

JS2-1:

## Evaluating community-environment relationships along fine to broad taxonomic resolutions reveals evolutionary forces underlying community assembly

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We propose a method for linking evolutionary process to community assembly by quantifying the strength of community-environment relationships hierarchically along taxonomic ranks. This approach explores the potential role of phylogenetic conservatism on habitat preferences: wherein, phylogenetically related taxa are expected to exhibit similar responses to environmental filtering if a niche is conserved over evolutionary time. Thus, the strength of community-environment relationships should not deteriorate with broadly-resolved taxonomic data. It therefore follows that broader taxonomic classification would even yield stronger associations with environmental factors by balancing potential spatiotemporal randomness in occurrences and abundances of finely-resolved taxa. In contrast, weaker community-environment relationships should be expected with broadening taxonomic resolution if niche is not phylogenetically conserved, since broadly-resolved taxa would combine finer taxa with distinct environmental responses. Here, we quantified the strength of community-environment relationships at fine to broad taxonomic resolutions using distance-based redundancy analysis, focusing on bacterial community composition (based on 454 pyrosequencing data of the 16S rRNA gene) of oceanic and soil samples. We found that among 4 cases, the amount of variation in community composition explained by environmental factors increased or remained constant with broadening taxonomic resolution from species- to order- or even phylum-level. This finding supports the hypothesis of phylogenetic conservatism in bacterial lineages and indicates that broadening taxonomic resolution may strengthen niche-related signals by removing potential uncertainty in quantifying the spatiotemporal distribution of finely-resolved taxa. Our results reinforce the current notion of ecological coherence in deep bacterial branches, emphasizing the role of niche conservatism in bacterial community assembly.

keywords:bacterial community composition,community-environment relationship,ecological coherence,phylogenetic conservatism,taxonomic resolution