frontiers | Frontiers in Ecology and Evolution

TYPE Editorial
PUBLISHED 01 February 2023
DOI 10.3389/fevo.2023.1061314

OPEN ACCESS

EDITED AND REVIEWED BY
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SPECIALTY SECTION
This article was submitted to
Population, Community, and Ecosystem Dynamics,
a section of the journal
Frontiers in Ecology and Evolution

RECEIVED 04 October 2022
ACCEPTED 23 January 2023
PUBLISHED 01 February 2023

CITATION
Modica MV, Furfaro G, Munari M and Locatello L (2023) Editorial: EVOLMAR 2020—The first Italian congress on marine evolution. *Front. Ecol. Evol.* 11:1061314. doi: 10.3389/fevo.2023.1061314

Editorial: EVOLMAR 2020—The first Italian congress on marine evolution

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KEYWORDS

proceedings, EVOLMAR Conference, marine evolution, populations and species, adaptation, macroevolution, biodiversity

Editorial on the Research Topic
EVOLMAR 2020—The first Italian congress on marine evolution

The First Italian Conference on Marine Evolution—EVOLMAR 2020—was held in a virtual format on 23–25th November 2020, with the support of the Stazione Zoologica Anton Dohrn (SZN Naples, Italy) and the Italian Society for Evolutionary Biology (SIBE-ISEB). The Conference germinated from the growth of interest in marine topics inside the Italian community of Evolutionary Biologists and the strong desire to maintain an active National and International exchange of ideas despite the severe limitations imposed by the COVID-19 pandemics. Organized in the four thematic areas of *Macroevolution*, *Populations and Species*, *Adaptation*, and *Biodiversity*, it gathered 287 participants from 29 countries. Oral presentations and posters spanned from the investigation of the evolutionary patterns accounting for marine species diversity and adaptations, to the plastic response of species and populations to a changing world, and to the consequences for their conservation. This special Research Topic in Frontiers in Ecology and Evolution represents the collection of six publications, from 38 authors belonging to 13 different Institutions in Italy, Germany, Portugal, United States, and China. As emerged from the Conference, the Topic emphasizes the value of multidisciplinary approaches to unveil novel scenarios for the study of evolution of marine biodiversity and to address future challenges in conservation and management of the biodiversity world heritage.

The group of marine invertebrates most represented in this Research Topic belongs to the Nudibranchia order, with three contributions focused on it, confirming the emerging interest on these shell less gastropod molluscs. Nudibranchs are characterized by unique defensive strategies and interesting specialized biological adaptations with very attractive potential applications. Garzia et al. here propose, for the first time, the use of the nuclear Internal Transcribed Spacer 2 as a powerful tool to delimit species in the eolid taxa. This innovative tool allows to enrich the suite of available molecular markers for species identification that, as highlighted throughout the EVOLMAR Conference, nowadays prompts for the use of integrative approaches combining morphological and molecular characters. This study calls the attention on the importance of developing cutting-edge molecular tools for a reliable assessment of biodiversity, a key basic step to also further understand the evolution of complex traits in this invertebrate group, such as photosymbiosis (i.e., the association between a heterotrophic host and microalgae). As introduced by Rola et al. in their Review, photosymbiosis is best studied in cnidarians, whereas in most other animals the mechanisms of establishing photosymbiosis, the physiological basis, and the evolution of a photosymbiotic life history remain poorly understood. Following Rola et al., the presence of both photosymbiotic and non-photosymbiotic species in Cladobranchia makes them a good model group to investigate the genomic adaptations underlying the evolution of a mutualistic photosymbiosis in sea slugs and to understand if photosymbiosis evolved independently or from a recent common ancestor in the different lineages. Clavijo et al., by investigating the gene expression profile in the cladobranch *Berghia stephanieae* (Valdés, 2005) which is unable to maintain symbiosis for more than a couple of days, show that in nudibranchs the mechanism of photobiont recognition is similar to those adopted by cnidarians. However, they also identify some additional candidate genes involved in this mechanism that might be molluscan specific, and unravel the factors that accounts for the unstable symbiosis in this slug.

Gene expression is also the focus of Gerdol et al. in their study on the patterns of DNA methylation and the complex role played by this mechanism in regulating genome activity in the bivalve mollusc *Mytilus galloprovincialis* Lamarck, 1819. This epigenetic mechanism, which contribute to modify gene expression independent of DNA sequence alterations, has been mainly studied in vertebrate and plants but can play a key role also in invertebrates organisms' resistance and plasticity to environmental stressors by increasing the adaptive potential (Roberts and Gavery, 2012). The study of Gerdol et al. identify the DNA methylation-related genes through a genome-wide analysis, their phylogenetic relationships and their expression pattern in different adult tissues in comparison with other bivalves. These early insights pave the way for further in-depth investigations on the mechanisms underpinning DNA methylation and the functional role of this process in molluscs, which can serve as a model to better understand how the environment and emerging contaminants can influence DNA methylation patterns in marine invertebrates. The role of ecological traits appears to be of large importance also in the evolution of genome size, as shown by Iannucci et al. in their study on the relationships between genome size and specific eco-physiological and morphological features in decapod crustaceans. A correlation between genome size and cytological traits has been proven to occur across a variety of taxa (Cavalier-Smith, 1985; Lynch, 2007), but the expected patterns of correlation become more unpredictable when life-history and eco-physiological traits are considered. Indeed, the study of Iannucci et al. shows that while developmental complexity emerges as the most powerful variable affecting genome size across all decapods, other multiple eco-physiological and life-history traits, including habitat, correlate with genome size when considering the sub-groups of Anomura, Astacidea, and Brachyura.

Developmental strategies are also the focus of the study of Muffet et al. that test the impacts of light and food availability on the ephyrae developmental stage of *Cassiopea xamachana* Bigelow, 1892. As evidenced by the Authors the investigation of early developmental stages resistance to extreme environmental conditions is of key importance to understand the high invasive potential of cnidarian species, especially scyphozoans and hydrozoans. Survival in extreme condition of podocysts, polyps and planulocysts is well documented, whereas starvation tolerance and robustness in the motile ephyra stage is less studied. Muffet et al. address this dearth and show that ephyrae of *C. xamachana* are tolerant of food and light stress and may be a sturdy life cycle stage with potential for species introduction.

Evolution in marine organisms is a truly complex and transversal field of study and the contributions to this Research Topic, and to the EVOLMAR Conference, highlight the need of increase the knowledge in this field by investigating the biodiversity at multiple levels, spanning from genes to populations and ecosystems. Advancing in our understanding of the drivers and mechanisms underlying marine evolution at all these levels is, indeed, imperative to improve current predictions on the fate of global biodiversity, and particularly timely in the framework of the United Nations Decade of Ocean Science for Sustainable Development (2021–2030). In this scenario new molecular, morphological and machine learning approaches are emerging as important tools for a more comprehensive assessment of global biodiversity.

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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