Pedosphere **20**(4): 466–478, 2010
ISSN 1002-0160/CN 32-1315/P

Published by Elsevier Limited and Science Press

PEDOSPHERE

www.elsevier.com/locate/pedosphere

Microbial Community Characteristics in a Degraded Wetland of the Yellow River Delta*[1]

WANG Zhen-Yu[1,*2], XIN Yuan-Zheng[1], GAO Dong-Mei[1], LI Feng-Min[1], J. MORGAN[2] and XING Bao-Shan[2]

[1] *College of Environmental Science and Engineering, Ocean University of China, Qingdao 266100 (China)*
[2] *Department of Plant, Soil and Insect Sciences, University of Massachusetts, Amherst, MA 01003 (USA)*

(Received January 26, 2010; revised March 23, 2010)

ABSTRACT

Five different sites with a soluble salt gradient of 3.0–17.7 g kg^{-1} dry soil from the coast to the inland were selected, and the microbial population size, activity and diversity in the rhizospheres of five common plant species and the adjacent bulk soils (non-rhizosphere) were compared in a degraded wetland of the Yellow River Delta, Shandong Province, China to study the effects of soil environment (salinity, seasonality, depth, and rhizosphere) on microbial communities and the wetland's ecological function, thus providing basic data for the bioremediation of degraded wetlands. There was a significant negative linear relationship between the salinity and the total number of microorganisms, overall microbial activity, or culturable microbial diversity. Salinity adversely affected the microbial community, and higher salinity levels resulted in smaller and less active microbial communities. Seasonal changes were observed in microbial activity but did not occur in the size and diversity. The microbial size, activity and diversity decreased with increasing soil depth. The size, activity and diversity of culturable microorganisms increased in the rhizospheres. All rhizospheres had positive effects on the microbial communities, and common seepweed had the highest rhizosphere effect. Three halophilic bacteria (*Pseudomonas mendocina*, *Burkholderia glumae*, and *Acinetobacter johnsonii*) were separated through BIOLOG identification, and common seepweed could be recommended for bioremediation of degraded wetlands in the Yellow River Delta.

Key Words: microbial activity, microbial diversity, rhizosphere, salinity, soil microorganisms

Citation: Wang, Z. Y., Xin, Y. Z., Gao, D. M., Li, F. M., Morgan, J. and Xing, B. S. 2010. Microbial community characteristics in a degraded wetland of the Yellow River Delta. *Pedosphere.* **20**(4): 466–478.

Microbial activity is important in wetland environments and for organic matter decomposition. Microorganisms can change the physical and chemical characteristics of a wetland soil, and play a vital role in soil organic matter dynamics, energy transfer, and elemental biochemical cycling (Angeloni *et al.*, 2006). In coastal wetlands, microbial decomposition prevents pollutants from entering into oceans (Liu *et al.*, 2007). In addition, different microbial species and communities provide different genetic resources and functions (Liu *et al.*, 2007). As a transition between terrestrial and aquatic ecosystems, wetlands provide a unique habitat for a diverse range of microbial species. High microbial diversity contributes to the genetic diversity of microbial populations and has a positive effect on the efficiency of nutrient cycling and important ecosystem processes, ensuring that all organic compounds are recycled (Loreau, 2001). At the same time, microorganisms are very sensitive to environmental changes. Some studies investigated the impacts of soil salinization on the microbial community and found that increasing salt levels had a significant negative impact on microbial populations: Yuan *et al.* (2007) found that there was a significant negative exponential relationship between soil salinity and soil microbial biomass and basal soil respiration. Sardinha *et al.* (2003) demonstrated a strong decline in the produc-

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[*1] Supported by the National Natural Science Foundation of China (No. 30570340), the National Key Technology R&D Program of China (No. 2006BAC01A13), the Program for New Century Excellent Talents in University, China (NCET-06-0599), and the Cheung Kong Scholar Program of the Education Ministry of China.

