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Organic carbon accumulation capability of two typical tidal wetland soils in Chongming Dongtan, China

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Abstract

We measured organic carbon input and content of soil in two wetland areas of Chongming Dongtan (Yangtze River Estuary) to evaluate variability in organic carbon accumulation capability in different wetland soils. Observed differences were investigated based on the microbial activity and environmental factors of the soil at the two sites. Results showed that the organic carbon content of wetland soil vegetated with *Phragmites australis* (site A) was markedly lower than that with *P. australis* and *Spartina alterniflora* (site B). Sites differences were due to higher microbial activity at site A, which led to higher soil respiration intensity and greater carbon outputs. This indicated that the capability of organic carbon accumulation of the site B soils was greater than at site A. In addition, petroleum pollution and soil salinity were different in the two wetland soils. After bio-remediation, the soil petroleum pollution at site B was reduced to a similar level of site A. However, the culturable microbial biomass and enzyme activity in the remediated soils were also lower than at site A. These results indicated that greater petroleum pollution at site B did not markedly inhibit soil microbial activity. Therefore, differences in vegetation type and soil salinity were the primary factors responsible for the variation in microbial activity, organic carbon output and organic carbon accumulation capability between site A and site B.

Key words: Chongming Dongtan; organic carbon accumulation; wetland soil; microbial activity

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Introduction

Wetland eco-systems provide substantial economic benefits to human societies and also have important ecological and environmental functions such as atmospheric regulation (Mitsch and Gosselink, 2000). Natural wetlands, which are primary carbon sinks, are usually characterized by high biomass, low temperature, high humidity, weak microbial activity, and hence a low carbon dioxide release rate (Friborg and Soegaard, 2003). Previous studies of wetlands as carbon sources and sinks have primarily focused on inland wetlands, especially inland peat wetlands in high latitudes of the northern hemisphere (Strom *et al.*, 2007; Bubier and Moore, 1994). As concern about global warming has intensified, however, scientists have become interested in the soil respiratory processes and carbon sinks of coastal salt marsh wetlands. Heinsh *et al*. (2004) reported that net ecosystem exchange and gross ecosystem production ranges from –7.3 to 12.3 g CO_2/(m^2·day) (net gain of CO_2). Liu *et al.* (2007) and Moreno-Mateosa *et al.* (2008) reported that soil organic carbon input of *Spartina alterniflora* salt marsh and *Phragmites australis* wetlands is similar, at about 0.771 and 0.653 g/m^2 per year, respectively.

Chongming Dongtan wetland is an important young tidal wetland of the Yangtze River Estuary. Recent studies on the ecological functions of Chongming Dongtan have focused on biodiversity conservation and carbon storage capacity of wetland vegetation, as well as soil organic carbon content (Gan *et al.*, 2009; Guo *et al.*, 2009). Chen *et al.* (2005) evaluated the effects of *S. alterniflora* invasions on the benthic macro-invertebrate community at Chongming Dongtan and found they reduced species diversity and changed the nutritional group structure significantly. Mei and Zhang (2007) found that *P. australis* had better carbon fixing ability than *Scirpus mariqueter*, which is dominant in early successional vegetation stages. Other studies found that surface sediments of the Yangtze Estuary salt marsh had total organic carbon levels of 0.1%–0.7%, with organic sediment matter predominantly controlled by the organic particulates in the Changjiang Estuary (Zhou *et al*., 2006, 2007). In addition, the vegetation type and siltation/erosion characteristics of tidal wetlands

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in different parts of Dongtan have been studied (Gao and Zhao, 2006; Chen *et al.*, 2004). In Chongming Dongtan, *P. australis* and *S. mariqueter* show zonal distribution due to the invasion of *S. alterniflora* (Li *et al.*, 2006), which promotes siltation due to its developed root systems (Li *et al.*, 2006). Accordingly, wetlands in northern Chongming Dongtan, which are dominated by *S. alterniflora*, have better siltation ability than the southern Dongtan wetlands of Chongming Island, which are dominated by *P. australis* (Li *et al.*, 2005).

