

# Patterns and drivers of microbiome in different rock surface soil under the volcanic extreme environment

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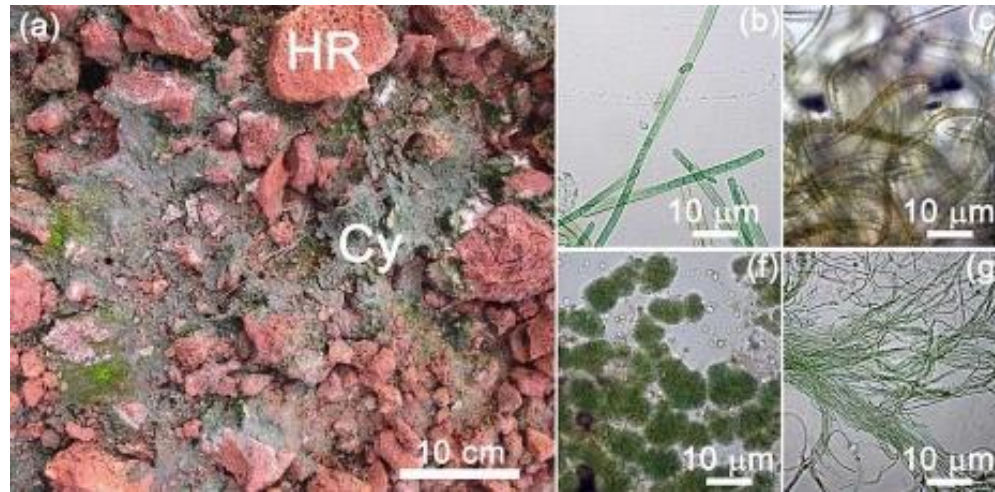
Chen, Jin, Zishan Li, Daolong Xu, Qingchen Xiao, Haijing Liu, Xiaoyu Li, Lumeng Chao, Hanting Qu, Yaxin Zheng, Xinyan Liu, Pengfei Wang, and Yuying Bao. 2023. "Patterns and drivers of microbiome in different rock surface soil under the volcanic extreme environment." *iMeta*. e122. <https://doi.org/10.1002/imt2.122>

# Introduction

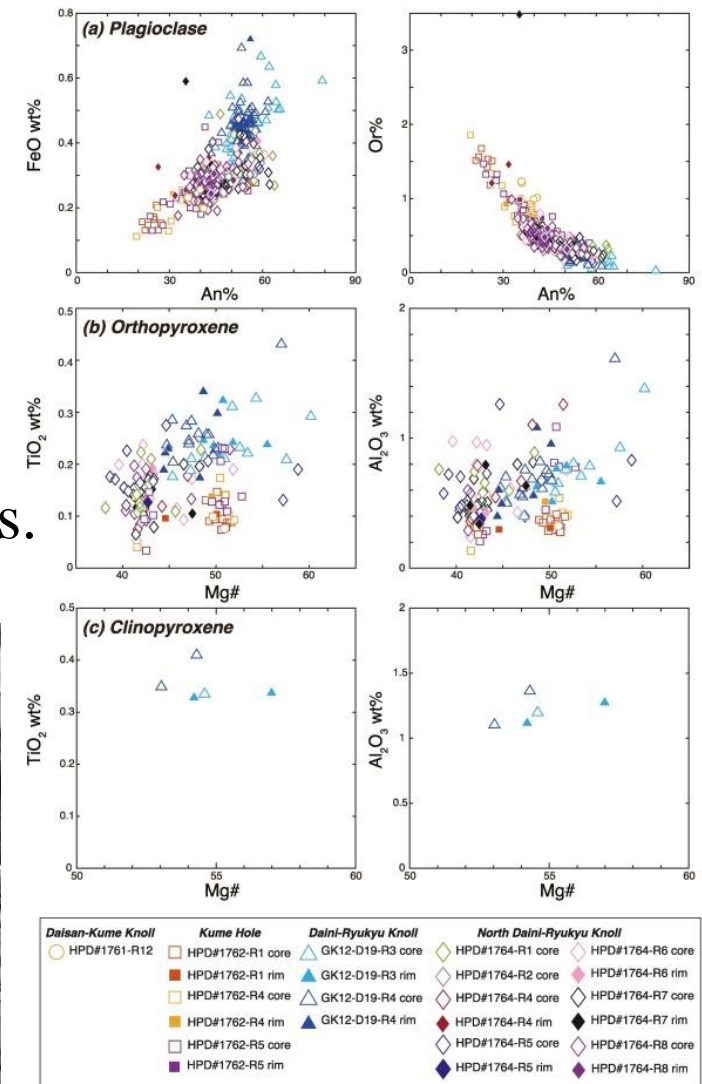
- Volcanic activity will cause the destruction of the original ecological environment;
- In the extreme environment of the volcano, the initial microorganisms will search for habitat on the rock;
- Different rock types have different physical and chemical properties.



