African Journal of Biotechnology Vol. 10(80), pp. 18425-18432, 14 December, 2011
Available online at http://www.academicjournals.org/AJB
DOI: 10.5897/AJB11.1911
ISSN 1684–5315 © 2011 Academic Journals

Full Length Research Paper

Seasonal changes in and relationship between soil microbial and microfaunal communities in a *Tamarix chinensis* community in the Yellow River Delta

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Accepted 21 September, 2011

The plant *Tamarix chinensis* is distributed along the coast of the Yellow River Delta in soils with high salinity. As the dominant local halophyte, it plays a unique role in modifying the local soil microenvironment. We investigated the effects of *T. chinensis* vegetative cover and the seasons on the soil microbe and microfauna communities in the Yellow River Delta. In April, June and October 2010, soil samples were taken from an estuary of the Yellow River. We measured microbiomass (using the soil chloroform fumigation extraction method), substrate induced respiration (SIR), and phospholipid fatty acids (PLFA). Microbe community structure and soil nematode species richness exhibited distinct seasonal variation. The levels of PLFAs, soil microbial biomass carbon (SMBC), microbial biomass nitrogen (SMBN) and SIR were lower in April than in October in *T. chinensis* sites. In June, there was a slight increase in the total abundance of PLFA and soil nematode diversity in *T. chinensis* sites. Stepwise regression analysis indicated that plant-feeding nematodes were a dominant factor for changes in soil microbial community composition, and soil moisture, soil organic carbon and fungal-feeding nematode capacity were secondary factors. The distinct seasonal changes in the soil microbe community composition were likely driven by changes in nematode trophic groups, soil moisture and soil organic carbon.

Key words: Microbial biomass, phospholipid fatty acids (PLFA), community diversity, nematode.

INTRODUCTION

Plants and soil microorganisms generally have a strong functional linkage as producers and decomposers, respectively. Plants can affect the soil biota by influencing the quantity and quality of organic substrates that reach the soil (Viketoft et al., 2005). On the other hand, the soil microbial community plays a central role in nitrogen fixation, nutrient cycling, production of phytohormones, and soil formation in terrestrial ecosystems (Allena and Schlesinger, 2004). In addition, the activity and diversity of soil microorganisms are directly influenced by changes in the soil environment, nutrient availability, soil texture, and type of vegetation cover (Jangid et al., 2008). Therefore, clarifying the function and role of soil biota is critical to understanding the effects of various disturbances on ecosystem-level processes.

The Yellow River Delta is the youngest wetland ecosystem in the warm-temperate zone in China. The Yellow River Delta is unique among wetlands: it is being formed by the deposition of silt from the new wetlands, with an annual growth rate of 20 to 30 km^2. The area is covered mainly by wet and saline soil low in nutrients, and the amount of evaporation is greater than the amount of precipitation (Cui et al., 2009). Therefore, large areas of saline soil remain to be developed in Yellow River Delta.

T. chinensis is one of the dominant salt tolerant plant species in the Yellow River Delta. It adapts to saline soils by regulating its salt balance through excretion of excess salts through foliar glands (Decker, 1961), and it promotes soil de-salinization around the plant (Glenn et al., 1998). In addition, *T. chinensis* can induce the

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formation of “fertile islands” with more favorable environmental conditions than the bare soil from which is derived.

Although, many studies have examined the effects of *T. chinensis* on soil parameters such as soil salinity, pH and nutrient availability, the effects of these soil parameters and microfauna on the microbial communities in *T. chinensis* areas have received less attention (Lesica and Miles, 2004). Over time, plants can alter their edaphic environment through the addition of organic matter and nutrient cycling (Ladenburger et al., 2006). The specific objectives of our experiment were (1) to examine the impact of *T. chinensis* communities on soil nematode and soil microbial properties; (2) to assess the effect of seasonal change on soil microbial parameters, and (3) to identify the main factors affecting the soil microbes.

