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Using microbial community functioning as the complementary environmental condition indicator: A case study of an iron deposit tailing area

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ABSTRACT

Various indices of soil microbial community and physiochemical properties at an iron deposit tailing area were investigated to evaluate the use of microbial community behavior as a complemental indicator of soil condition to traditional quality indices. Besides basal respiration rate and microbial carbon, the BIOLOG® method was applied to estimate the microbial ability in utilizing different carbon sources. Ordination methods to obtain a biological characterization of sampling sites, and principal response curve methods to reveal the carbon utilizing ability during the whole cultivating process were utilized in this study. The Nemerow composite index, which was used to assess the heavy metal contamination based on six total metal contents, hardly detected the overall discrepancy. However, there were significant differences in microbial functioning parameters at the five sampling plots, which provided more information about the environmental condition. The increases of certain metal contents and pH were accompanied by higher basal respirations (BAS). The increase of BAS did not correspond with the increase of carbon utilization and the higher level of microbial carbon contents. On the whole, these findings indicated that microbes can provide complementary information about different degrees of contamination and can be regarded as a usefully environmental indicator.

1. Introduction

Microbial communities have the ability to acclimatize, physiologically and evolutionally, to the changes in the environment [1]. The microbial characteristics have been receiving worldwide attention, especially in the aspect of environmental monitoring [2,3]. Numerous studies have focused on microbial community behavior under different types of land use, long-term farming management regimes, and polluted mining areas [1,4–6]. When focusing on the microbe response to metal contamination, many studies have demonstrated the suppressive effect of heavy metals on the microbial community [7–9] while other studies have reported the discovery of stimulating influences on microbial indices [10,11]. Taking into account the specific habitats of these studies, there is a functional redundancy of microbial communities which has correlation with these differences [12]. Total microbial community behavior such as respiration rates and microbial biomass tends to have local specific characteristics, and does not usually react in the same way when facing the same external influences [9]. For example, in metal-contaminated areas, the microbial functions in a highly polluted area may not be the same as those found in a mildly polluted region [13]. The potential of microbial functioning in assessing pollution in various tailing areas should be further investigated because it has the ability to sensitively reflect environmental changes.

Mine tailings have various negative effects on the environment, and their relationships with the microbial community have been discussed several times [7,14]. However, contrary to a constant concern about nonferrous metal deposits with serious toxic effects (such as those in Cu, Pb, and Zn mines), normal deposits like iron have been somehow neglected, even though their environmental effect have specific features. In our previous study, the functional diversity of microbial communities and microbial biomass was found to change significantly with certain kinds of metal concentrations in a gold mining area [13].

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In this paper we focused on the functioning of microbial communities in an iron tailing area, where great amounts of tailings and different kinds of heavy metals exist compared with nonferrous metal mines. In China, tailing sands and iron deposit rocks are mostly stacked directly on the ground [15]. These tailing dumps could bring harmful environmental influences through erosion, fluvial redeposition, and surface runoff. Soils in these areas are usually contaminated with toxic metals, including Cu, Zn, Pb, and Cd. Surface soil composition can be changed by running off from overburdened dumps. These negative effects on soil result in substantial loss of native vegetation and cause significant threats to human life [16]. Heavy metals from tailings also decrease the taxonomic diversity of soil communities and influence certain functional activities such as respiration or nitrification rate [9]. The microbial community plays an important role in element cycling, energy flow, and organic matter turnover in ecosystems [4]. Therefore, the influences of metals on ecosystems should be carefully investigated. In this study, we explore the reaction of microbial communities in an iron mine metal pollution area and their potential in giving external information about metal contamination.

The investigation was carried out to examine microbial functions in the biggest iron tailing area in Shandong Province, China. Besides basal respiration (BAS) rate and microbial carbon, the BIOLOG® method was applied to estimate the ability of microbes in utilizing different carbon sources [17]. We also tried to explore the community-level physiological profile (CLPP) change of microbes when facing iron tailing pollution and the simultaneous effects of other environmental factors such as pH, CEC and organic carbon contents. The main purpose was to assess the effects of heavy metal pollution on the microbial community and evaluate their indicative functions to the environmental condition in a typical iron deposit tailing area.