Ferlito, 2018, *Earth-Science Reviews*



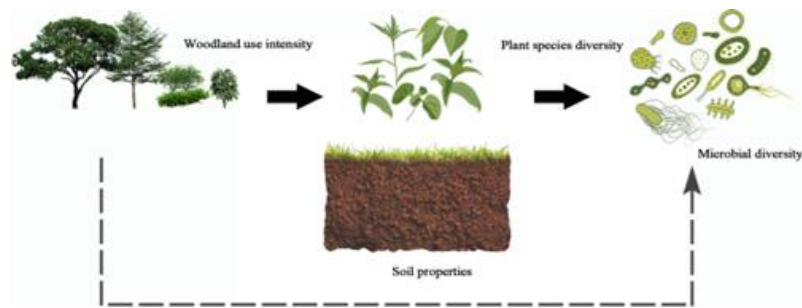
Oleg S. Vereshchagin et al., 2023, *Catena*



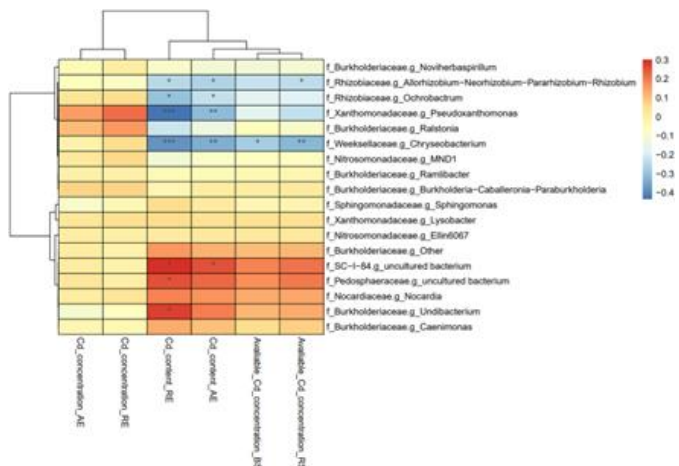
Yumiko Harigane et al., 2023, *Mar. Geol.*

# Introduction

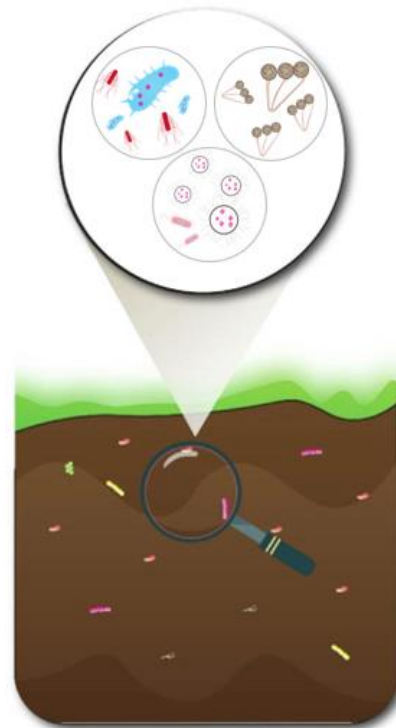
- Soil microorganisms play an important role in regulating soil environmental restoration and promoting plant growth;
- External environmental factors will have a certain impact on soil microorganisms.



Li et al., 2022, *Sci. Total Environ.*



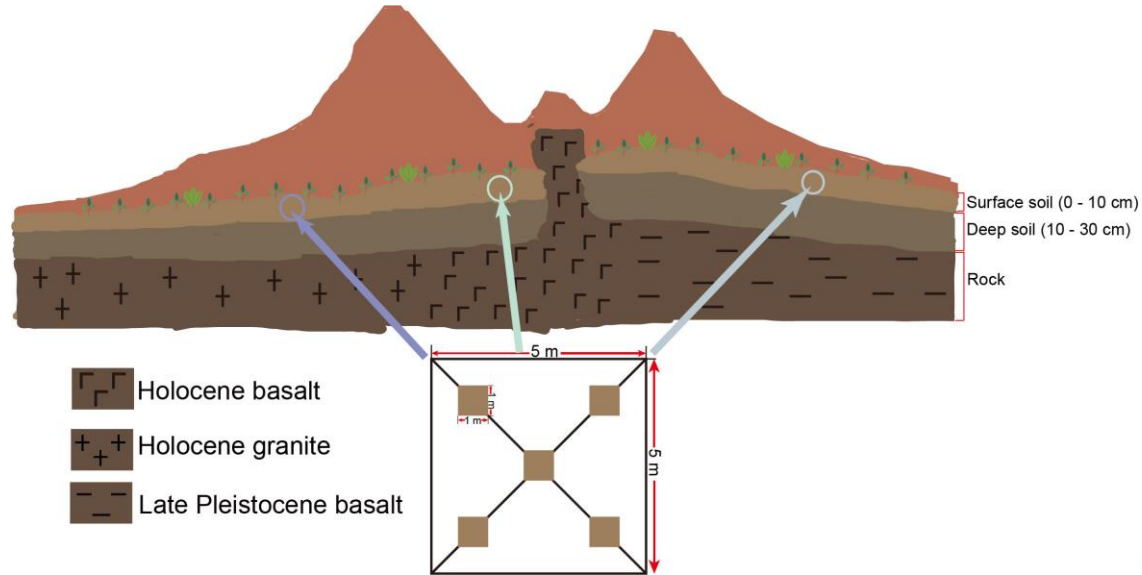
Huang et al., 2023, *Sci. Total Environ*



