***New Phytologist* Supporting Information**

Article title: Embracing mountain microbiome and ecosystem functions under global change

Authors: Jianjun Wang, Ang Hu, Fanfan Meng, Wenqian Zhao, Yunfeng Yang, Janne Soininen, Ji Shen, Jizhong Zhou

Article acceptance date: 07 February 2022

The following Supporting Information is available for this article:

Table S1 Summary of our literature review on elevational diversity patterns of microorganisms across global mountains. The critics for literature searching are shown in Figure 1. 'NA' indicates a study or dataset did not provide data on elevational biodiversity patterns. (See separate file.)

Table S2 Summary of the references for meta-analysis of the strength of elevational distance-decay pattern. We considered microbial communities across taxonomic groups and habitat types, as shown in Figure S2. (See separate file.)

Table S3 Summary of the categorised terms of different abiotic and biotic variables in shaping microbial elevational patterns for terrestrial or aquatic ecosystems. These terms are used in Figure 4a. For instance, the term "Temperature" for terrestrial ecosystems includes eight variables reported in literature: mean annual temperature, average temperature warmest quarter, mean temperature in season, monthly mean air temperature, annual mean temperature, annual temperature, temperature and soil temperature.

	Categorised terms	**Used variables in literature**	
		Terrestrial ecosystem	**Aquatic ecosystem**
Climate	**Temperature**	1) Mean annual temperature; 2) Average temperature warmest quarter; 3) Mean temperature in season; 4) Monthly mean air temperature; 5) Annual mean temperature; 6) Annual temperature; 7) Temperature; 8) Soil temperature.	1) Mean annual temperature; 2) Mean temperature of the warmest quarter; 3) Mean July temperature; 4) Temperature annual range; 5) Water temperature.
	Precipitation	1) Mean annual precipitation; 2) Precipitation; 3) Rainfall; 4) Annual precipitation; 5) Average annual precipitation.	/
Nutrients	**Carbon**	1) Total carbon; 2) Total organic carbon; 3) Soil carbon; 4) % Carbon; 5) Soil organic matter; 6) Colored dissolved organic matter (cDOM); 7) Dissolved organic carbon; 8) Carbon content; 9) Organic matter; 10) Soil organic matter.	1) Colored dissolved organic matter (cDOM); 2) Dissolved organic carbon.

	Nitrogen	1) Total nitrogen; 2) Available nitrogen; 3) Soil nitrate content; 4) NO_3^--N; 5) Dissolved organic nitrogen; 6) NH_4^+-N; 7) Dissolved total nitrogen; 8) % Nitrogen.	1) Total nitrogen; 2) NH_4^+-N; 3) NO_2^--N.
	Phosphorus	1) Total phosphorus; 2) Soil available phosphorus; 3) Olsen phosphate; 4) Soil phosphorus; 5) Resin-extractable Phosphorus; 6) Phosphorus content.	1) Total phosphorus; 2) Phosphate concentrations; 3) PO_4^--P.
Vegetation	**Plant**	1) Vegetation types; 2) Vegetation cover; 3) Cover type; 4) Plant cover degree; 5) Plant richness index; 6) Tree species richness; 7) Vegetation diversity; 8) Vegetation composition; 9) Vegetation features; 10) Plant characteristic; 11) Plant age; 12) Tree height; 13) Plant diversity; 14) Plant functional diversity; 15) Vegetation biomass.	1) Shading; 2) Normalized difference vegetation index (NDVI).

Table S4 Reference list for the relative importance of deterministic versus stochastic processes underlying microbial communities. These references are summarized regarding the two dimensions of ecological processes and publication year as shown in Figure 4b.

