

Review of: "The Role of Metabolic Strategies in Determining Microbial Community Diversity along Temperature Gradients"

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Potential competing interests: No potential competing interests to declare.

This study aimed to understand how microbial species diversity responds to natural and human-induced temperature changes by integrating ecological metabolic theory with a community assembly model. The goal was to predict patterns of microbial diversity across temperature gradients and to identify the mechanisms influencing these patterns, particularly through traits like carbon use efficiency (CUE) and generalist-specialist trade-offs. The study found that microbial community diversity follows a unimodal pattern with temperature, peaking at approximately 10-15 °C along global geological temperature gradients. This peak is driven by species sorting that favors communities with high mean and low variance in species-level CUEs. The results suggest that microbial diversity and CUE responses to temperature can be reliably predicted using life-history traits, enabling links between microbial diversity and carbon cycling across various temperature gradients.

The study is well-written and well-executed. I have no substantive comments on the methodology or model construction; however, I do have a few minor recommendations:

"The taxonomic diversity of microbial communities encodes the diversity of functional traits and therefore plays a critical role in determining their functional ability" - This statement may be overly assertive, as taxonomic diversity does not always correlate with functional diversity. Functional redundancy within the soil microbiome, along with intraspecies differences in functional gene composition, can influence this relationship. Strains within the same species may show significant differences in metabolism and functional gene composition. Additionally, horizontal gene transfer enables taxa adapted to higher temperatures to transfer genetic material to those with lower carbon use efficiency.

"This constant ecological selection in species with relatively high CUE is possibly due to a general lack of abiotic stress and resource limitation in our simulated environment" — This observation could be generalized to state that most soils typically exhibit this pattern, as soil is generally an oligotrophic environment for microbial communities.

I also recommend that the authors address which data on soil microbiome species composition should be used to model CUE dynamics. For instance, relying solely on NGS data and species' genomic features may be problematic, as only a small fraction of the microbial community is actively involved in carbon transformation. A significant portion of the genetic material may derive from dormant or dead cells and extracellular DNA, which could introduce noise into the data.

Therefore, I suggest that the authors include a section discussing the potential limitations of their approach and possible solutions for addressing them.