Differences in characteristics, such as vegetation type, in areas of Chongming Dongtan may lead to differences in microbial activity and intensity of soil respiration, resulting in variation in organic carbon cumulative capability and carbon sink and atmospheric regulation abilities in the wetlands. To date, however, few studies have been conducted to evaluate the variability in organic carbon accumulation capability of different types of wetland soils in Chongming Dongtan.

Carbon accumulation in wetland soil is determined by differences in carbon input and output. If organic carbon input from vegetation is similar among different types of wetlands, the organic carbon cumulative capability of different types of wetland soils can be determined by analyzing the soil's organic carbon content. Carbon output capability of different soils can be determined by soil respiration intensity, which is dominated by microbial respiration and activity (Wang *et al.*, 2003).

In this study, two Chongming Dongtan wetlands with different soil deposition characteristics and vegetation types were selected to evaluate variability in organic carbon cumulative capability. In addition, possible reasons for differences were identified. Our results will provide valuable information for management decision-making and improvement of carbon sink capability in the Chongming Dongtan wetlands.

1 Materials and methods

1.1 Field study and sampling

Chongming Dongtan is located in the east of Chongming Island (121˚050′E–122°005′E, 31°025′N–31˚038′N), China, and is the largest and youngest natural tidal wetland in the Yangtze River Estuary. It has a northern subtropical ocean climate, with an average annual temperature and precipitation of 15.3°C and 1117.1 mm, respectively. Chongming Dongtan is a typical herbaceous temperate tidal salt marsh wetland, with a general community succession from the beach to a *Scirpus mariqueter* community, and to a *S. alterniflora* and *P. australis* community.

A field survey was conducted from January to March, 2007. The two study sites were selected based on deposition conditions and vegetation distribution (sites A and B; Fig. 1), which differ substantially. Partly eroded Site A is located at Tuanjiesha in southeastern Dongtan and is dominated by *P. australis*. Silted Site B is located at Beibayao in northern Dongtan and consists of a mixture of *S. alterniflora* and *P. australis*. The average particle diameter of the sandy soil at site A and B is 6–17 and 4–12 μm, respectively. The selected sites were appropriate to evaluate the natural biological capability of different wetland types.

As sediments of the two areas were all from the Yangtze River, parent soil material at site A and B are similar (Hou, 1992). According to the results of Li *et al.* (2009) and Yang *et al.* (1990), average annual dry weight of the aboveground biomass from *P. australis* and *S. alterniflora* in the Yangtze River Estuary salt marsh was about 1.96 and 1.91 kg/m^2 per year during the period of 1990–2008, respectively. In addition, Liu *et al.* (2007) and Moreno-Mateosa *et al.* (2008) reported that soil organic carbon input of *S. alterniflora* salt marsh and *P. australis* wetlands is about 0.771 and 0.653 g/m^2 per year, respectively. From this we assumed that soil carbon input at site A and B was about 0.712 and 0.653 g/m^2 per year, respectively, if the proportion of *S. alterniflora* and *P. australis* was 1:1 in area B. Obviously, there is little difference in the soil's organic carbon input among different wetland sites in Chongming Dongtan.

Three parallel transects with an interval of approximately 100 m were set up at each study site. Four sampling sites were selected along each transect from the levee to the sea, including sites located in the upper tidal zone, middle tidal zone, lower tidal zone, and the tidal flat zone.

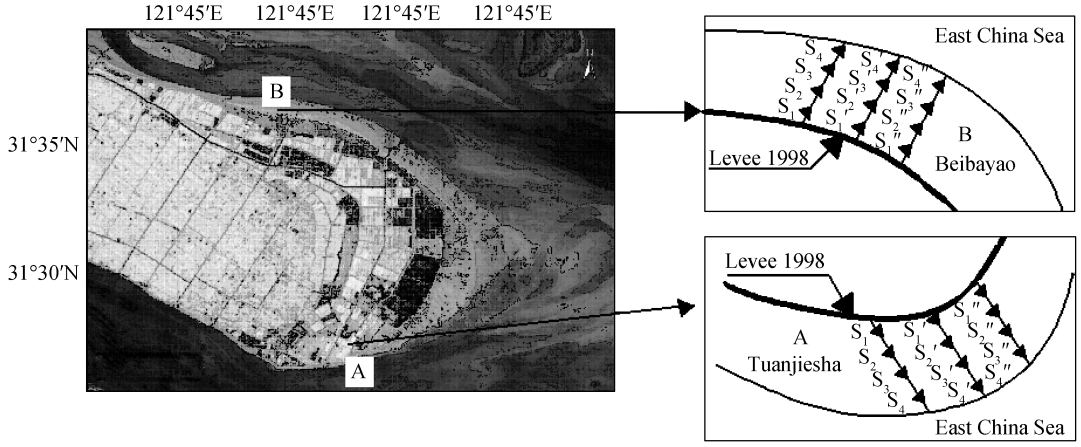

Fig. 1 Map of Chongming Island and study sites.

