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Marine bacterioplankton consortia follow deterministic, non-neutral community assembly rules

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ABSTRACT: The Bermuda Atlantic Time-series Study site provided an opportunity to study bacterial community assembly processes at 2 different depths, the surface and 200 m, in the upper mesopelagic, just below the euphotic zone. Over 100 monthly bacterioplankton DNA samples, from each depth, were analyzed using 16S rRNA gene sequences parsed with the custom software package PhyloAssigner. Co-occurrence networks, filtered for potential autocorrelation artifacts, were constructed for each depth. Network characteristics for the 2 depths were remarkably similar, and network parameters, such as connectance, were in the same range as previously published for ecological networks. Spectral clustering applied to similarity matrices based on exact connections revealed clusters of nodal taxonomic units (NTUs) that peaked at similar times, supporting deterministic, niche-based assembly. An algorithm that used hierarchical Dirichlet processes (HDPs) to model neutral communities based on learned parameters indicated that community assembly processes fit niche-based models at the metacommunity level for both depths. However, HDP analyses restricted to SAR11, SAR86, or SAR202 NTUs supported the neutral assembly hypothesis, suggesting that neutral process models may apply within some phylogenetic domains. To understand whether phylogenetically related taxa can substitute for one another in networks, we created a new metric, phylogenetically weighted connectivity, which considered the similarity of connections among near phylogenetic neighbors. This analysis suggested that phylogenetically similar lineages share similar network connections. Overall, our findings show that niche-based community assembly models are the best fit at both depths but that the neutral model may apply at some phylogenetic scales.

KEY WORDS: Community assembly · Network analysis · Marine bacterioplankton · Bermuda Atlantic Time-series Study

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