## Problem to be solved:

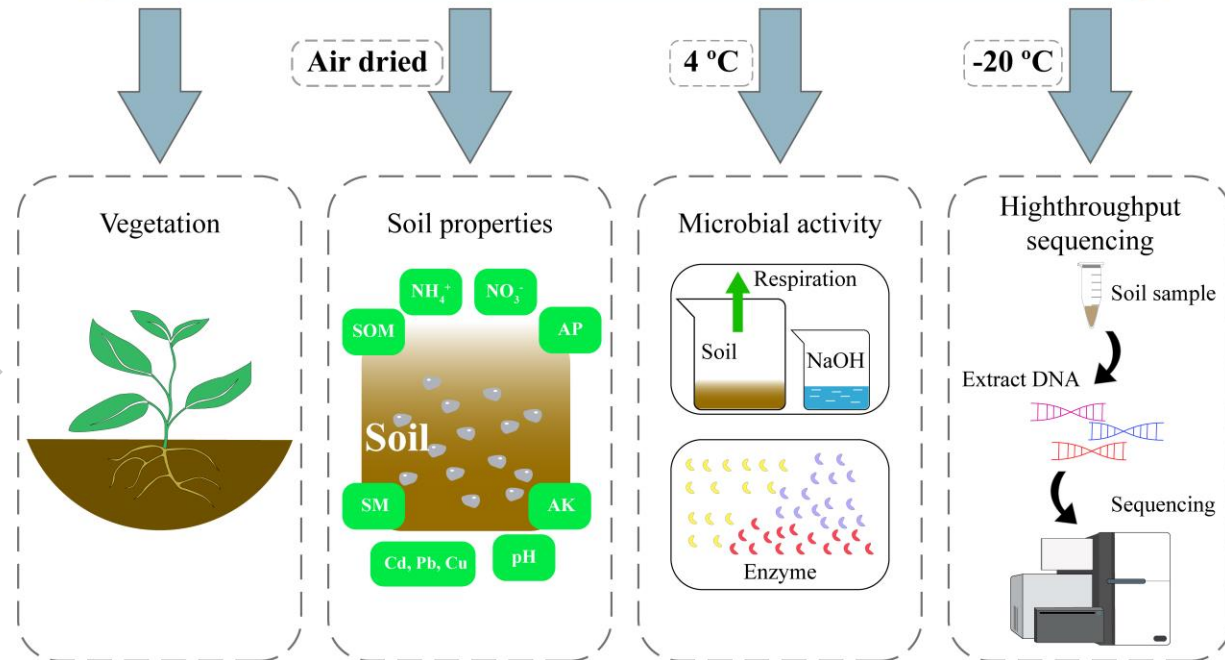
- How do microbial diversity and structure respond to the surface soil environment of volcanic rocks?
- What are the key species in the microbial communities of volcanic rock surface soil?
- Which environmental factors have an important impact on the microbial community in the surface soil of volcanic rocks?

