

Plant colonization mediates the microbial community dynamics in glacier forelands of Tibetan Plateau

Yang Liu¹, Mukan Ji*¹, Wenqiang Wang¹, Tingting Xing^{2,3}, Qi Yan¹,
Belinda Ferrari⁴, Yongqin Liu^{1,2,3}

1. Center for Pan-third Pole Environment, Lanzhou University,
Lanzhou 730000, China

2. State Key Laboratory of Tibetan Plateau Earth System, Resources
and Environment (TPESRE), Institute of Tibetan Plateau Research,
Chinese Academy of Sciences, Beijing 100101, China

3. University of Chinese Academy of Sciences, Beijing 100039, China

4. School of Biotechnology and Biomolecular Sciences, Australian Centre for
Astrobiology, UNSW Sydney, Randwick, New South Wales 2052, Australia

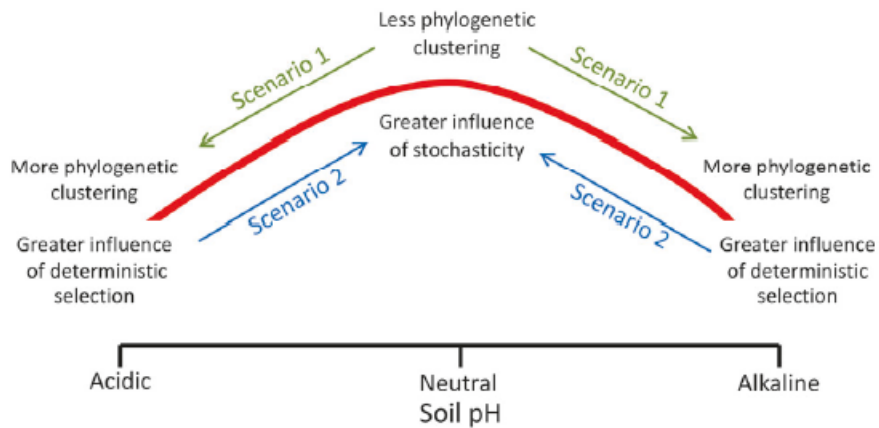


Yang Liu, Mukan Ji, Wenqiang Wang, Tingting Xing, Qi Yan, Belinda Ferrari, Yongqin Liu. 2022. Plant colonization mediates the microbial community succession in glacier forelands. *iMeta*

<https://mc.manuscriptcentral.com/imeta>

Introduction

- ◆ Glacier foreland is the product of glacier retreat
- ◆ **Microorganisms** as **pioneer species** for glacial foreland colonization