[*2] Corresponding author. E-mail: wang0628@ouc.edu.cn.

tion of adenosine-triphosphate (ATP) and ergosterol by microorganisms with salinity. Also, Rietz and Haynes (2003) reported a significant decrease in enzyme activity as soil salinity increased. In addition, Mühammad *et al.* (2008) concluded that a decrease in salinity can improve the accessibility of soil organic matter to the soil microbial community. Furthermore, other studies confirmed that soil organic matter, depth, and vegetation affect microbial communities. Understanding these effects is important as they affect soil quality and can be especially important for the remediation of degraded soils (Zak *et al.*, 2003; Zhou and Li, 2003; Ibekwe *et al.*, 2003, 2007). Environmental changes that alter microbial communities are serious threats to the stability and health of soil ecosystems (Riis *et al.*, 2003; Joeckel and Clement, 2005; Dong *et al.*, 2006; Lee and Liu, 2006; Chen *et al.*, 2007; Lin *et al.*, 2008). Therefore, the microbial community has been used as an indicator of soil quality (Zhang *et al.*, 2005).

The Yellow River Delta, located in the northern part of Shandong Province, has been characterized as the largest and youngest wetlands in the warm temperate zone of China (Xu *et al.*, 2004). In the Yellow River Delta, wetlands suffer acreage loss and degradation because of reclamation and human disturbance, *e.g.*, water recurrence changed or broken by banking up, diffluence and oil contamination. Global climate change is also a potential threat to the wetland's function and structure (Peng *et al.*, 2003). Soil salinity is a problem in this coastal wetland. The salinization may be the result of excessive exploitation, drying of the Yellow River, rising sea levels, and seashore erosion (Chen *et al.*, 2003). As the wetland further degrades and soil salinization progresses, breeding places for rare animal and plant species are threatened, and even destroyed (Chen *et al.*, 2003). Vegetative communities will also degrade, and the ability for humans to utilize the wetland benefits would be lost. These damaging effects can change the overall structure and function of the regional ecosystem (Xu *et al.*, 2004). While the effects of salinity on the physical and chemical properties of the soil and vegetation are well documented, some investigations on the soil microbiology have been undertaken in naturally saline soils (Rietz and Haynes, 2003; Sardinha *et al.*, 2003; Tripathi *et al.*, 2006; Yuan *et al.*, 2007). However, saline soil microbial community in this degraded wetland needs more attention.

There have been some researches about using vegetation for the bioremediation of saline soils in the Yellow River Delta, but less attention has been paid to the microbial community in the rhizosphere. Rhizosphere is the interaction center of plant, soil and microorganisms. Rhizosphere microorganisms can increase soil fertility, improve rhizosphere environment, promote the roots' growth, thus helping the protection of wetland vegetation and preventing wetland degradation. As rhizosphere microbial diversity decreases, plant growth may be affected (Ibekwe *et al.*, 2007). Therefore, it is hard to reach the bioremediation aim without considering the microorganism.

Accordingly, the aim of our research was to study the characteristics of microbial communities in the Yellow River Delta and the effects of soil salinity, seasonality, depth, and rhizosphere conditions on the size, activity, and diversity of soil microorganisms. Since there is lack of reports on the microbial community characteristics of wetland in the Yellow River Delta, this research can provide basic data for comparison with future data from the long-term observation of soil quality variation in the Yellow River Delta. The changes in the characteristics, structure and distribution of the microbial community due to environmental factors will be documented in an effort to identify the microbial resources in the Yellow River Delta. Knowledge of the seasonal and spatial fluctuation of microbial community will be helpful to identifying microorganisms with bioremediation potential. We also worked on the halophilic microorganisms which distributed broadly in the Yellow River Delta of the whole year. These microorganisms may be cultured in bulk and then introduced to the saline soil since they can survive in the saline environment. Therefore they can increase the soil fertility and be used to protect these wetland areas.

MATERIALS AND METHODS

Site description and soil sampling

The study was conducted in wetlands of the Yellow River Delta, Shandong Province, China. The