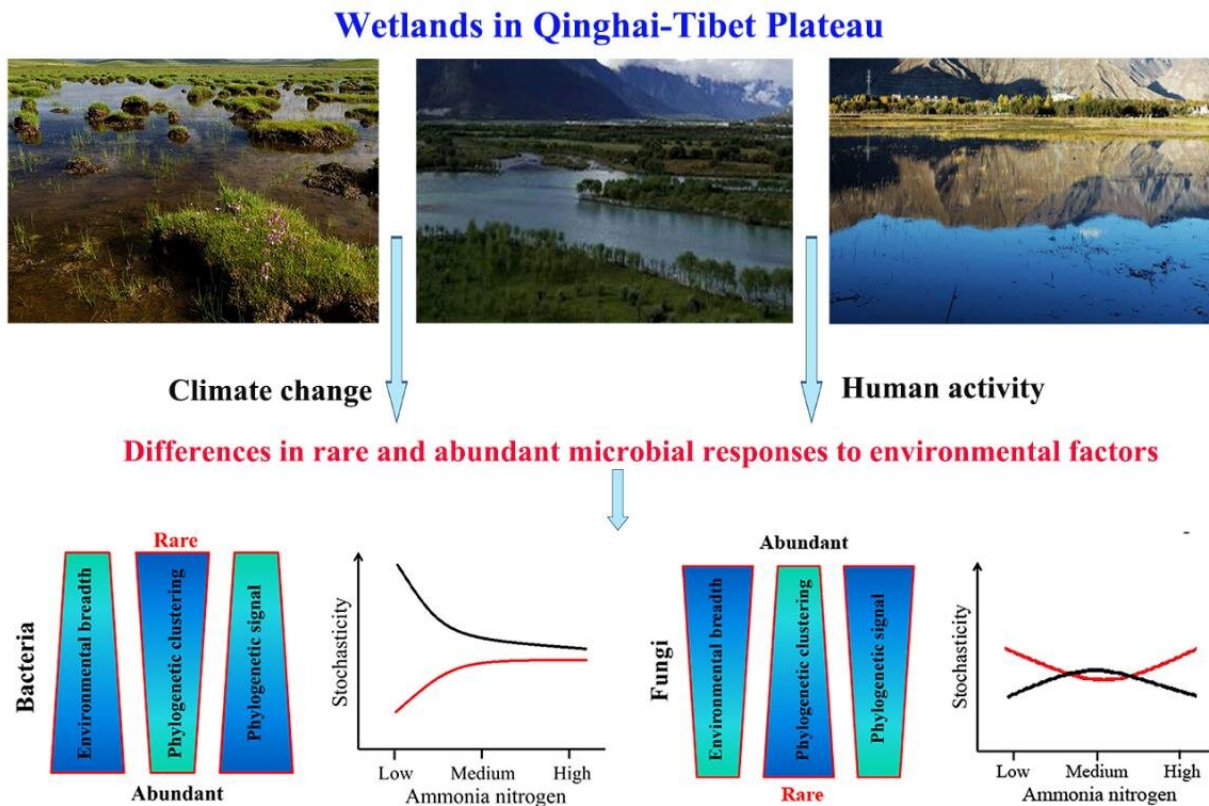


Researchers find maintenance mechanism of microbial diversity in Tibet wetlands

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Abundant bacteria and fungi exhibit broader environmental breadths and stronger phylogenetic signals of ecological preference than corresponding rare ones. Rare microbial taxa show closer phylogenetic clustering than abundant microbial taxa. Soil ammonia is the decisive factor in shaping the balance between community assembly processes of rare and abundant microbial taxa, showing distinct changes in stochasticity with higher ammonia content. Credit: WBG

Microorganisms participate in biogeochemical cycles of key elements (e.g., carbon, nitrogen, phosphorus, and sulfate), and their diversity is closely correlated with soil ecosystem functions. Disentangling the geographic distribution pattern and microbial diversity maintenance mechanism is of significance to estimate diversity-driven ecosystem functions and potentials. However, study on the maintenance mechanism of microbial diversity in the wetland ecosystems is poorly understood.

Associate professor Wan Wenjie, professor Yang Yuyi and professor Liu Wenzhi from Wuhan Botanical Garden, collaborated with professor Geoffrey Michael Gadd of the Dundee University in UK and professor GU Jidong of the Hong Kong University, took Qinghai-Tibet Plateau as the research object, and determined community composition and diversity of both bacteria and fungi along with environmental gradient.

The researchers employed multiple statistical analysis approaches to calculate environmental breadths, phylogenetic signals, phylogenetic clustering, and ecological community assembly processes.

Abundant bacterial and fungal subcommunities show broader environmental breadths and stronger phylogenetic signals of ecological preference than corresponding rare bacterial and fungal subcommunities. On the contrary, rare microbial subcommunities exhibit closer phylogenetic clustering than abundant microbial subcommunities.

In addition, deterministic processes dominate in the rare bacterial subcommunity, while stochastic processes govern abundant bacterial subcommunity, and rare and abundant fungal subcommunities.

The variation partitioning analysis and neutral model analysis further validates that abundant taxa are less environmentally constrained. Soil ammonia is crucial for shaping the balance between community assembly processes of rare and abundant microorganisms, showing

distinct changes in stochasticity with higher ammonia content.

These findings provide new insights and statistical methods for assessing the maintenance mechanism of microbial [diversity](#) in wetland [ecosystems](#), and enriches the theoretical basis for the environmental protection of wetland ecosystems in Qinghai-Tibet Plateau.

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More information: Wenjie Wan et al, Environmental adaptation is stronger for abundant rather than rare microorganisms in wetland soils from the Qinghai-Tibet Plateau, *Molecular Ecology* (2021). [DOI: 10.1111/mec.15882](#)

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