MATERIALS AND METHODS

Study site and soil sampling

The study site was located in the Zhanhua City, in the northern region of the Yellow River Delta (37°46′47.4 to 37°56′21.4N, 118°11′36.9 to 118°12′16.0E). The Yellow River Delta has a temperate continental monsoon climate. The annual average temperature is 12.9°C, and the frost-free period lasts 196 days. The annual average rainfall is 596.9 mm, with annual evaporation of 1900 to 2400 mm (Li et al., 2009). The soil texture in the study sites was predominantly light and medium loam. The plant community composition was simple, and the aquatic vegetation was dominated by halophytes, which constituted over 85% of species present. Typical halophyte species in the wetland included Phragmites australis, *T. chinensis*, Suaeda salsa, and Aeluropus sinensis, and the distribution of vegetation was mainly determined by the degree of soil salinization. Five random areas dominated by *T. chinensis* and five corresponding control sites (free of vegetation) were sampled in April, June, and October 2010. The five sites under *T. chinensis* were located at 1 km intervals along a transect perpendicular to the coastline that extended from the coast to the inland. The open areas between *T. chinensis* plants were almost free from vegetation, and five sites were selected as controls. Each area was subsequently divided into four sub-areas for sampling. Soil samples were collected at depths of 0 to 40 cm in the center of each sub-area using a soil auger (inner diameter: 7.5 cm). In total, 120 soil samples were included in the analysis. After removal of stones and large plant residues, samples were placed into plastic bags and then transferred immediately into the sterile cooling boxes. The fresh soil samples were sieved with a 2 mm diameter mesh. One sub-sample of the composite soil was frozen at 4°C until nematode extraction and analysis of soil moisture, SMBC, SMBN, and SIR. Another sub-sample was frozen at -20°C until PLFA analysis. A third sub-sample was dried and subjected to soil parameter analyses within four weeks of sampling.

Soil parameter analysis

Soil pH was measured in 1:2.5 soil: distilled H_2O suspensions using a glass electrode (Thomas and Sparks, 1996). The soil moisture content of each sample was determined gravimetrically by weighing and drying in an oven at 105°C for 12 h. Soil organic carbon (SOC), NH_4^+-N, and NO_3^--N concentrations were determined using a Continuous Flow Analyzer (Skalar Scan^{++}). The concentration of available phosphorus (AP) was measured using the method described by Bray and Kurtz (1945).

Nematode extraction and examination

Nematodes were extracted from 100 g (fresh weight) of soil for each sample using a modified Baermann method, and the nematode population was expressed per 100 g dry weight soil. Before extraction in the Baermann funnels, each soil sample was briefly soaked in water to dissolve soil aggregates and facilitate active emigration of the nematodes. The sample was then quickly and carefully passed through a cascade of four sieves (50 µm each) to remove water and very fine soil particles. After extraction (48 h), nematodes were killed by heat and preserved in 4% formaldehyde (Hohberg, 2003). The extracted nematodes in each sample were counted and identified to the genus level, when possible, using an inverted compound microscope. Nematode genera were assigned to “trophic groups” according to Yeates et al. (1993): Bacterial-feeding, fungal-feeding, plant-feeding, and omnivores.

SMBC, SMBN and SIR analysis

SMBC and SMBN were measured using a fumigation extraction method (Brookes et al., 1985; Vance et al., 1987). If the soil moisture content was lower than 40%, it was adjusted to 55% prior to chloroform fumigation (Ocio and Brookes, 1990). Each sample was the equivalent of 25 g of soil (dry weight). Three samples were fumigated with ethanol-free $CHCl_3$ vapour for 24 h at 25. Following fumigant removal, the soil was treated with 100 ml of 0.5 M K_2SO_4, shaken for 1 h at 200 rpm and then filtered. At the same time, the other three non-fumigated portions were also extracted. The filtrates were analyzed for organic carbon using the dichromate oxidation method and for total N using the alkaline potassium persulphate digestion UV spectrophotometer method (Shi et al., 2006).

SIR was measured using an O_2 microcompensation apparatus (Scheu, 1992). The microbial respiratory response was measured at hourly intervals for 24 h at 22°C. SIR was calculated from the respiratory response to D-glucose (Heal et al., 1997).

