

Integrating molecular genomic and palaeobiological data on the evolution of the *Gephyrocapsa-Emiliana* clade

El Mahdi Bendif, Bruno Nevado, Edgar Wong

University of Oxford, Department of Plant Sciences, Oxford, UK; elmhidi@gmail.com, bruno.nevado@plants.ox.ac.uk, edgar.wong@linacre.ox.ac.uk

Kyoko Hagino

Kochi University, Center for Advanced Marine Core Research, Kochi 783-8502, Japan; kyokohagino@kochi-u.ac.jp

Ian Probert

Sorbonne University, Roscoff Marine Station, CNRS, 29680 Roscoff, France; probert@sb-roscoff.fr

Jeremy R. Young

University College London, Department of Earth Sciences, London WC1E 6BT, UK; jeremy.young@ucl.ac.uk

Rosalind E. M. Rickaby

University of Oxford, Department of Earth Sciences, Oxford, UK; rosaling.rickaby@earth.ox.ac.uk

Dmitry A. Filatov

University of Oxford, Department of Plant Sciences, as above; dmitry.filatov@plants.ox.ac.uk

Most Quaternary and modern coccolithophore assemblages are dominated by the Noelaerhabdaceae, especially the genera *Gephyrocapsa*, *Emiliana* and *Pseudoemiliana*. They include key bloom-forming species, underpin Quaternary biostratigraphy, and have been extensively studied in cultures. The combination of their rapid recent evolution, enormous abundance in both the fossil record and the modern ocean, and ready accessibility for laboratory study make them a very attractive study group for microevolutionary studies. Indeed, they are one of the most accessible groups for integrating molecular and palaeontological approaches to plankton evolution. However, molecular genetic studies have long proven to be problematic. Studies of slow-evolving genes, such as 18S rRNA, have failed to produce any useful data because well-established species, such as *Gephyrocapsa oceanica* and *Emiliana huxleyi*, have proved to have identical gene sequences. Conversely, studies of fast-evolving genes have produced contradictory results and suggestions of complex interactions of hybridisation and inherited polymorphism (e.g. Bendif et al., 2014).

However, new data from whole-genome sequencing has largely resolved these problems. Whole-genome sequencing allows evolutionary inferences from hundreds of genes to be compared and, from this work, a clear synthesis has emerged. On one hand, the classic extant morphospecies are well supported. On the other hand, the entire set of extant species is closely related, and a molecular clock interpretation, based on the well-established first occurrence of *E. huxleyi*, suggests that the clade diversified from a common ancestral population ca. 500 ka ago. This suggests that the generic distinctions are inflated and arguably untenable. More significantly, the evolutionary pattern inferred from molecular genetic data can be directly compared to that from the fossil record (e.g. Samtleben, 1980; Matsuoka & Okada, 1990). It appears that the size-reduction event (extinction of *Gephyrocapsa omega*/*Gephyrocapsa* sp. C), which has been observed in multiple geological studies, corresponds to the base of the radiation of the modern *Gephyrocapsa-Emiliana* clade. By extension, it appears highly likely that previous size-reduction events in the reticulofenestrifid record were similarly significant macroevolutionary events. Moreover, the pattern suggests that evolutionary turnovers were both abrupt and occurred via sympatric, rather than allopatric, evolution.

References

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