



Deforestation decreases spatial turnover and alters the network interactions in soil bacterial communities



Jing Tian^{a,b}, Nianpeng He^{a,b}, Weidong Kong^{c,b}, Ye Deng^{d,b}, Kai Feng^{b,d}, Sophie M. Green^e, Xiaobo Wang^f, Jizhong Zhou^{g,h}, Yakov Kuzyakov^{i,j}, Guirui Yu^{a,b,*}

^a Key Laboratory of Ecosystem Network Observation and Modeling, Institute of Geographic Sciences and Natural Resources Research, Chinese Academy of Sciences, Beijing, 100101, China

^b College of Resources and Environment, University of Chinese Academy of Science, Beijing, 100049, China

^c Key Laboratory of Alpine Ecology and Biodiversity, Institute of Tibetan Plateau Research, Chinese Academy of Sciences, Beijing, 100101, China

^d Key Laboratory for Environmental Biotechnology, Research Center for Eco-Environmental Sciences, Chinese Academy of Sciences, Beijing, 100085, China

^e Geography, College of Life and Environmental Sciences, Amory Building, University of Exeter, Rennes Drive, Exeter, EX4 4QD, UK

^f Erguna Forest-Steppe Ecotone Research Station, Institute of Applied Ecology, Chinese Academy of Sciences, Shenyang, 110016, China

^g Institute for Environmental Genomics, University of Oklahoma, Norman, OK, 73019, USA

^h State Key Joint Laboratory of Environment Simulation and Pollution Control, School of Environment, Tsinghua University, Beijing, 100084, China

ⁱ Department of Agricultural Soil Science, University of Göttingen, Göttingen, 37077, Germany

^j Institute of Environmental Sciences, Kazan Federal University, Kazan, 420049, Russia

ARTICLE INFO

Keywords:

Deforestation
Bacterial community structure
Spatial turnover rate
Microbial network interactions
Distance-decay relationship

ABSTRACT

Despite important progress in understanding the influence of deforestation on the bacterial α diversity and community structure at local scales, little is known about deforestation impacts in terms of spatial turnover and soil bacterial community network interactions, especially at regional or global scales. To address this research gap, we examined the bacterial spatial turnover rate and the species networks in paired primary and secondary forest soils along a 3700-km north-south transect in eastern China using high-throughput 16S rRNA gene sequencing. The spatial turnover rate of bacterial communities was higher in primary forests than in secondary, suggesting deforestation increased biotic homogenization at a large geographic scale. Multiple regression on matrices analysis revealed that both geographic distance and soil properties (especially soil pH and organic matter availability) strongly affected bacterial spatial turnover. Through the phylogenetic molecular ecological network approach, we demonstrate that the bacterial network of primary forests was more intricate than in secondary forests. This suggests that microbial species have greater niche-sharing and more interactions in primary forests as compared to secondary forests. On the other hand, the bacterial network in secondary forests was more modular, and the taxa tended to co-occur, with positive correlations accounting for 82% of all potential interactions. In conclusion, our findings demonstrate that anthropogenic deforestation has clear effects on bacterial spatial turnover and network interactions, with potential for serious consequences such as microbial diversity loss in primary forests.

1. Introduction

More and more primary forests are being cleared or strongly disturbed globally by human activities to make free areas for agriculture, wood production, human habitation and industry (Gómez-Acata et al., 2016). With increasing intensity of anthropogenic perturbations, more attention is being placed on secondary forests, since they may act as buffer zones and serve as a habitat for forest plants, animals and microorganisms displaced from destroyed primary forests (Brearley et al.,

2004). Soil microbial communities are engineers of important biogeochemical processes and play a critical role in regulating the functions and stability of an ecosystem (Naeem and Li, 1997; Fuhrman, 2009). Many studies showed that deforestation changed soil bacterial α diversity, composition and community structure on local scales (Jesus et al., 2009; Bastida et al., 2015; Gómez-Acata et al., 2016; Wood et al., 2017). However, little is known about the effects of deforestation on spatial turnover and species interactions of bacterial community at a large spatial scale, e.g. regional, continental or global.

* Corresponding author. Key Laboratory of Ecosystem Network Observation and Modeling, Institute of Geographic Sciences and Natural Resources Research, Chinese Academy of Sciences, Beijing, 100101, China.

E-mail address: yugr@igsnr.ac.cn (G. Yu).

<https://doi.org/10.1016/j.soilbio.2018.05.007>

Received 4 January 2018; Received in revised form 8 May 2018; Accepted 10 May 2018

Available online 15 May 2018

0038-0717/ © 2018 Elsevier Ltd. All rights reserved.