested the different influences of plant type on archaeal and bacterial abundance.

Influence of plant type on wetland microbial richness and diversity

Several previous studies have revealed the considerable influence of plant type on bacterial community richness and diversity in CW systems treating high salinity tannery wastewater (Calheiros et al. 2009, 2010), domestic wastewater (Zhang et al. 2015b), and triclosan-containing synthetic wastewater (Liu et al. 2016). Moreover, Menon et al. (2013) suggested that plant type could affect sediment bacterial community richness in CW mesocosm fed with groundwater. To date, although a few previous studies have investigated bacterial community richness and diversity and their shifts in CW systems purifying polluted surface water (Guan et al. 2015; He et al. 2016; Ligi et al. 2014; Tu et al. 2014; Yin et al. 2009; Zhi et al. 2015), the links between plant and bacterial community richness or diversity in surface water CW have not been addressed. In this study, Illumina high-throughput sequencing was applied to characterized microbial communities in five CW systems that were vegetated with different plant species. Bacterial community richness and diversity were found to vary remarkably among CW systems with different plant species. Wetlands planted with *V. zizanioides* or *J. effusus* L. had much higher bacterial richness and diversity than other

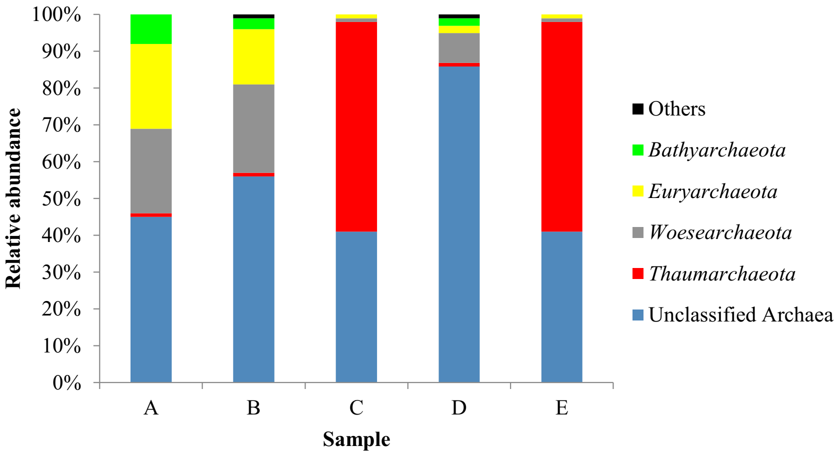

Fig. 8 Comparison of the quantitative contribution of the sequences affiliated with different archaeal phyla to the total number of archaeal sequences from wetland samples. Others include the archaeal phyla with the relative abundance less than 1 % in each sample

wetlands. Therefore, to the authors' knowledge, the present study provided the first evidence for the influence of plant type on bacterial community richness and diversity in surface water CW system.

Two recent studies suggested the influence of plant type on archaeal community richness and diversity in natural wetland ecosystem (Lee et al. 2015; Lliros et al. 2014), yet information on the links between plant and archaeal community richness or diversity in CW system is still lacking. In the present study, archaeal community richness and diversity illustrated a considerable variation in the five CW systems with different plant species. CW systems planted with *V. zizanioides* or *J. effusus* L. illustrated much lower archaeal richness and diversity than the other ones. Hence, plant type could affect archaeal community richness and diversity in surface water CW system. Moreover, the results obtained in this study indicated that the plantation with *V. zizanioides* or *J. effusus* L. in surface water CW system favored bacterial richness and diversity but disfavored archaeal richness and diversity, suggesting that the influences of plant type on bacterial and archaeal richness and diversity might be different. In addition, in the present study, bacterial community was found to have much higher richness and diversity than archaeal community. This was in agreement with the results observed in CW systems treating polluted pond water (He et al. 2016) and domestic wastewater (Adrados et al. 2014; Bouali et al. 2013) and in natural wetland (Dorador et al. 2013).

Influence of plant type on wetland microbial community structure

The profound influence of plant type on bacterial community structure has been found in CW systems used for the treatment of various waters, such as high salinity tannery wastewater (Calheiros et al. 2009, 2010), domestic wastewater (Zhang et al. 2015b), metal polluted wastewater (Arroyo et al. 2013), and triclosan-containing synthetic wastewater (Liu et al. 2016). Menon et al. (2013) also suggested the strong influence of plant type on bacterial community structure in CW fed with groundwater. However, to date, there has been no report available on the influence of plant type on bacterial community structure in surface water CW system. Moreover, the strong influence of plant type on archaeal community structure has been documented in a variety of natural wetland ecosystems (Lee et al. 2015a; Lliros et al. 2014; Rietl et al. 2016; Tian et al. 2012a,b), while the links between plant and CW archaeal community structure remain unknown. In this study, the results of both UPGMA clustering and phylogenetic analysis indicated the remarkable difference of both bacterial and archaeal community structures in surface water CW systems with various plant species. Moreover, only a small proportion of microbial OTUs was shared among all CW systems, which further confirmed the strong influence of plant type on microbial community structure in surface water CW.

