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ORIGINAL PAPER

Effects of electron donors on anaerobic microbial debromination of polybrominated diphenyl ethers (PBDEs)

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Abstract Polybrominated diphenyl ethers (PBDEs) are a class of widely used flame retardants that have been highly accumulated in sediments. It is reported that microorganisms play an important role in the reductive debromination of PBDEs in anaerobic sediments. However, little is known about the effects of electron donors on the microbial community structure and their debromination capacity in PBDE transformation. In this study, alternate carbon substrates were used as electron donors to enrich the PBDE-debrominating microbial consortia to evaluate the effects of electron donors on PBDE microbial debromination. Decabromodiphenyl ether (BDE-209) was found to be the dominant (more than 50%) PBDEs congener in all consortia, and the percentage of BDE-209 was deceased by 12% (methanol), 11% (ethanol), 8% (acetate), 9% (lactate), 5% (pyruvate), and 11% (no electron donors), while the relative abundances of most lesser-brominated PBDEs increased after 90-day incubation compared to the initial profile of PBDEs. Substantial shifts in the microbial community structure among different amendments were observed based on denaturing gradient gel electrophoresis results. *Pseudomonas* spp. were identified to be the predominant organisms and the abundances of Band R, which was associated with *Pseudomonas* sp. SCSWA09, was well correlated with the biodegradation rate of BDE-209. Finally, the microbial community structure was highly correlated with the concentration of deca-BDE, octa-BDE and total nitrogen. These results provide insights into in situ bioremediation of environments contaminated by PBDEs and our understanding of microbial ecology associated with PBDE-debromination.

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Introduction

Polybrominated diphenyl ethers (PBDEs), a group of brominated flame retardants used widely in products such as electronic equipment and furniture (de Wit 2002), have been detected in environmental samples around the world, including China (Chen et al. 2006; Mai et al. 2005; Wang et al. 2010), Canada (Gauthier et al. 2008), and the US (Lorber 2008). The concentrations of PBDEs at Guiyu, which have been involved in e-waste "recycling" for ~10 years in southeast Guangdong Province, China, are among the highest found in environmental media in the world, up to 33,000–97,400 μg g^{-1} soil (dry wt) (Leung et al. 2007; Yang et al. 2010).

It is known that PBDEs are persistent in the environment and accumulated in the biota. Many studies investigated the distribution of PBDEs in the environment and their potential toxicity to humans and environments during the past 10 years (Chen et al. 2006; Leung et al. 2010; Sjodin et al. 2008). More and more evidences showed that biodegradation could be an important way for PBDEs transformation (Lee and He 2010; Yen et al. 2009) and PBDEs could be debrominated to less brominated congeners by pure cultures and microbial consortia. Gerecke et al. (2005) found that 15% of added decabromodiphenyl ether (BDE-209) (10.0 μmol) was transformed into BDE-208 and BDE-207 by anaerobic sludge without the addition of alternative electron acceptors within 238 days. *Dehalococcoides*-containing culture could transform octa-BDE to a variety of hepta-through di-BDE but without any effects on BDE-209 (He et al. 2006). Some of 28 samples collected from different places showed the occurrence of debromination when spiked with octa-BDE (Lee and He 2010). Currently, researchers have studied microbial communities and dehalo-bacteria involved in the process of PBDE degradation (Lee and He 2010; Shin et al. 2010; Yen et al. 2009). Biotransformation of deca-BDE by an indigenous bacterium isolated from PBDEs contaminated environment have been reported (Deng et al. 2011). However, little is known about the correlation between the supply of electron donors and the microbial community structure during PBDEs degradation. A better understanding of this relationship will provide guidance on in situ bioremediation of PBDEs-contaminated environments.

The objective of this study was to evaluate the effect of electron donors on the PBDEs debromination capacity of microbial consortia. To our knowledge, this is the first study concerning the effect of electron donors on PBDEs-debrominating microbial community structures and their debromination capacities.

Materials and methods

Materials

Commercial deca-BDE containing more than 98% BDE-209 was purchased from TCI (Tokyo, Japan). 21 PBDE congeners selected for quantitative analysis were purchased from AccuStandards (New Haven, CT), including BDE-28, -47, -66, -77, -85, -99, -100, -138, -153, -154, -181, -183, -196, -197, -202, -203, -205, -206, -207, -208, and -209. All organic solvents, neutral silica gel (80–100 mesh) and alumina (100–200 mesh) were pretreated by redistill and Soxhlet extraction according to the previous description by Mai et al. (2005), respectively. Sodium sulfate was baked at 450°C for 2 h and stored in sealed containers.

