

Rates of phenotypic evolution in coccolithophores

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By studying coccolithophores and their fossil coccoliths, we may gain detailed knowledge about the actual workings of phenotypic evolution. However, despite many efforts to describe the tempo and modes of evolution from the fossil record, it remains difficult to identify the processes responsible for the patterns observed. Fossil coccolith time series offer some of the most detailed and well-sampled records of evolutionary change spanning millions of years which can also be readily compared to proxy records of past climates to address a range of process-oriented questions. Much work has been done to document the patterns of past diversification and phenotypic change in coccolithophores, and several working hypotheses have been formulated that address distinct macroevolutionary coccolith size changes in terms of speciation and climatic adaptation. Yet, concerted efforts to understand what actual processes and rates of evolution underpin the observed patterns have only just begun, and to date, studies mainly focus on one single coccolithophore family, namely that of the ubiquitous species *E. huxleyi* and its closest relatives within the Noëlaerhabdaceae family. Here, we present an analysis of the rates of phenotypic evolution in several coccolithophore lineages, and explore why these vary across timescales. We use a range of statistical models to describe and discuss “bursts of evolution” as well as the more stationary trait dynamics during “evolutionary stasis”.