

分类号: Q14

学校代码: 10269

密 级: _____

工 号: 20164066



華東師範大學

博士后研究工作报告

土壤微生物多样性及其在不同人类干扰梯 度下的群落构建

博士后姓名: 刘兰
合作导师: 张健 教授
流动站(一级学科): 生态学
院系(所): 生态与环境科学学院
研究工作开始时间: 2016 年 9 月
研究工作完成时间: 2021 年 4 月

华东师范大学(上海)
2021 年 4 月

土壤微生物多样性及其在不同人类干扰梯度下的群落构建

Soil microbial diversity and the assembly rules of soil microbial
communities along different human disturbance gradients

博 士 后 姓 名 刘 兰

流动站（一级学科）名称 华东师范大学生态学博士后流动站

专 业（二级学科）名称 生态学

研究工作起始时间 2016 年 9 月 6 日

研究工作期满时间 2021 年 4 月 31 日

华东师范大学（上海）

2021 年 4 月

内 容 摘 要

土壤微生物在生物地球化学循环、生态系统稳定性和植被恢复等过程中起到重要作用。然而目前关于土壤微生物多样性的分布格局和群落构建机制，尤其在人类世背景下，土壤微生物多样性和群落结构是否和怎样响应人类干扰、影响生态系统功能和植被恢复等问题还难以回答。本工作首先从土壤微生物和植物功能相关性角度，分析了全球尺度上土壤微生物和植物多样性相关性的格局，以揭示全球尺度上土壤微生物多样性的分布现状及其影响因子。检验不同人类干扰梯度中土壤微生物多样性和群落结构变化，并结合群落构建机制的分析，以期揭示土壤微生物是否和怎样响应人类干扰、影响生态系统功能。主要研究结果包括：

(1) 基于全球尺度上 84 个研究，3900 多个取样点的分析，土壤微生物多样性与植物多样性具有弱的正相关关系 ($r = 0.333$, $CI = 0.220-0.437$)。这一相关性在不同的微生物类群和研究尺度上存在显著差异，在中等的纬度和海拔跨度范围和热带地区具有较高的正相关。在检验的环境因素中，土壤 pH 值与全球尺度上土壤微生物与植物多样性负相关。在相对贫瘠和具有较为松散结构的土壤中，微生物-植物的相关性对土壤因子的变化更为敏感。

(2) 在两个亚热带森林干扰后恢复的演替序列的研究发现，从演替早期的灌丛和针叶林到演替顶级的常绿阔叶林，土壤原核生物和真菌的群落在不同演替阶段上显著差异，并且演替早期通常具有更高的群落结构变异。检验群落构建过程随演替的变化，确定性过程主导了土壤中原核生物和真菌的群落构建，但随机性过程的相对重要性在演替恢复后期增加。检验环境因子的影响，植物群落结构的差异与群落构建过程相对重要性随演替的变化显著相关。在植物群落结构差异较大的土壤中，原核生物和真菌的群落受到越强的确定性选择的影响。

(3) 在上海市这一高度人类干扰的城市，基于 258 个取样点的土壤微生物与植物多样性数据的分析发现，增加的人类干扰与土壤原核生物、总真菌和丛

枝菌根真菌群落同质化正相关，也与增加的土壤原核生物、总真菌的多样性正相关。在相对较高的（如~70%城市化用地覆盖）和较低的人类干扰（如~30%城市化用地覆盖）下，多种土壤微生物的相对多度分别表现出显著的增加和降低的趋势。土壤 pH 是影响土壤微生物多样性和群落结构变异的主要因子，但人类干扰单独的解释了一部分土壤微生物的变异。另外，从群落构建过程的角度解释微生物群落的变异，人类干扰可能通过增加随机过程影响土壤微生物群落结构。

以上研究表明在不同的微生物类群、尺度跨度范围和生态系统中，土壤微生物与植物多样性的相关性存在差异；人类干扰环境中，土壤微生物能够响应变化的生物和非生物环境，可能具有可预测的规律；高强度的人类干扰的城市生态系统可能通过改变土壤环境的选择过滤、增加随机过程等作用影响微生物分布与群落结构。这些研究结果对揭示人类干扰怎样影响土壤微生物群落和扰动后生态系统恢复的研究至关重要。

关键词：微生物生物地理学，次生演替，城市生物多样性，随机过程，确定性过程， β 多样性

Abstract

Soil microbes play crucial roles in biogeochemical cycles, ecosystem stability, and ecosystem recovery. However, our knowledge of the diversity and underlying mechanisms of their distribution, particularly in human-disturbed ecosystems, is insufficient. Based on the functional linkage between soil microbes and plants, we first investigated the relationship between soil microbial diversity and plant diversity globally, which made it possible to understand the global distribution of soil microbial diversity and the environmental factors underlying it. We then investigated the diversity, community composition, and assembly processes of soil microbial communities along different human disturbance gradients to explore how and to what extent soil microbes respond to human disturbance. The following results were obtained:

(1) Based on the correlations between plant diversity and soil microbial diversity from 84 studies covering more than 3900 natural terrestrial samples globally. We found that microbial richness displayed a modest but positive correlation with plant diversity ($r = 0.333$, $CI = 0.220-0.437$). In spite of variability among taxonomic groups and their relationship with plant diversity, positive correlations were more pronounced in the intermediate sampling extent of latitude and elevation coverage, and tropical forests. Among examined environmental factors, soil pH was negatively associated with the plant and soil microbial relationships at large spatial scales. The plant-microbial correlation appears more sensitive to edaphic factor variation in the poor nutrients and soil less compact systems.