Collection and enrichment of sediment samples

Sediment samples were collected in October 2009 using a stainless steel shovel at a depth of 5–15 cm at the riverside of Lianjiang River at Guiyu, an Electronic Waste Recycling Town in China. Collected samples were stored in a jar and kept at 4°C. Sediment samples were enriched in the defined medium containing 5.7 mM Na_2HPO_4, 3.3 mM KH_2PO_4, 18.0 mM NH_4Cl, vitamin solution and mineral solution (Wolin et al. 1963), 0.2 g l^{-1} of yeast extract and 10 mM of electron donor. The electron donors used in this study included methanol, ethanol, acetate, lactate and pyruvate. 10 μM of BDE-209 resolved in dichloromethane was added to the serum bottle (250 ml) and

evaporated in the darkness. 20 g sediments (wet weight) and 150 ml defined medium were then added to each glass bottle, purged with pure nitrogen gas for 5–10 min, and incubated at 30°C in anaerobic gloveboxes without shaking. The culture medium was exchanged every 2 weeks. All experiments were conducted in duplicate.

Chemical analyses

To determine the debromination rate, 2 ml of the culture medium were taken out every 2 weeks. Pretreatments to remove organic matters and heavy metals were performed before analysis with Ion chromatograph (IC) (Dionex-ICS2000) equipped with AS19 column. Quantification of bromides was analyzed by establishing six-point calibration curves (Y peak area, X bromide concentration):

$$Y = 0.0023X - 0.0025 \left(5 - 100\,\mu g l^{-1}, r = 0.9996\right);$$
$$Y = 0.0029X - 0.0228 \left(100 - 2000\,\mu g l^{-1}, r = 0.9999\right).$$

The sediment samples were freeze-dried, ground, and homogenized by sieving through a stainless steel 100-mesh (0.5-mm) sieve and stored in glass containers at −20°C until extraction. The extraction procedures were modified from the previous study (Mai et al. 2005), and 24 h was used for the extraction time of Soxhlet extractor. PBDE congeners were detected by a Shimadzu Model 2010 gas chromatograph coupled with a Model QP200 mass spectrometer (MS) and the analytical procedures were almost the same as previously described by Mai et al. (2005).

For quantitative determination, standard curves of PBDEs were prepared by diluting the stock solution standard of PBDEs with *n*-hexane to 0.01, 0.025, 0.075 and 0.125 μg ml^{-1} and analyzed with gas chromatography-electron capture detection (GC-ECD). Linear regression equations with r^2 were obtained by plotting the integration area (y) versus PBDE concentration (x) for calculating the analyst.

PCR-denaturing gradient gel electrophoresis (DGGE) analysis

Genomic DNA was extracted from 2 ml of anaerobic culture medium using a Soil gDNA kit (Biomiga Inc, USA) and then stored at −20°C. 16S rRNA genes were amplified from the extracted DNA with primers 1401R (5′-CGGTGTGTACAAGACCC-3′) and 968F-GC (5′-CGCCCGCCGCGCGCGGCGGGCGGGGCGGGGGCACGGGGGGAACGCGAAGAACCTTAC-3′). The reaction mixture (25 μl) contained 50 ng of the purified DNA as the template, 1 U Taq polymerase, 20 pmol of each primer, and 10 nmol of dNTP. PCR was performed by preheating at 94°C for 10 min, followed by 30 cycles of denaturation at 94°C for 1 min, annealing at 55°C for 1 min, and extension at 72°C for 1 min. Duplicate PCR products were then used for DGGE analysis. DGGE was performed according to the standard protocol (Muyzer 1993) using the Bio-Rad Dcode system (Bio-Rad Laboratories, Hercules, CA). DNA fragments for major bands in the DGGE gels were cut from the gels and eluted in TE buffer overnight at 4°C. Each eluted DNA was re-amplified by PCR using the primers 968F (without a GC-clamp) and 1401R under the conditions described above, and then sequenced by BGI (Guangzhou, China). Identity analysis of the sequences was performed on the NCBI website (http://blast.ncbi.nlm.nih.gov).

Data analysis

DGGE data were analyzed by unweighted pair-group method using arithmetic averages (UPGMA) and the similarity was calculated by coefficient of DICE, using the Quantity One software (Bio-Rad, USA). The UPGMA method was employed to reveal the structure of bacterial community during incubation. Principal component analysis (PCA) was used to determine the changes of microbial communities. Redundancy analysis (RDA), associated with forward selection and unrestricted Monte Carlo permutation test based on 999 random permutations, were used to select the minimum number of environmental variables explaining the largest amount of variation in microbial communities. In order to evaluate the specific contribution of each significant variable, a variation partitioning analysis was run with the variables of interest as explanatory variables and the other significant variables as covariables (Ramette and Tiedje 2007; Xu et al. 2010). PCA, RDA and variation partitioning analysis were performed with the package CANOCO 4.5 (Biometris/Plant Research International, Wageningen, The Netherlands). To identify patterns of variation among microbial communities, we normalized

environmental variables by subtraction of the mean and division by standard deviation before performing multivariable analyses.