# Method



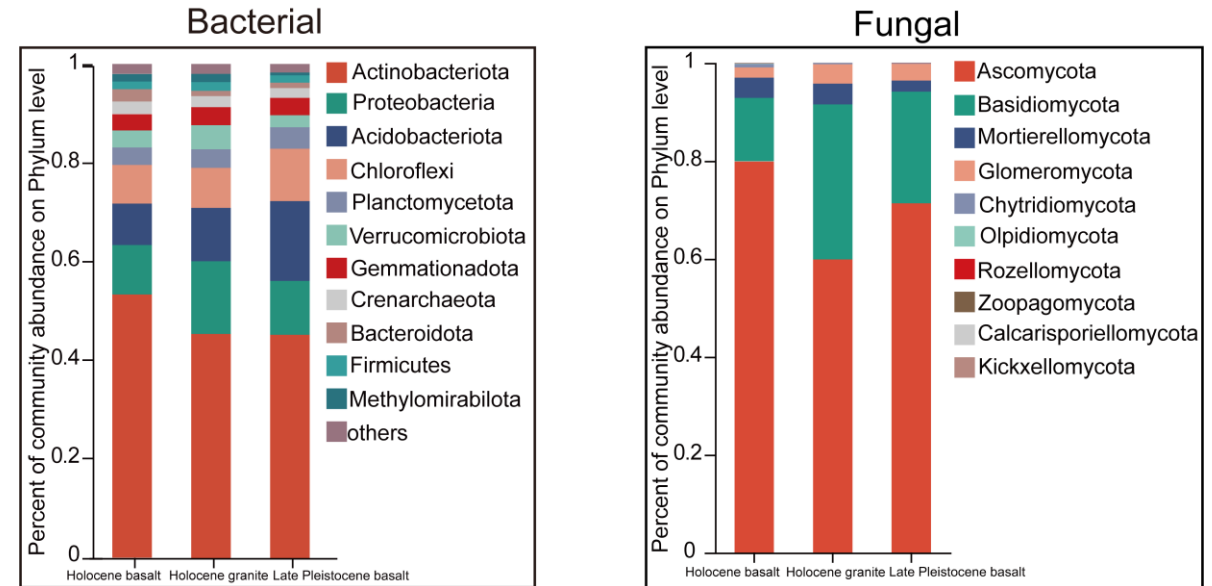
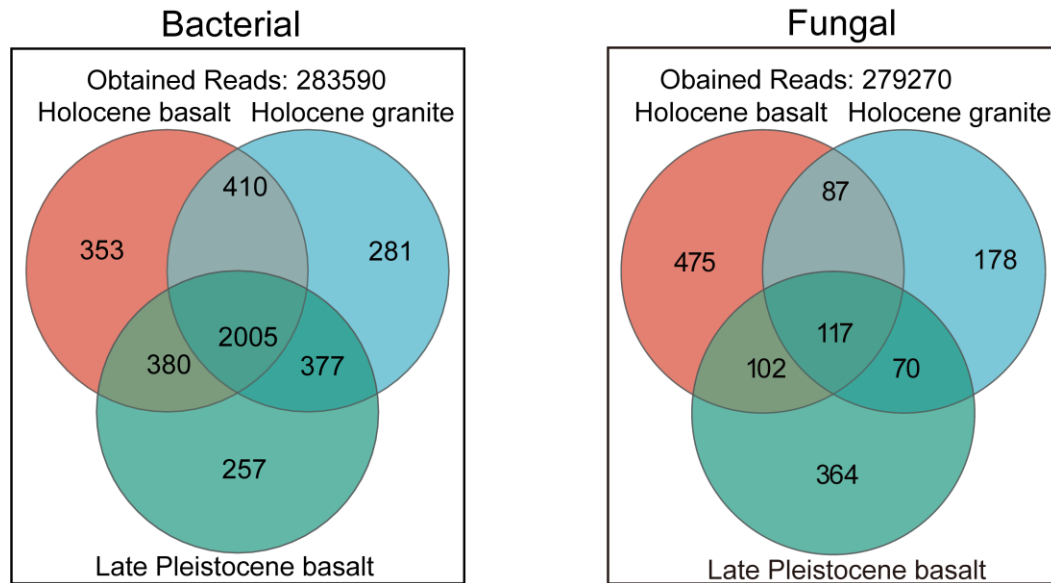
Sample collection

Soil treatment



# Results

## Microbial composition of different rock surface soil

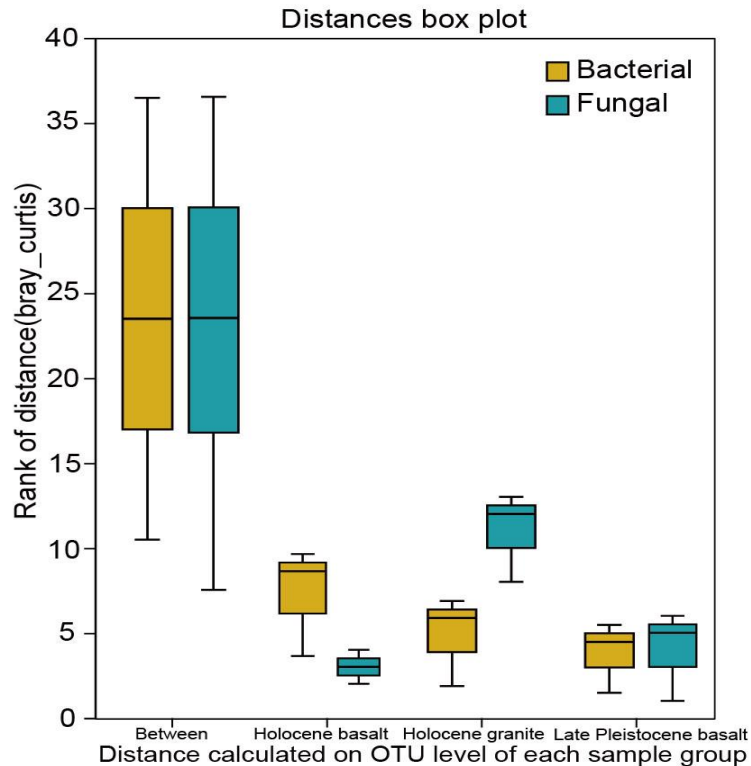


- The obtained reads by bacteria were greater than that by fungi;
- Among the bacteria, the number of OTUs in the Holocene basalt was the largest, and 2005 OTUs were shared among the three plots.
- Among the fungi, the number of OTUs in the Holocene basalt was the largest, and 117 OTUs were shared in the three plots.

