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Effect of land cover on biodiversity and composition of a soil macrofauna community in a reclaimed coastal area at Yancheng, China

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Abstract: Reclamation was considered the primary factor that caused coastal wetland loss in China. Along with land conversion, there were different types of land cover on the reclaimed coast. In early March 2012, we selected 5 habitats with different land cover from a reclaimed coastal area at Yancheng City that was diked about 30 years before, and the biodiversity and composition variations in soil macrofauna communities were studied. We found that higher biodiversity values appeared in the uncultivated land, the poplar forest, and the metasequoia forest, while lower values occurred in the wheat farm and bulrush land. By multivariate statistical analysis, significant differences in comparisons of soil macrofauna communities were detected, except for in the comparison between the poplar forest and the metasequoia forest. Our findings indicated that the biodiversity of macrofauna was significantly affected by habitat characters and the vegetation cover was strongly related to soil macrofauna distribution patterns and community composition in the reclaimed coastal area.

Key words: Reclamation, coastal ecosystem, soil evolution, soil macrofauna, wetlands

1. Introduction

Coastal wetlands are disappearing worldwide at an alarming rate; the loss has been 70%–80% in the last 50 years in some countries, such as in China, Japan, and the Netherlands (Duke et al., 2007; Wolanski, 2007). Because of economic development in the past decades, land resources have become more precious in some areas of China, and in eastern coastal areas the direct method to get new land was reclamation (Wang et al., 2012). The reclaimed land was used for urbanization, rice farms, forests, and shrimp ponds, such as in Yancheng, which is a city in the process of urbanization (Ge et al., 2012). The land cover has been greatly changed since the wetlands were reclaimed, but a mismatch between science and policy in coastal zone ecosystem management has been discussed (Paterson et al., 2011), such as in biodiversity conservation (Mora and Sale, 2011). Normally, coastal wetlands have high biodiversity and offer very important ecological services, and biodiversity patterns in reclaimed lands change with land use/cover conversions (Wolanski, 2007).

Land use/cover change has been considered as one of the most important factors affecting biodiversity in the ecosystem (Falcucci et al., 2007). It could eliminate the local species, degrade natural habitats and ecosystem functioning, and affect the biodiversity and provision of the ecosystem (Martínez et al., 2009), especially when massive land conversion occurs (Reidsma et al., 2006). The soil macrofauna are used to indicate the ecological health of soils (Barros et al., 2002), while land cover has a strong influence on the overall abundance, biodiversity, and community composition of soil macrofauna (Barrios et al., 2005; Azul et al., 2011).

Here, we addressed the question of the effect of land cover change on the biodiversity distribution pattern at coastal areas. We selected a coastal wetland which was diked about 30 years ago, and then evaluated and analyzed the biodiversity and composition variation of soil macrofauna communities in the habitats with different vegetation covers.

2. Methods

2.1. Study areas

Yancheng City is located in Jiangsu Province, China, on the west coast of the Pacific where the transition of subtropical and temperate zones occurs. Its average annual rainfall is 900 to 1100 mm.

A diked dam was built in the 1980s on the coast at Yancheng, and most of the diked land has been used for

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forests, farms, and shrimp ponds. In early March 2012, we selected 5 different types of land use/cover (uncultivated land, bulrush land, wheat farm, poplar forest, and metasequoia forest) for evaluating the biodiversity and composition variation in soil macrofauna (Figure 1), and the vegetation cover was described for each habitat (Table 1). The study area was diked from tidal zones about 30 years ago, and the soil in the study area is Fluvisols (FAO/UNESCO Taxonomy) or Inceptisols (Soil Taxonomy).

2.2. Sampling and identification

At each type of habitat, a sample plot was established; 5 soil blocks of 25 cm × 25 cm with a depth of 15 cm were collected and sorted. Sampling units were located 5-m apart and distributed randomly in the plot. The soil blocks were removed from the ground, and hand-sorted for soil macrofauna. Each soil block was hand-sorted for about 60 min and any macrofauna encountered were counted for abundance, preserved in 70% ethanol, and identified to order level (Pauli et al., 2011).

2.3. Data analysis

The Shannon–Weaver diversity index (*H'*) (Shannon and Weaver, 1949) and Margalef's richness index (*R*) (Margalef, 1957) were used to determine the biodiversity of communities. The diversity indices were usually adopted in the analysis of macrofauna communities, identifying the soil macrofauna at the order/class level (Pauli et al., 2011).

To detect the distribution variation in macrofauna communities among different habitats, one-way ANOVA was used in taxonomic richness and abundance comparisons, and then the Student–Newman–Keuls (SNK) test would be used if significant differences occurred (all datasets passed Levene's test in this study). Based on the community composition data, classification analysis (Bray–Curtis similarity) was used to analyze differences among communities from different habitats. Based on the Euclidean distance created from the community composition data, one-way ANOSIM (with the number of permutations as 9999) was used for testing the statistical significance among communities.

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

3. Results

A total of 16 soil macrofauna taxa (orders) were identified belonging to arthropods (13 groups), mollusks (2 groups), and annelids (1 group). Isopoda and Hymenoptera (all of which were ants) were the dominant groups (Table 2).