Results

Debromination by enriched microbial consortia

It is reported that PBDEs can be debrominated under anaerobic conditions by microorganism (He et al. 2006; Lee and He 2010) associated with the production of bromide ion. Figure 1 showed the formation of bromide ion by the consortia, which were enriched on the defined medium supplied with five different electron donors (methanol, ethanol, acetate, lactate, and pyruvate). The concentration of bromide ion increased from 100 to 500 μg l^{-1} approximately over the course of 90 days. No obvious increase in the concentration of bromide ion was detected in the control. After 90 days incubation, the concentrations of bromide ion were 425 μg l^{-1} (methanol), 445 μg l^{-1} (ethanol), 463 μg l^{-1} (acetate), 480 μg l^{-1} (lactate), 420 μg l^{-1} (pyruvate), 501 μg l^{-1} (no electron donors), respectively. The addition of exogenous electron donors in the medium did not enhance the debromination of PBDEs (Fig. 1). The enriched microbial consortium from sediment without any electron donor added produced more bromide ion than those with additional electron donors. The results indicate that most of the microorganisms in the sediment involved in PBDEs debromination were oligotrophic and the amount of carbon source in sediment was enough to support the PBDEs debromination.

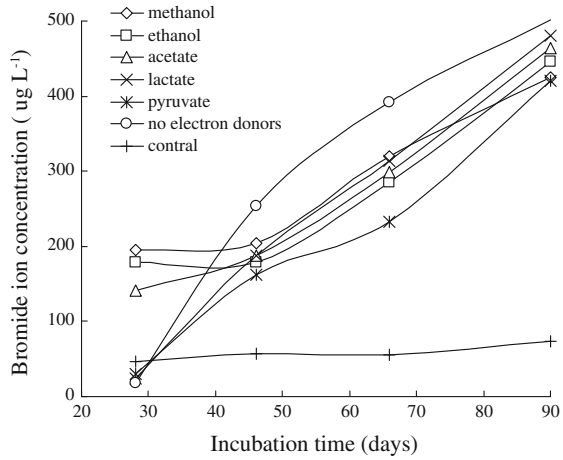

Fig. 1 Bromide production by consortia enriched on five different electron donors over the course of 90 days

Products of PBDEs and electron donors on the degradation of PBDEs

The products of PBDEs were monitored during a 90-day incubation, and showed that PBDEs were debrominated to lower brominated congeners by microorganism in the time course of 90 days. Obvious differences in the profile of PBDEs were observed among the consortia enriched on different electron donors (Fig. 2). No new PBDE congeners were found except BDE-154 in the consortia enriched on a variety of electron donors. BDE-154 was only observed in methanol, ethanol, and acetate enrichments. Deca-BDEs (BDE-209) was found to be the dominant (more than 50%) PBDEs congener in all consortia, and the percentage of BDE-209 was decreased by 12% (methanol), 11% (ethanol), 8% (acetate), 9% (lactate), 5% (pyruvate), and 11% (no electron donors) after 90-day incubation compared to the initial profile of PBDEs. Meanwhile, less-brominated congeners such as nona-BDE, octa-BDE and hexe-BDE were increased by the same proportions as BDE-209 decreases (Fig. 3), while the relative abundance of most lesser-brominated PBDEs, such as nona-BDE, octa-BDE, hepta-BDE, hexa-BDE, or penta-BDE, deceased when electron donors added. The results suggested that elelctron donors had different impacts on the degradation of PBDEs and the degradations of lesser-brominated PBDEs were stimulated, although the addition of acetate, lactate or pyruvate inhibited BDE-209 biodegradation in some degree.

DGGE analysis

DGGE was chosen as an assessment tool to evaluate major changes in the diversity of microbial communities of enrichments as it has been widely used in the study of microbial ecology. DGGE analysis revealed significant shifts in the community structure among different treatments (Fig. 4). PCA was used to examine the overall variation among those six different consortia. The PCA plot based on the DGGE profiles showed a difference in the first component among those enrichments (Fig. 5). PC1 explained 58.6% of