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The distance between each sample site was 50–100 m. Sub-surface soil samples (from –5 to –20 cm depth) were collected from each sampling site in April (spring), July (summer), September (autumn) and December (winter) (Cater and Gregorich, 2007).

The fresh soil samples were stored in valve bags (10#, 240 mm × 340 mm, Shanghai Ancheng Plastic Science Technologies Co., Ltd., China) at 4°C. Aliquots of each soil sample were used to determine the culturable microbial biomass, soil respiration intensity, and soil microbial diversity. The remainder of each soil sample was air-dried, and the roots, visible plant remains, and anthropogenic materials were removed. The samples were then ground and screened through a 100 mesh soil sieve and stored at 4°C for determinations of organic carbon content, soil invertase activity, petroleum content, and total water-soluble salt.

1.2 Soil bioremediation study

Soil polluted by petroleum was collected from site B and stored at 4°C. To simulate the environmental conditions of *in-situ* remediation, the bioremediation experiment was conducted in outdoor pots under conditions similar to the Yangtze River Estuary in December 2007, which had an average temperature and rainfall of 7.2°C and 205 mm, respectively. Petroleum pollution in the wetland soil was remediated using high efficiency petroleum degradation microorganisms isolated from vicinal contaminated soil, with a degradation capability of 640 mg /(L·day) petroleum (Wang *et al.*, 2006). Specifically, approximately 1 kg of soil collected in autumn 2007 was set in a pot and inoculated with 1% (*V*/*W*) (1.7×10^6 CFU/g) of highly efficient petroleum degrading microbial inoculum. The culturable microbial biomass, organic carbon content, and enzyme activity were analyzed after bioremediation was conducted for different time periods. The pot bioremediation experiment was conducted in triplicates and soil from site B not inoculated with high efficiency petroleum-degradation microorganisms was used as a control.

1.3 Analytical methods

1.3.1 Physical and chemical indices

Soil salinity and moisture content were determined according to standard methods (Carter and Gregorich, 2007). Soil particle diameter was measured using an EyeTech Particle size and shape analyzer (Hao *et al*., 2009).

Organic carbon content was determined using a TOC elemental analyzer (Shimadzu, TOC-VCPN, Japan) (Haeryong and Heechul, 2003). Briefly, the air-dried soil samples were titrated with 0.1 mol/L of hydrochloric acid in a sample boat, placed in an oven (105–110°C) for 4 hr, and then maintained at room temperature for 24 hr. The samples were then directly analyzed using the TOC elemental analyzer.

1.3.2 Microbial activity indices

Culturable microbial biomass is closely related to total microbial biomass in soil, and soil invertase activity is an indicator of microbial activity. Microbial respiration intensity is a comprehensive index that reflects organic carbon degradation capacity resulting from microbial metabolism. Therefore, culturable microbial biomass, soil invertase activity, and microbial respiration intensity were all tested to determine microbial activity of the two wetland soils.

Culturable microbial biomass of the soils was determined by colony forming units (CFU) using the Dilution plate method (Sutton, 2006). The microorganisms were cultured on Salmonella-Shigella medium at a constant temperature of 30°C for 3 days, after which the colonies were counted.

Soil invertase activity was determined using chemical methods (Gopal, 2007).

Aerobic soil microbial respiration intensity was determined at 28°C over 3 days using gas chromatography (GC214B, Shimadzu, Japan). After the logarithmic growth phase, the microbial numbers in the culture bottle gradually became stable and eventually reached a constant value, which implies that microbial respiration intensity was stable. In this study, the period of logarithmic growth phase was selected to measure respiration, and the amount of carbon dioxide released from the microorganism per hour per gram of soil was calculated. The anaerobic respiration intensity was determined by CO_2 production using gas chromatography after the soil samples were incubated for 16 days at 28°C under anaerobic conditions.