Tripathi et al., 2018

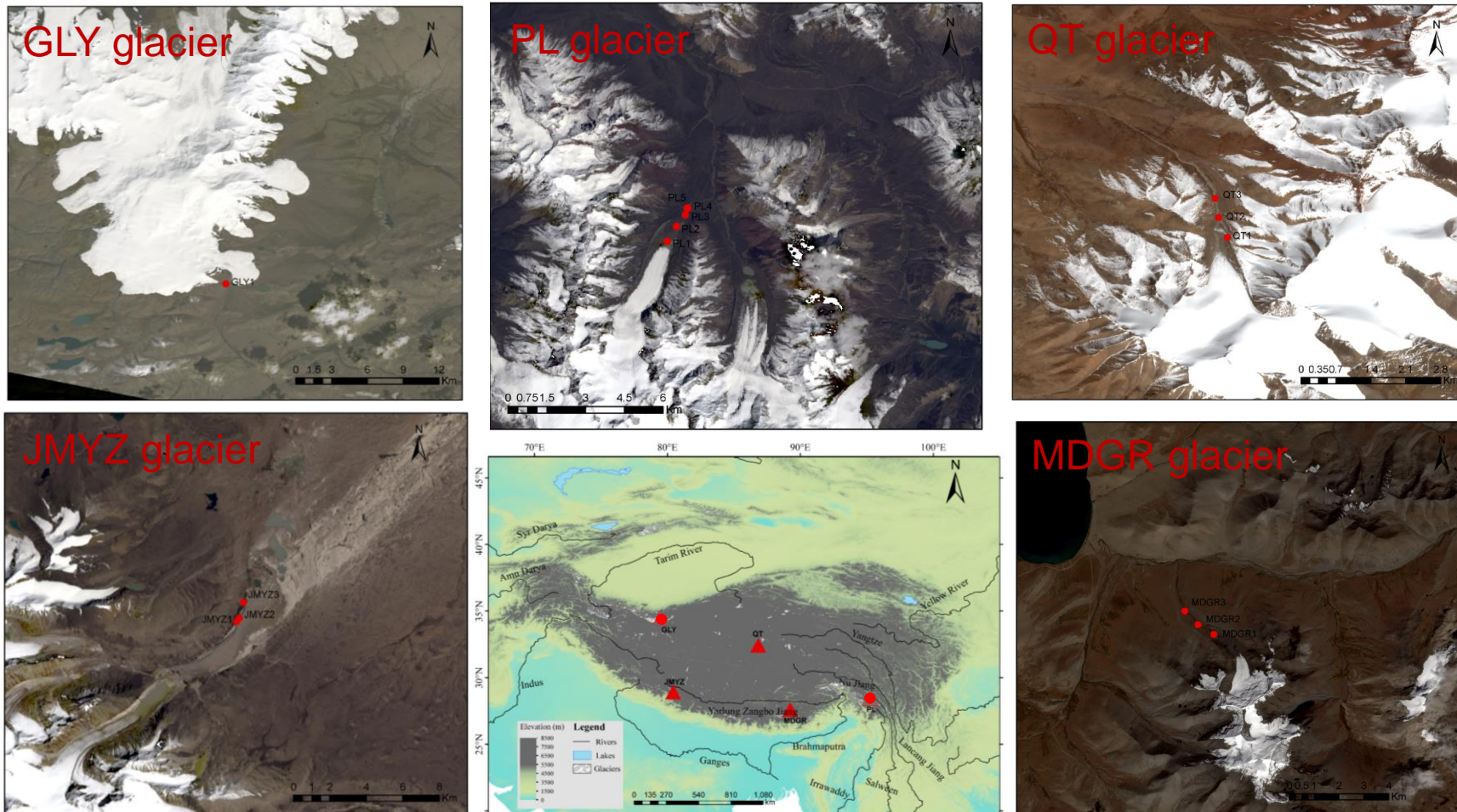
Hypothesis:

- ◆ The impact of pH on microbial community only occurs after plant colonization, while carbon consistently explains microbial community both before and after plant colonization
- ◆ As bacteria and fungi follow different successional trajectories and are explained by different soil physicochemical properties, their diversity and community structure changing patterns to plant colonization could also be different

- ◆ pH and Soil organic carbon (SOC) are the main drivers of microbial community succession
- ◆ Plant colonization lowers soil pH and increased SOC
- ◆ Could plant colonization be the master control of community dynamics in glacier foreland?