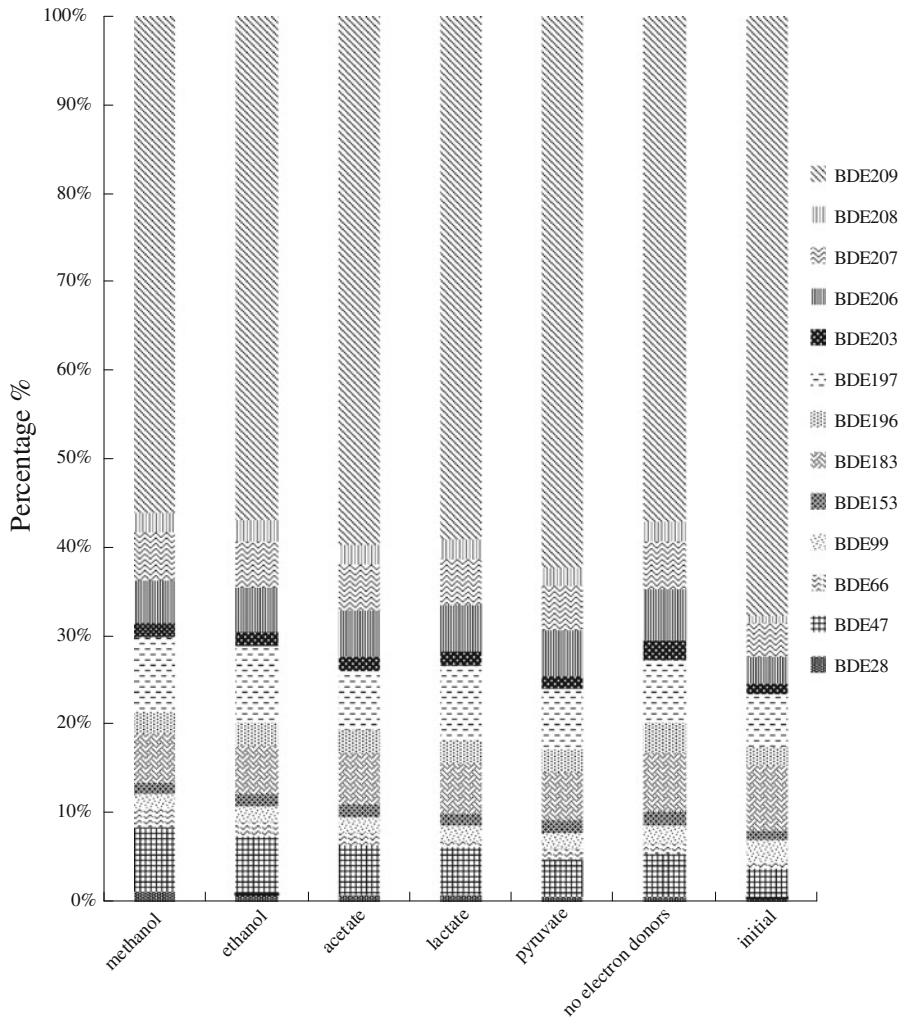

Fig. 2 PBDEs congeners profile of consortia under different treatments after incubation for 90 days. Initial represent day zero

the total variance, while PC2 explained 22.5%. The results of PCA suggested that the bacterial community structure was significantly affected by the addition of electron donors. The consortium enriched on methanol was similar to ethanol, but differed from acetate, lactate and pyruvate, indicating that electron donor has different effects on the growth of microbes presented in the sediment.

A total of 19 dominant bands were excised from DGGE gels, and their nucleotide sequences were determined and compared with 16S rRNA gene databases (Table 1; Fig. 4). A phylogenetic tree of the 16S rRNA gene clones detected and their relatives retrieved from the databases is shown in Fig. 6. The samples of methanol, ethanol, acetate, lactate and pyruvate contained 18, 19, 15, 23, 17 and 12 dominant bands, respectively. Six dominant bands, Band A, D, I, Q, R and S, were uniform in all consortia (Fig. 4). Within these six bands, Band I and S are related with the bacteria involved in dechlorination (Dong et al. 2011; Rowe et al. 2008), Band Q and R are associated with *Pseudomonas* spp., Band A is associated with uncultured *Acidobacteria* clone 356G isolated from hydrocarbon contamination soil, while Band D is closely related with Acetoanaerobium noterae strain ATCC 35199. Band F and band G, associated with *Alcaligenes* sp. and unknown species, were only observed in pyruvate enrichment, while band J, associated with clone IA19 from chlorobenzenes degrading bacterial consortia, was only observed in