Reference ID	Publication year	Ecosystems	Studied groups	Methods	References
[1]	2008	Terrestrial	Acidobacteria	Phylogenetic structure, phylogenetic beta diversity	Bryant et al. (2008)
[2]	2012	Aquatic	Bacteria	Phylogenetic structure	Wang et al. (2012)
[3]	2013	Aquatic	Bacteria	Phylogenetic structure, phylogenetic beta diversity	Wang et al. (2013a)
[4]	2013	Aquatic	Bacteria	Phylogenetic structure	Wang et al. (2013b)
[5]	2014	Terrestrial	Ectomycorrhizal fungi	Mid-domain null model	Miyamoto et al. (2014)
[6]	2017	Aquatic	Bacterioplankton	Phylogenetic structure	Li et al. (2017)
[7]	2018	Terrestrial	Bacteria	Phylogenetic structure, phylogenetic beta diversity	Zhang et al. (2018)
[8]	2019	Terrestrial	Bacteria	Phylogenetic structure, phylogenetic beta diversity	Cho et al. (2019)
[9]	2019	Terrestrial	Diazotrophs	Phylogenetic beta diversity	Wang et al. (2019)
[10]	2019	Terrestrial	Bacteria	Phylogenetic structure, phylogenetic beta diversity	Shen et al. (2019)
[11]	2019	Terrestrial	Bacteria	Paup-Crick null model	Luo et al. (2019)
[12]	2019	Terrestrial	Fungal endophyte	Discussion	Cobian et al. (2019)
[13]	2020	Terrestrial	Bacteria, fungi	Phylogenetic structure	Li et al. (2020)
[14]	2020	Terrestrial	Bacteria	Phylogenetic beta diversity	Zhu et al. (2020)
[15]	2020	Aquatic	Bacteria, diatoms	Paup-Crick null model	Wang et al. (2020)
[16]	2020	Aquatic	Bacterioplankton	Phylogenetic beta diversity	Aguilar and Sommaruga (2020)
[17]	2020	Terrestrial	Bacteria, fungi	Phylogenetic beta diversity	Cai et al. (2020)
[18]	2021	Terrestrial	Diazotrophs	Phylogenetic beta diversity	Wang et al. (2021)
[19]	2021	Terrestrial	Methanotrophs	Phylogenetic beta diversity	Li et al. (2021)
[20]	2021	Terrestrial	Bacteria, archaea, fungi	Partial Mantel test	Liu et al. (2021)

Table S5 Detailed key questions for the proposed seven perspectives.

1 Biodiversity hypotheses
(1) Are there biodiversity theories specifically for mountain microbes? (2) How do human activities affect elevational diversity patterns and the underlying processes? (3) Can we predict vertical variations in the assembly of microbial communities?
2 Novel drivers underlying biodiversity variations
(4) Which geodiversity variable best explains mountain microbial diversity patterns? (5) How important is geodiversity compared to well-recognized drivers? (6) How does geodiversity affect elevational diversity patterns?
3 Ecological interactions between terrestrial and aquatic ecosystems
(7) What mechanisms are underlying the terrestrial-aquatic interactions on mountainsides: environmental filtering vs. mass effects? (8) How will global change influence terrestrial effects on aquatic communities? (9) How can the meta-ecosystem framework improve our understanding of terrestrial-aquatic interactions?
4 Trait-based ecology
(10) How can we identify microbial traits and their variability on mountainsides for a practical framework of trait-based ecology? (11) How important are functional traits in maintaining microbial diversity and ecosystem functioning? (12) What new technologies would advance trait-based microbial ecology?
5 Manipulative field experiments
(13) How can we experimentally disentangle the direct influence of climate change on microbial diversity and ecosystem functions? (14) How can we experimentally quantify the joint influences of climate and other factors? (15) How applicable are field experiments from terrestrial to aquatic ecosystems?
6 Biodiversity and ecosystem functioning relationships
(16) How does microbial biodiversity link ecosystem functions along elevational gradients? (17) How do microbial biodiversity-ecosystem functioning (BEF) relationships change across tropical levels and ecosystem boundaries? (18) How will interplay of multiple global change drivers influence BEF relationships?
7 Modelling and prediction of global change responses
(19) How can we project the global change consequences of microbial dynamics using elevational gradients? (20) How can we integrate biotic interactions into models of global change? (21) To what extent do novel drivers and microbial species traits improve model accuracy?