Phospholipid fatty acids analysis

Microbial community composition was determined using extracting PLFA analysis with the method described by Frostegård et al. (1993). The soil samples were extracted and fractionated to collect the PLFAs, which were then transmethylated to their fatty acid methyl esters using alkaline methanolysis. With methyl non deaconate fatty acid (19: 0) as internal standard, the samples were analyzed on a Hewlett Packard 5890 gas chromatograph equipped with a flame ionization detector. The PLFA nomenclature used is presented by Rinnan et al. (2007). The relative abundance of each fatty acid was expressed as percentage of the peak area to the sum of total peak area in the chromatograph (mol %). The PLFA 18:2ω6, 9 was used to as a measure of fungal biomass, while the sum of PLFAs i15:0, a15:0, 15:0, i16:0, 16:1v9, i17:0, a17:0, 17:0, cyclo-17:0, 18:1v7 and cyclo-19:0 was used as a measure of bacterial biomass (Frostegård and Bååth, 1996).

Statistical analysis

Statistical analysis was performed using SPSS V.10.0 for Windows. In addition, PLFA profiles were analyzed by principal components analysis (PCA). The rest of the data were analyzed using one-way ANOVA followed by Duncan tests ($p \leq 0.05$). Relationships between

Table 1. Changes in soil characteristics in the *T. chinensis* community and control sites.

Site	Range	pH	Moisture (%)	NO_3-N (mg kg^{-1})	$NH4^+$-N (mg kg^{-1})	Available P (µmol$h^{-1}g^{-1}$OM)	SOC (mg kg^{-1})
T. chinensis	Apr	8.38 (0.04)	1.25 (0.02)	1.385 (0.013)	5.107 (0.034)	3.66 (0.27)	2.40 (0.15)
	Jun	8.38 (0.04)	1.51 (0.05)	1.817 (0.025)	5.423 (0.136)	7.45 (0.21)	2.86 (0.11)
	Oct	8.32 (0.03)	1.17 (0.09)	2.899 (0.017)	6.106 (0.074)	8.54 (0.27)	3.66 (0.18)
Control Sites	Apr	8.62 (0.02)	1.46 (0.04)	1.385 (0.008)	5.076 (0.050)	2.34 (0.13)	2.20 (0.23)
	Jun	8.66 (0.03)	1.64 (0.07)	2.263 (0.016)	5.489 (0.132)	4.28 (0.12)	2.13 (0.26)
	Oct	8.62 (0.02)	1.13 (0.09)	2.662 (0.011)	6.300 (0.049)	4.05 (0.10)	2.04 (0.13)

soil parameters and soil microbial community composition were analyzed using stepwise regression analysis.

RESULTS

Soil parameters

The soils were moderately alkaline to neutral, and the pH was significantly lower in the plant-covered soil than in the bare control sites (Table 1). Soils collected from different sites exhibited pH values ranging from 8.29 to 8.69. There was no significant seasonal change in the soil pH at *T. chinensis* sites or control sites. Compared to the control sites, both soil NO_3^--N and soil NH_4^+-N concentrations were higher in *T. chinensis* sites. The average NO_3^--N and NH_4^+-N levels soil in October were significantly higher than that in the other two months. The AP content was significantly lower in the control sites than in *T. chinensis* sites. The highest levels of AP activity were detected in October in the *T. chinensis* sites. The SOC content averaged 2.55g mg kg^{-1} soil across all sites. The levels of SOC were significantly greater in soils from *T. chinensis* sites than the control sites on the same dates as AP activity was sampled. From April to October, there was a significant increasing trend in SOC content under *T. chinensis*.