Methods

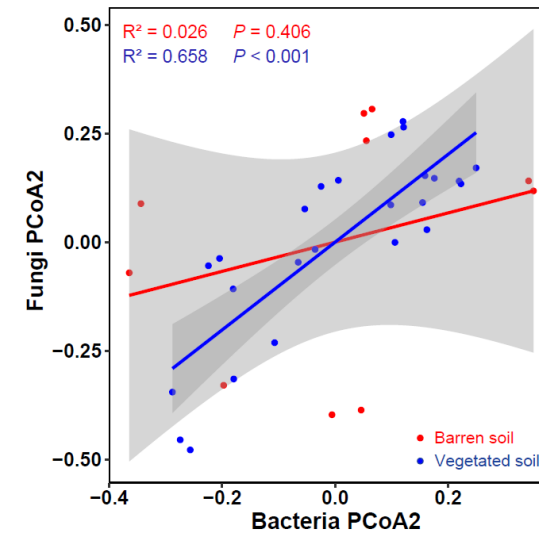
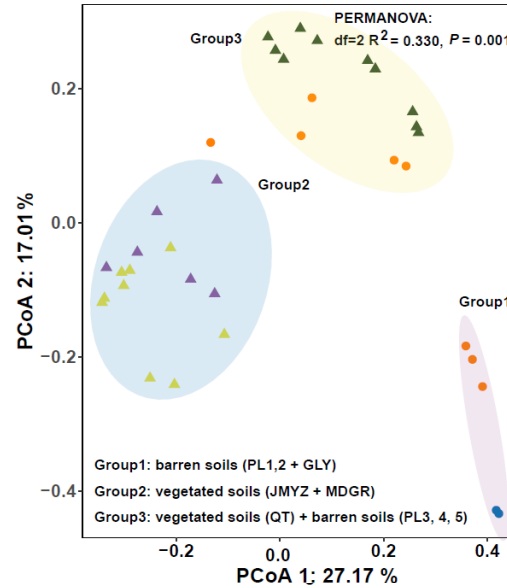
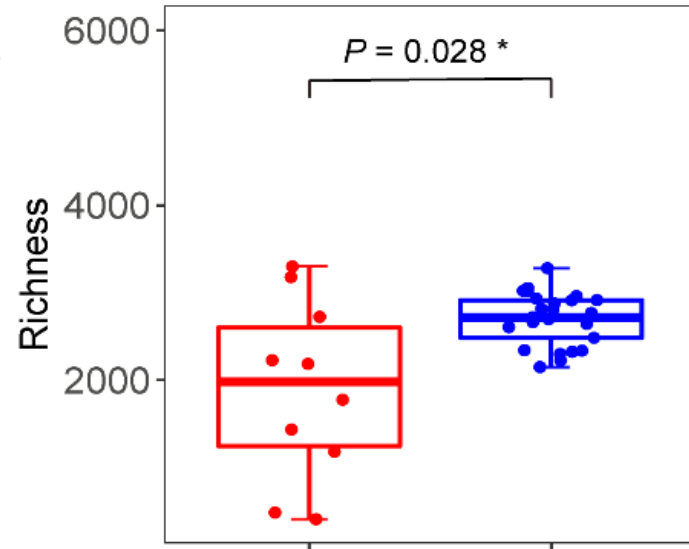
- ◆ Collected soil from **five glacier forelands** across the Tibetan Plateau
- ◆ The soil samples were grouped into **barren** and **vegetated groups**
- ◆ **Amplicon sequencing** was used to study the changes of **bacterial and fungal community structure**



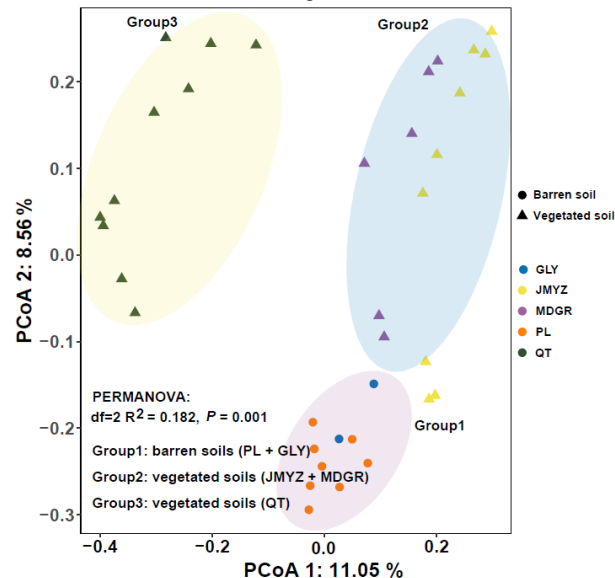
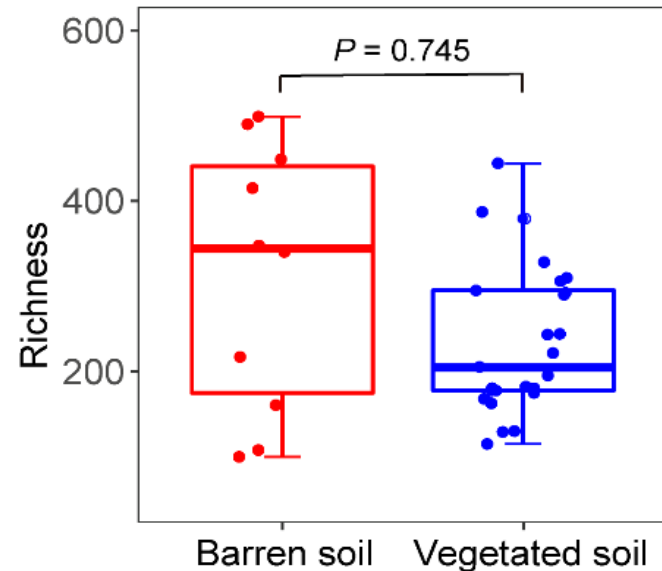
Results

