Effects of changing temperature regimes on soil microbiomes: a metagenome comparison between dynamic cold and hot sites

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Résumé

Environmental change has drastic effects on the ecology of soil microbial communities, affecting their structure and functions supporting ecosystem services. Exploring how large-term environmental changes, like altered temperature regimes, affect soil microbiomes is important for understanding and predicting the consequences of climate change for soil functions.

We compared the dynamics of soil microbial community metagenome profiles under two distinct warming disturbances to understand how changing temperature regimes influence their ecology. First, we analyzed metagenomes of bacterial communities in active layer and permafrost soils over 2 months of experimental thawing in Fairbanks, Alaska USA. Second, we analyzed metagenomes of bacterial communities collected over seven years of recovery after temperate soils were heated by an underground coal seam fire in Centralia, Pennsylvania USA. While these two studies represent opposite thermal disturbances (*i.e.,* thawing of $>$ 1,000-year-old permafrost and cooling of temperate soils heated for decades, respectively), comparing them provides insights into broad effects of changing temperature on soil microbial ecology. We hypothesized that both frozen permafrost and fire-affected soil communities experience similar selection pressures for genomic traits and functions distinct from those of thawed and unheated soils. However, we also expected distinct genomic characteristics in each site that reflect differences in their warming regimes.

Between these systems, we found notable similarities and differences in relationships between metagenome structure and temperature. Average genome size was smaller in frozen permafrost and fire-heated soils compared to active layer and reference soils, but trended larger as soil temperatures approached typical surface temperatures for their regions. Regarding nutrient cycle functions, potential nitrogen fixers (*i.e.,* metagenome assembled genomes encoding the *nifH* gene), were more abundant in the permafrost and heated soils with decreasing

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[*] Intervenant

abundance as soils thawed or cooled respectively. However, while the average number of carbohydrate active enzyme (CAZyme) genes within MAGs were lower in frozen permafrost compared to active layer soils and increased during thawing, CAZyme gene investment was higher in fire-affected compared to reference soils with no significant shift as soils cooled.
Overall, our results demonstrate that long-term temperature changes from either warm or cool ”extremes” towards ambient affect the genomic traits and functional potential of naturally occurring soil microbiomes. This work provides insights into how microbial community structure and functions may be altered by long-term temperature changes given climate change.

Mots-Clés: Soil, Microbiology, Climate change, Permafrost, Centralia, Metagenomics, Heating