2. Materials and methods

2.1. Study area and soil sampling

The study area, Jinling iron mine, is located in Zibo City, Shandong Province, China (Fig. 1). The Jinling mining area has dozens of deposits consisting mostly of skarn, which has simple ore properties. A large deposit in the Jinling mining area, named Black Iron Hill deposit, was chosen as our soil sampling site. This deposit has been explored for about 60 years and formed typical gradients from tailing core to farm land. Throughout the years of exploring and grinding, ore tailings were stacked on the ground and gradually became a little hill, now measuring approximately 4 km^2. The sampling area were located between 36°50′39″North, 118°09′45″East to 36°50′37″North, 118°09′24″East (Fig. 1).

With the gradual but continuous accumulation of the tailing hill, differences between plant arrangement and coverage were found at various restoration stages. According to the distinct gradient, soil samples were collected in April at five sampling sites with three samples from each. Site 1 was set in the center of the tailing area where *Phragmites australis* communities are the dominant species. Plots 2 to 5 were all covered with pinaster and other shrubs. Soil samples were collected at a depth of 2–20 cm in 5 sites, each of which containing 3 replicated samples (Fig. 1). Each sample was the mixture of samples from four to six sites located at the corners of a 2 × 2 m square. Fifteen samples were transported to the laboratory sealed in sterile plastic bags. The soil of each sample was divided into two. One part was passed through a 2-mm sieve and stored at 4 °C for the BIOLOG® test, a 1-mm sieve for soil pH, and a 0.125-mm sieve for cation exchange capacity (CEC), organic C (C_{org}), total nitrogen (N_{t}), and analyses of metal contents. BIOLOG® tests were started as soon as possible after collection (storage temperature 4 °C).

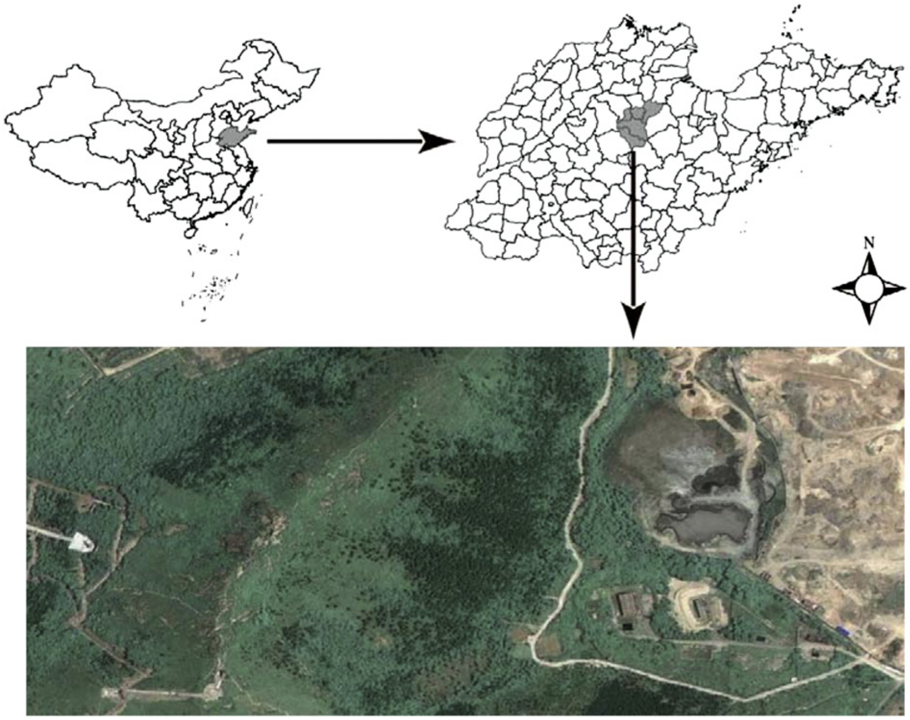

Fig. 1. Schematic representation of sampling sites. ZB represented the city of the studied area Zibo, ZB1 to ZB5 stand for the five sampling sites that the distances increase away from the tailing center.