➤ The influences of plant colonization on bacterial and fungal communities

Bacteria



Fungi

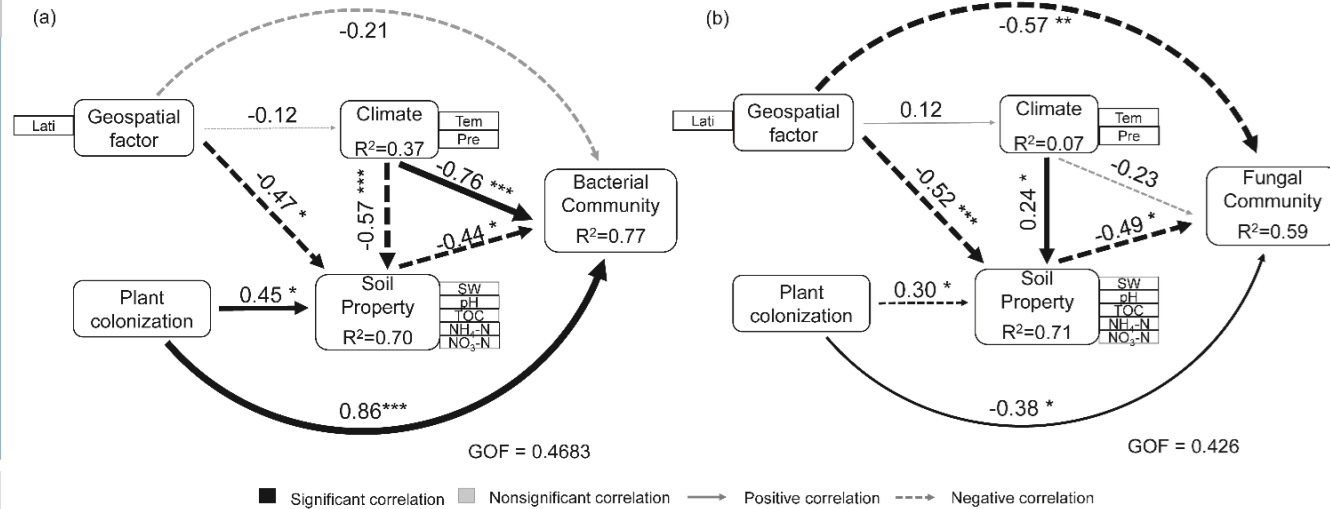
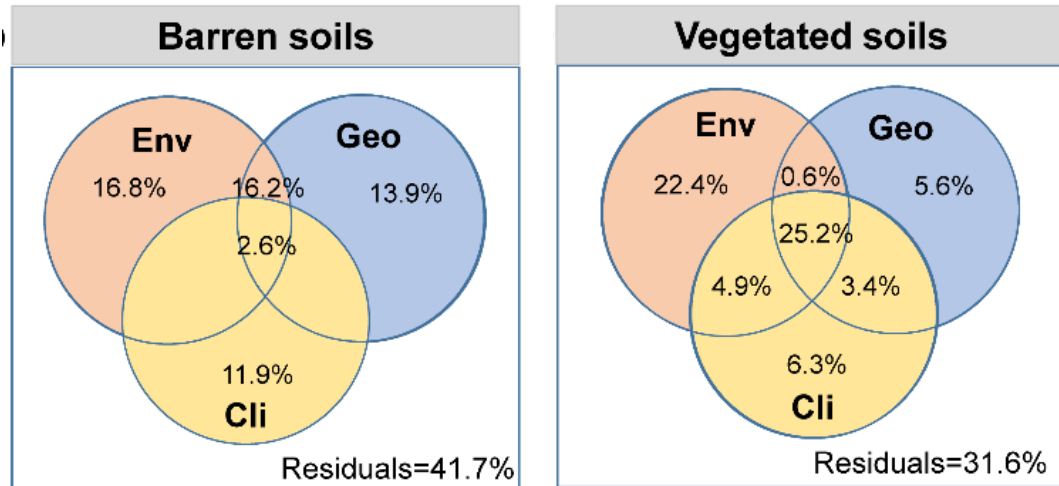


