

Impact of dike age on biodiversity and functional composition of soil macrofaunal communities in poplar forests in a reclaimed coastal area

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Abstract: Four patches of poplar forest with different dike histories (about 30 to 200 years) were selected from the coastal area of Yancheng, China, for detecting the effect of dike age on soil macrofauna. A total of 825 individuals belonging to 21 taxonomic groups were collected. Omnivorous, phytophagous, predaceous, and saprophagous groups were classified on the basis of diet. Higher biodiversity values were observed in the forests with longer dike histories (100 and 200 years) than in those with shorter dike histories (30 and 50 years). By principal coordinate analysis, the soil macrofaunal communities from the forests were distinguished as three groups with shorter or longer dike histories (30 years, 50 years, and above 100 years). One-way ANOSIM analysis revealed significant differences among soil macrofaunal communities ($P < 0.050$), except for those with longer dike histories (100 and 200 years, $P = 0.217$). The groups of omnivorous and predaceous macrofauna showed no significant differences in taxonomic richness and abundance among habitats, while significant differences were observed between the other functional groups. A significant difference in functional composition between the soil macrofaunal communities in the forests with dike ages of 30 and 100 years was found with the chi-square test ($P = 0.027$). The biodiversity and functional composition of soil macrofauna was significantly affected by dike age in the reclaimed coast.

Key words: Dike history, community succession, functional group, soil evolution, reclamation

1. Introduction

Coastal areas are an important kind of habitat for humans; over 1/3 of the world's human population resides in coastal areas and on small islands, which account for only 4% of the total land area on earth (Brown et al., 2006). Coastal wetlands disappeared worldwide at an alarming rate of 70%–80% over the past five decades (Duke et al., 2007; Wolanski, 2007). In response to the demand for land resources, reclamation has been accepted as a direct strategy to obtain new land from the coastal wetlands along some coastal countries and regions (Wang et al., 2012). Reclamation in coastal areas has been practiced for thousands of years and continues to be employed on a global scale (Ellis and Atherton, 2003; An et al., 2007). Reclamation is responsible for the loss of over half of the natural coastal wetlands in China between 1950 and 2000 (An et al., 2007). The coastal wetlands in East China were reclaimed by diking to create urban areas, rice farms, forests, and shrimp ponds; for example, Yancheng City was diked from the coast thousands of years ago and is presently undergoing urbanization (Ge et al., 2012). Coastal areas have undergone significant changes with a long diking history. However, the science and policies behind coastal

zone ecosystem management show inconsistencies (Paterson et al., 2011) in terms of biodiversity maintenance and conservation (Mora and Sale, 2011).

Diked coastal areas are an important source of native biodiversity, although the habitats are highly modified and disturbed (Gaston et al., 2004; Martínez et al., 2009). The sustainable management of vast reclaimed lands along shorelines can be affected by land uses (Cui et al., 2012a). Most of the reclaimed lands in eastern China are used for agricultural purposes, some are used for forests, and the rest are used for other purposes, such as those in Yancheng City (Ge et al., 2014a). Soil fauna is a vital group of plant mutualisms that has attracted attention in biodiversity research because of its active role in soil processes and its sensitive response to soil system changes (Rainio and Niemelä, 2003; Sauberer et al., 2004). The biodiversity of soil fauna is highly sensitive to any disturbances because the soil environment serves as their habitat and source of requirements (Lavelle et al., 2006). Soil fauna can be described in terms of size (macro-, meso-, and microfauna), taxonomic composition (order, family, genus, or species), guild structure, or trophic level; this classification indicates the structural and functional

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diversity of soil fauna (Lavelle et al., 2006). A guild is a species group that exploits the same class of environmental resources (Brussaard, 1998). The structural and functional diversity of soil fauna communities indicates the diversity of a biogenic soil structure; it also regulates the physical properties and processes of soil, and it allows material recycling (De Bruyn, 1997). In particular, the abundance, biodiversity, and functional composition of soil macrofauna can reflect the changes in soil properties after reclamation (Barrios et al., 2005; Azul et al., 2011).