1.3.3 Analysis of microbial diversity

As viable but not culturable microorganisms were present in soil, PCR-DGGE was used to analyze prokaryotic microbial diversity of the soils, which was determined by identification of the 16S rDNA fingerprint (Wang *et al.*, 2008). Briefly, total soil DNA was extracted using a soil DNA kit (D5625-01, OMIGA, USA) according to the manufacturer's instructions. The 16S rDNA V3 region of total soil DNA was PCR amplified using universal primers 341f (5′-CGCCCGCCGCGCGCGGCGGGCGGGGCGGGGGCACGGGGGGCCTAGGGGAGGCAGCAG-3′) and 534r′ (5'-ATTACCGCGGCTGCTGG-3′), which produced a fragment of about 190 base pairs. The primers were produced by the Shanghai Sangon Biological Engineering Technology & Services Company, China. The reaction was conducted by subjecting the reaction mixture (25 μL of 10× PCR buffer; one unit of Taq DNA Polymerase; 1.0 μL of each DNTP (2.5 mmol/L), the mixture of equal amount ATP, TTP, GTP and CTP; 0.5 μL of each primer (10 μmol/L), and 50 ng DNA (as the template) to the following conditions: 94°C for 3 min, followed by 30 cycles at 94°C for 30 sec, 56°C for 30 sec, 72°C for 30 sec and a final extension at 72°C for 10 min. The obtained PCR product was then analyzed by denaturing gradient gel electrophoresis (DGGE) using the D-Code system (Bio-Rad, USA) with a 10% polyacrylamide gel and 40%–65% denaturing gradient (100% denaturing was equivalent to 7 mol/L urea and 40% deionized formamide). Each lane contained 25 μL of PCR product (about 800 ng DNA), and electrophoresis conditions were 60°C, 100 V, 1×

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TAE (diluted by 50 × TAE, 242 g Tris base, 57.1 mL glacial acetic acid, 100 mL 0.5× EDTA, pH 8.0). After 16 hr of electrophoresis, the gel was stained with ethidium bromide (EB) for 15 min and then photographed by UV light. The DGGE fingerprints were then analyzed using Smart View software and the bio-diversity of each sample was evaluated based on the Shannon index, determined as follows:

$$H = -\sum_{i=1}^{S} P_i \log P_i$$

where, H is the Shannon-Weiner Index, S is the number of bands in the gel, and P_i is the relative abundance of the ith phenotype fraction.

Petroleum content was determined by ultrasound-UV extraction (Li and Li, 1999). All indices for each sample were measured in triplicates.

1.4 Statistical analysis

All data were analyzed using SPSS 13.0 software. Differences in organic carbon content, culturable microbial biomass, and invertase activity between the two wetland soils were analyzed using paired *t*-tests. Errors were indicated as standard deviation (SD) of the mean of triplicate parallel samples for each site.

2 Results

2.1 Soil organic carbon content and reserving capability of different types of wetlands

Soil organic carbon includes all animal and plant residues and various organic substances decomposed by microorganisms in the soil, and reflects the net difference between organic carbon inputs (from original sediments and the death of plants and animals) and organic carbon outputs (soil respiration).

Soil organic carbon content at site B was higher than at site A throughout the year (Fig. 2). Specifically, organic carbon content of soil at site B (approximately 2.74%) was much higher than the organic carbon content at site A (approximately 1.81%) (F = 4.475, P = 0.039). The organic carbon content of the two types of wetland soils varied seasonally.

Organic carbon content of both soils was highest in spring and lowest in summer and autumn. In addition, soil organic carbon showed a decreasing trend from the upper tidal to the tidal flat zone. A possible reason for this may be that lower tidal mudflat soils had little vegetation and a long water-logging time; therefore, organic carbon inputs of the lower tidal soils were very low. Organic carbon inputs into the high tide flat soils were, however, much higher. Another reason may be due to different clay content in the upper tidal to the tidal flat zone soils (Yang *et al.*, 2008). Our results showed that organic carbon of the upper tidal zone soil was higher than the lower tidal zone soil. The soil clay content in the upper tidal zone was higher than the lower tidal zone, which may result in higher organic carbon inputs in the soil of the upper tidal zone.

