



Soil bacterial community response to vegetation succession after fencing in the grassland of China



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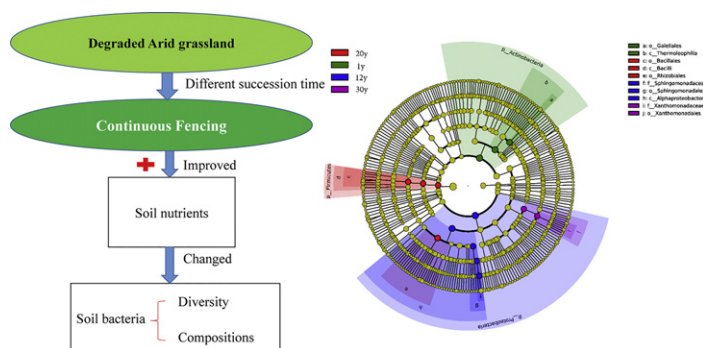
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HIGHLIGHTS

- Secondary succession after fencing significantly affected soil nutrients and plant coverage.
- Succession had no influence on soil bacterial diversity.
- Soil copiotrophic bacterial composition increased across succession.
- Soil nutrients and soil bacterial composition altered incongruously.

GRAPHICAL ABSTRACT



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ABSTRACT

Natural succession is an important process in terrestrial system, playing an important role in enhancing soil quality and plant diversity. Soil bacteria is the linkage between soil and plant, has an important role in aboveground community dynamics and ecosystem functioning in terrestrial ecosystems, driving the decomposition of soil organic matter and plant litter. However, the role of soil bacteria in the secondary succession has not been well understood, particularly in the degraded soil of Loess Plateau. In this study, we investigated soil nutrients and soil bacterial community during the secondary succession after a long-term fencing in the grassland, in the Yunwu Mountain, northwest China. The chronosequence included 1 year, 12 years, 20 years and 30 years. The soil bacterial community composition was determined by the Illumina HiSeq sequencing method. The data showed that soil bacterial diversity had no significant changes along the chronosequence, but soil bacterial community compositions significantly changed. Proteobacteria, Acidobacteria and Actinobacteria were the main phyla in all the samples across succession. With the accumulation of soil organic matter and nutrients, the relative abundance of Actinobacteria decreased, whereas Proteobacteria increased. These shifts may be caused by the increase of the available nutrients across the secondary succession. In the younger sites, soils were dominated by oligotrophic groups, whereas soil in the late-succession site were dominated by copiotrophic groups, indicating the dependence of soil bacterial community composition on the contents of soil available nutrients.

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1. Introduction

Plant secondary succession is a common phenomenon in the degraded areas, and has been proved that it is a useful and effective

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method to enhance soil quality and plant diversity in the world (Cheng et al., 2012; Knelman et al., 2015; Lozano et al., 2014; Van Hall et al., 2017; Zhang et al., 2016). Studying chronosequences improves well understand the function of underground and aboveground systems (Hannula et al., 2017). Plant is the driver of succession in restored areas, affecting soil chemical and physical properties through root growth and the input of plant litter and root exudates (Van Der Heijden et al., 2008). Some studies revealed that the long term plant succession had positive soil nutrients and enhanced plant diversity (Deng et al., 2014; Lozano et al., 2014; Sojneková and Chytrý, 2015). For example, Lozano et al. (2014) showed that a continuous increase in plant diversity and plant cover along a 84-year succession. The increase in plant diversity and cover with succession subsequently enhanced soil nutrients via root exudates and plant litter decomposition (Berg, 2014; Bertin et al., 2003). In turn, better soil nutrients improve the growth of plant and develop a sustainable system. Plant succession is essential for the interaction between plants and soil microorganism (Kuramae et al., 2011). In the below and above ground systems, soil nutrients and plant diversity along a succession have been well studied, but the role of soil bacteria is still far lag behind, especially in arid ecosystems (Cline and Zak, 2015; Lozano et al., 2014).

Soil bacteria are the linkage between soil and plant, driving the decomposition of soil organic matter and plant litter. Thus, soil bacteria play vital roles in soil element cycling, especially for carbon cycling and global warming. Little changes in microbial processes would cause a central effect on the global fluxes of greenhouse gases (Singh et al., 2010). Therefore, understanding the variations along a succession is essential to model and manage the restoration of degraded environments (Kirk et al., 2004). Across the secondary succession, some researchers have reported soil microbial diversity changed with the changes of plant diversity in different areas (Cline and Zak, 2015; Cutler et al., 2014; Zhang et al., 2016). These studies were partly indicated the changes of microorganism across the succession, but the function of different microbial communities in the soil were still unknown. Because soil is complex, it varies from nutrients to plant species. Thus investigating the role of soil microorganisms across the succession in the dryland is necessary and will guide the management of degraded pasture.

