Biodiversity Variations of Soil Macrofauna Communities in Forests in a Reclaimed Coast with Different Diked History

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Abstract.- A long history of reclamation has affected the coast of east China. This factor has been recognized as the most important cause of coastal wetland loss in the country. In August 2012, we selected six forest patches, each with ages after diking ranging between 30 and 200 years, occupied by planted poplar and metasequoia in the reclaimed coast at Yancheng city. We assessed the biodiversity and the taxonomic composition variation of soil macrofauna communities among these habitats. Hymenoptera, Isopoda, Haplotaxida, and Lepidoptera groups constituted 57.13% of the total macrofauna from the six habitats. The higher biodiversity values, expressed as Margalef's richness index (R) and Shannon-Weaver diversity (H'), were observed in the forests with a longer diked history, whereas lower values occurred in the forests in recently-reclaimed coasts. Ordination analysis (non-metric multi-dimensional scaling) demonstrated that soil macrofauna community parameters are determined by the diked age of the plots. One-way ANOSIM analysis showed significant differences between soil macrofauna community characteristics of the sample forest patches ($P<0.050$), with the exception of poplar forest compared to metasequoia forest diked approximately 30 years ago ($P=0.558$). The findings indicated that the biodiversity of soil macrofauna was significantly affected by the diked history, and the soil macrofauna distribution pattern was strongly related with soil development after reclamation.

Keywords: Coastal ecosystem, reclamation, soil chronosequence, soil macrofauna, wetlands

INTRODUCTION

The wetlands supply certain important ecological services and functions for the world, such as hydrologic flow, biogeochemical cycling, and transformations of elements on the landscape (Richardson, 1994). Coastal wetlands should be the most important habitat for human beings. Studies have reported that more than one-third of the world's human population lives in coastal areas and small islands, which together comprise just 4% of total land area on Earth (Brown *et al.*, 2006). The cumulative effects of mining waste, dams, land use change, and urbanization have left few watersheds intact. Reclamation of coastal wetlands has been practiced for thousands of years (An *et al.*, 2007; Ellis and Atherton, 2003). Reclamation has been accepted as a direct way to obtain new land from the coastal wetlands (Wang *et al.*, 2012). This tradition has been continued on a global scale. Coastal wetlands are disappearing at an alarming rate. In the

last five decades the loss is 70% to 80% in certain countries (Duke *et al.*, 2007; Wolanski, 2007). In China, 51.2% of the natural coastal wetlands were lost from 1950 to 2000, and reclamation was recognized as the most important factor for wetland loss (An *et al.*, 2007). Considering the recent Chinese economic development, land resources became more valuable in certain areas, especially in the coastal areas of east China, where the demands of land for urbanization, forest, rice farms and shrimp ponds drive the reclamation of coastal wetlands. One such coastal area is Yancheng city, which is a city that was diked from the coast thousands of years ago, and is presently in the process of urbanization (Ge *et al.*, 2012).

Reclamation significantly increased soil organic matter, phosphorus, and nitrogen concentrations, and soil properties approached a relatively stable level nearly 30 years after reclamation, as observed in Eastern Asia (Li *et al.*, 2014). Sustainable management of the vast reclaimed lands along shorelines showed different soil dynamics under the influences of various agricultural land uses (Cui *et al.*, 2012a). Although the environments have been highly modified and

