

Comparative genomics of the Isochrysidales

El Mahdi Bendif

Université du Québec à Rimouski, Institut des sciences de la mer de Rimouski (ISMER), Rimouski, Canada; University of Oxford, Department of Earth Sciences, Department of Biology, Oxford, UK; ElMahdi_Bendif@uqar.ca

<https://doi.org/10.58998/jnr3208>

Coccolithophores constitute one of the ecologically important phytoplankton groups, yet their evolutionary and diversity patterns remain unclear due to limited observations. This is particularly true for the Order Isochrysidales, despite it containing several ecologically and economically key taxa, such as *Gephyrocapsa huxleyi* and *Tisochrysis lutea*. This study provides a triptych overview of the relationships between Isochrysidales species by examining their macroevolutionary phylogenetic context and conducting finer scale studies of intraspecific morphogenetic variability and biogeographic structuring, as inferred from comparative genomics. First, obtaining a stable phylogenetic tree for all haptophytes using single-gene phylogenies remains very challenging. Despite extensive sequencing efforts, several deep branches in the haptophyte phylogenetic tree remain unresolved and statistically unsupported. For example, do the Isochrysidales form an independent and basal divergence, or do they cluster with the Zygodiscales in the Calcihaptophycidae? To address this, I propose employing a phylogenomic approach based on a large transcriptomic dataset that covers most of the haptophyte groups, although this may not necessarily resolve all nodes of haptophyte phylogeny. Second, the integration of Isochrysidales diversity with recent genomic research has been successfully linked to the fossil record. This linkage has been well demonstrated for the genus *Gephyrocapsa*, particularly at a fine scale for the species *G. huxleyi*. Such studies have provided insights into the evolutionary history and adaptive strategies of these organisms over geological timescales. Can similar analyses be extended to *G. oceanica* to uncover comparable patterns? Specifically, can we identify evolutionary events in *G. oceanica* that correspond to changes observed in the fossil record? Additionally, what can these findings reveal about the environmental factors that have influenced the evolution of *G. oceanica*, and how do these factors compare to those affecting *G. huxleyi*? Third, to what extent do both *G. oceanica* and *G. huxleyi* differ in terms of adaptability conferred by their genetic features? This question aims to explore the genetic basis of their adaptability to varying environmental conditions. What specific genes or genetic mechanisms contribute to the resilience or vulnerability of each species in different habitats? How do these genetic features influence their capacity to respond to environmental stressors such as ocean acidification, temperature fluctuations, and nutrient availability? Moreover, are there differences in the ploidy levels or gene content between *G. oceanica* and *G. huxleyi* that explain their distinct adaptive strategies? Understanding these genetic differences can provide deeper insights into the evolutionary processes that shaped the diversity and ecological success of these key phytoplankton species. Overall, this study sheds light on the biocomplexity and microevolution of phytoplankton and highlights the importance of considering microdiversity when studying their ecological and biogeochemical roles in the global ecosystem.