Nematode abundance and trophic groups

A total of 3,068 nematodes from 45 genera were identified in the nematode suspensions (Table 2). Soil under *T. chinensis* had greater nematode abundance than control sites. A total of 3,022 nematodes and 45 genera were found in *T. chinensis* sites. The dominant genera were Acrobeloides, Hoplolaimus, Paratylenchus, and Hemicycliophora. A few juveniles of genera Eucephalobus, Plectus, Aphelenchus, Pratylenchus, Amplimerlinius, Caenorhabditi, Tylenchus, Malenchus, Trichodorus, and Gracilacus were found only at *T. chinensis* sites. Total nematode abundance significantly differences by season (ANOVA: df=2, F=3.941, p=0.042), and the abundance of soil nematodes under *T. chinensis* was significantly differences between seasons (ANOVA: df=2, F=3.499, p=0.035). The Shannon-Wiener diversity index (1.76±0.48), species richness (2.68±0.55) and enrichment index (0.44±0.23) were significant difference in *T. chinensis* sites compared to the control sites (ANOVA: df=2, F=1.945, p=0.223).

The dominant trophic group was the plant-feeding nematodes (76.41%), but bacterial-feeding were also abundant in the *T. chinensis* and control sites (Figure 1). Fungal-feeding and omnivores were rare at both types of sites, with very low population densities.

Microbial biomass

Levels of PLFAs, SMBC and SIR were lower in April (PLFA: 3.0 ugg^{-1}dw; SMBC: 141.768 mg/kg; SMBN: 23.51 mg/kg; SIR: 17.8 O_2 $h^{-1}g^{-1}$dw) than in October (PLFA: 8.3 ugg^{-1}dw; SMBC: 159.408 mg/kg; SMBN: 28.76 mg/kg; SIR: 35.4 O_2 $h^{-1}g^{-1}$dw) under *T. chinensis* (Table 3). Furthermore, the levels of PLFAs, SMBN and SIR in soil samples collected from *T. chinensis* sites were positively correlated with each other (PLFA and SMBN: R= 0.927, p<0.01; PLFA and SIR: R=0.940, p<0.01; SMBN and SIR: R=0.848, p<0.01).

Levels of SMBC differed considerably between control sites and vegetated sites (Table 3). In April, *T. chinensis* had slightly higher levels of PLFAs compared to the control sites. During the vegetative period (June), microbial biomass on the vegetated sites increased, in contrast to control sites with slow microbial growth. In October, both control and *T. chinensis* sites reached the highest levels of PLFAs. Consequently, PLFAs and SIR were at higher concentrations on vegetated sites compared to control sites in October (PLFA: F=0.149, p=0.162; SMBC: F=7.486, p=0.015; SMBN: F=5.005, p=0.04; SIR: F=5.005, p=0.040).

Microbial community composition

Since different subsets of microorganisms have different PLFA compositions, the PLFA pattern of an environmental sample should reflect the microbial community composition (Vance et al., 1987). Comparing the two sampling dates (control sites and *T. chinensis* community

Table 2. Relative abundance (%) of genera and trophic groups of the soil nematode community sampled in April, June and October under *T. chinensis* and control sites.