Dominant microbial groups

Microorganisms within bacterial phylum *Proteobacteria* are able to participate in various biogeochemical processes, including biodegradation of organic pollutants (Cheng et al. 2014; Liu et al. 2014b; Zhang et al. 2014). The dominance of *Proteobacteria* has been commonly found in surface water CW system (Guan et al. 2015; He et al. 2016; Ligi et al. 2014; Zhi et al. 2015). To date, the influential factors governing the proteobacterial proportion in CW bacterial community remain elusive. In this study, Illumina sequencing analysis illustrated the dominance of proteobacterial organisms in CW systems treating polluted river water, which suggested that proteobacterial organisms might be actively involved in the biological processes in surface water CW. Moreover, the proteobacterial proportion in CW bacterial community was found to be related to plant type. This suggested the influence of plant type on the proteobacterial proportion in surface water CW. However, the links between the CW proteobacterial proportion and TOC removal remain unclear.

Cyanobacteria was usually a minor bacterial group or even not detected in surface water CW (Guan et al. 2015; He et al. 2016; Ligi et al. 2014; Zhi et al. 2015). However, Guan et al. (2015) revealed the high proportion of *Cyanobacteria* organisms in surface water CW filled with natural zeolite but not in CW filled with sand or fine gravel. The influential factors governing the *Cyanobacteria* proportion in CW bacterial community remain unclear. In this study, the *Cyanobacteria* proportion illustrated a considerable variation in the five studied surface water CW systems, and *Cyanobacteria* organisms displayed the dominance in surface water CW planted with *J. effusus* L. This suggested the influence of plant type on the *Cyanobacteria* proportion in surface water CW.

Microorganisms within archaeal phylum *Thaumarchaeota* can contribute to ammonia oxidation in both natural and man-made ecosystems (Bouali et al. 2012, 2013; He et al. 2016; Hugoni et al. 2015; Lee et al. 2015b; Liu et al. 2015a,b; Sauder et al. 2011). So far, information on *Thaumarchaeota* in CW system is still very limited. The dominance of *Thaumarchaeota* organisms in archaeal community has been found in CW systems treating domestic wastewater (Bouali et al. 2012, 2013). *Thaumarchaeota* was also found to be a major archaeal phylum group in surface water CW (He et al. 2016). In this study, *Thaumarchaeota* organisms predominated in surface water CW systems planted with *V. zizanioides* or *J. effusus* L., which might account for the very high ammonia removal in these two CW systems. However, *Thaumarchaeota* was found to be a minor archaeal group in other CW systems. Therefore, the present study showed, for the first time, that the proportion of *Thaumarchaeota* organisms in archaeal community might be affected by plant type.

Microorganisms within archaeal phylum *Euryarchaeota* are involved in methane production (He et al. 2016; Quemeneur et al. 2015; Roske et al. 2014). *Euryarchaeota* was found to be a minor archaeal group in CW system treating domestic wastewater (Bouali et al. 2012, 2013), while Liu et al. (2015a) revealed the dominance of *Euryarchaeota* organisms in CW system treating the mixture of domestic wastewater and reservoir water. He et al. (2016) also indicated that *Euryarchaeota* was a major archaeal group in CW system treating polluted pond water. To date, information on the influential factors governing the proportion of *Euryarchaeota* organisms in archaeal community in CW system is still lacking. In this study, *Euryarchaeota* organisms were much more abundant in CW systems planted with *C. papyrus* or *C. indica* L., suggesting their potential roles in the reduction of organic matter in these two CW systems. In addition, the considerable variation of the *Euryarchaeota* proportion in the five studied CW systems suggested the potential effect of plant type on *Euryarchaeota* organisms.

Woesearchaeota organisms were present in various ecosystems, such as marine water and sediment (Merkel et al. 2015; Nunoura et al. 2012), saline shallow lake (Casamayor et al. 2013), and nitrogen-/phosphate-removing wastewater treatment sludge (Kuroda et al. 2015), yet the role of *Woesearchaeota* organisms in the environment is still elusive. Moreover, previous studies showed the absence of *Woesearchaeota* organisms in CW systems (Bouali et al. 2012, 2013; He et al. 2016; Liu et al. 2015a). In contrast, in the current study, *Woesearchaeota* was found to be a major archaeal group in CW systems planted with *C. papyrus* or *C. indica* L. The considerable variation of the *Woesearchaeota* proportion in the five CW systems suggested the potential influence of plant type on *Woesearchaeota* organisms.

Conclusions

Plant species could have a considerable effect on microbial abundance in surface water CW system. *Archaea* had much lower community size than *bacteria*. Illumina high-throughput sequencing analysis illustrated the considerable variation of microbial community richness, diversity, and structure in surface water CW systems with different plant species. Compared with *bacteria*, *archaea* had relatively lower community richness and diversity. *Proteobacteria* usually predominated in CW bacterial community. *Thaumarchaeota* was dominant in archaeal communities in CW systems planted with *V. zizanioides* or *J. effusus* L., while *Woesearchaeota* and *Euryarchaeota* were the major archaeal groups in CW systems planted with *C. papyrus* or *C. indica* L.

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Compliance with ethical standards

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

Ethical statement The work has not been published previously and is not under consideration for publication elsewhere.

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