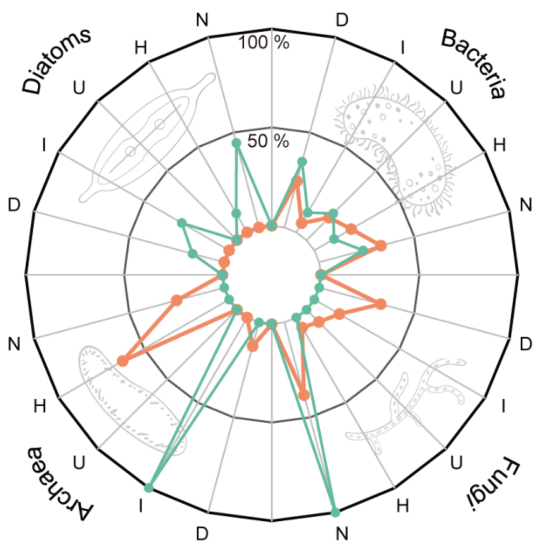

Fig. S1 Radar plot for the percentages of datasets with typical elevational patterns in alpha diversity. These patterns are decreasing (D), increasing (I), hump-shaped (H), U-shaped (U) or no discernable (N) patterns for bacteria, fungi, archaea and diatoms in terrestrial (light brown) or aquatic (dark green) ecosystem.

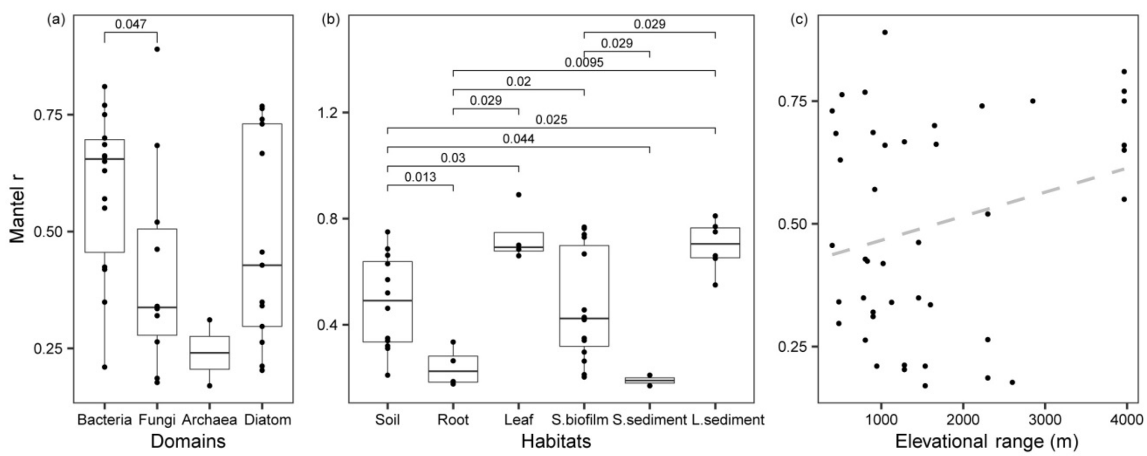

Fig. S2 The strength of elevational distance-decay patterns of microbial communities across taxonomic groups (a) and habitat types (b), and their relationships with elevational ranges (c). The strength was quantified by the Mantel correlation coefficient *r* between compositional dissimilarities and elevational change. The differences in Mantel r between pairwise taxonomic groups or habitat groups were tested using the Wilcoxon test, and only significant differences ($P < 0.05$) are shown above the boxplots. The dots in the boxplots are the Mantel *r* for individual datasets. We included 48 datasets from 20 studies that have Mantel tests for elevational distance-decay relationships. Furthermore, we examined the effects of habitat type (or taxonomic group) with taxonomic group (or habitat type) as random factors using meta-analysis via linear mixed-effects meta-regression models (Viechtbauer, 2010). The Waldtype test was used to evaluate model significance, and we found only the significant effects of habitat type when taxonomic group being random factor. S.biofilm: Stream biofilm; S.sediment: Stream sediment; L.sediment: Lake sediment. Statistical non-significance of linear model fits in (c) was indicated by a dotted ($P > 0.05$) line. Components of the box are: top of the box, upper hinge; midline of box, median; bottom of box, lower hinge.

References

Aguilar P, Sommaruga R. 2020. The balance between deterministic and stochastic processes in structuring lake bacterioplankton community over time. *Molecular Ecology* **29**(16): 3117-3130.

Bryant JA, Lamanna C, Morlon H, Kerkhoff AJ, Enquist BJ, Green JL. 2008. Microbes on mountainsides: contrasting elevational patterns of bacterial and plant diversity. *Proceedings of the National Academy of Sciences* **105**(Supplement 1): 11505-11511.

Cai Z, Wang X, Bhadra S, Gao Q. 2020. Distinct factors drive the assembly of quinoa-associated microbiomes along elevation. *Plant and Soil* **448**(1-2): 55-69.