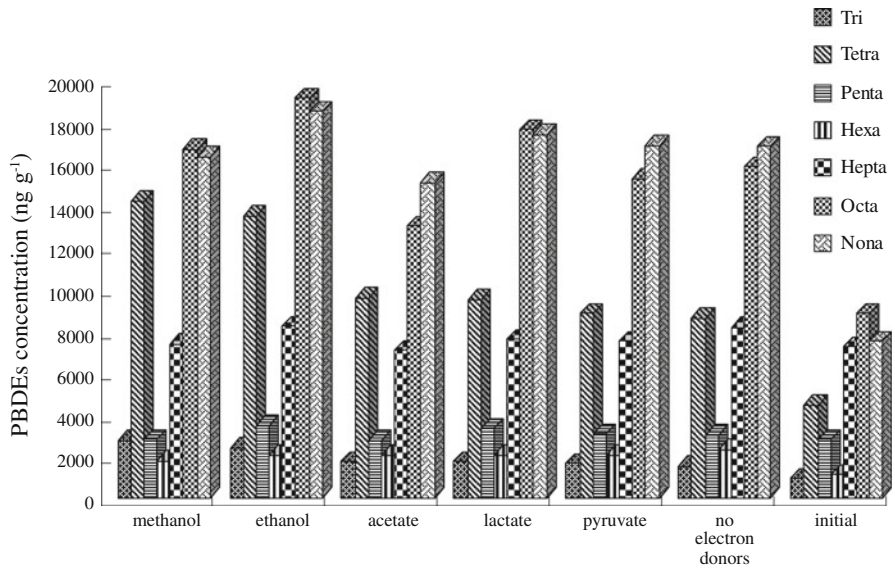

Fig. 3 PBDEs congeners profile of consortia under different treatment after incubation for 90 days. Initial represent day zero

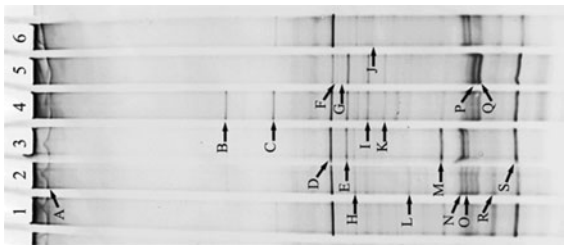

Fig. 4 DGGE profiles of 16S V6 rRNA genes derived from different electron donors-amended consortia. The DGGE bands designated A–S were purified and subjected to sequence analysis (see Table 1)

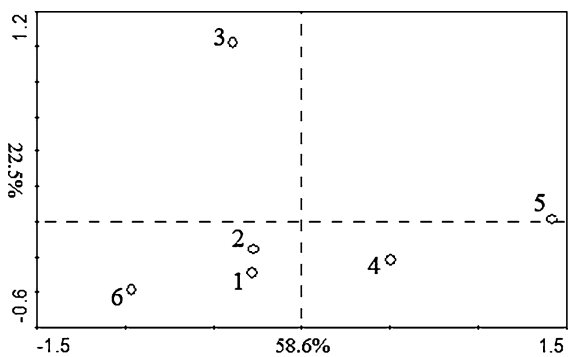

Fig. 5 Ordination plot produced from PCA of six different enrichments represented by *open circles*. *Number 1–6* represent methanol, ethanol, acetate, lactate, pyruvate, and no electron donor, respectively

the enrichment without any electron donors added. Band C, associated with PCE degrading enrichment cultures, was more abundant (accounted for 6.36%) in lactate enrichment, but less abundant in methanol enrichment (0.88%) and the control (1.9%), and completely disappeared in ethanol, acetate and pyruvate enrichments (Table 1; Fig. 4). Within the 19 dominant bands detected by DGGE gels, six of them were identified as *Pseudomonas* spp. (Band E, L, O, P, Q, R) (Table 1) and the abundance of Band R was correlated with the biodegradation rate of BDE-209 in different consortia. The results suggest electron donors have substantial impacts on the composition and structure of enriched microbial communities and the bacteria closely related with *Pseudomonas* spp. may play key role in PBDEs biotransformation.

Relationship between microbial communities and hydrogeochemical parameters

To better understand the relationships between the functional community structure and the hydrogeochemical parameters, RDA was performed using DGGE data and environmental parameters for each sediment sample as covariables. The microbial community composition could be affected by hydrogeochemical parameters such as pH, total organic carbon (TOC), total nitrogen (TN), chemical oxygen demand