- ◆ Plant colonization increased bacterial diversity, but not fungal diversity
- ◆ Bacterial and fungal communities exhibited similar clustering patterns
- ◆ Plant colonization enhanced the community covariations in bacteria and fungi

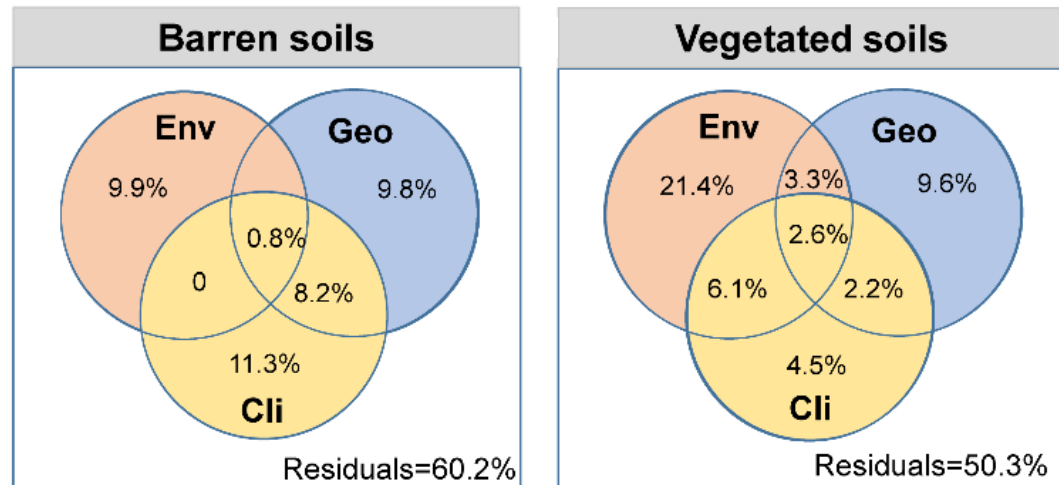
Results

➤ Bacterial and fungal communities response to environmental, geospatial and climate factors