Significant differences were detected in taxonomic richness ($F_{4, 20} = 24.373$, $P < 0.001$), abundance ($F_{4, 20} = 95.590$, $P < 0.001$), *H'* index ($F_{4, 20} = 20.357$, $P < 0.001$), and *R* index ($F_{4, 20} = 11.522$, $P < 0.001$) of soil macrofauna among different habitats (Figure 2).

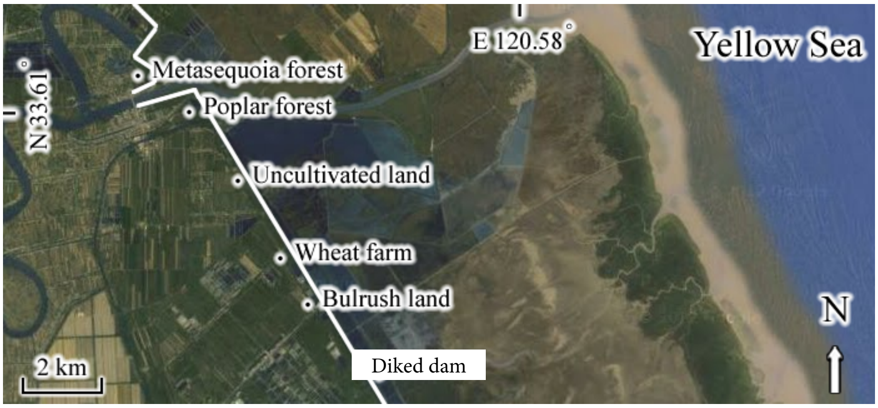

Figure 1. The distribution of sample sites on the reclaimed coast.

Table 1. The characters of selected habitats in the study.

Habitats	Vegetative characters	
	Arbor (coverage)	Herbage (coverage)
Uncultivated land	none	*Cynodon dactylon*, *Sonchus oleraceus, Chenopodium glaucum* (30%)
Bulrush land	none	*Phragmites communis* (90%)
Wheat farm	none	*Triticum aestivum* (80%)
Poplar forest	*Populus euramericana* (40%)	*Setaria viridis*, *Conyza canadensis* (40%)
Metasequoia forest	*Metasequoia glyptostroboides* (60%)	*Stellaria media, S. chinesis* (50%)

Table 2. Number of soil macrofauna (identified to order level) collected in the investigation from different habitats.

Order	Uncultivated land	Bulrush land	Wheat farm	Poplar forest	Metasequoia forest	Total	Frequency %
Hymenoptera	25	12	5	28	25	95	27.6
Isopoda	28	0	0	14	15	57	16.6
Lepidoptera	12	0	9	10	14	45	13.1
Coleoptera	6	0	6	10	8	30	8.72
Araneida	5	4	1	6	5	21	6.1
Haplotaxida	0	0	7	7	4	18	5.23
Hemiptera	3	0	0	7	7	17	4.94
Diplura	0	0	0	8	8	16	4.65
Diptera	0	5	0	3	3	11	3.2
Mesogastropoda	0	9	0	0	0	9	2.62
Orthoptera	2	0	0	2	4	8	2.33
Stylommatophora	4	0	0	2	2	8	2.33
Scolopendromorpha	1	0	0	1	1	3	0.87
Geophilomorpha	3	0	0	0	0	3	0.87
Opiliones	2	0	0	0	0	2	0.58
Scutigeromorpha	0	0	0	1	0	1	0.29
Total	91	30	28	99	96	344	100

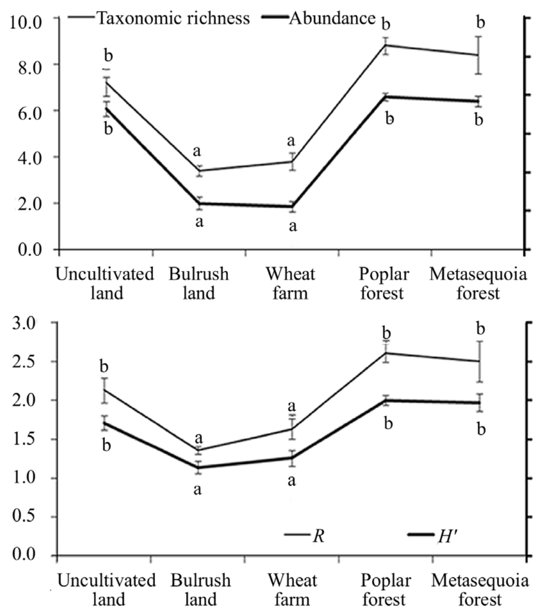

Figure 2. One-way ANOVA on taxonomic richness and abundance, Margalef's richness index (*R*) and Shannon-Weaver diversity index (*H'*) among different habitats (Mean ± SE). The means with different scripts are significantly different by SNK test, α = 0.05.

The cluster dendrogram (Figure 3) indicated that the communities could be divided into 3 groups (similarity at 0.6). The soil macrofauna communities from the poplar forest and the metasequoia forest were similar, and only one sample from uncultivated land mixed with the samples from the forests.

