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Effects of thinning intensity on understory vegetation and soil microbial communities of a mature Chinese pine plantation in the Loess Plateau

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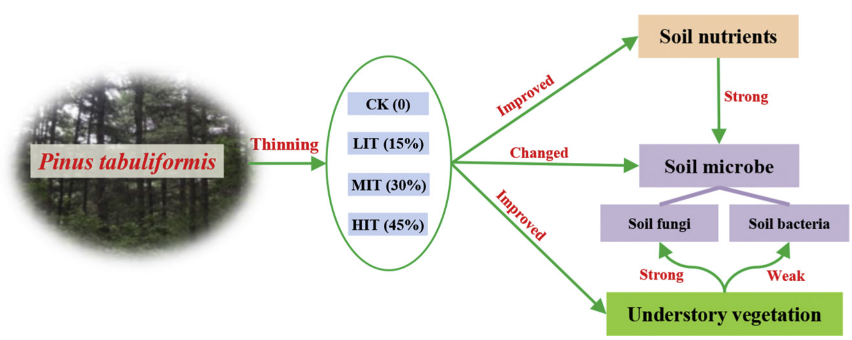
HIGHLIGHTS

- Thinning increased understory plant diversity and soil nutrients after 11 years.
- Thinning intensity had no significant influence on soil microbial diversity.
- Soil copiotrophic bacteria increased with increasing thinning intensity.
- Understory vegetation affect fungi more strongly than bacteria after thinning.

GRAPHICAL ABSTRACT



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ABSTRACT

Thinning can effectively improve forest production and maintain ecological stability. However, the changes in soil microbial community compositions after thinning are still not well understood. In this study, we investigated the changes in the soil microbial community of mature Chinese pine (*Pinus tabuliformis*) plantations in the Loess Plateau after 11 years of four different thinning intensity treatments. Furthermore, the responses of the soil microbial community to changes in understory plants and soil properties were analyzed. The ratios of wood removal investigated were 0 (CK), 15% (LIT), 30% (MIT) and 45% (HIT). Compared with the CK, thinning significantly increased the Shannon index, species richness, coverage and biomass of the understory plants, and these values were highest for the HIT. The soil organic carbon (SOC), total nitrogen (TN), total phosphorus (TP), nitrate nitrogen (NO_3^--N) and available phosphorus (AP) concentrations increased with increasing thinning intensity. Thinning intensity did not significantly affect soil microbial community diversity indices. With respect to the dominant bacterial groups, the relative abundance of Proteobacteria was much higher in the HIT, while that of Acidobacteria was much higher in the LIT and CK. For the dominant fungal groups, the relative abundance of Basidiomycota was lowest in the HIT, while that of Ascomycota was highest in the same treatment. Redundancy analysis (RDA) showed that SOC, TN, and AP significantly correlated with soil bacterial communities and that SOC, TN, TP, AP and NO_3^--N significantly correlated with soil fungal communities. The understory vegetation influenced soil fungal communities rather than soil bacterial communities. These findings suggest that the aboveground vegetation diversity and soil nutrients were improved with the increased thinning intensity after 11 years. The copiotrophic groups (e.g. Proteobacteria) and oligotrophic groups (e.g. Acidobacteria) differed significantly among the four thinning treatments, indicating a dependence of the soil microbial community composition on soil nutrients.

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1. Introduction

Thinning practices have been widely employed in forest management to protect forest biodiversity, improve the quality of regenerated tree products, and maintain ecosystem function (Chen et al., 2015; Trentini et al., 2017). This silvicultural treatment can directly or indirectly influence the above- and belowground forest characteristics (Taki et al., 2010; Vesterdal et al., 1995). Furthermore, changes in these characteristics, such as plant communities and soil abiotic factors, may affect soil microbial communities in the forest ecosystems (Barg and Edmonds, 1999). For example, changes in plant communities directly affects litter, roots and plant exudates that indirectly affects SOC and other edaphic properties that influence soil microbial community structure and diversity (Prescott and Grayston, 2013; Urbanová et al., 2015). Soil microorganisms may strongly react to the growth of plants because of released mineral elements near the rhizosphere (Singh et al., 2004; Zhang et al., 2016). Thus, Above- and belowground plant and microbial communities interact to influence community- and ecosystem-level processes and properties in terrestrial ecosystems (Wardle et al., 2004). Understanding the relationships between understory vegetation, soil properties and soil microbial communities will therefore be undoubtedly necessary for forest thinning research.

