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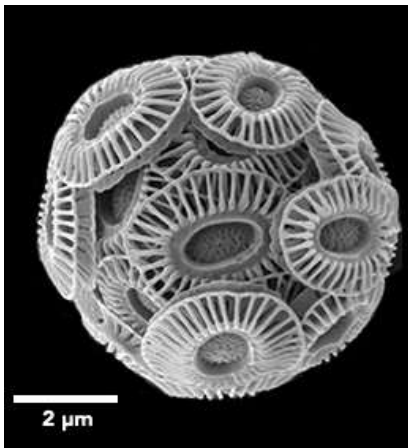
Orientation: Ocean Observation and Global Change

Specialization Area: Ocean Observation

Research Area: 1.4 Biological Oceanography

PhD project: **Response of the coccolithophore *Emiliana huxleyi* to future ocean acidification conditions: from gene expression to physiological rates**

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Summary: After the Industrial Revolution, the CO₂ produced by humans and emitted to the atmosphere has been increased exponentially. Around a quarter of this anthropogenic CO₂ is sequestered by the ocean, driving the process known as ocean acidification (OA). This OA will impact to the calcifying marine phytoplankton group of coccolithophores, which are amongst the most important marine primary producers and contribute significantly to the oceanic calcium carbonate precipitation. Since their importance at biogeochemical level, a lot of studies have assessed their response under OA conditions using mostly *Emiliana huxleyi*. These studies indicate that while decreases in calcification seem to be a general response under future OA conditions, photosynthetic rates show more variable responses. This variability has been attributed to culture conditions, inter- and intra-species variability and adaptive processes of clones maintained for a long time in the laboratory, though, until now any physiological mechanism has been described to understand this variability of responses.

A better understanding of the responses of marine phytoplankton to OA conditions has been achieved thanks to the introduction of molecular techniques, indicating a generalized down-regulation of their carbon concentrating mechanisms (CCMs) under OA conditions. Other studies also reported a broader cell impact to OA, not only constrained to CCMs. These metabolic rearrangements under future OA conditions have been explained in diatoms and chlorophytes by conceptual models such the Sobrino et al. (2014) which proposes that under acclimated future OA conditions, phytoplankton down-regulate their CCMs promoting a cascading cellular response that triggers a decrease of cellular energy-consuming pathways finally translating into an optimization of growth rate. Based on this, in this thesis we hypothesized that like other taxonomic groups of phytoplankton, in future OA conditions, coccolithophores operate with a down-regulated cellular metabolism. In order to test this hypothesis, the response of *E. huxleyi* metabolic pathways to future OA conditions from gene expression to physiological rates was studied.

The results of this thesis demonstrated that, like other taxonomic groups of marine phytoplankton, the metabolic responses of coccolithophorids under OA conditions can also be explained by the conceptual model of Sobrino et al. (2014), i.e. during acclimated OA conditions the carbon metabolism of *E. huxleyi* is down-regulated. This down-regulation ultimately affects an increase in cell efficiency, translating into an increase in biomass. On the contrary, in this thesis it is also observed that when these acclimated cells of *E. huxleyi* to OA conditions are disturbed, carbon metabolism is up-regulated, impacting the total biomass, which is reduced. However, the calcification response of this species always decreases regardless of metabolic conditions, this being reflected in cellular carbon allocation. This down- and up-regulation of metabolism as a function of CCM activity contradicts the commonly assumed "fertilizing effect" of CO₂, demonstrating the relevance of considering CCM activity to predict the response of phytoplankton to future climate conditions at biogeochemical scale. Moreover, this thesis also demonstrates that the cellular response to increased CO₂ involves extensive reprogramming at the cellular level, including even those that are supposed to be invariant, such as the actin gene. The variability in the gene expression of actin gene observed in this thesis carried out in *E. huxleyi* under OA conditions is also important from a methodological perspective since this gene is widely used in studies of phytoplankton under OA conditions evaluating the quantification of gene expression by relative methods.