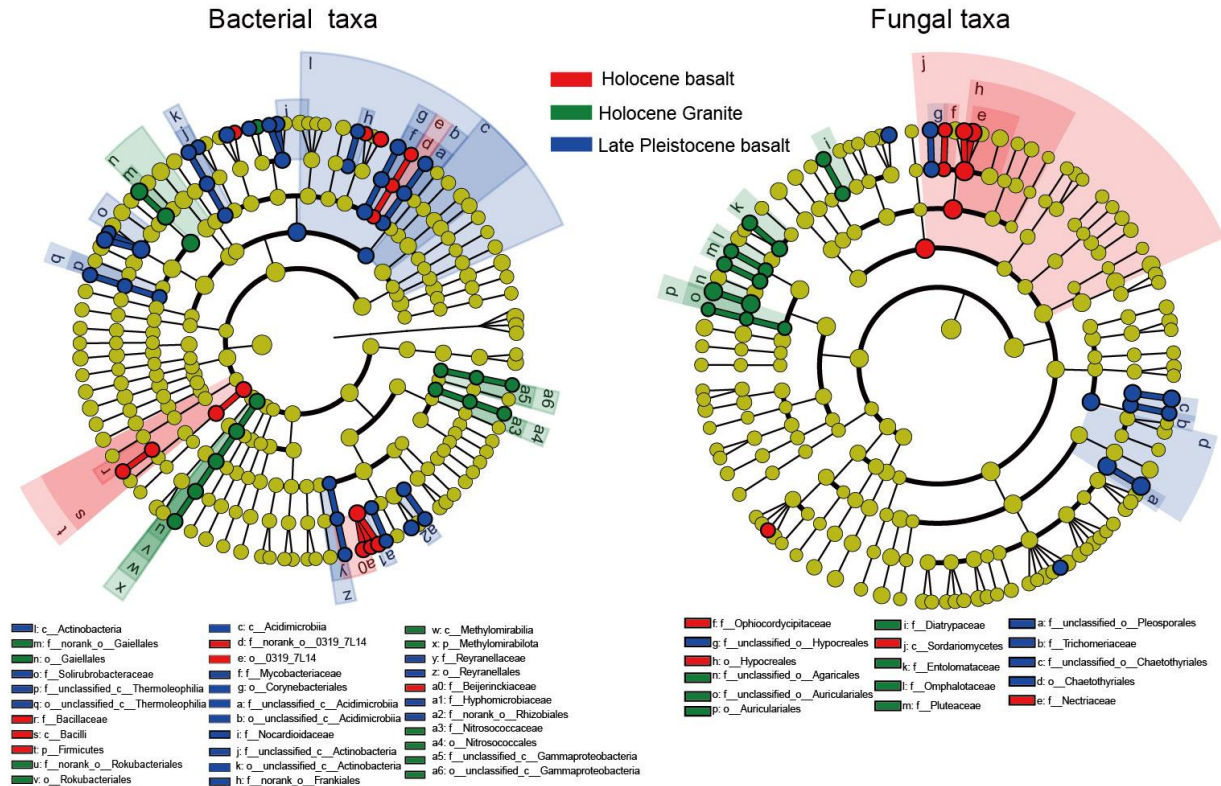
- Among the bacteria, the abundance of Actinobacteria ( 46.70-52.90 % ) was the highest; Among the fungi, Ascomycota had the highest abundance ( 58.30-79.21% ).
- With the passage of time, the microbial composition of basalt in two different periods is also different.
- Among the three plots, the abundance of Proteobacteria and Basidiomycota in granite was the highest, and the abundance of Actinobacteria and Ascomycota was the lowest.