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disturbed, the unique environments have recently been identified as an important source of native biodiversity (Gaston *et al.*, 2004). Plant mutualisms are widespread and are thought to maintain the structure and diversity of natural communities, influencing the performance of land cover but also altering soil traits, plant productivity, and biogeochemical cycling (Smith and Read, 2008; Tahir and Butt, 2009). Soil fauna is an important group of mutualistic plants; it is gaining importance in biodiversity assessment studies due to its active role on soil processes and its sensitive response to changes in the soil system (Rainio and Niemelä 2003; Sauberer *et al.*, 2004). The diversity of organisms and the functions that the fauna community perform in the soil combine to create the diversity of biogenic soil structure, as well as help regulate physical properties and processes of soil and material recycling. Furthermore, this diverseity provides a host of ecosystem services that help increase soil heterogeneity and the soil ecosystem's resilience and resistance to ecological disequilibria (Brown *et al.*, 2002). The biodiversity of soil fauna is highly sensitive to any disturbances because the soil environment is their habitat and the source of all the resources they need (Lavelle *et al.*, 2006). Several representatives of the soil macrofauna have been proposed as bioindicators of soil health (Barros *et al.*, 2002); their overall abundance, biodiversity, and community composition can be used to reveal the conversion of land use and variation of soil traits (Barrios *et al.*, 2005; Azul *et al.*, 2011).

Studying soil macrofauna responses to habitat changes is of considerable interest, because certain investigations on soil macrofauna after reclamation showed that soil macrofauna can be used as indicators of environmental conditions (Wu *et al.*, 2002, 2005; Römbke *et al.*, 2009). However, few studies have addressed how the soil macrofauna community would change under long-term diked history, especially at a time scale of centuries. A better understanding of how the composition and diversity of soil macrofauna change over time would provide important scientific bases for sustainable land use. Here, we hypothesized that in the biological community affected by the diked history in the reclaimed coast, following soil development, the soil macrofauna would be more complex and maintain higher biodiversity in the new lands with a longer reclamation history.

MATERIALS AND METHODS

Study areas

Yancheng City is located at the West Pacific coast, which is the transition of subtropical and temperate zones in Jiangsu Province, China. Annual rainfall averages between 900 and 1,100 mm. The youngest diked dam was built in the 1980s at the coast, filled with clay and mud until the desired height was well above the high tide. It has been used as a road after the land was reclaimed. From the dam to inland, the lands were diked in different historical periods mostly for forest and agricultural use. The soil in the study area was Fluvisols (FAO/UNESCO Taxonomy). In August 2012, we selected forest patches with diked age ranging from 30 to approximately 200 years occupied by planted poplar or metasequoia (Fig. 1), and we sampled the soil macrofauna from the habitats for evaluating the biodiversity and composition variation to test our hypothesis. The vegetation cover and the habitat characters were described for each patch (Table I).
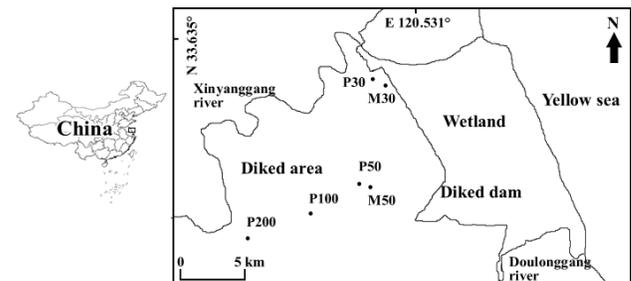
Fig. 1. The distribution of sample sites on the reclaimed coast.

Sampling and identification

A sample plot was settled at each patch, then five soil blocks of 25 cm × 25 cm with 15 cm depth were collected and sorted. Sampling units were located 5 m apart and distributed randomly in the plot. Totally 30 blocks were removed from the ground and hand-sorted for soil macrofauna. The macrofauna were then preserved in 70% ethanol and identified to order level (Yin, 2000; Pauli *et al.*, 2011).

Table I.- The characters of selected habitats in the study.