However, only a few studies have investigated the changes in soil macrofaunal communities under long-term dike histories (Wu et al., 2002; Frouz et al., 2006). Research on the manner by which the diversity and functional composition in soil macrofauna change over time may provide crucial scientific bases for sustainable land use. We hypothesized that the complexity and biodiversity of soil macrofauna in reclaimed coastal lands increase with dike history. In this study, we determined the effect of dike age on the biodiversity distribution pattern and functional composition of soil macrofauna in a reclaimed coast.

2. Materials and methods

2.1. Study area

Yancheng City is located at the transition of subtropical and temperate zones in Jiangsu Province, China, with an average annual precipitation between 900 and 1100 mm. The youngest dike dam was built at the coast in the 1980s; the diked area was filled with clay and mud until the desired height was well above the high tide. The lands from the dam to the inland were diked in different historical periods mostly for forest and agricultural uses. The soil in the study area was Fluvisol by the classification of FAO taxonomy. We selected four patches from poplar forests with dike ages ranging from about 30 to 200 years in August 2013 (Figure 1). The diked area shared the same land-use pattern; the lands were used for paddy rice and upland cropping from about 4 to 5 years later after being diked, and then they were used for poplar forest after 1998. We sampled the soil macrofauna from the forests to evaluate biodiversity and composition variation for hypothesis testing. The vegetation cover and the habitat characters are described in Table 1 (Ge et al., 2014a).

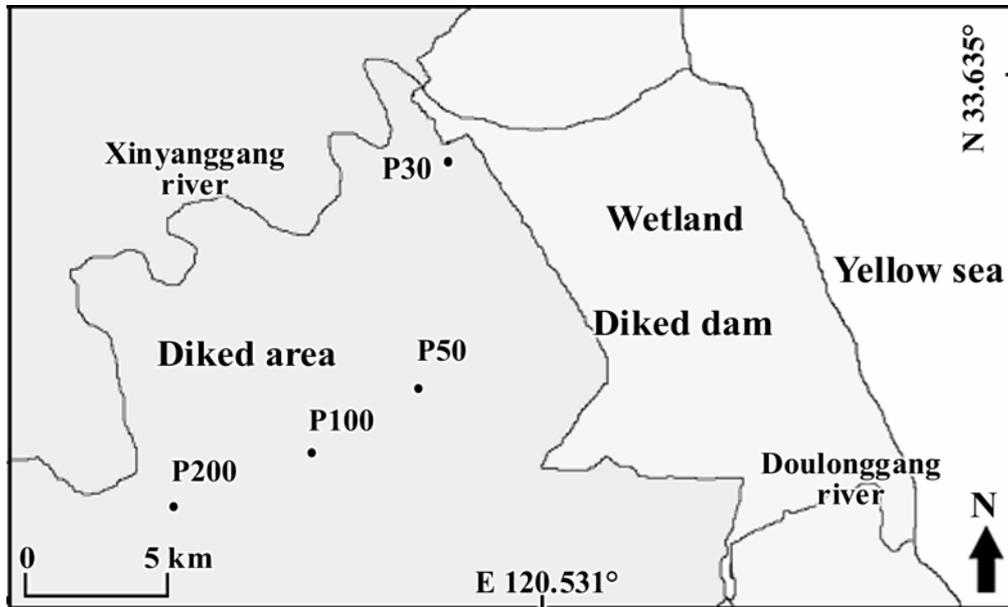


Figure 1. Distribution of sample sites on the reclaimed coast.

Table 1. Habitat codes and characteristics of selected poplar forests.

Habitat code	Dominant vegetation species		Trees' age	Dike age
	Arbor (coverage)	Herbage (coverage)		
P30	<i>Populus euramericana</i> (90%)	<i>Cynodon dactylon</i> , <i>Chenopodium glaucum</i> (50%)	13 years	~30 years
P50	<i>P. euramericana</i> (90%)	<i>C. dactylon</i> , <i>Sonchus oleraceus</i> , <i>C. glaucum</i> (60%)	16 years	~50 years
P100	<i>P. euramericana</i> (80%)	<i>C. dactylon</i> , <i>S. oleraceus</i> , <i>C. glaucum</i> (60%)	14 years	~100 years
P200	<i>P. euramericana</i> (80%)	<i>Setaria viridis</i> , <i>C. dactylon</i> , <i>S. oleraceus</i> (50%)	14 years	~200 years

