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Community assembly processes as a mechanistic explanation of the predator-prey diversity relationship in marine microbes

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Abstract

Predator and prey α-diversity are often positively associated; yet, underlying mechanisms remain unclear. We attempt to address this issue by deciphering how α-diversity of predator and prey influences each other's community assembly processes and subsequently determines α-diversity. The occurrence of assembly processes were indicated by the mean pairwise taxonomic index within a community (*aMΠTI*), assuming assembly processes left traceable imprints on species' phylogeny. Specifically, *aMΠTI* quantifies deviations of observed phylogenetic distances from that of random, thus indicating that non-random/deterministic assembly processes are in action. Less negative *aMΠTI*, which hints at the occurrence of weaker homogeneous deterministic assembly processes, is expected to increase α-diversity of the community. We hypothesize that higher predator and prey α-diversity make each other's *aMΠTI* less negative, which then increases their α-diversity. To test the hypothesis, we calculated Shannon diversity and *aMΠTI* for heterotrophic nanoflagellates (HNF; predator) and bacteria (prey) communities in the East China Sea. The HNF Shannon diversity was found to make the *aMΠTI* of bacteria less negative, which then increased bacterial Shannon diversity. In contrast, bacterial Shannon diversity did not affect HNF's *aMΠTI*. We provide evidence that top-down control underpins the positive α-diversity association among trophic levels in microbes of the East China Sea.

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