The forest management practice of thinning can affect understory biodiversity due to changes in canopy densities and forest microclimate parameters (Ares et al., 2010; Taki et al., 2010; Tang et al., 2007). Thinning exerts positive (Taki et al., 2010), negative (Metlen and Fiedler, 2006) or neutral (Lei et al., 2007) effects on understory vegetation because of variations in deforestation time and intensity, thinning site conditions, and stand ages (Fulé et al., 2005; Lei et al., 2007). Thinning practices also promoted the coexistence and development of different shade-tolerant species once a certain gap size forms after thinning (Wang and Liu, 2011; Wang et al., 2017). Despite the extensive research on understory plants have been done, how thinning affects soil microbes is still unclear. Because soil microorganisms are important in the regulation of nutrients cycling between above- and belowground communities, they have great influence on ecosystem processes (Wall and Moore, 1999). Thinning practices influence understory plants in forest ecosystems (Kerr, 1999), thereby affecting the functions of the microorganisms in belowground ecosystems (Bengtsson et al., 2000). Previous studies investigated the effects of thinning on soil nutrients cycling (Vesterdal et al., 1995), soil microbial biomass and enzymes (Boerner et al., 2008; Thibodeau et al., 2000), and soil and microbial respiration (Akburak and Makineci, 2015; Tang et al., 2005). Several studies have studied the response of soil microbial community structures to thinning practices (Lin et al., 2016; B. Yang et al., 2017). However, most of the methods used in these studies, such as PCR- denaturing gradient gel electrophoresis (DGGE), and phospholipid fatty acid (PLFA), have limitations that prevent an accurate, detailed description of the microbial community compositions. The development of next-generation sequencing technology, also known as high-throughput sequencing technology, has allowed for a much greater phylogenetic resolution to be achieved than previous methods, such as cloning libraries, DGGE and phospholipid fatty acid (PLFA) analyses (Liu et al., 2014; Baldrian et al., 2012; Nacke et al., 2011). The use of this method is therefore advantageous to understanding the aboveground-belowground feedback for the forest management of plantation ecosystems. However, knowledge of the relationships between understory vegetation, soil abiotic characteristics and microorganisms in plantations after thinning is very poor.

Chinese pine is a major conifer tree species that grows over large areas in northern China that have been afforested for ecological restoration. However, after decades of growth, many plantations have become seriously degraded due to a number of problems, including the presence of high stand density, low forest species diversity, and poor regeneration capacity, especially in the Loess Plateau region, which has a fragile ecosystem and serious soil and water erosion (Ma et al., 2007; Cao et al., 2009). Thinning has been implemented since 2005 to improve the biological diversity and ecosystem stability in the Loess Plateau plantations. Observations of the effects of thinning on Chinese pine plantation ecosystems have primarily concentrated on aboveground characteristics such as plant diversity and seedling regeneration, and belowground environmental factors such as soil properties (Chen and Cao, 2014; Wen-juan et al., 2012; Yun-chang et al., 2013). Research on soil microbial community compositions and their relationships with plant communities and soil abiotic factors is still scarce. However, this information is essential to understanding the fundamental ecological processes in Chinese pine plantations after a decade of thinning. Furthermore, such research has practical implications for the appropriate management and conservation of the environment.

In this study, we explored the changes in understory vegetation properties, soil physicochemical properties and microbial community compositions in 55-year-old Chinese pine plantations with four thinning treatments after 11 years. The study aimed to (1) assess the changes in understory vegetation, soil properties and soil microbial community composition and diversity after thinning; and (2) explore the relationships among understory plants, soil properties and soil microbial communities in thinned plantations. We hypothesized that the thinning of Chinese pine plantations after 11 years would change the soil microbial community structures and that these microbial communities would be associated with the understory plant communities and soil physicochemical properties.

2. Materials and methods

2.1. Study area description

The study was conducted in Chinese pine plantations located in the Caijiachuan forest area of Huanglong county (35°28′–36°02′N, 109°38′–110°12′E), which is located in the southern Loess Plateau, Northwest China. This region in the Loess Plateau that typically exhibits hills and gullies with an elevation of 1100–1300 m. The region has a warm, temperate, continental monsoon climate with a mean annual temperature of 8.6 °C with 611.8 mm of precipitation, 2369.8 h of sunshine, and a frost-free period of 158 days each year. The soil in this region is classified as cinnamon soil according to the national standards of China (China soil classification and code GB/T 17296–2009).

2.2. Soil sampling and plants investigation

The experiments were conducted in August 2016 and four sites subjected to four thinning treatments were selected for sampling. The four treatments were no thinning (CK, control), low-intensity thinning (LIT, 15% of the trees removed), moderate-intensity thinning (MIT, 30% of the trees removed) and high-intensity thinning (HIT, 45% of the trees removed). Three replicate plots (20 × 20 m) with similar slopes, gradients and altitudes were established at each site. Each plot was surrounded by buffer zones (5 m) to reduce potential edge effects. The standard plots are adjacent and are at least 100 m apart from one another. The stand characteristics, including stand density, canopy density, mean height and diameter at breast height (DBH) were measured for the four different thinning treatments sites (Table 1).

For each triplicate plot, nine soil corns of topsoil (0–10 cm) were collected with an "S" shape after removing the litter layer and then mixed to form one sample. A stainless-steel corer with a 4.5-cm inner diameter was used to collect soil. These standard plots are adjacent and are at least 100 m apart from one another. Overall, twelve samples (four stand sites × three plots) were collected. All the samples were sieved quickly with 2 mm mesh, and the roots and other debris were removed. Next, the samples were divided into two subsamples and immediately transported to the laboratory on ice. One set of subsamples was stored at −80 °C for later DNA extraction, while the second set was air-dried