Table 1 Phylogenetic assignment of DGGE clones isolated from microcosms

Band	Phylum	Closest relative	Accession no.	Similarity (%)
A	Acidobacteria	Uncultured bacterium clone 356G, hydrocarbon contamination soil	AY571789.1	90
B	Unknown	Clone 37B_038, anaerobic microbial degrading short-chain fatty acids	EU156224.1	97
C	Unknown	Clone DPF04, PCE degrading enrichment cultures	GQ377124.1	100
D	Firmicutes	Acetoanaerobium noterae strain ATCC 35199	GU562448.1	99
E	Gammaproteobacteria	*Pseudomonas aeruginosa* strain ZFJ-5	EU931560.1	99
F	Betaproteobacteria	Biodegradation of dichloromethane in an estuarine environment	AF430122.1	95
G	Unknown	Anaerobic microbial community degrading short-chain fatty acids	EU156224.1	99
H	Clostridia	Direct biological conversion of electrical current into methane	EU812216.1	99
I	Unknown	Bacterium culture clone DPF35, PCE degrading enrichment cultures	GQ377131.1	91
J	Unknown	Clone IA19, chlorobenzenes degrading bacterialconsortia	AJ488072.1	94
K	Gammaproteobacteria	UASB_TL22, 4-methylbenzoate-degrading methanogenic consortium	AF254403.1	93
L	Gammaproteobacteria	*Pseudomonas balearica* strain EH58	GU339285.1	98
M	Lentisphaerae	Uncultured Lentisphaerae bacterium clone 283ZH04	GQ451984.1	99
N	Gammaproteobacteria	Gamma proteobacterium enrichment culture clone BP8-1	GU594668.1	99
O	Gammaproteobacteria	*Pseudomonas* sp. Pyr41	GU951459.1	99
P	Gammaproteobacteria	*Pseudomonas* sp. BCBo7	EU140960.1	99
Q	Gammaproteobacteria	*Pseudomonas* sp. CB8	EU482912.1	98
R	Gammaproteobacteria	*Pseudomonas* sp. SCSWA09	FJ461426.1	98
S	Deltaproteobacteria	*Syntrophus* sp. clone D2CL_Bac_16S_Clone10, dechlorinating culture	EU498376.1	99

(COD), the concentrations of bromide and sulfate. The major geochemical parameters related to microbial activity on the 90th day were shown in Table 2. Three hydrogeochemical parameters, groundwater TN, the amounts of octa-BDE and deca-BDE, were selected from 18 parameters based on a forward selection procedure and variance inflation factors with 999 Monte Carlo permutations. The RDA ordination plot (Fig. 7) was well consistent with the PCA ordination patterns based on microbial community data, indicating that hydrogeochemical parameters well explained the variation among different samples. The consortia from control without electron donor amended and from methanol and ethanol enrichments were grouped together with 56.9% ($P = 0.049$) of the first axis explanation and 20.5% ($P = 0.0570$) of the second axis explanation, respectively. Within these three hydrogeochemical parameters selected, deca-BDE was identified as the most important factor, which was significantly and independently explained 40% ($P = 0.049$) of total variance, while octa-BDE and TN could explained 25% and 17% of total variance, respectively. These results suggest that the groundwater TN and the amounts of deca-BDE and octa-BDE appear to be key factors shaping microbial communities for PBDE-debromination.

Discussion

Biostimulation with the amendment of electron donor is a promising strategy for bioremediation of contaminated environment. PBDEs have become ubiquitous environmental contaminants due to their widespread use. Although microbial reductive debromination of PBDEs has been studied previously, there is no information about the effect of electron donors on the degradation of PBDEs. In this study, five common electron donors were used to analyze the effects of electron donor on the microbial structures and their PBDEs-debromination capacities, and the relationship between microbial community structure and hydrogeochemical parameters were also detected.

It was found that the initial sediment contained enough carbon sources to support the debromination of PBDEs for 90 days and the supplementary of