# Results

## Differences in microbial communities in different rock surface soils



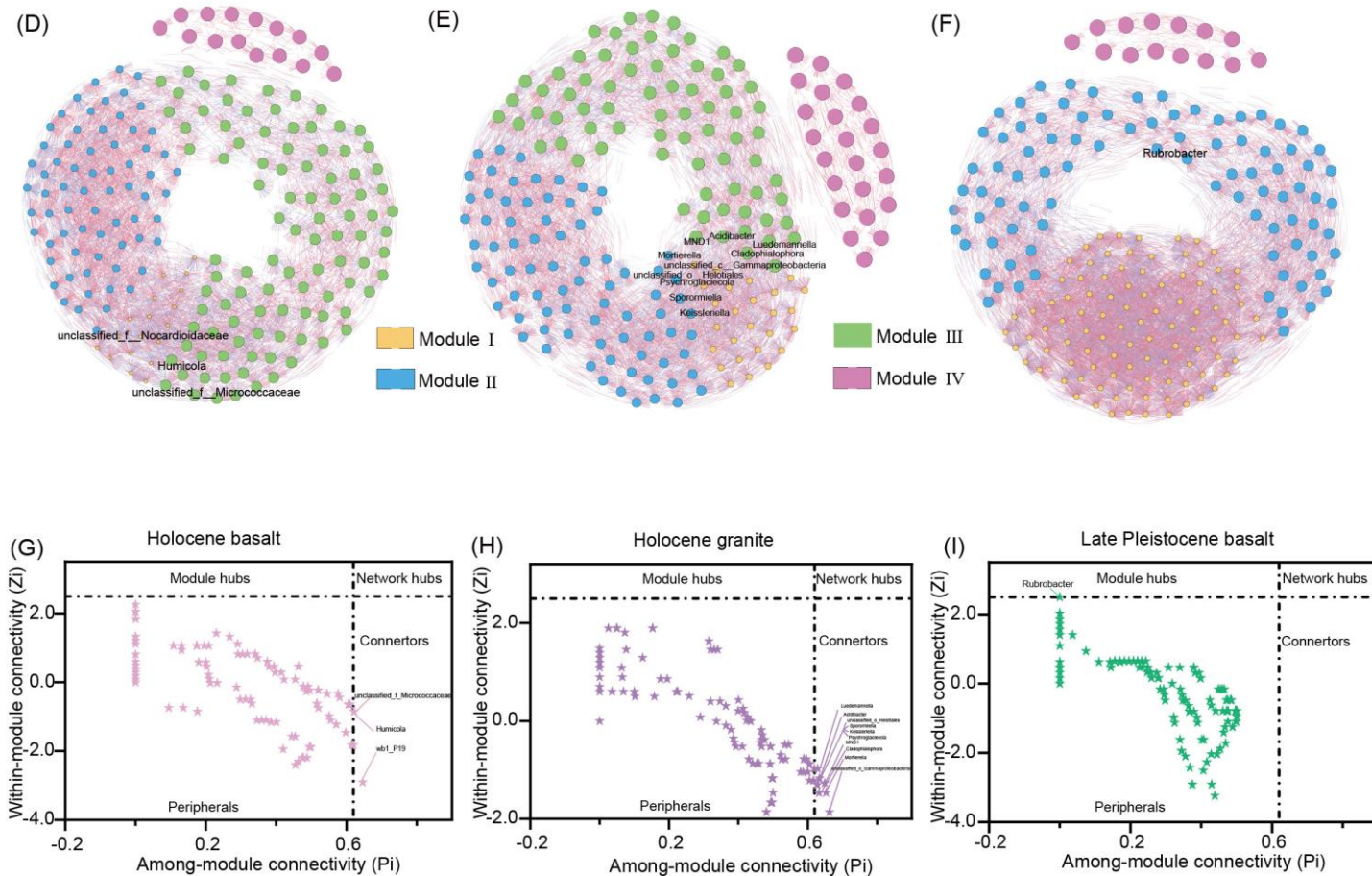
- Bacterial community is more stable than fungi.



- The LEfSe results revealed 63 clades in the bacterial community and 32 clades in the fungal community;
- Bacteria had more biomarkers than fungi;
- There were more biomarkers in Holocene basalt.