Bacteria



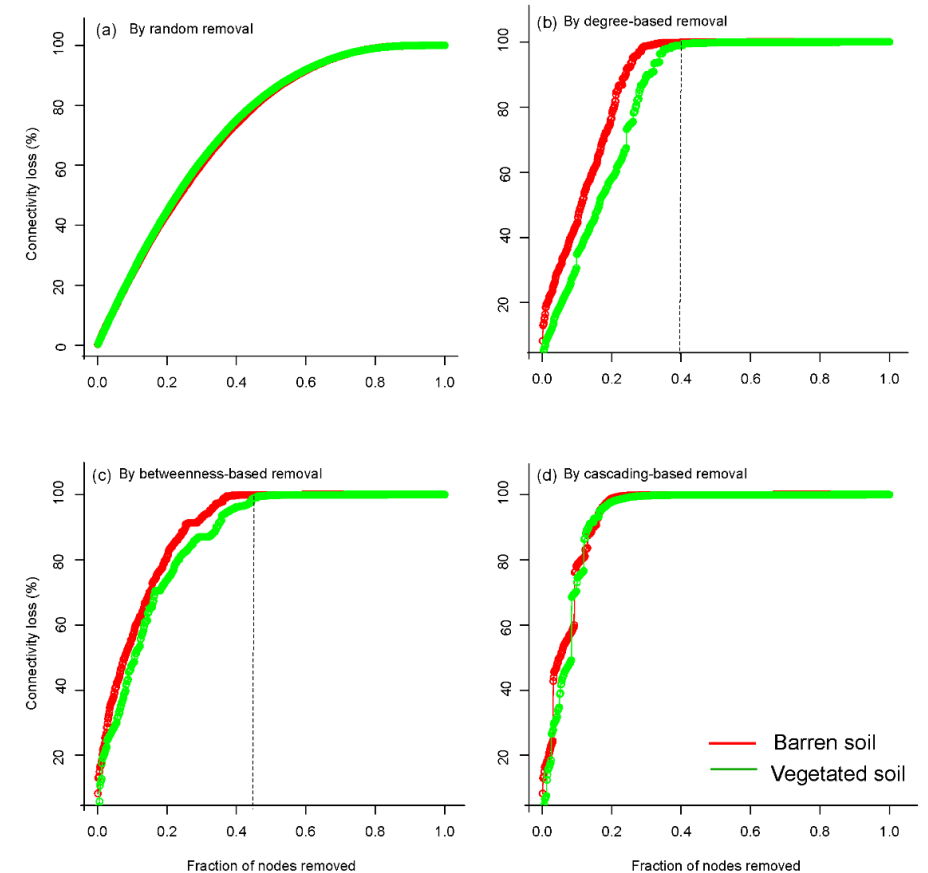
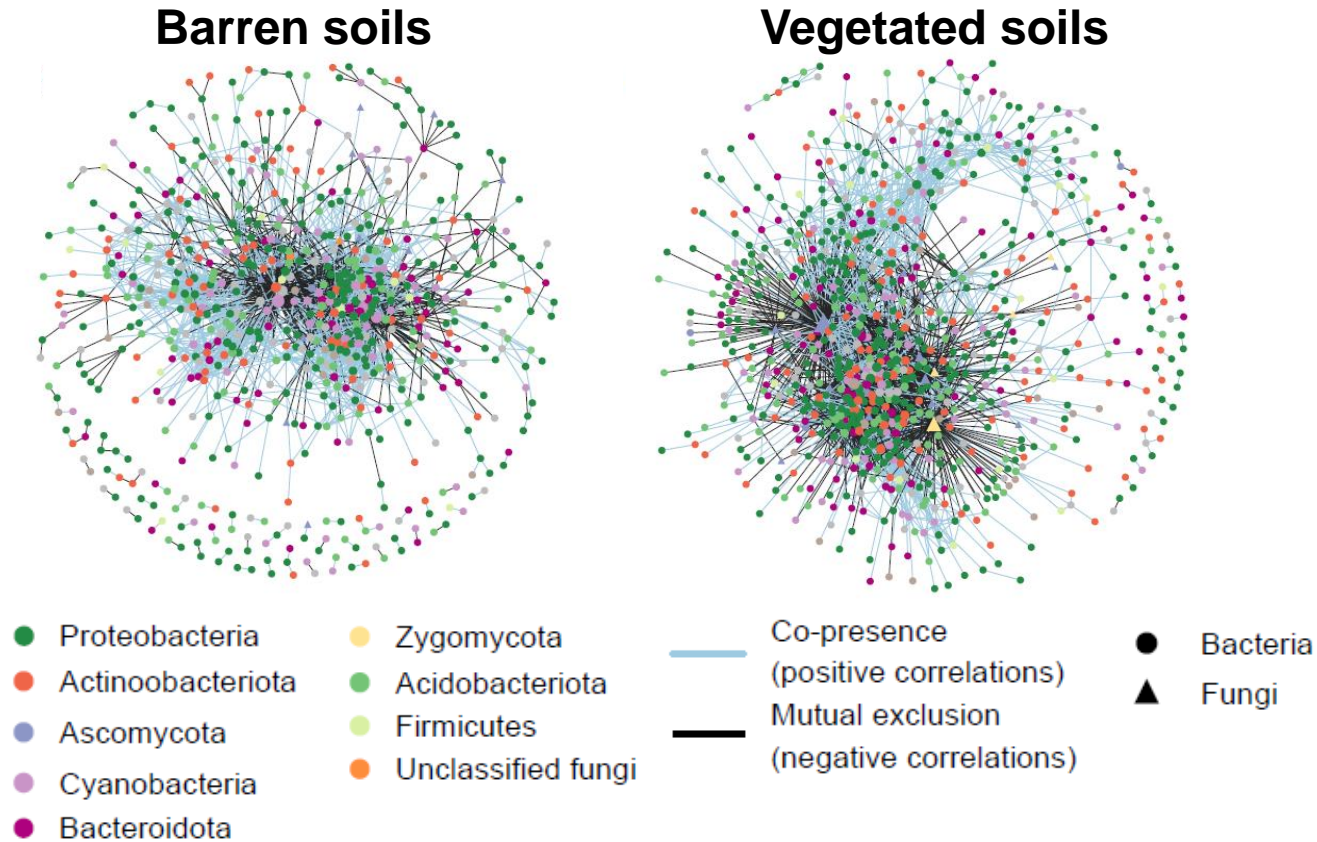
Fungi



