frontiers | Frontiers in Marine Science

TYPE Editorial
PUBLISHED 02 March 2023
DOI 10.3389/fmars.2023.1166708

Editorial: Biological models for the study of ocean acidification: From molecules to ecosystems

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KEYWORDS

ocean acidification, biological models, stress ecology, marine invertebrates, plasticity

OPEN ACCESS

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SPECIALTY SECTION
This article was submitted to Global Change and the Future Ocean, a section of the journal Frontiers in Marine Science

RECEIVED 15 February 2023
ACCEPTED 21 February 2023
PUBLISHED 02 March 2023

CITATION
Della Torre C, Gambi MC, Freitas R and Munari M (2023) Editorial: Biological models for the study of ocean acidification: From molecules to ecosystems. *Front. Mar. Sci.* 10:1166708. doi: 10.3389/fmars.2023.1166708

Editorial on the Research Topic
Biological models for the study of ocean acidification: From molecules to ecosystems

The increase of CO_2 emissions in the atmosphere is considered one of the main drivers of global climate change. Higher atmospheric CO_2 concentrations generate the ocean acidification phenomenon (OA), occurring at the global ocean scale (Vargas et al., 2022), which is posing a risk to ocean biodiversity and ecosystem functioning (Nagelkerken and Connell, 2015). For this reason, there has been an increase in research on OA and important conceptual and methodological efforts in the last decade, in order to better understand how organisms would cope with OA and to foster conservation and restoration of marine ecosystems in a high-pCO_2/low pH scenario. Studies carried out under laboratory conditions have described detrimental effects due to OA across many taxa, highlighting strong species/population-specific sensitivity (Kroeker et al., 2010; Asnicar et al., 2021). Although most of the research has been focused on short/middle-term laboratory/mesocosm experiments usually on single species or a single stage of their life cycle, they have proved useful to understand the physiological effects of OA and the plasticity of individual species/populations. On the other hand, lab simulation experiments do not allow comprehensive predictions of the effects on ecological processes. In this respect, studies carried out in naturally acidified systems (e.g., hydrothermal vent systems and ice melting fronts) help to fill this gap, highlighting the ability of some organisms to survive and thrive under high-pCO_2/low pH conditions (Foo et al., 2018; Palombo et al., 2023).

There is now mounting evidence that the response of organisms to OA is a complex puzzle of mechanisms and processes at different scales of biological organization, from genetic (Pespeni et al., 2013) and molecular modifications (Wäge et al., 2018) to ecophysiological performances (Calosi et al., 2013) and the biological traits of the organisms (Gambi et al., 2016), up to ecological interactions such as facilitation, competition (Kroeker et al., 2013; Nagelkerken et al., 2017), and predatory/prey interactions (Ghedini and Connell, 2017), which are still largely unknown and mostly considered singularly.

In this view, the aim of the current topic was to collect papers that could help to identify model species to study the effects of OA on different biological hierarchical levels, from genes to populations, using different approaches in order to better predict how this phenomenon may influence population structure and species interactions, shaping marine communities in the future ocean of the Anthropocene.

The main outcomes of papers submitted to this Research Topic are:

1 The tolerance to high pCO$_2$/low pH is energy-consuming and might occur at the expense of other physiological functions

This consideration has been achieved in two papers of the Research Topic. The first was carried out using the polychaete *Platynereis* spp. as a model species and investigating a population inhabiting the CO_2 vents system of Castello Aragonese on the island of Ischia (Italy), which is considered to be adapted to OA (Signorini et al.). Through the application of the metabolomic approach, it was possible to observe a downregulation of purine and pyrimidine metabolism and a reduction in the content of fatty acids in polychaetes subjected to OA compared to controls. This suggests that an expenditure of energetic reserves is necessary to maintain the basic metabolism under stressful conditions. The second study focused on the calcifying mollusk *Ameghinomya antiqua*, which was exposed in the laboratory to OA and thermal stress (Martel et al.). Clams were able to persist during the 90 days of exposure, but in this case the survival under stressful conditions implied an investment of energy at the expense of growth and shell formation, potentially also affecting the ecosystem services related to the harvest of this species.

2 Epigenetic modifications as a molecular mechanism potentially underpinning tolerance to OA

The paper on *Platynereis* spp. from the CO_2 vents system on the island of Ischia (Signorini et al.) provided the first evidence of the potential involvement of histone posttranslational modifications (in particular acetylation) in promoting tolerance to OA. This information contributes to increasing the current understanding of the role of epigenetic variations as molecular mechanisms underlying acclimatization/adaptation to environmental stressors in marine species.

3 OA impacts negatively on coral reef carbonate accretion rates

Another study employed a natural wide-scale gradient of OA represented by the coral reefs associated with the US Pacific Islands (Barkley et al.). A decennial (2010-19) variation of the aragonite saturation state (Ωar) was correlated with several metrics such as the benthic cover, genera, and morphology of coral communities, as well as the net carbonate accretion. In this natural OA gradient, the authors did not find a correlation between Ωar variation and the composition of reef communities. Conversely, the decrease in net carbonate accretion was strongly correlated with Ωar. The study pointed out that the measurements of calcification and accretion rates are effective tools for monitoring the adverse impacts of OA on reef ecosystems, and they are more sensitive than other metrics related to benthic community composition.

4 The evolution of the DIC carbon isotope signature under OA and its implication for laboratory culturing of marine organisms

This represents a methodological paper where the stable isotope approach is used to better understand the physiological processes contributing to the response of organisms to ocean acidification (Zhang et al.). To simulate OA in laboratory cultures, the direct bubbling of seawater with CO_2 is a preferred method because it adjusts pCO$_2$ and pH without altering the total alkalinity. Frequently, the dissolved inorganic carbon (DIC) in the initial seawater culture has a distinct $^{13}C/^{12}C$ ratio, which is far from the equilibrium expected with the isotopic composition of the bubbled CO_2, and this aspect is sometimes ignored. To overcome this problem, the authors have proposed a numerical model that can well predict the DIC carbon isotope ratio and its evolutions during bubbling, which can be traced during the experiment. Their simulations show that, if not properly accounted, CO_2 bubbling can lead to large errors in estimated carbon isotope fractionation between seawater and biomass or biominerals, consequently affecting interpretations and hampering comparisons among different experiments.

Author contributions

All authors listed have made a substantial, direct, and intellectual contribution to the work and approved it for publication.

Conflict of interest

The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

Publisher's note

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