Despite the parent materials of site A and B soil being similar (soil particle diameter in site A and B range from 6–7 and 4—12 μm) and organic carbon inputs not differing significantly (Hou, 1992), carbon outputs from the soil at site B were lower than that at site A. The wetland soil at site B with mixed *P. australis* and *S. alterniflora* had a higher ability to retain organic carbon, while the wetland soil at site A with *P. australis* had a better ability to decompose organic carbon.

Soil respiration provides the main contribution to carbon outputs from soil, especially microbial respiration (Sicardi *et al.*, 2004). To determine the reasons for variation in organic carbon retention capability of different wetland soils, microbial activity and carbon output capability were studied.

2.2 Soil microbial activity of different types of wetlands

The average culturable microbial biomass and invertase activity of the soil from the two study sites (A and B) across the four seasons are shown in Fig. 3. The average culturable microbial biomasses of soil in sites A and B were 5.82×10^7 and 3.99×10^7 CFU/g, respectively, while the invertase activity was 0.24 mL of 0.05 mol/L $Na_2S_2O_3$/g and 0.10 mL of 0.05 mol/L $Na_2S_2O_3$/g, respectively. Both culturable microbial biomass and invertase activity were significantly higher at site A than site B (P = 0.033 and 0.005, respectively). The average soil microorganism respiration intensity (including both aerobic and anaerobic respiration) of site A (at 0.523 mg C/(g soil·day)) was also greater than that of site B (0.450 mg C/(g soil·day)).

Obviously, the higher microbial activity and soil microorganism respiration intensity at site A may result in higher soil organic carbon output, and hence lower soil organic carbon content.

The DGGE fingerprint and Shannon diversity index for each sample are shown in Fig. 4 and Table 1. According to the DGGE fingerprint, average band densities of site A (45) and B (36.5) were significantly different (P = 0.021). This indicated that the dominant microorganisms at site A were more diverse than at site B. Average Shannon diversity index at sites A and B was 3.246 and 2.026, respectively.

The results shown in Fig. 4 and Table 1 suggest there were differences in the prokaryotic microbial community

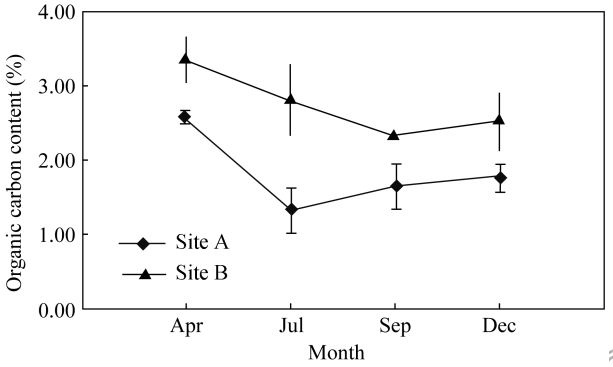

Fig. 2 Seasonal variation in organic carbon content. Organic carbon content at each point is the average of 12 samples (four points and three replicates).

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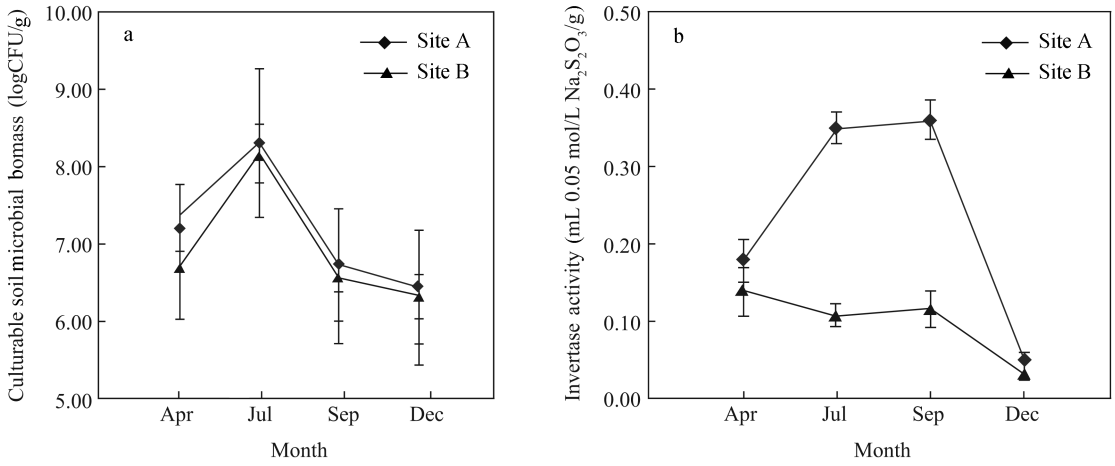

