

Modeling microbial functional trait-environment interactions at the continental scale

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Abstract text:

Inferring linkages between microbial metabolism and dissolved organic matter (DOM) across environmental gradients is a promising avenue to improve biogeochemical predictions at large spatial scales. Despite decades of metagenomic studies identifying microbial functional trait-environment patterns at small spatial scales, general patterns at continental or global scales that may improve large-scale models remain unresolved. Recent influx of multi-omics datasets that represent diverse environmental conditions has enabled scalable analyses linking microbial metabolic niche breadths with key environmental processes, such as carbon and nutrient transformations.

Here, we leveraged publicly available microbial metagenome assembled genomes (MAGs) derived from the Worldwide Hydrobiogeochemistry Observation Network for Dynamic River Systems (WHONDRS) data paired with metabolomic (FTICR-MS) and sediment chemistry data to link microbial metabolic potential with organic chemistry. We annotated 1,384 MAGs representing 65 sites using the R tool microTrait, which categorizes functional traits under the YAS (growth yield-resource acquisition-stress tolerance) framework. Following Hutchinsonian niche theory, we modeled microbial trait combinations as n-dimensional hypervolumes and observed trait-DOM patterns at the continental scale, showing microbial functional tradeoffs along gradients of organic carbon. We expect that at the continental scale, microbial trait profiles will be distinct across climatic regions, and that niche breadth (i.e. the size of individual hypervolumes in trait space) will correlate with DOM/metabolite diversity. The results of this work will distill generalizable patterns of microbe-DOM availability and diversity at large spatial scales, thus identifying information to improve current biogeochemical models.

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