2.2. Sampling and identification

A sample plot was settled at each patch; five soil blocks of 25 cm × 25 cm with 15 cm depth were collected and sorted. Sampling blocks were located 5 m apart and randomly distributed in the plot. Twenty blocks were removed from the ground and hand-sorted for soil macrofauna. The macrofauna were preserved in 70% ethanol and categorized by family level (Yin, 2000; Pauli et al., 2011), while the Araneae were identified just by order level. The macrofauna were classified into different functional groups on the basis of diet. Saprophagous, phytophagous, predaceous, and omnivorous groups were considered in this research (Lefebvre and Gaudry, 2009).

2.3. Data analysis

Margalef’s richness index *R* (Margalef, 1957) and Shannon–Weaver diversity index *H'* (Shannon and Weaver, 1949) were used to determine the biodiversity of the communities. Diversity indices are usually employed in the analysis of macrofaunal communities (Pauli et al., 2011).

Taxonomic richness, abundance, and *R* and *H'* comparisons were subjected to one-way ANOVA to identify the distribution variation of macrofaunal communities across different habitats. The least significant difference (LSD) test was used if a significant difference was observed and if Levene’s test was passed, whereas Dunnett’s T3 test

was used if Levene’s test was not passed (in this study, Dunnett’s T3 test was used for the datasets of individuals and groups). On the basis of community taxa composition data, principal coordinate analysis (PCoA) with Euclidean similarity index was used to analyze the differences among communities from different habitats. One-way ANOSIM analysis (with the number of permutations as 10,000) was used to test the statistical significance among communities on the basis of the Gower distance created from the community composition data (Ge et al., 2014b).

One-way ANOVA was used for taxonomic richness and abundance to detect the differences in functional composition among groups. The chi-square (χ^2) test was then utilized to determine significant differences between the expected and observed frequencies in the abundance of functional groups. Pearson’s χ^2 test was used in 2 × 2 crosstabs, where total abundance was >40 and minimum expected frequency was >5.

SPSS 16.0 (SPSS Inc.) and PAST (freeware, Hammer et al., 2001) were employed for statistical analysis.

3. Results

3.1. Composition and biodiversity

A total of 825 individuals belonging to 21 taxonomic groups were included in our research (Table 2). Formicidae

Table 2. Composition of soil macrofauna from different habitats.

Functional group	Order	Family	Habitat code				Total	Frequency (%)
			P30	P50	P100	P200		
Omnivorous	Hymenoptera	Formicidae	27	44	51	69	191	23.15
Omnivorous	Orthoptera	Gryllidae	4	7	15	14	40	4.85
Phytophagous	Coleoptera	Scarabaeidae	0	3	16	19	38	4.61
Phytophagous	Hemiptera	Pentatomidae	7	8	9	10	34	4.12
Phytophagous	Lepidoptera	Pieridae	11	35	15	18	79	9.58
Phytophagous	Orthoptera	Acrididae	2	2	16	16	36	4.36
Phytophagous	Julida	Julidae	0	0	6	5	11	1.33
Phytophagous	Mesogastropoda	Cyclophoridae	0	0	3	5	8	0.97
Phytophagous	Stylommatophora	Ariophantidae	0	0	1	1	2	0.24
Phytophagous	Stylommatophora	Bradybaenidae	0	3	5	8	16	1.94
Predaceous	Coleoptera	Carabidae	16	17	9	12	54	6.55
Predaceous	Coleoptera	Staphylinidae	8	8	10	12	38	4.61
Predaceous	Coleoptera	Coccinellidae	1	1	2	1	5	0.61
Predaceous	Araneae	Not identified	2	5	7	13	27	3.27
Predaceous	Geophilomorpha	Geophilidae	0	2	3	0	5	0.61
Predaceous	Scolopendromorpha	Scolopendridae	1	2	3	7	13	1.58
Saprophagous	Dermaptera	Forficulidae	8	9	6	10	33	4.00
Saprophagous	Pauropoda	Scutigereillidae	0	2	1	2	5	0.61
Saprophagous	Isopoda	Armadillidiidae	18	22	15	27	82	9.94
Saprophagous	Isopoda	Porcellionidae	3	0	12	13	28	3.39
Saprophagous	Haplotaxida	Lumbricidae	0	17	30	33	80	9.70
		Total	108	187	235	295	825	100.00