# Results

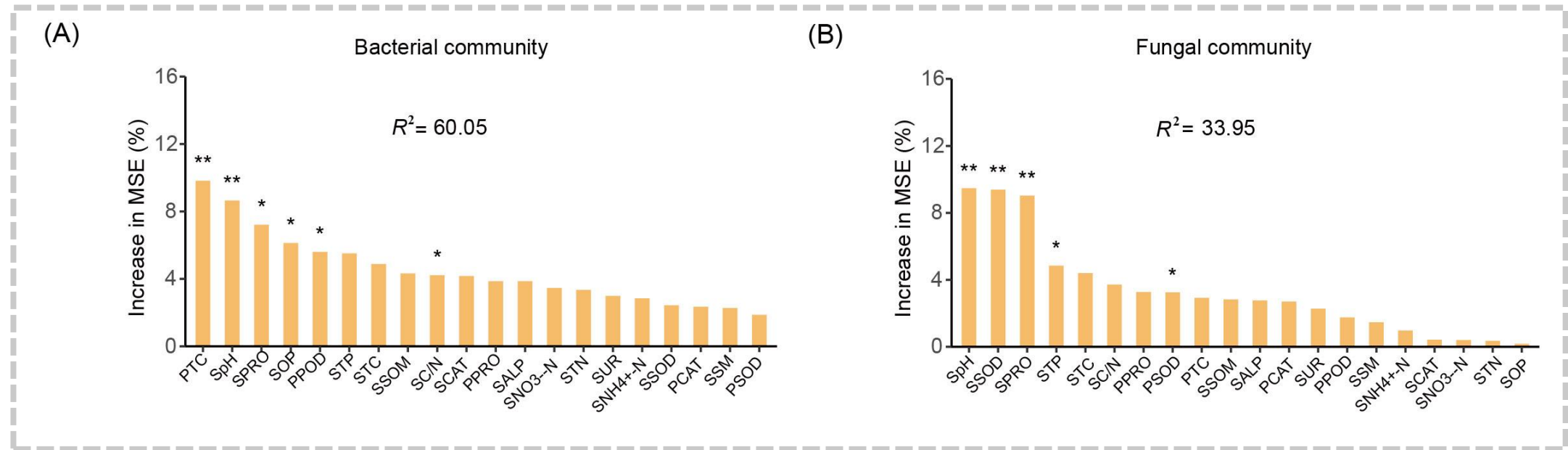
## Microbial co-occurrence network of different rock surface soils



- Late Pleistocene basalts had a more complex microbial networks than Holocene basalts; Granite had a more complex microbial network than basalt.
- Holocene basalts had four keystones; granite had 11 keystones; the Late Pleistocene basalts had one keystone.

# Results

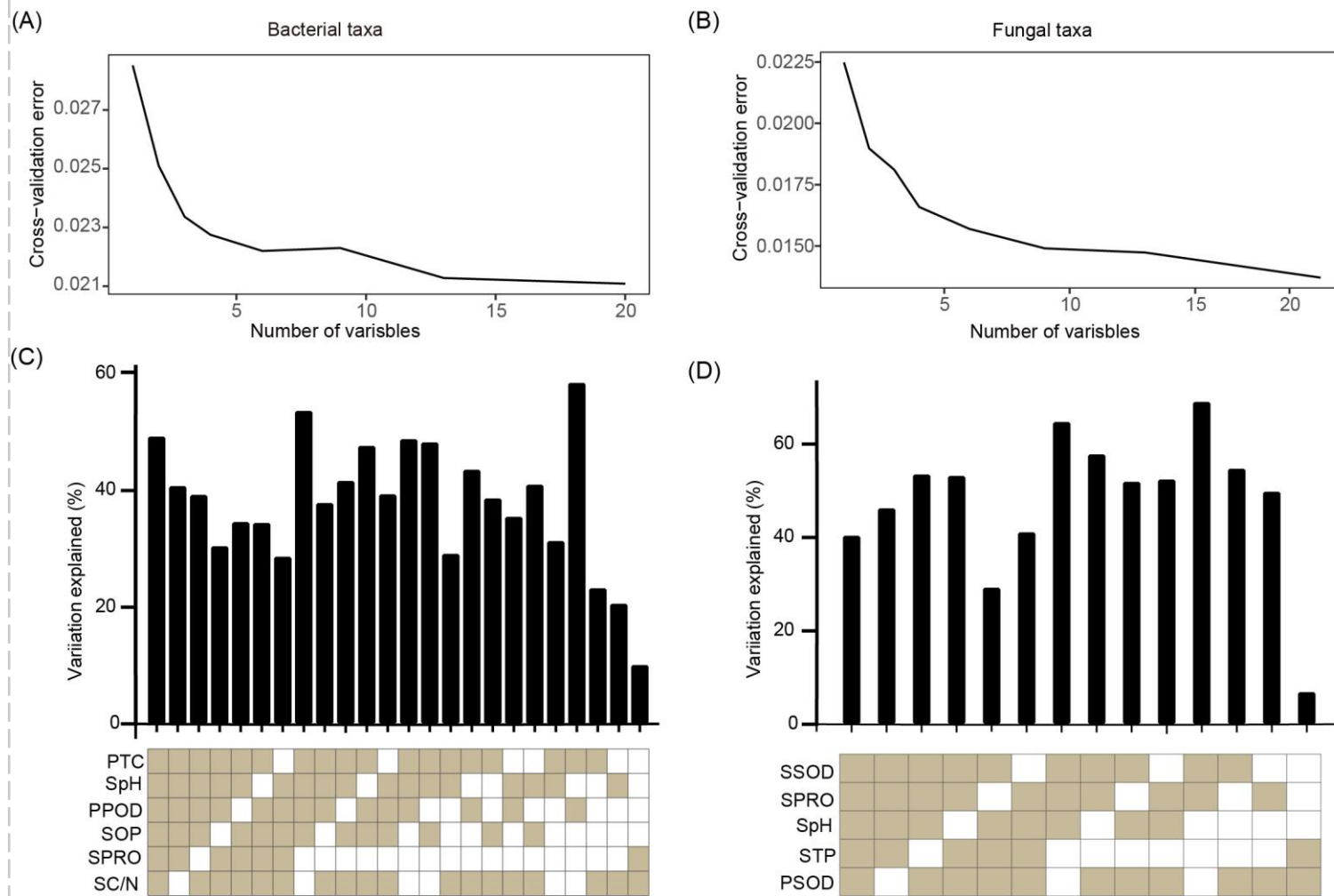
## Full random forest model prediction of bacterial and fungal communities



