Reply to Brun et al.: Fingerprint of evolution revealed by shifts in realized phytoplankton niches in natural populations

Irwin et al. (1) show that the realized niches of many phytoplankton species shifted over a 15-y time period at the CARIACO (Carbon Retention in a Colored Ocean) Ocean Time-Series Station. The realized niche is a restricted version of the fundamental niche arising from at least three factors: biotic interactions, dispersal limitation, and the absence of some of the fundamental niche from the environment. At CARIACO, changes in the realized niches of phytoplankton species tracked a decadal-scale rise in average temperature and an increase in average irradiance in the upper mixed layer related to the deepening of the nutricline. The magnitudes of the changes in realized niches were proportional to the change in the mean environmental conditions, revealing a fingerprint of evolution. In contrast, changes in nitrate niches divided species into two categories: A minority of species shifted to lower nitrate niches, and the majority of species exhibited fixed niches in response to decreasing nitrate concentration. It is likely more difficult for phytoplankton to adapt to decreasing nitrate concentrations than modest changes in temperature or irradiance. We hypothesize that the changes we observed in realized niches were a result of evolution because of the structure in the changes of the realized niches. Laboratory studies have shown that microalgae can adapt to new environments in a few hundred generations, demonstrating the potential for rapid evolution in natural communities (2).

Brun et al. (3) argue that evolutionary adaptation must be recorded in a change in the fundamental niche and that this change will have a direct translation into the realized niche. The fundamental niche is the set of all conditions under which a species persists. The authors conclude that a 0.45 °C increase in the mean of the realized niche would require an 8 °C change in the mean of the fundamental niche. This conclusion relies on a model of the effects of evolution on the fundamental niche, which assumes the niche has a specific shape, constant width, and a simple translation of the fundamental into the realized niche. Although the realized and fundamental niches are related (4), it is not straightforward to predict one from the other. We lack the data required to quantify changes in the fundamental niches of phytoplankton from time-series data. Evolution can change both the fundamental niche and the species interactions that shape the realized niche.

Brun et al. (3) propose that reductions in abundance of the phytoplankton species provide an alternative explanation for the observed shifts in realized niches, but they don't explain how this mechanism would lead to the observed changes in realized niches. The MaxEnt method was appropriate for documenting changes in the realized niche because it uses presence-only data, not abundance data, and thus would not be biased by changes in the abundance of species (5). Our observations are consistent with the hypothesis that phytoplankton communities adapted to the changes in temperature and irradiance observed over a decade. This hypothesis should be tested with genomic and transcriptomic profiling of species from time-series studies and we recommend this approach be implemented widely to test for evolution in natural communities (6).

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