was the dominant group ($\geq 10.00\%$); Carabidae, Forficulidae, Gryllidae, Acrididae, Pentatomidae, Pieridae, Scarabaeidae, Staphylinidae, Armadillidiidae, Araneae, Julidae, Porcellionidae, Scolopendridae, Lumbricidae, and Bradybaenidae were the frequent groups ($\geq 1.00\%$, $< 10\%$). The dominant and frequent groups constituted 96.97% of the total abundance and macrofauna. Coccinellidae, Scutigereidae, Ariophantidae, and Geophilidae were the rare groups ($< 1.00\%$). In this study, four functional groups were identified: omnivorous, phytophagous, predaceous, and saprophagous. The omnivorous group included Formicidae and Gryllidae; the phytophagous group included Scarabaeidae, Pentatomidae, Pieridae, Acrididae, Julidae, Cyclophoridae, Ariophantidae, and Bradybaenidae; the predaceous group included Carabidae, Staphylinidae, Coccinellidae, Araneae, Geophilidae, and Scolopendridae; and the saprophagous group included Forficulidae, Scutigereidae, Armadillidiidae, Porcellionidae, and Lumbricidae.

Significant differences were detected in the taxonomic richness ($F_{3,16} = 37.683$, $P < 0.001$), abundance ($F_{3,16} = 168.709$, $P < 0.001$), H' index ($F_{3,16} = 8.853$, $P < 0.001$), and R index ($F_{3,16} = 17.039$, $P < 0.001$) of the soil macrofauna across different habitats. The taxonomic richness, abundance, and biodiversity indices were higher in the forest lands with long dike histories than in those with short dike histories, whereas communities were simpler

in the young forest lands than in the old forest lands. The soil macrofaunal communities in the poplar forest patches designated as P100 and P200 were similar in biodiversity analysis, and the soil macrofaunal communities from the young diked lands (P30 and P50) showed the same characteristics, except for abundance (Figure 2).

3.2. Ordination and analysis of similarity

The PCoA ordinal configuration by Euclidean distance similarity index indicated that the communities can be divided into three groups, with the soil macrofaunal communities sorted following the history of reclamation in coordinate 1 (Figure 3). The soil macrofaunal communities from forests can be distinguished in terms of dike history. The plots were gathered as three groups, which were labeled as 30 years, 50 years, and above 100 years (Figure 3).

One-way ANOSIM revealed significant differences between communities ($R = 0.711$, $P < 0.001$). Pairwise comparisons also revealed significant differences between communities ($P < 0.050$), except for those from P100 and P200 ($R = 0.160$, $P = 0.217$) (Table 3).

3.3. Functional group composition

The omnivorous and predaceous groups showed no significant differences in taxonomic richness ($F_{3,16} = 1.000$, $P = 0.418$) or abundance ($F_{3,16} = 2.740$, $P = 0.078$). In contrast, significant differences in taxonomic richness and abundance were observed in the other groups among the habitats with different dike ages ($P < 0.050$; Table 4).

The χ^2 results showed significant differences in the functional composition between soil macrofaunal communities from P30 and P100 ($P = 0.027$, $\chi^2 = 9.202$); significant differences were also observed in all other comparisons ($P > 0.050$) (Table 5).

4. Discussion

Land conversion significantly affected the ecosystem of coastal zones in the past decades (Etter et al., 2006; An et al., 2007). The history of land use intensely modified the relationship between soil fauna and soil ecosystem (Salamon et al., 2008; Liiri et al., 2012). The present study analyzed the structures of soil macrofaunal communities, which showed remarkable increases in abundance, taxa richness, and diversity with dike age. We observed lower taxonomic richness, abundance, and biodiversity indices in the soil macrofaunal communities from forest patches with short dike histories than in those from forest patches with long dike histories (Figure 2). These results indicate that dike age significantly affects the composition of soil macrofaunal communities, which supports the results of Thomas et al. (2004) and Cui et al. (2012a).