Trophic type	Genus	*T. chinensis*			Control site		
		April	June	October	April	June	October
Bacterial-feeding	*Acrobeles*	0	0	0.13 (0.01)	0	0	4.35 (1.13)
	Acrobeloides	12.15 (1.16)	10.48 (1.63)	1.76 (0.13)	14.37 (2.45)	0	0
	Cervidellus	0	2.18 (0.31)	0.90 (0.07)	0	0	0
	Chiloplacus	6.54 (0.91)	0.22 (0.12)	0.07 (0.13)	0	0	4.35 (0.32)
	Rhabaditis	4.67 (0.73)	3.28 (0.54)	0.17 (0.01)	5.86 (1.09)	0	0
	Cephalobus	0	0.87 (0.61)	0.60 (0.21)	0	0	0
	Eucephalobus	0	0.44 (0.22)	0	0	24.51 (3.91)	0
	Brevibucca	0	0.44 (0.29)	0.03 (0.00)	0	0	0
	Caenorhabditis	0	0	0.03 (0.01)	0	0	0
	Plectus	0	0.22 (0.20)	0	0	0	0
Fungal-feeding	*Aphelenchoides*	0	1.09 (0.18)	0.07 (0.02)	0	0	0
	Aphelenchus	0	0.22 (0.10)	0	0	0	0
	Paraphelenchus	0	0.66 (0.37)	0	0	16.30 (2.85)	13.14 (1.05)
	Ditylenchus	0	0.87 (0.12)	0.20 (0.01)	0	0	0
Plant-feeding	*Helicotylenchus*	0	1.53 (0.46)	3.46 (0.47)	0	0	13.04 (1.82)
	Rotylenchus	0.94 (1.57)	39.31 (3.86)	35.58 (2.59)	0	0	0
	Pararotylenchus	0	2.62 (1.01)	9.61 (1.32)	0	0	0
	Scutellonema	0	2.18 (1.12)	7.05 (2.41)	5.86 (1.27)	0	0
	Hoplolaimus	33.64 (2.14)	0	5.45 (1.85)	0	0	0
	Tylenchus	0	0	1.10 (0.38)	0	0	0
	Boleodorus	0	0.22 (0.07)	4.39 (1.26)	0	8.2 (1.29)	0
	Malenchus	15.88 (1.38)	0.87 (0.10)	1.63 (0.34)	0	0	0
	Filenchus	1.87 (0.24)	1.53 (0.24)	1.60 (0.27)	0	8.2 (1.07)	21.74 (2.37)
	Lelenchus	0	0.66 (0.36)	2.00 (0.15)	0	24.52 (3.28)	17.39 (1.09)
	Miculenchus	0	0.22 (0.11)	1.13 (0.56)	0	0	4.35 (0.45)
	Aglenchus	0.94 (0.35)	0.44 (0.22)	0.03 (0.00)	0	0	0
	Heterodera	0	4.15 (1.31)	2.49 (0.19)	0	16.30 (2.57)	0
	Tylenchorhynchus	0	3.71 (1.63)	0	54.98 (4.73)	0	0
	Pratylenchus	0	1.97 (0.92)	0	0	0	0
	Trichodorus	0	0.22 (0.11)	6.55 (0.73)	0	0	0
	Paratylenchus	0	0	7.05 (1.95)	20.00 (2.98)	0	0
	Malenchus	0	0	1.00 (0.39)	0	0	0
	Pratylenchus	0	0.22 (0.10)	0.90 (0.17)	0	0	0
	Trichodorus	0	0	1.26 (0.68)	0	0	0
	Gracilacus	0	0	0.13 (0.01)	0	0	0
	Paratylenchus	12.15 (1.11)	10.48 (1.55)	1.76 (0.17)	0	0	0
	Hirschmanniella	0	2.18 (1.26)	0.90 (0.28)	0	0	0
	Sclerogryllus	6.54 (1.53)	0.22 (0.12)	0.07 (0.00)	0	0	8.70 (1.19)
	Hemicycliophora	4.67 (0.74)	3.28 (1.21)	0.17 (0.03)	0	0	4.82 (0.84)
	Merlinius	0	0.87 (0.53)	0.60 (0.25)	0	0	0
	Amplimerlinius	0	0.44 (0.27)	0	0	0	0
	Aorolaimus	0	0.44 (0.31)	0.03 (0.00)	0	0	0
Omnvores	*Dorylaimus*	0	0.22 (0.12)	0	0	0	4.82 (0.51)
	Aporcelaimus	0	1.09 (0.31)	0.07 (0.02)	0	0	4.82 (1.19)