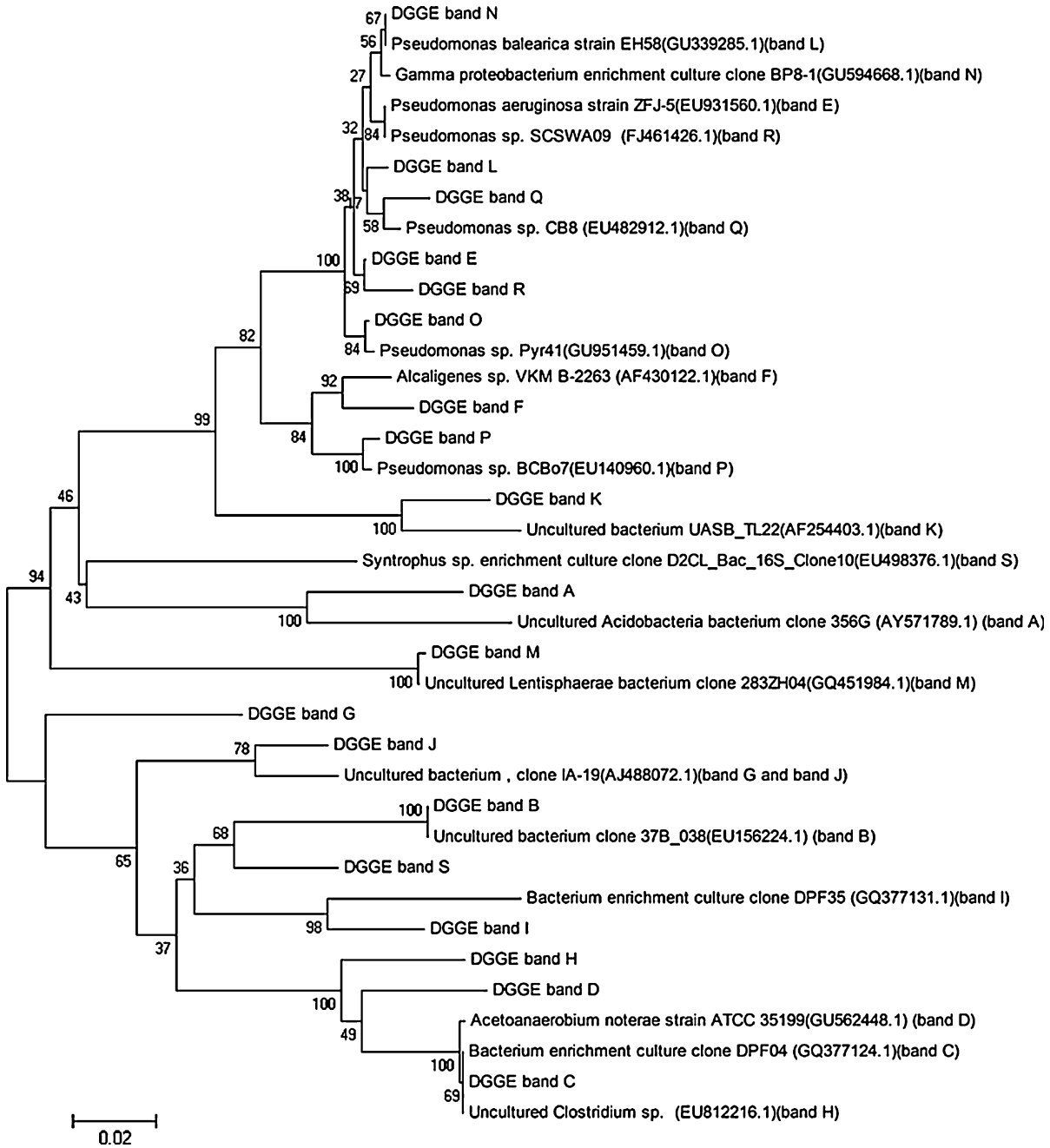

Fig. 6 A phylogenetic tree of the 16S rRNA gene clones detected and their relatives retrieved from the databases

electron donor did not improve even inhibit the biodebromination rate. Obvious differences in the profile of PBDEs degradation products were observed in the consortia with different electron donor treatments, and BDE-154 was only detected in the treatments added with methanol, ethanol or acetate. For the most dominant and highest brominated PBDE, BDE-209, obvious degradation was detected after 90-day incubation compared to the initial profile of PBDEs. However, lower degradation rates of BDE-209 were observed when acetate, lactate or pyruvate was added. This phenomenon is consistent with the

Table 2 Major geochemical parameters of different amendment microcosms (day 90)

Parameters	Abbreviation	Eletron donors					
		Methanol	Ethanol	Acetate	Lactate	Pyruvate	No electron donors
Supernatant							
pH	pH	6.93	6.711	7.11	6.816	6.702	7.046
Conductivity	U-cond	3800.00	4000.00	4600.00	4600.00	4600.00	4000.00
TOC (mg/l)	U-TOC	97.68	358.08	385.53	568.60	413.10	91.65
COD (mg/l)	U-COD	249.00	1105.00	960.00	1745.00	1185.00	478.50
TN (mg/l)	U-TN	256.28	240.58	261.90	253.00	266.70	254.43
Bromide (μg/l)	U-bromide	425.22	445.22	463.48	480.87	420.87	501.30
Sulfate (mg/l)	U-sulfate	5.25	1.44	9.98	10.02	0.64	1.059
Nitrate–N (μg/l)	U-nitrate	0.042	0.04	0.04	0.05	0.08	0.37
Nitrite-N (μg/l)	U-nitrite	0	0	0.92	0	0	1.76
Sediment							
TOC (mg/l)	S-TOC	12.40	10.95	10.90	11.30	10.90	10.10
Tri-BDE (μg/g)	Tri	2757.70	2373.73	1742.65	1744.91	1646.82	1502.24
Tetra-BDE (μg/g)	Tetra	14141.05	13441.46	9575.62	9480.50	8821.96	8566.82
Penta-BDE (μg/g)	Penta	2792.07	3450.02	2766.98	3306.89	3055.04	3030.12
Hexa-BDE (μg/g)	Hexa	1794.75	2054.73	2051.94	2042.88	2015.24	2290.64
Hepta-BDE (μg/g)	Hepta	7338.80	8196.41	7040.32	7550.34	7475.59	8132.81
Octa-BDE (μg/g)	Octa	16617.64	19081.08	12956.94	17574.26	15221.95	15782.64
Nona-BDE (μg/g)	Nona	16306.20	18465.62	15036.27	17329.28	16807.46	16776.99
Deca-BDE (μg/g)	Deca	74088.71	84074.53	71380.43	81252.33	86408.22	71212.52