Fig. 3 Seasonal variation in soil culturable microbial biomass (a) and soil invertase activity (b). Soil culturable microbial biomass and invertase activity at each point is the average of 12 samples (four points and three replicates).

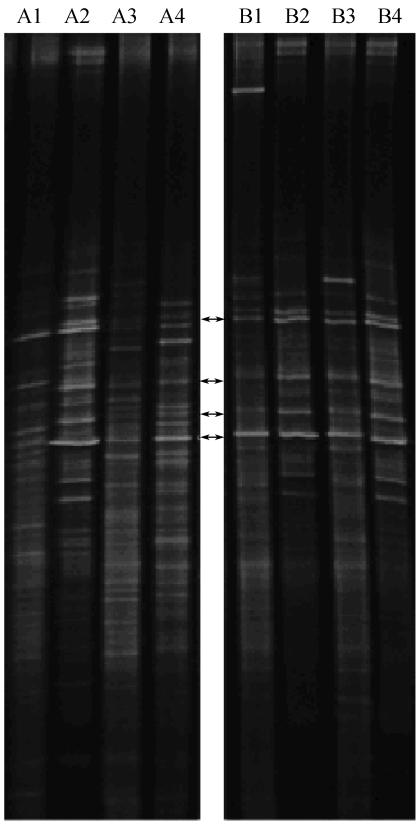

Fig. 4 PCR-DGGE fingerprint atlas. Sample A*i* and B*i* are the mixed sample of S_i, S_i' and S_i", of which *i* is the serial number of the samples in Fig. 1. Same bands are indicated by the black arrows in the middle of the two pictures.

structure between the soils at the two sites, with site A more diverse and abundant than site B.

In addition, the prokaryotic microbial diversity index from the lower beach to the upper tidal zone at the two sites was different, which may be related to differences in vegetation type, density, and fertility.

Increased culturable microbial biomass and prokaryotic microbial diversity implied that environmental conditions at sites A may be more suitable for the growth of microbial species, resulting in its higher microbial enzyme activity, soil respiration intensity, and organic carbon output.

Table 1 Analysis of DGGE fingerprint atlas

Sample	DGGE band	Shannon index
A1	31 ± 2	2.43 ± 1.05
A2	30 ± 1	2.91 ± 0.39
A3	42 ± 3	4.16 ± 1.20
A4	37 ± 3	3.49 ± 1.48
Average Shannon index at site A		3.25 ± 0.91
B1	47 ± 5	3.18 ± 0.17
B2	21 ± 2	1.42 ± 0.38
B3	32 ± 2	2.07 ± 0.29
B4	17 ± 1	1.44 ± 0.59
Average Shannon index at site B		2.03 ± 1.15

Each value was the average of three samples. Sample A*i* and B*i* are the mixed sample of S_i, S_i' and S_i", of which *i* is the serial number of the samples in Fig. 1.

2.3 Environmental factors influencing soil microbial activity

Different vegetation types can result in differences in soil microbial properties (Saetre, 1999; Kaiser *et al.*, 1992). In addition to vegetation type, however, soil microbial activity is also correlated with other factors such as soil pollutant concentrations and salinity (Jonas *et al.*, 2004).

To investigate other environmental factors affecting soil microbial activity and carbon output, petroleum concentrations and soil salinity at sites A and B were measured. The petroleum pollutants at site A and B, which primarily consisted of alkanes and a small amount of aromatics, are shown in Fig. 5. Both the concentration of petroleum hydrocarbons and the salinity of the soil at site B were greater than those at site A. These results indicated that the higher concentrations of petroleum pollutants and salt in site B soil might decrease microbial activity to a certain extent.

