Impacts of environmental factors on the whole microbial communities in the rhizosphere of a metal-tolerant plant: *Elsholtzia haichowensis* Sun

Songqiang Deng, Tan Ke, Longtai Li, Shenwen Cai, Yuyue Zhou, Yue Liu, Limin Guo, Lanzhou Chen, Dayi Zhang

**A B S T R A C T**

Rhizospheric microbes play important roles in plant growth and heavy metals (HMs) transformation, possessing great potential for the successful phytoremediation of environmental pollutants. In the present study, the rhizosphere of *Elsholtzia haichowensis* Sun was comprehensively studied to uncover the influence of environmental factors (EFs) on the whole microbial communities including bacteria, fungi and archaea, via quantitative polymerase chain reaction (qPCR) and high-throughput sequencing. By analyzing molecular ecological network and multivariate regression trees (MRT), we evaluated the distinct impacts of 37 EFs on soil microbial community. Of them, soil pH, HMs, soil texture and nitrogen were identified as the most influencing factors, and their roles varied across different domains. Soil pH was the main environmental variable on archaeal and bacterial community but not fungi, explaining 25.7%, 46.5% and 40.7% variation of bacterial taxonomic composition, archaeal taxonomic composition and alpha-diversity, respectively. HMs showed important roles in driving the whole microbial community and explained the major variation in different domains. Nitrogen (NH4-N, NO3-N, NO2-N and TN) explained 47.3% variation of microbial population composition and 15.9% of archaeal taxonomic composition, demonstrating its influence in structuring the rhizospheric microbiome, particularly archaeal and bacterial community. Soil texture accounted for 10.2% variation of population composition, 28.9% of fungal taxonomic composition, 19.2% of fungal alpha-diversity and 7.8% of archaeal alpha-diversity. Spatial distance had stronger influence on bacteria and archaea than fungi, but not as significant as other EFs. For the first time, our study provides a complete insight into key influential EFs on rhizospheric microbes and how their roles vary across microbial domains, giving a hand for understanding the construction of microbial communities in rhizosphere.

© 2017 Elsevier Ltd. All rights reserved.

1. Introduction

Heavy metals (HMs) in soils have become a serious environmental problem for degrading environmental quality, affecting food security and threatening human health (Li et al., 2014). HMs contamination is covert, persistent and irreversible, leaving technical challenges and attracting numerous physical and chemical approaches to remediate HMs contaminated soils (Wang et al., 2014).
Among them, phytoremediation has gained special attention as a cost-effective and environmentally friendly technology (Pilon-Smits, 2005). However, phytoremediation application is limited by its relatively low efficiency and long treatment cycle, owing to the low availability of HMs in soils and the slow growth of plants (Ma et al., 2011). The important roles of rhizospheric microbes in promoting plant growth and HMs transformation have therefore drawn particular attention. Microbial compositions, diversities and functions in rhizosphere are widely investigated in phytoremediation practices (Bolan et al., 2014; Jiang et al., 2016).

Rhizospheric microbes consist of several important populations including bacteria, fungi and archaea. They play different roles in phytoremediation (Buee et al., 2009; Ma et al., 2011). Rhizospheric bacteria affect the HMs transformation through changing soil pH, excreting chelating substances and altering redox potentials (Giller et al., 1998). They are also able to increase plant productivities via secreting plant hormones and improving nutrient availability (Verma et al., 2001). Rhizospheric fungi are reported to increase the surface area of plant root, benefiting the uptake and acropetal translocation of nutrients and HMs from soils. They can also ameliorate HMs toxicity in their plant hosts (Khan et al., 2000). Archaea are the key players in nitrogen cycle for their roles in soil ammonification, building up a mutual relationship with plants (Leininger et al., 2006). Therefore, rhizospheric microbes possess great potential for the success of phytoremediation.

