



Climatic forcings on algal cell size through the Cenozoic

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Marine phytoplankton constitute the base of the marine food chain and are fundamental components in biogeochemical cycles. A better understanding of both the mechanisms and the rates of climatic adaptation by marine phytoplankton remains a critical challenge in predicting future impacts of climate change. Using coccolithophores (a prominent group of calcifying unicellular algae) as an example, we explore why different species respond differently to environmental change, and determine what climatic parameters drive changes in cell size over geological time scales. We use comprehensive time series of coccolith size – a proxy for cell size – over the Cenozoic, targeting the ancestry of extant taxa that have revealed distinct physiological responses in culture experiments. We employ a novel, information-theoretic method to quantify the relative influence of different environmental variables on coccolith size. This model-free technique detects the significance and relative strength of the causal influence of multiple climatic forcing variables (including non-linear relationships), while correcting for possible common causal interactions among the forcings. Our analyses suggest that the macroevolutionary size decrease within the *Reticulofenestra* lineage (the ancestry of today's most prolific bloomer *Emiliania huxleyi*) primarily reflects a physiological adaptation to CO₂ limitation. In contrast, macroevolutionary size variability within the *Coccolithus* lineage (the ancestry of *Coccolithus pelagicus* and *C. braarudii*), while influenced by long-term trends in ocean temperature, is not affected by changes in CO₂. Improved understanding of such heterogeneity within ecosystem functional groups, including taxon-specific climatic adaptation strategies, will be of fundamental importance to the assessment of future climate change impact and mitigation.