Cho H, Tripathi BM, Moroenyane I, Takahashi K, Kerfahi D, Dong K, Adams JM. 2019. Soil pH rather than elevation determines bacterial phylogenetic community assembly on Mt. Norikura. *FEMS microbiology ecology* **95**(3): fiy216.

Cobian GM, Egan CP, Amend AS. 2019. Plant-microbe specificity varies as a function of elevation. *The ISME journal* **13**(11): 2778-2788.

Li C, Tu B, Kou Y, Wang Y, Li X, Wang J, Li J. 2021. The assembly of methanotrophic communities regulated by soil pH in a mountain ecosystem. *Catena* **196**: 104883.

Li H, Zeng J, Ren L, Wang J, Xing P, Wu QL. 2017. Contrasting patterns of diversity of abundant and rare bacterioplankton in freshwater lakes along an elevation gradient. *Limnology and Oceanography* **62**(4): 1570-1585.

Li J, Li C, Kou Y, Yao M, He Z, Li X. 2020. Distinct mechanisms shape soil bacterial and fungal co-occurrence networks in a mountain ecosystem. *FEMS microbiology ecology* **96**(4): fiaa030.

Liu L, Zhu K, Krause SMB, Li S, Wang X, Zhang Z, Shen M, Yang Q, Lian J, Wang X, et al. 2021. Changes in assembly processes of soil microbial communities during secondary succession in two subtropical forests. *Soil Biology and Biochemistry* **154**: 108144.

Luo Z, Liu J, Zhao P, Jia T, Li C, Chai B. 2019. Biogeographic Patterns and Assembly Mechanisms of Bacterial Communities Differ Between Habitat Generalists and Specialists Across Elevational Gradients. *Frontiers in microbiology* **10**: 169.

Miyamoto Y, Nakano T, Hattori M, Nara K. 2014. The mid-domain effect in ectomycorrhizal fungi: range overlap along an elevation gradient on Mount Fuji, Japan. *The ISME journal* **8**(8): 1739-1746.

Shen C, Shi Y, Fan K, He JS, Adams JM, Ge Y, Chu H. 2019. Soil pH dominates elevational diversity pattern for bacteria in high elevation alkaline soils on the Tibetan Plateau. *FEMS microbiology ecology* **95**(2): fiz003.

Viechtbauer W. 2010. Conducting meta-analyses in R with the metafor package. *Journal of statistical software* **36**(3): 1-48.

Wang J, Legendre P, Soininen J, Yeh CF, Graham E, Stegen J, Casamayor EO, Zhou J, Shen J, Pan F. 2020. Temperature drives local contributions to beta diversity in mountain streams: Stochastic and deterministic processes. *Global Ecology and Biogeography* **29**(3): 420-432.

Wang J, Shen J, Wu Y, Tu C, Soininen J, Stegen JC, He J, Liu X, Zhang L, Zhang E. 2013a. Phylogenetic beta diversity in bacterial assemblages across ecosystems: deterministic versus stochastic processes. *The ISME journal* **7**(7): 1310-1321.

Wang J, Soininen J, He J, Shen J. 2012. Phylogenetic clustering increases with elevation for microbes. *Environmental Microbiology Reports* **4**(2): 217-226.

Wang J, Soininen J, Shen J. 2013b. Habitat species pools for phylogenetic structure in

microbes. *Environmental Microbiology Reports* **5**(3): 464-467.
Wang Y, Li C, Shen Z, Rui J, Jin D, Li J, Li X. 2019. Community assemblage of free-living diazotrophs along the elevational gradient of Mount Gongga. *Soil Ecology Letters* **1**(3): 136-146.
Wang Y, Li C, Tu B, Kou Y, Li X. 2021. Species pool and local ecological assembly processes shape the β-diversity of diazotrophs in grassland soils. *Soil Biology and Biochemistry* **160**: 108338.
Zhang Q, Goberna M, Liu Y, Cui M, Yang H, Sun Q, Insam H, Zhou J. 2018. Competition and habitat filtering jointly explain phylogenetic structure of soil bacterial communities across elevational gradients. *Environmental Microbiology* **20**(7): 2386-2396.
Zhu B, Li C, Wang J, Li J, Li X. 2020. Elevation rather than season determines the assembly and co-occurrence patterns of soil bacterial communities in forest ecosystems of Mount Gongga. *Applied Microbiology and Biotechnology* **104**(17): 7589-7602.