- ◆ In barren soils, bacterial and fungal communities were more heavily influenced by environmental filtering and dispersal limitation, respectively
- ◆ The influence of pH and SOC on microbial community in glacier foreland was the results of plant colonization

Results

➤ Plant colonization and microbial community stability

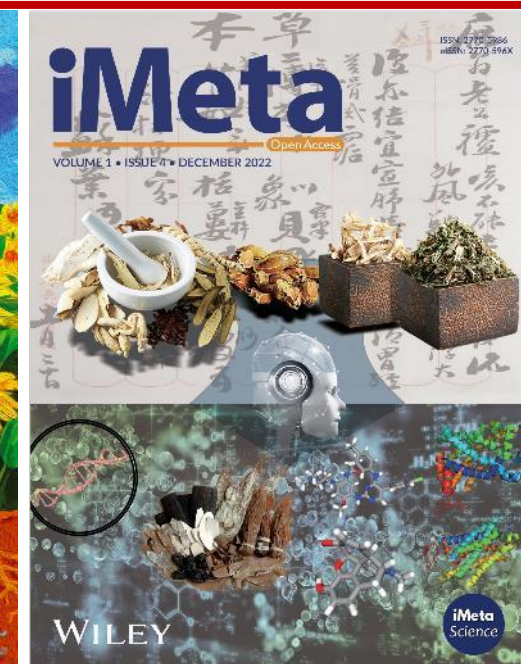


◆ Plant colonization increased microbial network stability and enhanced resistance to disturbance

Summary

- ✓ The influence of pH on bacterial community in glacier foreland results from plant colonization
 - ✓ Plant colonization increases bacterial diversity, but fungal diversity is unchanged
 - ✓ In barren soils, bacterial community is more strongly influenced by environmental filtering, while fungal community is more strongly influenced by dispersal limitation
 - ✓ Plant colonization enhances community co-variations in bacteria and fungi
 - ✓ Plant colonization enhances microbial community stability
- Plant colonization is a strong environmental filtering factor for the biogeography of the microbial community at glacier foreland

Yang Liu, Mukan Ji, Wenqiang Wang, Tingting Xing, Qi Yan, Belinda Ferrari, and Yongqin Liu. 2023. Plant colonization mediates the microbial community dynamics in glacier forelands of the Tibetan Plateau. *iMeta*. e91.
<https://doi.org/10.1002/imt2.91>



“***iMeta***” is an open-access Wiley partner journal launched by iMeta Science Society consist of scientists in bioinformatics and metagenomics world-wide. iMeta aims to promote microbiome, and bioinformatics research by publishing research, methods/protocols, and reviews. The goal is to publish high-quality papers (top 10%, IF > 15) targeting a broad audience. Unique features include video submission, reproducible analysis, figure polishing, APC waiver, and promotion by social media with 500,000 followers. Four issues were released in [March](#), [June](#), [September](#), and [December](#) 2022. Index by [Google Scholar](#), [Crossref](#), [Dimensions](#), [PubMed\(partial\)](#), [DOAJ](#) and [Scopus](#).



Society: <http://www.imeta.science>

Publisher: <https://wileyonlinelibrary.com/journal/imeta>

Submission: <https://mc.manuscriptcentral.com/imeta>



office@imeta.science



[Promotion Video](#)



[iMetaScience](#)



[iMetaScience](#)