results observed by Chang et al. (2004), which also found that the addition of acetate, lactate or pyruvate inhibited nonylphenol biodegradation. We also found that the abundances of most PBDEs, such as nona-BDE, octa-BDE, hepta-BDE, hexa-BDE, or penta-BDE, deceased when electron donors added. As we know that reductive debromination of BDE-209 could provide a significant source of lesser-brominated PBDEs, which is considered more toxic than deca-BDE (Lorber 2008), although the risk assessments of BDE-209 is still continuing. These results suggest that the addition of electron donor will affect the transformation rate of PBDEs, especially stimulate the degradation of lesser-brominated PBDEs, although the addition of acetate, lactate or pyruvate will inhibit BDE-209 biodegradation in some degree.

Knowledge of microbial community composition and structure in relation to the addition of electron donors and environmental parameters is important for designing successful bioremediation strategy. It is previously reported that the bacterial communities changed immediately and irreversibly with the amendment of BDE-153 or -154 and the addition of trichloroethene (TCE) (Lee and He 2010) and primer compounds (e.g.,4-bromobenzoic acid) improved PBDEs degradation (Gerecke et al. 2005). In this study, PCR-DGGE analysis showed the difference in microbial community structure among different communities enriched with different electron donors. The consortia enriched on methanol were similar to those on ethanol due to similar chemical characteristics of the electron donors. This result was also confirmed by PCA analysis based on the DGGE profile. Most of dominant DGGE bands were identified to be closely related with *Pseudomonas* spp., the powerful organisms for degrading the recalcitrant organic compounds, such as dibenzothiophene (Caro et al. 2008), *p*-chlorobiphenyl, 2- and 4-bromobiphenyl (de Boer et al. 2000). Our recent results also show that *Pseudomonas* spp. have the capacity for BDE-209 debromination (unpublished data), which suggested that *Pseudomonas* spp. may be the predominant

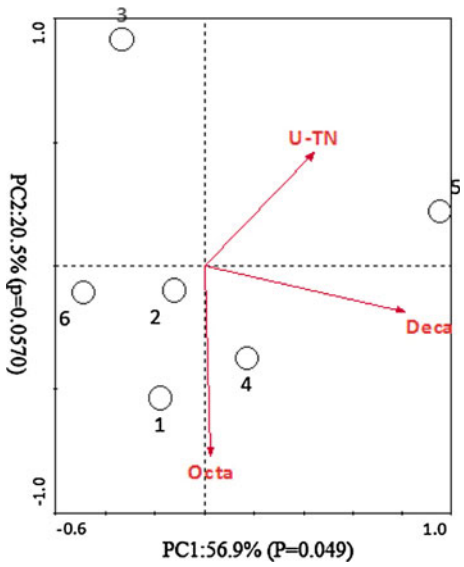

Fig. 7 Biplot of RDA of the consortia enriched by five different electron donors on day 90. *Open circles* represent samples collected from six consortia. Descriptors (*arrows*) are the concentration of geochemical parameters TN in supernate, deca-BDE, octa-BDE in sediment. Number *1–6* represent methanol, ethanol, acetate, lactate, pyruvate, and no electron donor treatments, respectively

bacteria for PBDEs degradation. No *Dehalococcoides* species was detected by DGGE in our study, although *Dehalococcoides* was found to be responsible for the biodegradation of many kinds of organohalide compounds (He et al. 2006). The microbial community structures detected by DGGE could be well explained by deca-BDE, octa-BDE and TN. Deca-BDE is the most dominant congener in all of the culture systems, octa-BDE is one of the most toxic congeners (de Wit 2002), and the TN in system will be the important nutrient for microorganism growth coupling PBDEs degradation.

In conclusion, this study showed that the addition of exogenous electron donors could affect the biotransformation rate of PBDEs by changing the microbial community composition and structure. The concentrations of deca-BDE, octa-BDE and TN in the system may be the important factors shaping the microbial community structures. To our best knowledge, this is the first study on the effects of electron donor on microbial PBDEs transformation. To well understand the relationships between microbial community structure and environmental parameters, high throughput sequencing approach was needed to reveal the microbial composition.

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