Code	Dominant vegetation species		Tree age (years)	Diked age (years)
	Arbor (coverage)	Herbage (coverage)		
P30	*Populus euramericana* (90%)	*Cynodon dactylon, Chenopodium glaucum* (50%)	12	30
M30	*Metasequoia glyptostroboides* (90%)	*Stellaria chinesis, Chenopodium glaucum* (60%)	12	30
P50	*Populus euramericana* (90%)	*Cynodon dactylon, Sonchus oleraceus, Chenopodium glaucum* (60%)	15	≈50
M50	*Metasequoia glyptostroboides* (90%)	*Stellaria media, Stellaria chinesis* (80%)	15	≈50
P100	*Populus euramericana* (80%)	*Cynodon dactylon, Sonchus oleraceus, Chenopodium glaucum* (60%)	13	≈100
P200	*Populus euramericana* (80%)	*Setaria viridis, Cynodon dactylon, Sonchus oleraceus* (50%)	13	≈200

Data analysis

Margalef's richness index *R* (Margalef, 1957) and Shannon-Weaver diversity index *H'* (Shannon and Weaver, 1949) were used to detect the biodiversity of the communities. The diversity indices are usually employed in the analysis of macrofauna communities (Pauli *et al.*, 2011).

In order to detect the distribution variation of macrofauna communities among different habitats, one-way ANOVA analysis was used in taxonomic richness and abundance comparison, and then the Student-Newman-Keuls (SNK) test was used if a significant difference occurred and if Levene's test was passed, whereas Dunnet's T3 test was used if Levene's test was not passed (in this study, Dunnet's T3 test was used for the dataset of individuals). Based on the community taxa composition data, ordination analysis (non-metric multi-dimensional scaling, nMDS) was used to analyze the differences among communities from different habitats. Based on the Euclidean distance created from the community composition data, one-way ANOSIM analysis (with the number of Permutations as 9999) was used for testing the statistical significance among communities.

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

RESULTS

Composition and biodiversity

A total of 807 individuals were collected, with 18 soil macrofauna taxa (orders) identified as belonging to arthropods (15 groups), mollusks (2 groups), and annelids (1 group). In the study area, Hymenoptera (all of which were ants), Isopoda, Haplotaxida and Lepidoptera were the dominant groups (≥10.00%), with frequency of 23.92%, 12.02%, 10.66%, and 10.53%, respectively (Table II). Mesogastropoda, Opiliones, Geophilomorpha, Polydesmida and Anoplura were the rare groups (<1.00%). The rest of the nine orders were the frequent groups. In forest patches with longer dike history, more taxa, such as Opiliones. Mesogastropoda, only occurred in habitats coded as P100 and P200, whereas Stylommatophora, Symphyla, Geophilomorpha, Polydesmida and Anoplura did not occur only in habitats coded as P30 and M30.

Significant differences were detected in taxonomic richness ($F_{5,24}$=56.433, P<0.001), abundance ($F_{5,24}$=235.566, P<0.001), *H'* index ($F_{5,24}$=29.396, P<0.001), and *R* index ($F_{5,24}$=33.044, P<0.001) of soil macrofauna among different habitats (Fig. 2). It showed that the higher values of taxonomic richness, abundance, and biodiversity indices occurred in the forests patches with longer diked history, while the communities were simpler in the forests on the younger lands. In the earlier diked land, the soil macrofauna communities from poplar forest patches (P100 and P200) were similar in the biodiversity analysis. In the younger land, the soil macrofauna communities had similar biodiversity characteristics with the same diked age (*e.g.* P30 and M 30; P50 and M 50).

Communities ordination

Using the two-dimensional nMDS ordinal configuration with Bray-Curtis similarity method

Table II.- Number of soil macrofauna (identified to order level) collected in the investigation from different habitats.

Order	P30	M30	P50	M50	P100	P200	Total	Frequency (%)
Hymenoptera	24	25	32	22	38	52	193	23.92
Isopoda	15	15	13	14	13	27	97	12.02
Haplotaxida	0	0	13	10	30	33	86	10.66
Lepidoptera	11	14	18	11	13	18	85	10.53
Coleoptera	9	8	10	12	9	8	56	6.94
Dermaptera	8	8	9	13	6	10	54	6.69
Orthoptera	2	4	2	12	16	16	52	6.44
Hemiptera	7	7	8	10	9	10	51	6.32
Araneida	5	0	5	4	7	13	34	4.21
Diptera	3	0	6	1	7	7	24	2.97
Stylommatophora	0	0	3	5	6	8	22	2.73
Symphyla	0	0	3	0	6	6	15	1.86
Scolopendromorpha	1	1	2	0	3	6	13	1.61
Mesogastropoda	0	0	0	0	3	4	7	0.87
Opiliones	0	0	0	0	2	3	5	0.62
Geophilomorpha	0	0	2	0	3	0	5	0.62
Polydesmida	0	0	0	1	3	0	4	0.50
Anoplura	0	0	1	0	1	2	4	0.50
Total	85	82	127	115	175	223	807	100

