

# Puzzling speciation and adaptive patterns in the *Gephyrocapsa* complex

## El Mahdi Bendif

University of Oxford, Department of Plant Sciences, Oxford OX1 3RB, UK; elmhidi@gmail.com

## Ian Probert

Station Biologique de Roscoff, 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

## Colomban de Vargas

Station Biologique de Roscoff, 29680 Roscoff, France; vargas@sb-roscoff.fr

The haptophyte genus *Gephyrocapsa* comprises a complex of widely distributed bloom-forming coccolithophore species that have played a key role in global marine carbon fluxes over the last 3Ma. The most abundant species in modern oceans is *Gephyrocapsa huxleyi*, which has colonized very diverse ocean surface habitats, while its close relatives have remained more ecologically restricted. *Gephyrocapsa huxleyi* appears to have lost the ability to reproduce sexually in environments with low biotic/environmental pressures. This loss of sexual reproduction appears to have been a rapid microevolutionary process as compared to the establishment of the major phylogenetic groups within the *Gephyrocapsa* complex. Here, we present an attempt to describe the global diversity of *Gephyrocapsa* by coupling barcoding and phylogenomics approaches to metagenomics and relating physiological traits to an assessment of ecological niches. Data retrieved

from several cruises highlight the existence of two major mitochondrial haplogroups within *G. huxleyi*, alpha and beta, respectively, which are associated with warm and cold (bipolar) water systems. At a finer phylogenetic level, haplotypes were related to hydrographic structures, especially to subtle changes in nutrient and carbonate species concentrations. Furthermore, multi-barcode and phylogenomic analyses revealed a deep phylogenetic divergence that is related to thermal clines with a slight incongruence when compared to mitochondrial barcodes, suggesting the potential for hybridization between alpha and beta haplogroups. Considering actual scenarios of global warming and ocean acidification, this study provides a relevant diversity baseline for future monitoring that aims to evaluate whether an important climate-regulating organism has the intrinsic ability to adapt and thus continue to modulate our climate.