- Six key environmental predictors were identified in the bacterial community, with the major predictors being plant total chlorophyll content (plant TC), followed by soil pH, soil total protein (soil PRO), soil organic phosphorus (soil OP), plant peroxidase (plant POD), and soil carbon-to-nitrogen ratios (soil C/N).
- Five key environmental predictors were identified in the fungal community, with the major predictors being soil pH, soil superoxide dismutase (soil SOD), soil PRO, soil total phosphorus (soil TP), and plant superoxide dismutase (plant SOD).

# Results

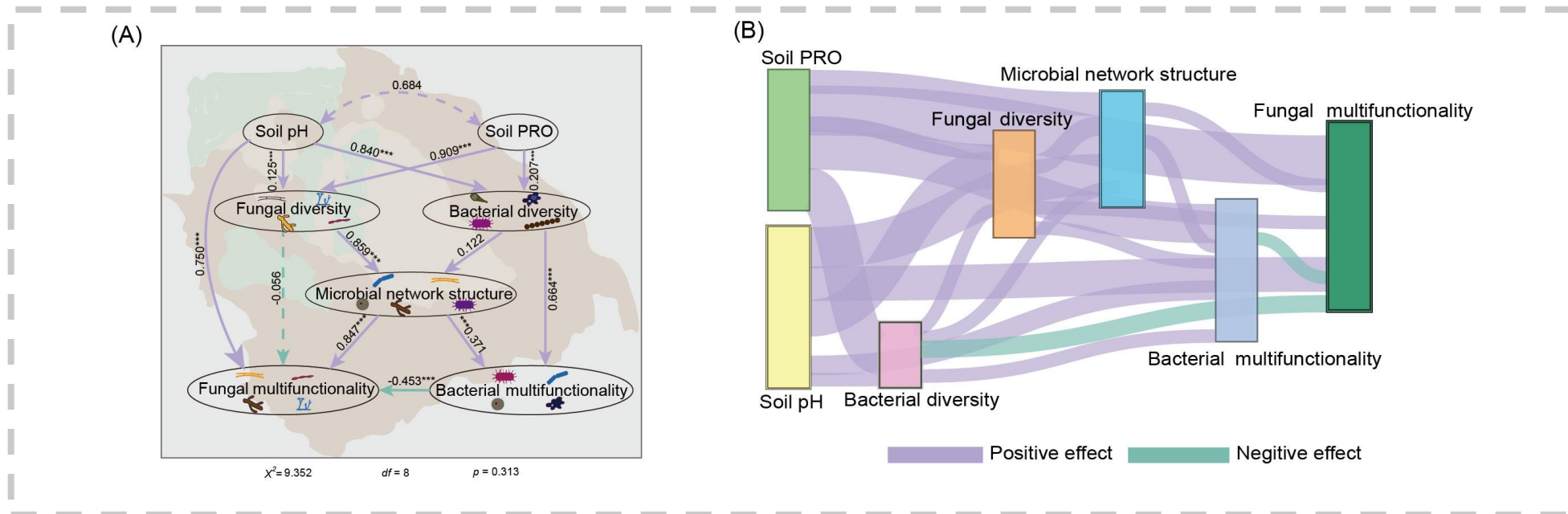
## Bacterial and fungal partial random forest model prediction



- The cross-validation error was minimal when four variables were included in bacterial the model; the cross-validation error was minimal when five variables were included in the fungal model.
- Soil microbial diversity was closely associated with soil pH and soil PRO.

# Results

## Environmental factors mediate microbial diversity and versatility



- Soil pH and soil PRO had a significant positive effect on bacterial and fungal community diversity;
- Soil pH was a major contributor to fungal multifunctionality and fungal diversity contributed most to the microbial network structure.

# Summary



Holocene basalt

- There were significant differences in the composition of microbial communities among the Holocene basalt, granite, and late Pleistocene basalt surface soils;



Holocene granite

- There were significant differences in the composition of microbial communities among the Holocene basalt, granite, and late Pleistocene basalt surface soils;



Late Pleistocene basalt

- Soil PH and total protein had significant effects on soil microbial communities in the Holocene basalt, granite, and late Pleistocene basalt.

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