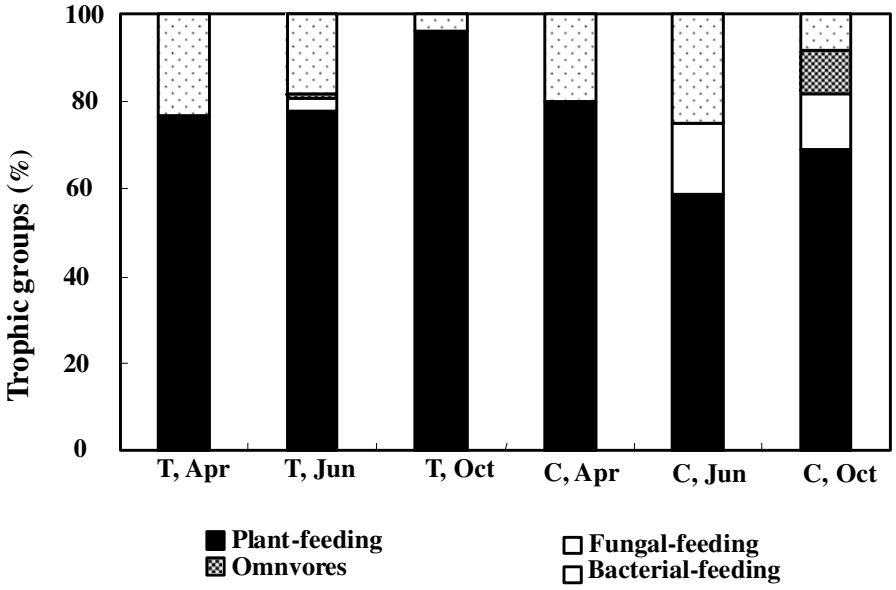

Figure 1. Relative abundance of nematode trophic groups in different months in *Tamarix chinensis* (T) and control sites (C).

Table 3. Average levels of phospholipid fatty acids (PLFA), microbial carbon (SMBC), microbial nitrogen (SMBN) and substrate induced respiration (SIR) in *T. chinensis* (n =40) and control sites (n =40) in different months.

Vegetation	Range	PLFA (ug g^{-1}dw)	SMBC (mg kg^{-1})	SMBN (mg kg^{-1})	SIR ($O_2h^{-1}g^{-1}$dw)
T. chinensis	Apr	3.0 (1.3)	140.768 (12.184)	23.51 (1.98)	17.8 (1.3)
	Jun	3.9 (1.1)	142.330 (11.311)	24.71 (2.41)	25.8 (2.8)
	Oct	8.3 (1.2)	159.408 (15.149)	28.76 (3.29)	35.4 (2.5)
Control site	Apr	2.9 (0.3)	34.717 (3.241)	14.29 (0.78)	7.6 (0.6)
	Jun	3.0 (0.4)	33.203 (2.199)	13.45 (1.19)	12.9 (1.1)
	Oct	6.1 (0.8)	32.714 (2.471)	14.42 (1.32)	13.1 (1.9)

sites), principal component 1 and principal component 2 explained 72.72 and 20.04% of the variation in the microbial community, respectively (Table 4). In April and June, control sites differed along principal component 1 ($F= 0.95$, $p< 0.05$; $F= 0.81$, $p< 0.05$). Control sites and *T. chinensis* community sites differed in April ($F= 9.14$, $p < 0.05$) and June ($F= 9.15$, $p < 0.05$).

Averaged over all sites, Gram-negative bacteria dominated the microbial communities. Their relative abundance (as percentages of the total) ranged from 65.3% (April) to 66.5% (October) (Table 5). In June, there was a small decrease in the percentage of Gram-negative bacteria under *T. chinensis*. Gram-positive bacteria and fungi contributed little to PLFAs levels. Gram-positive bacteria outnumbered fungi, and the proportion of Gram-positive bacteria was higher in April (25.2%). In contrast, the proportion of fungi was significantly higher in June (9.3%), during the growing season, at both sites. The Shannon index was significantly lower in April than in October ($F= 74.13$, $p < 0.001$).

Stepwise regression analysis between soil parameters and soil microbial community composition

The results of stepwise regression analysis between the soil microbial community composition, the two soil parameters and the three nematode trophic groups are shown in Table 6. There was a high linear correlation between each index and the five main soil parameter factors ($P<0.01$). Among the absolute values of the three regression coefficients, soil moisture, SOC, bacterial-feeding nematodes and plant-feeding nematodes were higher than other indices. The results indicate that plant-

Table 4. Summary of the principal components analysis (PCA) for different plots (*T. chinensis* and control) combined for different months.