(2) We characterized soil prokaryotic and fungal communities to determine their assembly patterns, along two chronosequences with early to later successional subtropical forests. Prokaryotic and fungal community composition was more variable in early successional forests but converged in the later successional forests. The

community composition was governed by deterministic processes in the early stages, while the relative influence of stochasticity increased in the later stages. Among examined environmental factors, the compositional dissimilarity of plant communities strongly predicted the relative influences of the two processes during succession. Heterogeneous plant communities led to the deterministic assembly of soil microbial communities.

(3) Using Shanghai as an example of the highly disturbed ecosystem, we investigated how human activities impacted soil microbial diversity and its assembly processes. Based on a large sampling effort across 258 sites covering various environmental gradients in the city, we revealed that increased disturbance was associated with slightly homogenized communities of prokaryotes, total fungi, and arbuscular mycorrhizal fungi. The diversity of soil prokaryotes and total fungi were weakly but positively related to disturbance as well. For the abundance of microbial phylotypes along disturbance, we observed synchronous increases and decreases of many phylotypes at relatively high and low strength of disturbance, respectively. Among the examined factors, the contribution of soil properties in explaining microbial variances in diversity and composition were generally larger than that of human disturbance, while disturbance explained an independent part of the variances. Further, we suggested that human disturbance might increase the relative influence of stochastic processes in producing the homogenized communities of soil microbes.

To sum up, our results point to key differences across taxonomic groups, spatial scales, and biomes in the relationship between soil microbial and plant diversity. In human-disturbed ecosystems, soil microbes respond to the modified biotic and abiotic environments and may display predictable trends in assembly processes. Human disturbance in urban ecosystems could impact microbial communities by the changes in the selective pressures from soil environments and increasing stochastic processes.

These findings shed light on our deep understanding in how soil biodiversity responds to human disturbance and effective management of ecosystem recovery.

Keywords: microbial biogeography, secondary succession, urban biodiversity, stochastic process, deterministic process, β diversity

目 录

内 容 摘 要.....	i
Abstract.....	iii
目 录.....	vi
第一章 绪 论.....	1
1.1 土壤微生物与植物的功能联系	1
1.2 土壤微生物多样性对人类干扰的响应	3
1.3 土壤微生物多样性随人类干扰后的恢复	4
1.4 人类干扰环境中土壤微生物的群落构建机制	5
1.5 科学问题和研究内容	6
第二章 微生物类群和尺度影响土壤微生物与植物多样性的相关性.....	9
2.1 Introduction	9
2.2 Material and methods	12
2.2.1 Database	12
2.2.2 Data analysis	14
2.3 Results	17
2.2.1 Data structure	17
2.2.2 Impacts of biome and sampling extent on the correlations of plant diversity and microbial diversity.....	18
2.2.3 Correlations between plant diversity and microbial diversity varied among taxonomic groups	19
2.2.4 Impacts of climatic and edaphic factors	20
2.4 Discussion.....	28
第三章 土壤微生物群落构建机制在亚热带森林次生演替过程中的变化.....	34
3.1 Introduction	34
3.2 Material and methods	36
3.2.1 Study sites	36
3.2.2 Soil sampling and woody plant survey	38
3.2.3 Molecular analyses for soil microbes.....	38
3.2.4 Bioinformatics analyses	39
3.2.5 Statistical analyses.....	39
3.3 Results	41
3.3.1 Changes in soil microbial community composition.....	41
3.3.2 Relative influences of deterministic and stochastic processes	42
3.3.3 Impacts of environmental variables on microbial community assembly processes.....	43
3.4 Discussion.....	51

第四章 高强度人类干扰的城市生态系统中土壤微生物多样性与群落构建.....	55
4.1 Introduction	55
4.2 Material and methods	58
4.2.1 Study sites	58
4.2.2 The metrics of anthropogenic impacts	59
4.2.3 Soil sampling and soil physicochemical properties	59
4.2.4 Molecular analysis and sequence processing	60
4.2.5 Statistical analysis	61
4.3 Results	63
4.3.1 Urbanization gradient and microbial diversity	63
4.3.2 Relationships between urbanization and microbial diversity and community composition	65
4.3.3 Predictors of microbial diversity and community composition	66
4.4 Discussion.....	71
第五章 结论与展望.....	76
5.1 结论	76
5.2 展望	77
参考文献.....	78
致谢.....	94
博后个人简历.....	95
博士和博后期间发表的学术论文.....	96
博后期间主持和参与的科研项目	96