

Critical transition of soil bacterial diversity and composition triggered by nitrogen enrichment

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Abstract. Soil bacterial communities are pivotal in regulating terrestrial biogeochemical cycles and ecosystem functions. The increase in global nitrogen (N) deposition has impacted various aspects of terrestrial ecosystems, but we still have a rudimentary understanding of whether there is a threshold for N input level beyond which soil bacterial communities will experience critical transitions. Using high-throughput sequencing of the 16S rRNA gene, we examined soil bacterial responses to a long-term (13 yr), multi-level, N addition experiment in a temperate steppe of northern China. We found that plant diversity decreased in a linear fashion with increasing N addition. However, bacterial diversity responded nonlinearly to N addition, such that it was unaffected by N input below 16 g N·m⁻²·yr⁻¹, but decreased substantially when N input exceeded 32 g $N \cdot m^{-2} \cdot yr^{-1}$. A meta-analysis across four N addition experiments in the same study region further confirmed this nonlinear response of bacterial diversity to N inputs. Substantial changes in soil bacterial community structure also occurred between N input levels of 16 to 32 g N·m⁻²·yr⁻¹. Further analysis revealed that the loss of soil bacterial diversity was primarily attributed to the reduction in soil pH, whereas changes in soil bacterial community were driven by the combination of increased N availability, reduced soil pH, and changes in plant community structure. In addition, we found that N addition shifted bacterial communities toward more putatively copiotrophic taxa. Overall, our study identified a threshold of N input level for bacterial diversity and community composition. The nonlinear response of bacterial diversity to N input observed in our study indicates that although bacterial communities are resistant to low levels of N input, further increase in N input could trigger a critical transition, shifting bacterial communities to a low-diversity state.

Key words: acidification; bacterial community composition; bacterial diversity; life history; plant diversity; threshold.

INTRODUCTION

Human activities, such as industrialization of fossil fuel combustion and agricultural fertilizer application, have caused increasing nitrogen (N) deposition (Galloway et al. 2004), which poses a serious threat to terrestrial biodiversity (Butchart et al. 2010). This is especially

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true for grasslands, where N deposition leads to loss of plant diversity across the world (Stevens et al. 2004, Suding et al. 2005, Isbell et al. 2013, Zhang et al. 2019). Soil bacterial communities represent a large proportion of terrestrial biodiversity (Whitman et al. 1998, Delgado-Baquerizo et al. 2017). Both soil physiochemical properties (Fierer and Jackson 2006, Cruz-Martinez et al. 2009, Zhou et al. 2016) and plant community composition (Kowalchuk et al. 2002, Wardle et al. 2004) are known to influence soil bacterial diversity and composition. Yet, it remains largely unknown whether plant and