To determine whether petroleum pollution inhibited microbial activity at site B, high-efficient petroleum degrading bacteria were applied to bio-remediate the petroleum polluted soil. The microbial activity of the remediated soil was then compared with soil at site A.

Prior to bioremediation, the petroleum content of site B soil was about 22.23 μg/g. During bioremediation, the petroleum hydrocarbon content of soil gradually decreased

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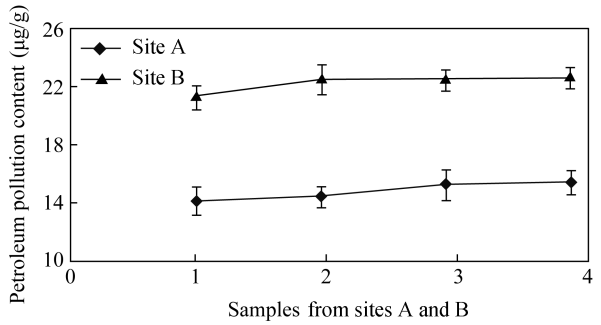

Fig. 5 Petroleum pollution content at sites A and B. Samples 1, 2, 3 and 4 on the X-axis are the samples from the upper tidal zone to the beach, and each points was the mixed sample of S_i, S_i' and S_i", of which *i* is the serial number of the samples in Fig. 1.

and became stable (14.88 μg/g) after remediation for 21–28 days. Although culturable microbial biomass in site B soil was higher after remediation than before, the extent of increase was likely not significant since the soil was inoculated with highly-efficient microorganisms (1.7×10^6/g soil) which can reproduce during remediation. Therefore, the culturable microbial biomass and invertase activity of site B soil after remediation were still lower than those of site A without remediation (Table 2).

These results imply that the extent of petroleum pollution at site B did not significantly inhibit soil microbial activity, and the higher salinity in site B may be the reason for the observed inhibition of microbial activity (Fig. 6).

The salinity at sites A and B differed markedly due to their location, with site A facing the Yangtze River and site B facing the East China Sea.

3 Discussion

3.1 Effect of soil microbial activity and community structure on soil organic carbon accumulation capacity

Soil microbes are important in regulating soil organic carbon content, degrading harmful compounds, biochemical cycling, and the development of soil structure, all of which relate to soil quality (Sicardi *et al.*, 2004; Zhao *et al.*, 2005). Thus, soil microbes are relevant to all soil processes and environmental effects (Groffman *et al.*, 2001).

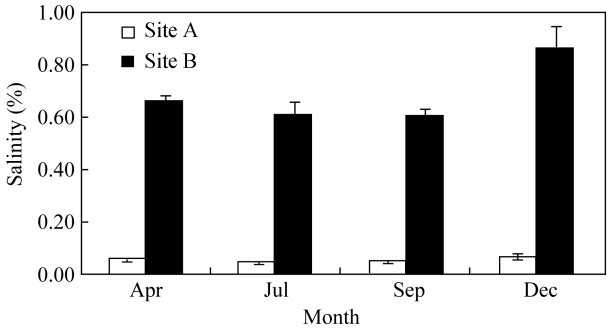

Fig. 6 Salinity of the wetland soils from sites A and B.

Generally, soil respiration intensity is stronger with increasing microbial biomass and higher microbial enzyme activity in the soil. Perucci (1992) reported that amylase, arylsulfatase, catalase, deaminase, dehydrogenase, phosphatase, and protease activity increased markedly with increasing microbial biomass. Shen *et al.* (1997) found that soil respiration rate was closely related to microbial biomass. In our study, soil CFU and microbial enzyme activity at site A was much higher than that at site B, resulting in higher soil respiration intensity at site A. Consequently, organic carbon output at site A was much higher than that at site B.

Rice (2002) indicated that differences in soil microbial community could affect the ratio of carbon converted to carbon dioxide or to soil organic carbon. Drenovsky (2004) found differences in the microbial community with changes in soil carbon and moisture content in California agriculture soils. In the present study, the prokaryotic microbial community structures of the two typical wetland soils were different, which may result in differences in the microbial carbon metabolism capacity. Specific species need to be identified, however, and their effects on carbon metabolism need to be studied further.