Some evidence demonstrates the direct relationship between rhizospheric microbial community and phytoremediation efficiency (Johnson et al., 2005; Fernandes et al., 2017; Thijs et al., 2017). Nevertheless, it is still questioned whether phytoremediation is attributed to the whole microbiome rather than a single taxon (Uhlik et al., 2009; Bell et al., 2011). Notwithstanding some microbes are individually capable of mineralizing, transforming or detoxifying pollutants, their real roles in situ are actually embedded within the whole microbial community. Other work suggests that the phytoremediation efficiency is determined by the whole microbial populations and their inter-species interactions (Thijs et al., 2017). Although bacterial consortiums could achieve high cadmium removal efficiency in phytoextraction, the dominant genera of the inoculated microbes faded after one year, indicating the instability of introduced non-indigenous microbial consortium (Li et al., 2014). So far, little information is available about the roles of EFs on the whole rhizospheric microbial communities of *E. haichowensis* at Cu mine sites. The importance of each individual EFs remains unclear on Cu phytoremediation. We hypothesize that some significant EFs can affect the whole microbial community in *E. haichowensis* rhizosphere but their importance is dependent on microbial domains. The present study therefore aimed to: 1) unveil the whole microbial communities in the rhizospheric and surrounding soils of *E. haichowensis*, including bacteria, fungi and archaea; 2) explore the influence of 37 EFs on the whole microbial communities in the rhizosphere of *E. haichowensis*; 3) identify key influential factors shaping rhizospheric microbial community, and distinguish the response of different microbial population to each EF. This study gives a first insight into the whole microbial community within *E. haichowensis* rhizosphere in situ and a hand for understanding the construction of microbial communities in rhizosphere.

2. Materials and methods

2.1. Soil samples collection

Sixty *E. haichowensis* rhizospheric soil samples were collected from three areas in June 2016 (details see Electronic Supporting Information [ESI], Fig. S1): 1) a well-known Cu mine (Tonglushan, Hubei Province, China), where the mining activities started 3000 years ago and the soils are seriously contaminated (Huang et al., 2011); 2) a young Cu mine (Fengjiashan, Hubei Province, China) located 5 km away from Tonglushan, where the soils are less contaminated; 3) a non-metalliferous area (Macheng, Hubei Province, China) located 130 km away from Tonglushan (Cai et al., 2014). *E. haichowensis* was found in these three areas and collected from five sites in each area (ESI, Table S1). At each site, the soils surrounding the rhizosphere (Eh-surrounding) were collected by digging individual *E. haichowensis* and gently shaking. The rhizospheric soils from *E. haichowensis* (Eh-rhizosphere) were sampled by brushing the roots. Rhizospheric soils from other plants with the closest distance (nonEh-rhizosphere) were collected following the same method as described above. The bulk soils were sampled near Eh-surrounding soils at each site without vegetation. For each soil, triplicates were combined from adjacent plants and then packed on dry ice for transportation. Soil samples were then sieved through a 2-mm sterile mesh and then split into two parts for soil property analysis and DNA extraction, stored at 4°C and –80°C, respectively.

2.2. Soil physicochemical analysis

Soil pH was determined in 0.01 M CaCl₂ suspension (1:5, m/v) by pH meter (Luo et al., 2005). Seven HMs, including Cu, Cd, Cr, Zn, Co, Ni and Pb, were measured in terms of total, extractable and available fractions. For the total HMs, the soils were treated with aqua regia digestion using HNO₃ and HCl, and the extractable HMs were pretreated with 0.01 M CaCl₂ extraction. Soil available HMs were measured by diffusive gradients in thin-films (DGT), following previously described method using a C-LSLM Loaded DGT device (DGT Research Limited Corporation, UK) (Yao et al., 2016). The details of analytical methods for other soil properties are listed in ESI.

2.3. DNA extraction, quantitative polymerase chain reaction and sequencing

Soil DNA was extracted using FastDNA Spin Kit for Soil (MP
دریافت فوری
متن کامل مقاله

امکان دانلود نسخه تمام متن مقالات انگلیسی
امکان دانلود نسخه ترجمه شده مقالات
پذیرش سفارش ترجمه تخصصی
امکان جستجو در آرشیو جامعی از صدها موضوع و هزاران مقاله
امکان دانلود رایگان ۲ صفحه اول هر مقاله
امکان پرداخت اینترنتی با کلیه کارت های عضو شتاب
دانلود فوری مقاله پس از پرداخت آنلاین
پشتیبانی کامل خرید با بهره مندی از سیستم هوشمند رهگیری سفارشات