Eigen value				Eigenvector					
PC	Value	PrVar	CumVar	*T. chinensis*			Control site		
				Apr	Jun	Oct	Apr	Jun	Oct
1	4.363	72.724	72.724	0.925	0.814	0.962	0.884	0.889	0.591
2	1.202	20.038	92.763	-0.228	0.470	0.065	-0.447	-0.339	0.781

Table 5. Properties of different microbial groups in *T. chinensis* (n =25) and control sites (n =25) in different months.

Vegetation	Range	Gram- (%)	Gram+ (%)	Fungi (%)	Not identified (%)	Gram-/Gram+ (%)	Shannon index
T. chinensis	Apr	65.3 (0.8)	25.2 (0.8)	5.3 (0.9).	2.1 (0.3)	2.59 (0.1)	2.71 (0.02)
	Jun	64.7 (1.6)	24.3 (0.2)	9.3 (0.7)	1.7 (0.2)	2.66 (0.5)	2.72 (0.01)
	Oct	66.5 (1.7)	23.5 (2.0)	8.0 (0.2)	1.5 (0.7)	2.83 (0.2)	2.78 (0.00)
Control site	Apr	56.3 (0.8)	34.0 (0.7)	4.2 (0.3)	3.1 (0.0)	1.66 (0.4)	2.71 (0.02)
	Jun	58.8 (0.9)	32.0 (0.2)	4.1 (0.1)	2.2 (0.3)	1.84 (0.5)	2.73 (0.01)
	Oct	60.6 (0.4)	30.8 (0.5)	4.0 (0.7)	2.3 (0.7)	1.97 (0.2)	2.75 (0.04)

Table 6. Stepwise regression analysis between soil parameters, trophic groups, and soil microbial community composition.

Y	Model	β_1	β_2	β_3	β_4	β_5	R^2	ANOVA test
PLFAs ug g^{-1}dw	$y=15.371+0.5175X_3+1.163X_5$			0.074		0.303	0.788	P<0.01
Gram-%	$y=56.364+0.052X_3+0.115X_5$			0.318		0.769	0.592	P<0.01
Gram +%	$y=15.788+2.863X_2$		0.782				0.611	P<0.01
Fungi%	$y=6.075+1.371X_1+0.570X_5$	0.659				0.637	0.471	P<0.01

X_1, Soil moisture; X_2, soil organic carbon; X_3, bacterial-feeding nematode; X_4, Fungal-feeding nematode; X_5, plant-feeding nematode. β_1-β_5: Standardize regression coefficients corresponding X_1-X_5. The greater the absolute β value, the stronger effect of the stress factor on physiological index. R^2: Square of total correlation coefficient.

feeding nematode capacity was a dominant factor, and that soil moisture, soil organic carbon and the bacterial-feeding nematode capacity were secondary.

DISCUSSION

Plant community effects on soil microbial parameter

Through variation in the quantity and quality of root exudates, plants can alter abiotic and biotic soil properties, affecting belowground ecosystems processes such as decomposition and nutrient cycling and influencing the composition and number of soil microorganisms (Bowen and Roviral, 1999; Orwin et al., 2006). In the present study, the soil under *T. chinensis* had a relatively higher abundance and species composition of nematodes and several microbial parameters compared to the control sites. This is likely due to the *T. chinensis* community's extensive root system, which can increase rhizodeposition and facilitate the transport of soil water and nutrients (Sanaullah et al., 2011). Rhizodeposition is also a nutrient resource for the soil microorganisms and nematodes, directly impacting the activity of soil microbial parameters.