(A)

(B)
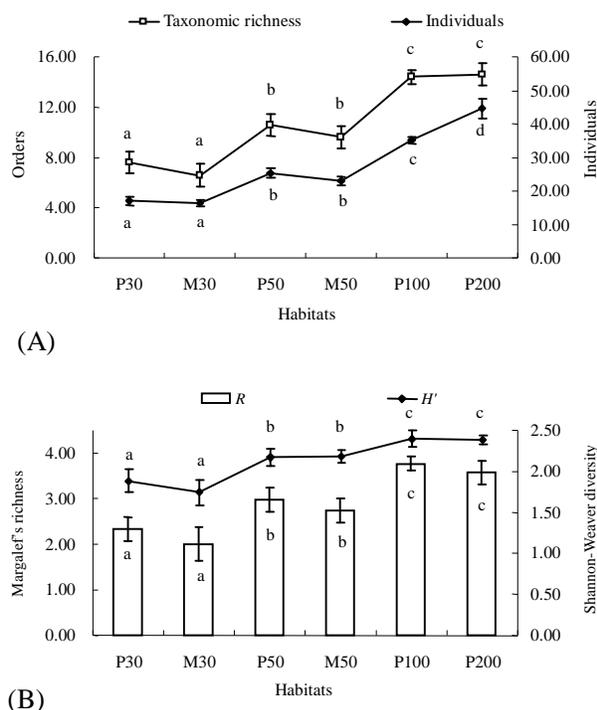
Fig. 2. One-way ANOVA on taxonomic richness and abundance (A), Margalef's richness index *R* and Shannon-Weaver diversity index *H'* (B) among different habitats (Mean±SE). The means with different scripts are significantly different by SNK test, α=0.050.

indicated that the communities can be divided into two groups, with the soil macrofauna communities sorted following the history of reclamation in coordinate axis 1 (Fig. 3). The communities' composition of soil macrofauna differed among habitats and the community groups corresponding to the diked history. We found that the soil macrofauna communities from forests can be distinguished from those with shorter diked history (30 and ≈50 years) or longer diked history (≈100 and ≈200 years).

The ANOSIM showed significant differences between communities (R=0.707, P<0.001), and the pairwise comparisons indicated no significant difference only between the communities from forests coded P30 and M30 (R=-0.028, P=0.558), whereas significant differences occurred in all other comparisons (P<0.050) (Table III).

DISCUSSION

History of land-use intensity has been proven to modify the relationship between complexity of the soil fauna and soil ecosystem (Salamon *et al.*, 2008; Liiri *et al.*, 2012). Our findings showed that a lower taxonomic richness and abundance of soil macrofauna occurred in samples from forest patches with shorter diked history, while a higher value

Table III.- **One-way ANOSIM analysis on similarity of soil macrofauna communities based on Euclidean distance.**

