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Bacterial communities drive the resistance of soil multifunctionality to land-use change in karst soils

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ABSTRACT

Bacterial communities play key roles in maintaining ecosystem multifunctionality. With increasing land use intensity, soil biogeochemical and microbial characteristics change significantly and may affect the multifunctionality of ecosystems. The relationship between soil microbial communities and resistance of multiple ecosystem functions under land-use change has not previously been assessed in the karst regions. Soils from four karst ecosystems (primary forest, secondary forest, abandoned land and cultivated land) were analyzed for microbial communities as predictor of multifunctional resistance to land use change by using high-throughput sequencing, structural equation modeling and random forest modeling. We evaluated the multifunctional resistance of soil ecosystems by measuring indicators related to soil carbon, nitrogen and phosphorus cycling. The resistance of Proteobacteria was the highest in the secondary forest, and that of Verrucomicrobia was the highest in the abandoned and cultivated lands. With increasing land-use intensity, C-cycling functional resistance decreased by 77% and nitrogen functional resistance increased by 17% in the abandoned land, compared with those in the secondary forest. Bacterial communities had the largest direct positive effect on multifunctional resistance and N-related functional resistance. Among bacterial communities, Verrucomicrobia and Chloroflexi were the two most important phyla that affected soil multifunctional resistance. Armatimonadetes_unclassified, Chloroflexia and OPB35_soil_group were the best predictor of total organic carbon, total nitrogen and total phosphorus content, respectively. Our results suggested strong links between microbial community composition and multifunctional resistance in various karst ecosystems, and provided insights into the importance of microbial community composition in the recovery of ecosystems following human intervention.

1. Introduction

Soil microbial communities play a vital role in the biogeochemical cycle of almost all terrestrial ecosystems. Microbial diversity and community composition will affect the decomposition of organic matter, nutrient cycling, plant diversity and productivity [1–4]. The increase in bacterial abundance in the soil can promote ecosystem multifunctionality response to environmental changes [5]. While a reduction in bacterial abundance reduced the multifunctionality of the ecosystem [3]. The resistance is an important part of ecosystem stability [6]. Current researches have shown changes in microbial properties, such as bacterial α -diversity can affect the multifunctional resistance of an

ecosystem [7] or in the global scale [8]. Therefore, microbial diversity has a positive linear relationship with the multifunctional resistance of ecosystems [7]. Land use change is a primary driver of changes in microbial diversity [9]. Human activities (such as land-use change) have threatened soil microbial diversity. Increasing human perturbation can reduce microbial diversity and result in biodiversity homogenization across time and space through the loss of endemic taxa [10]. Therefore, the impact of land-use change on soil microbial communities has the potential to affect soil ecosystem functions and stability [11].

Previous studies have reported that the conversion of forests to cultivated land reduced the diversity of fungi [12] and bacteria [13]. On the other hand, the restoration of cultivated land to forests increases the

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