Seasonal effects on soil microbial parameters

An influence of seasonal variation on microbial communities was indicated by the PLFA analysis. Changes in the PLFA pattern are usually interpreted as changes in community composition, that is, changes in species present (Rousk, 2010). Microbial biomass and activity were higher during the growing season (June) in *T. chinensis* sites, which correlate with increases in carbon

source availability due to root growth (Griffiths et al., 2003). However, with PLFA, the biomass of the micro-organisms actually increased 0.9 μg g^{-1}dw, with low rates in June due to the higher soil moisture due to the large amounts of precipitation during June in the Yellow River Delta. Soil moisture is an important resource for both plant growth and microbial activity (Williams and Rice, 2007). Changes in soil moisture may affect the function and structure of the soil microbial community through its effect on osmotic potential, transport of nutrients and energy, and cellular metabolism, as well as on the competitive interactions between microbial species (Kempf and Bremer, 1996). A significant change in the fungal community (9.3%) was also detected in June. Stepwise regression analysis showed that soil moisture was a dominant factor for soil fungi levels (Table 6).

Previous studies have shown that the activity of soil microorganisms is affected by soil salinity (Tripathi et al., 2006, 2007). *T. chinensis* is a typical salt-secreting plant which absorbs salt from soil and secretes salt from the leaves and shoots through the salt glands. The high level of precipitation in June caused the salt crystals on the leaf surfaces to return to the soil, increasing soil salinity. This may be the reason that microbiomass increased only at a low rate during the growing season.

Soil nutrient levels increased significantly in October under *T. chinensis* (Table 1). This may be correlated with increased growth of fine roots during the summer. In October, *T. chinensis* litter is easily degraded, and a large amount of root exudate becomes available to soil microorganisms. The increase in PLFA, SMBC and SIR probably resulted from the increase in soil nutrients. Stepwise regression analysis also showed that soil organic carbon was a dominant factor for Gram-positive bacteria content (Table 6). Habekost et al. (2008) also found that the effect of the source for carbon substrates on the proportion of microbial groups is more distinct in autumn.

Soil microbial community composition and microfaunal communities

To date, there has been little research that links the effects of the soil microbial community composition with nematode communities under *T. chinensis*. Our results show that there were consistent interactions between the soil microbe community composition and nematode communities. Despite the apparent disconnection between the nematode and microbial communities, the nematode components of the food web do affect microbial community composition in some ways, but it might be circumstantial and associated with particular abiotic factors, such as soil temperature, moisture, carbon, and nitrogen content (Papatheodorou et al., 2004). Stepwise regression analysis showed that the plant-feeding and bacterial-feeding nematodes were the dominant factors for the amount of PLFA, and the feedback between these two trophic groups and the amount of PLFA in this experiment seems to be mainly positive.

The soil organic carbon, plant-feeding nematodes, and bacterial-feeding nematodes were the dominant factors for soil bacteria content. Gram-positive bacteria are positively correlated with increasing organic carbon levels in soil. Kramer and Gleixner (2008) also found that the Gram-positive bacteria can use a greater number of derived carbon sources from soil organic matter, but Gram- negative bacteria prefer plant-derived carbon sources.

The plant-feeding nematode content and soil moisture content were the dominant factors for soil fungal content (Table 6). In the soil, fungal-feeding nematodes can feed on saprophytic, pathogenic and mycorrhizal fungi (Viketoft et al., 2005). As the main food predator, the fungal-feeding were not the dominant factors for the fungi content in the stepwise regression analysis. That is mainly because this factor has strong interaction with the other four factors which had a combined direct effect on the soil fungi content. Fungal-feeding nematodes were less abundant in the wetland in this study, reflecting the relationship between nematode community structure and available food resources (Connell and Slatyer, 1997). Fungi are aerobic organisms whose populations would be suppressed by the higher water content in the wetland ecological system.

Conclusions

The high salinity of the soil environment produced different degrees of inhibition of the population and activities of the micro-ecosystem. Plant halophytes can reduce rhizosphere salinity, thereby reducing the effects of salinity stress on soil microbes. The presence of the *T. chinensis* plant community increased soil substrates through release to root exudates, and the litter degradation improved the micro-ecological environment. *T. chinensis* has potential application in the remediation of salt pollution of the environment.

ACKNOWLEDGMENTS

This work was supported by Foundation of the Research center for Eco-Environmental Sciences of Yellow River Delta in Shandong Province (No. 2008KFJJ01).

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