

Abrupt permafrost thaw alters microbial structure and function

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Permafrost thaw could emit substantial carbon (C) into the atmosphere, and possibly trigger a positive feedback to climate warming. As the engine of biogeochemical cycling, soil microorganisms exert a critical



role in mediating the direction and strength of permafrost C-climate feedback. However, our understanding about the impacts of thermokarst (abrupt permafrost thaw) on microbial structure and function remains limited.

To resolve this issue, a research team led by Prof. Yang Yuanhe from the Institute of Botany of the Chinese Academy of Sciences explored the impacts of thermokarst on <u>soil microorganisms</u> and their drivers on the Tibetan Plateau.

Based on <u>metagenomic sequencing</u>, laboratory incubations and a twopool model, the researchers analyzed the changes in <u>microbial</u> <u>communities</u> and functional genes along a typical <u>permafrost thaw</u> sequence (one, 10 and 16 years since permafrost collapse), and also explored the functional potential associated with soil C decomposition.

They observed that thermokarst formation not only significantly altered the microbial community composition, α - and β -diversity, but also increased the abundance of functional genes involved in stable C decomposition over 16 years since permafrost collapse. Specifically, the functional genes involved in labile C degradation decreased while those for stable C degradation significantly increased at the late stage of permafrost collapse.

Consistent with the changes in functional genes, the two-pool model illustrated that microbial decomposition of stable C significantly increased 16 years after permafrost collapse.

They found that substrates rather than soil environment and vegetation were the dominant driver shaping the structure and function of microbial diversity in this permafrost ecosystem. These findings extend our understanding of the mechanism of the impacts of permafrost thawing on soil microorganisms.



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