Considering the large taxonomic diversity of soil fauna, some researchers aimed to simplify this relationship by grouping individuals on the basis of their shared

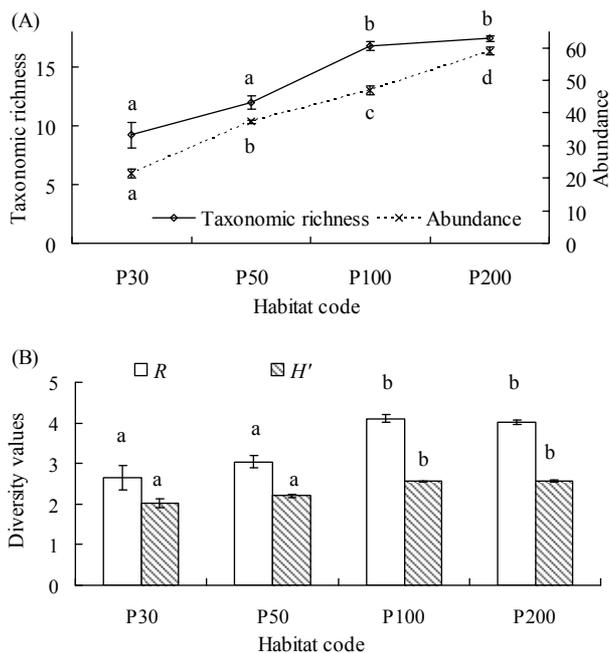


Figure 2. One-way ANOVA of taxonomic richness and abundance (A) and Margalef's richness index R and Shannon-Weaver diversity index H' (B) across different habitats (mean \pm SE). Means with different scripts are significantly different by Dunnett's T3 test (A) and LSD test (B), $\alpha = 0.05$.

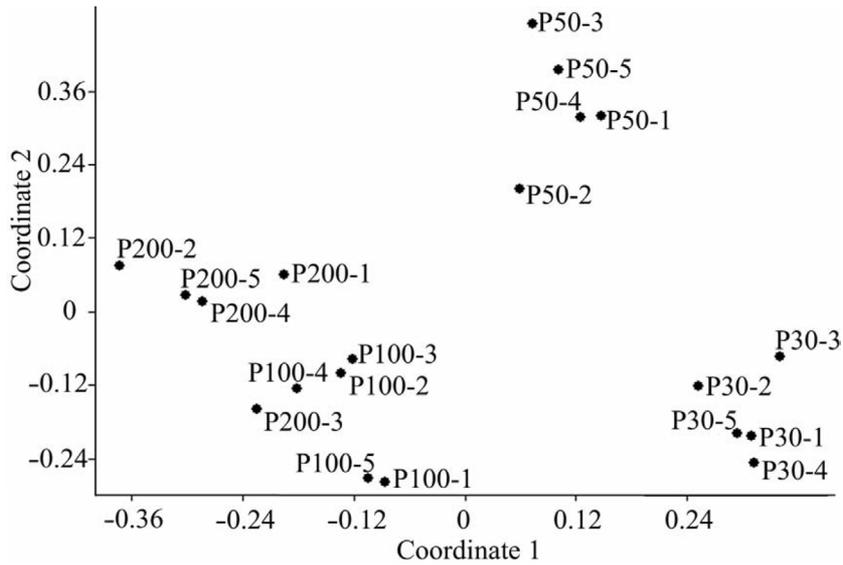


Figure 3. PCoA ordinal configuration of soil macrofaunal communities from different habitats by Euclidean distance similarity index. In the code of the samples, the prefix means the code of the habitat, and the suffix means the number of the sample.

Table 3. One-way ANOSIM analysis of similarity of soil macrofaunal communities based on Gower distance.

Habitat code	P50	P100	P200
P30	P = 0.009 R = 0.510	P = 0.009 R = 0.872	P = 0.007 R = 0.996
P50		P = 0.008 R = 0.896	P = 0.010 R = 0.964
P100			P = 0.217 R = 0.160

Table 4. Taxonomic richness and abundance of functional groups among different habitats (mean ± SE).