The study is designed to enhance the understanding of the effect of grazing exclusion and restoration sequence on the function of soil bacteria. The Yunwu Mountain reserve, excluded from grazing since 1982, is the only remaining grassland region of the Loess Plateau. The long-term (30 years) fencing has made it possible to better understand the effects of grazing exclusion on both soil properties and soil bacteria. Therefore, this study focused on four different restoration ages (30 years, 20 years, 12 years and 1 year) along a successional gradient in northwest China. Thus, we tested the following hypotheses: the diversity of soil bacteria and copiotrophic communities increased as the increase of soil nutrients across the succession. This study strengthens the understanding of the restoration of soil C, N and P sequestration and the changes of soil bacterial communities in degraded grasslands on the Loess Plateau.

2. Methods and materials

2.1. Studied areas

The experiment area is located in the Yunwu Mountain Reserve for Vegetation Protection and the Eco-environment in the city of Guyuan, Ningxia Province, China. Predominant soil of the experimental site is a loess based on the Chinese soil classification and Entisols, according to the U.S.A. taxonomy, respectively (Staff, 1999; Zeng et al., 2016). The primary plant species are herbaceous plants (i.e., *Androsace erecta*, *Artemisia capillaries*, *Artemisia frigid*, *Artemisia sacrorum*, *Heteropappus altaicus*, *Lespedeza davurica*, *Potentilla acaulis*, *Stipa bungeana*, *Stipa grandis*, *Thymus mongolicus*, etc.). The dominant plant species are *Stipa bungeana*, *Thymus mongolicus*, and *Artemisia vestita*. The reserve consists of three areas, including core area, buffer area and experimental area, which have comparatively similar geographical patterns and climate (Fig.1). The core area comprises approximately 1000 ha, which is totally enclosed and accounts for 25% of the total area. In the core area, the *Stipa bungeana* community is the most extensive; *Stipa grandis* and *Stipa bungeana* are the dominant grass species, and *Thymus mongolicus* and *Artemisia sacrorum* are the dominant forb species. The buffer area covers 1200 ha and also accounts for approximately 25% of the total area. The

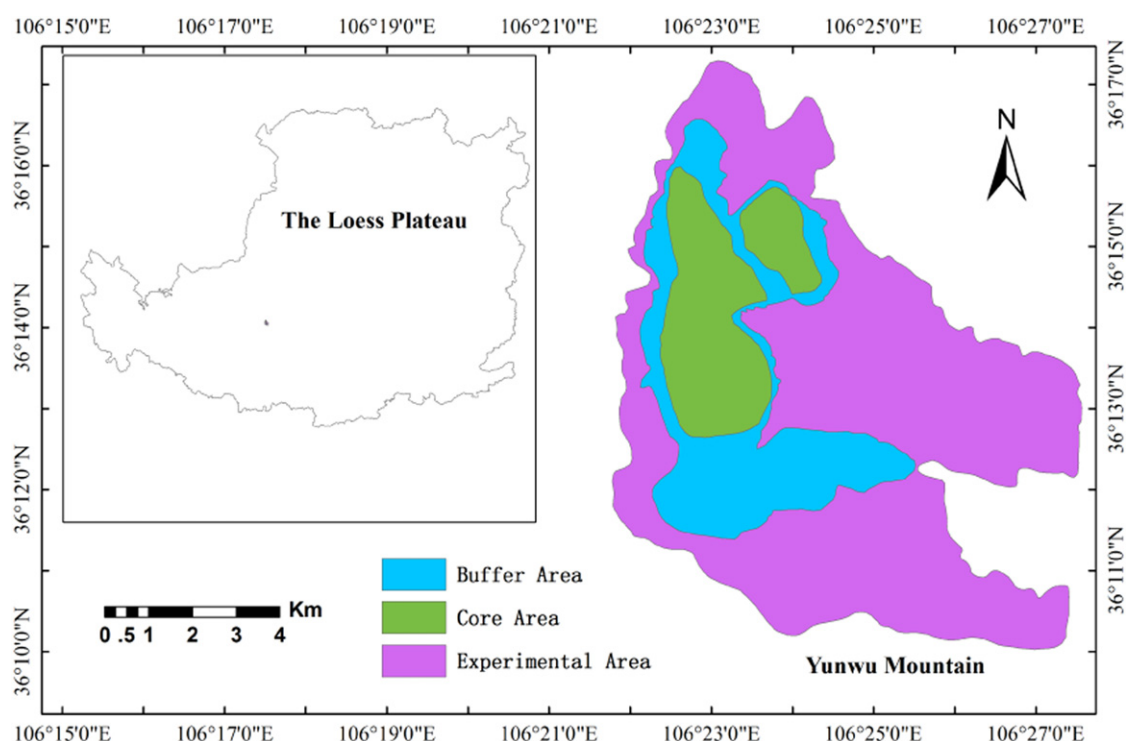


Fig. 1. The information of sampling site in the Yunwu Mountain, the Loess Plateau.

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