The microbial activity and community diversity observed in this study indicate that the vegetation at site A was more suitable for the growth and metabolism of microorganisms, which result in higher carbon output as the microorganisms convert organic carbon into microbial cells and CO_2. Considering the lower soil organic carbon content at site A than at site B and the similar organic carbon inputs between the two sites, weaker microbial activity is likely the primary reason for the higher organic carbon accumulation capability of the soil at site B. In other words, the silting wetland soil with *P. australis* and *S. alterniflora* (site B) had higher carbon accumulation capacity than the eroding wetland soil with *P. australis* (site A).

In addition, culturable microbial biomass and invertase activity in the two types of wetland soils showed similar seasonal variations, with higher levels from July to September and lower in December. This seasonal variation likely relates to the weather conditions in the Yangtze estuary. From July to September, the weather is suitable for soil microbe growth, which leads to large numbers of microbes, higher enzyme activity, and consequently higher soil respiration and lower soil organic carbon content

Table 2 Comparison of culturable microbial biomass and invertase activity before and after bioremediation of the samples collected in September

Experiments	Culturable microbial biomass ($\times 10^6$ CFU/g)	Invertase activity (mL 0.05 mol/L $Na_2S_2O_3$/g)	Organic carbon (%)	Oil content (μg/g)
Before bioremediation of site B soil	3.67 ± 1.78	0.12 ± 0.04	0.43 ± 0.04	22.23 ± 0.24
After bioremediation of site B soil	5.54* ± 1.89	0.10 ± 0.01	0.42 ± 0.06	14.70 ± 0.17
Site A	5.61 ± 2.01	0.35 ± 0.03	1.68 ± 0.03	14.88 ± 0.13

*The inoculated highly-efficient microorganisms were deducted but without considering their reproduction.

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during these months (Fig. 2). Another reason for this seasonal variation may be related to changes in nutrient content (such as N and P) in seawater, with higher levels accelerating microorganism growth during the summer months (Lopez *et al.*, 1998).

3.2 Effect of environmental factors on microbial activity and organic carbon outputs of the soil

Many studies have found that vegetation type markedly affects soil microbial activity. Smolander and Kitunen (2002) found that birch stands show higher values for soil microbial characteristics than coniferous stands. Vegetation types influence soil microbial community magnitude, structure and catabolic diversity (Han *et al.*, 2007). In our study, microbial activity and community differed significantly in soils from site A with *P. australis* than site B with a mixture of *S. alterniflora* and *P. australis*

Except for vegetation type, environmental factors such as harmful pollutants and salinity of the soil may also influence soil microbial enzyme activity. Labud *et al.* (2007) found that contamination of soil with oil hydrocarbons negatively affected soil ecosystems and microbial activity. Rietz and Haynes (2003) reported that soil salinity had extremely adverse affects on soil microbial biomass and activity. High chloride ion concentration associated with increased salinity may also affect microbial community and activity (Milan *et al.*, 2008).

Results from our study found, however, that the extent of petroleum pollution present did not inhibited microbial activity markedly. Consequently, the differences in microbial activity between sites A and B may be related to differences in vegetation type and salinity. Therefore, the soil, mixed vegetation of *P. australis* and *S. alterniflora*, and higher salinity may be the primary factors responsible for the lower microbial activity of soil at site B, and hence the higher soil organic carbon accumulation capability.

4 Conclusions

Organic carbon content in wetland soil with *P. australis* (site A in south Dongtan) was significantly lower than that with mixed *P. australis* and *S. alterniflora* (site B in north Dongtan), even though the carbon inputs of the two wetlands were the same. This implied that organic carbon accumulation capability of site B soil was greater than the soil at site A.

The high organic carbon accumulation capability of soil at site B was primarily due to its lower microbial activity, and hence soil respiration intensity. The soil conditions at site B were unfavorable for microbial growth and metabolism, and thus favorable for organic carbon retention and accumulation.

The petroleum pollution at site B might not markedly inhibit the microbial activity of the soil; therefore, differences in vegetation type and soil salinity are likely the main reasons for microbial activity differences between sites A and B soils, and hence the differences in organic carbon output and carbon accumulation capability of the soils from the two sites.

Acknowledgments

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