

Thermal niche evolution in the marine diatom genus *Cylindrotheca*

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To what extent closely related species are similar in their ecological niches is a major and recurring theme in evolutionary biology and ecology (Wiens *et al.*, 2010). Two extremes along a continuum of niche evolution can be distinguished: phylogenetic niche conservatism (PNC) and adaptive radiation (Ackerly, 2009). PNC is the tendency of species to retain aspects of their fundamental niche over time. Adaptive radiation can be defined as the evolutionary divergence of members of a single phylogenetic line into a variety of different adaptive forms. Given the paucity of data, it is at present not known how important PNC is, and more importantly to what degree organismal or environmental features influence the incidence of PNC.

Our views on evolutionary niche dynamics are biased towards macroscopic and often eye-catching species mainly from terrestrial communities; a selection often guided by natural history observations on striking ecological differentiation. Little is known about evolutionary niche dynamics in marine microbial species (Palumbi, 1994). Marine microbial populations are often believed to lack geographical barriers to gene flow (Cermeno and Falkowski, 2009) which would frequently lead to the dispersal of large numbers of cells into unfavourable environments. It has been hypothesized that marine communities are characterized by a widespread occurrence of ecological speciation, i.e. reproductive isolation caused by divergent natural selection (e.g. Ingram, 2011), but the importance of this mechanism is unknown in marine microbial communities.

We addressed the evolutionary niche dynamics within the globally distributed marine diatom genus *Cylindrotheca*. We collected strains from a wide range of marine habitats, from coastal plankton to sea ice and intertidal mudflats. We first inferred the evolutionary relationships of these strains using a multi-locus DNA dataset and obtained a well-resolved phylogeny. We then determined temperature preferences of these strains. Combining the molecular phylogeny with the thermal niches of lineages revealed a very weak phylogenetic signal in thermal niche characteristics. This indicates that closely related species tend to differ more in thermal niche than expected by a Brownian motion-based model. This seems to be caused by a combination of adaptive evolution and frequent shifts in environments in related lineages.

References

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