Case	Functional groups	P30	P50	P100	P200
Taxonomic richness	Omnivorous	1.80 ± 0.20 NS	2.00 ± 0.00	2.00 ± 0.00	2.00 ± 0.00
	Phytophagous	2.20 ± 0.37 a	2.80 ± 0.49 a	6.60 ± 0.24 b	6.80 ± 0.37 b
	Predaceous	2.80 ± 0.49 a	3.60 ± 0.24 ab	4.40 ± 0.24 b	4.20 ± 0.20 b
	Saprophagous	2.40 ± 0.24 a	3.40 ± 0.24 b	4.00 ± 0.00 bc	4.40 ± 0.20 c
Abundance	Omnivorous	6.20 ± 0.58 a	10.20 ± 0.37 b	13.20 ± 0.86 bc	16.60 ± 0.75 c
	Phytophagous	4.00 ± 0.32 a	10.20 ± 0.92 b	14.20 ± 0.37 c	16.40 ± 1.17 c
	Predaceous	5.60 ± 0.75 NS	7.00 ± 0.84	6.80 ± 0.80	9.00 ± 1.00
	Saprophagous	5.80 ± 0.92 a	9.80 ± 1.16 ab	12.8 ± 0.58 bc	17.00 ± 1.18 c

The means with different scripts are significantly different by multiple comparisons in rows, while NS means that no significant difference occurred (Dunnett's T3 test or LSD test), $\alpha = 0.050$.

Table 5. Chi-square test of the functional composition of soil macrofaunal communities.

Habitats	P30	P50	P100
P50	P = 0.273 $\chi^2 = 3.897$		
P100	P = 0.027 $\chi^2 = 9.202$	P = 0.683 $\chi^2 = 1.495$	
P200	P = 0.051 $\chi^2 = 7.776$	P = 0.790 $\chi^2 = 1.045$	P = 0.933 $\chi^2 = 0.435$

properties (Brussaard, 1998). Functional groups were also distinguished on the basis of food resources (Lefebvre and Gaudry, 2009). In forests with long dike histories, the abundance and taxa richness of the phytophagous and saprophagous groups increased, whereas the taxa richness of the omnivorous group and the abundance of the predaceous group did not significantly change (Table 4). These phenomena and the χ^2 results on the functional composition of soil macrofaunal communities (Table 5) suggest that soil environment provides different food resources in habitats with different dike histories, which cause significant changes in the functional composition of soil macrofaunal communities (Lefebvre and Gaudry, 2009).

In the present study, the ordination analysis (Figure 3) and functional group composition (Tables 3 and 4) of macrofaunal communities supported the idea that a dike age between 30 and 50 years should be a boundary of soil environmental changes. Similar findings were presented in a previous study of bacterial succession on Chongming Island (Cui et al., 2012b). The results of the present study suggest that another boundary (or more) that ranges from 50 to 100 years is needed. The absence of differences in the soil macrofaunal communities from P100 and P200 as revealed through ANOSIM proves that the environments of old habitats present similar development histories. However, soil characteristics vary among different forests because of their different land-use histories (Salamon et al., 2008; Zou et al., 2011).

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Large-scale land-use changes have been observed with economic development and urbanization in some developing countries that have undergone sharp changes in landscape pattern and composition (Dewan et al., 2012). In East Asia, the physicochemical properties of coastal saline soils significantly improved after reclamation, after which long-term fertilization and cultivation resulted in modified soil structure, which enhanced the capacity for preserving fertility and C sequestration (Li et al., 2014). Changes in functional groups can indicate soil environmental changes (Lefebvre and Gaudry, 2009). Dike age is an important factor that distinguishes diked coastal habitats. Therefore, soil macrofauna distribution and community composition are strongly related to land dike age (Ge et al., 2014a, 2014b). Most of the reclaimed land in the study area was used for agriculture (such as for grains) and tended to eliminate biodiversity components that depend on high-productivity environments, whereas forests and other marginal lands should be considered as the remaining reservoirs of biodiversity of reclaimed coasts (Huston, 2005; Ge et al., 2014b).

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