A significant difference was detected among communities by ANOSIM (R = 0.819, P < 0.001). Based on pairwise comparisons, there was no significant difference only between the communities from the poplar forest and the metasequoia forest (R = –0.192, P = 0.899), while a significant difference occurred in other comparisons (P < 0.050) (Table 3).

4. Discussion

Our results showed that there were significant differences in the habitats with different land covers, which could indicate the type of land use. It has been proved that the conversion of land use significantly affected the ecosystem of the coastal zone after decades (Etter et al., 2006; An et al., 2007). The results also indicated that the biodiversity was closely related to the complexity of the habitat, which was determined by the soil quality and vegetation

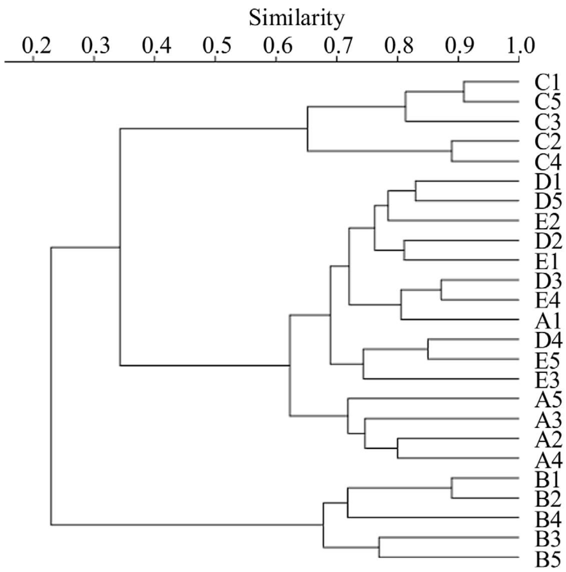

Figure 3. The dendrogram of cluster analysis on soil macrofauna from different habitats with Bray–Curtis similarity by paired groups method (A: Uncultivated land; B: Bulrush land; C: Wheat farm; D: Poplar forest; E: Metasequoia forest).

(Paoletti et al., 2009; Schöll and Devetter, 2013). The samples from the wheat farm and the bulrush land in this study had a lower taxonomic richness and abundance of soil macrofauna, while a higher value occurred in the uncultivated land, the poplar forest, and the metasequoia forest; then the biodiversity indices showed the same trend (Figure 2). Thus, our results support the idea that the type of land use has a significant effect on the composition of soil macrofauna communities (Smith et al., 2006; Ge et al., 2012), and the vegetation cover can be considered as a visual character to distinguish the type of land use (Tasser and Tappeiner, 2002; Dewan and Yamaguchi, 2009a, 2009b). The ecological function with land conversion would be caused by different land use (Drummond and Loveland, 2010).

We also find that the communities' composition of soil macrofauna differed among habitats and the community groups correspond to the types of land cover (Figure 3). By AMOSIM, we detected significant differences in comparisons of communities among different habitats with the soil macrofauna identified to order level, except between the poplar forest and the metasequoia forest (Table 3). The results showed that the vegetation cover was strongly related to patterns of soil macrofauna distribution and community composition (Wu et al., 2005; Pauli et al., 2011). The effect of trees on biodiversity should be especially considered (Barbier et al., 2008; Ge et al., 2012), which could affect the evolution processing of soil (Fernández et al., 2009).

Against the backdrop of economic development and urbanization in some developing countries, sharp changes in landscape pattern and composition along with large scale land use/cover change could be observed (Dewan et al., 2012). The habitats with different types of land use would offer different biodiversity in the coastal ecosystem following soil evolution after reclamation. Agricultural, industrial, and information/communication have been reported as 3 phases of land use change with different effects on biodiversity (Huston, 2005). In the study area, most of the reclaimed land was used for agriculture (such as for grains) and tended to eliminate those components of biodiversity that depend on high-productivity environments, while the forests and other marginal lands should be considered as the remaining reservoirs of biodiversity at the reclaimed coast (Huston, 2005). The biodiversity conservation at the reclaimed coast with the massive land conversion was important to the ecosystem health and services at regional scale (Reidsma et al., 2006; Martínez et al., 2009). Our results indicated the agricultural use of land would intensively affect the biodiversity in the reclaimed coast. We deemed that the type of land cover is an important factor that affects the biodiversity and composition variation in the soil macrofauna community in the study area.

Table 3. One-way ANOSIM on similarity of soil macrofauna communities based on Euclidean distance.

Habitats	Bulrush land	Wheat farm	Poplar forest	Metasequoia forest
Uncultivated land	R = 0.999 P = 0.009	R = 0.999 P = 0.009	R = 0.652 P = 0.008	R = 0.452 P = 0.008
Bulrush land		R = 0.996 P = 0.008	R = 0.996 P = 0.010	R = 0.999 P = 0.008
Wheat farm			R = 0.988 P = 0.008	R = 0.972 P = 0.007
Poplar forest				R = −0.192 P = 0.899

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