Habitat	M30	P50	M50	P100	P200
P30	R=-0.028 P=0.558	R=0.672 P=0.008	R=0.796 P=0.009	R=0.999 P=0.007	R=0.999 P=0.009
M30		R=0.648 P=0.007	R=0.790 P=0.007	R=0.999 P=0.009	R=0.999 P=0.007
P50			R=0.608 P=0.008	R=0.946 P=0.007	R=0.978 P=0.008
M50				R=0.954 P=0.006	R=0.996 P=0.007
P100					R=0.684 P=0.009
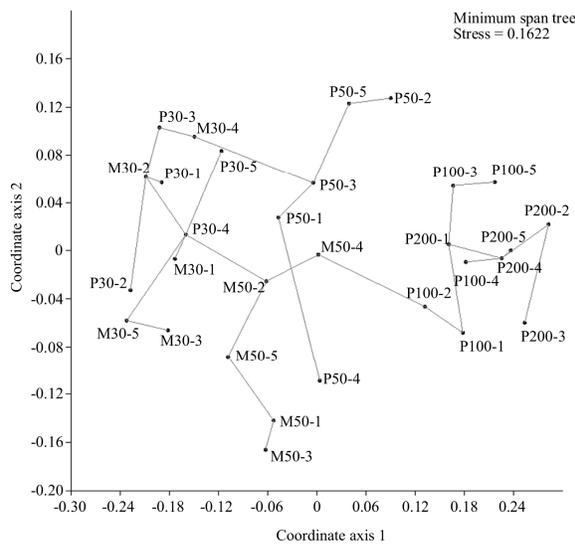
Fig. 3. The 2-dimensional nMDS ordinal configuration of soil macrofauna from different habitats with Bray-Curtis similarity method (In the code of the samples, the prefix means the code of habitat, the suffix means the number of sample).

occurred in forest patches with longer diked history, all of which reflect the same trends of biodiversity indices (Fig. 2). Thus, the results support the idea that the diked history has a significant effect on the composition of soil macrofauna communities, which could be affected by the soil chronosequence (Thomas *et al.*, 2004; Cui *et al.*, 2012a). Vegetation cover and soil characteristics could then be considered important factors to distinguish the habitats (Tasser and Tappeiner, 2002; Dewan and Yamaguchi, 2009; Ge *et al.*, 2014). The conversion

of land significantly affected the ecosystem of the coastal zone in the past decades (Etter *et al.*, 2006; An *et al.*, 2007).

Considering that soil fauna taxonomic diversity is huge, researchers want to simplify it by grouping together individuals by their shared properties. This work also addressed the lack of knowledge of taxonomy, such as functional guilds that were distinguished by food resources (Lefebvre and Gaudry, 2009). In the forest patches with longer diked history, most of the additional taxa of soil macrofauna were omnivorous or saprophagous (McGill *et al.*, 2006; Villéger *et al.*, 2008). Appearance of these taxa suggested that in such habitats soil environment provided sufficient food resources for these trophic groups (Brown *et al.*, 2002). Our results indicated that the biodiversity was closely related to the complexity of habitat, which was determined by the soil quality and vegetation environmental characters in the same soil chronosequence (Mathieu *et al.*, 2005; Paoletti *et al.*, 2009). No differences in soil macrofauna communities of M30 and P30 revealed by ANOSIM prove that the environment of younger habitats have a more similar history of development which is not yet overshadowed by the tree-species specific impacts on soil. (Table III). In other forests, the soil characteristics would be varied for the differences of the land use history and agricultural management practices (Salamon *et al.*, 2008; Zou *et al.*, 2011).

In the present study, the results of ordination analysis on macrofauna communities supported the conclusion that the diked age of 40 years should be the boundary of soil characteristic changes in the

study on the bacterial succession at Chongming Island (Cui *et al.*, 2012b). In Eastern Asia, the physicochemical properties of coastal saline soils significantly improved over the long term following reclamation. Long term fertilization and cultivation resulted in modified soil structure, enhancing the capacity for preserving fertility and C sequestration (Li *et al.*, 2014). Furthermore, soil organic carbon, total nitrogen and phosphorous was changed with the soil chronosequence, which could affect soil evolution processing (Fernández *et al.*, 2009; Cui *et al.*, 2012a). Here, we found that the patterns of soil macrofauna distribution and community composition were strongly related to land diked history. Our results proved that the reclaimed habitats with different diked history would maintain different biodiversity in the coastal ecosystem following soil evolution after reclamation.

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Statement of conflict of interest

There was no conflict of interest from the authors.

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