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# Editorial: Mediterranean coastal fish biology and ecology

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### Editorial on the Research Topic Mediterranean coastal fish biology and ecology

The Mediterranean Sea, known for its rich historical and cultural significance, also holds a unique and diverse marine ecosystem (Coll et al., 2010). Its coastal areas, in particular, represent critical habitats for various fish species, some of great economic importance. The biodiversity of Mediterranean coastal fish communities is influenced by a complex interplay of natural and anthropogenic factors (Tiralongo, 2021). In recent decades, human activities, environmental change and biological invasions have increasingly threatened the delicate balance of Mediterranean ecosystems (Katsanevakis et al., 2014). As the basin continues to face unprecedented challenges due to impacts of climate change, habitat degradation and biological invasions, the biology and ecology of coastal fish populations have become a focal point of scientific research and conservation efforts (Giangrande et al., 2020).

This Research Topic aims to provide some recent updates of the state of knowledge regarding Mediterranean coastal fish biology and ecology. It highlights some key factors shaping these communities, such as the interactions between fish and their microbiota, population structure of an exploited fish resource, fish community composition and expansion of thermophilic species. Moreover, the Research Topic highlights the need for interdisciplinary research to better understand the complex dynamics and interconnectedness of these ecosystems and support sustainable practices that can ensure the long-term health of Mediterranean coastal fisheries.

The work of Lipej et al. investigates the marine protected area of Mljet National Park in the southern Adriatic Sea, examining the structure of coastal fish assemblages associated with a temperate coral reef. The research aimed to provide baseline information on the occurrence and temporal distribution of fish species, highlighting the ecological significance of the coral reef to local ichthyofauna. Using non-destructive SCUBA-based visual census techniques, data were collected from 2013 to 2021 at two sites in Veliko jezero, a seawater lake connected to the sea with a narrow strait. This area is a protected no-take zone which hosts one of the biggest coral reefs in the Mediterranean composed of stony coral *Cladocora caespitosa*. In total, 38 fish taxa were recorded on the right bank, where the coral reef is present, and 36 species on the left bank. The presence of the coral reef, located at depths of 9 to 12 meters, was the key factor differentiating the fish fauna between the two sites, which otherwise share similar environmental conditions. A decline in fish diversity was observed at the coral reef site, with a steady regression documented from 2013 to 2021. This suggests potential degradation of the reef ecosystem, underscoring the need for continued monitoring and further research to investigate the factors influencing ichthyofaunal community within this marine protected area.

The study of Lilli et al. demonstrates the critical role of the gut microbiome in the health and homeostasis of fish. Despite the vast diversity and distribution of this vertebrate group, the intestinal microbiome has been thoroughly characterized in only a limited number of freshwater and marine fish species. In their work, the researchers analyzed the gut mucosal microbial communities of three commercially important Scorpaena species (n=125), using 16S rRNA gene amplicon data from four distinct locations across the Mediterranean Sea. Their findings revealed that the geographical origin of the individuals had a greater influence on the diversity and composition of the gut microbial communities than the phylogenetic relatedness between hosts. Additionally, a positive correlation between the gut microbiota composition and phylogenetic distance (known as phylosymbiosis) was observed. The study also described the core microbiota of each species both regionally and throughout the Mediterranean, highlighting that only a few bacterial genera were consistently found in the gut microbiota of scorpionfishes across the region: Photobacterium, Enterovibrio, Vibrio, Shewanella, Epulopiscium, Clostridium sensu stricto 1, and Romboutsia in S. notata; Clostridium sensu stricto 1, Cetobacterium, and Romboutsia in S. porcus; and only Clostridium sensu stricto 1 in S. scrofa. This study emphasizes the importance of investigating the gut microbiome across a species' geographical range, suggesting this methodology as a general approach to better understand the microbial ecology of fish species.

The study of Corti et al. provides valuable insights into the population structure of the common sole Solea solea in the Mediterranean Sea by employing a multidisciplinary approach that integrates genomic and otolith data. Through the use of single nucleotide polymorphism (SNP) markers, otolith shape, and trace element composition, the researchers delineated the population structure and explored the environmental factors driving these patterns. By correlating SNPs with environmental and spatial variables, they evaluated how these features impact population structure, applying a seascape genetics approach, including redundancy analysis (RDA) and genetic-environmental association (GEA) analysis, to identify loci potentially linked to local adaptation. Functional annotation analysis was conducted to detect genes associated with both neutral and adaptive genetic variation. The results revealed significant genetic divergence among putative populations of common sole, with a clear distinction between the western and eastern Mediterranean populations, and a separate genetic cluster corresponding to the Adriatic Sea. Fine-scale population structure was evident in the

western Mediterranean at the level of outlier loci, with further differentiation within the Adriatic. The study found that longitudinal and salinity variations were the primary drivers of both broad and fine spatial structure. GEA analysis detected significant outlier loci associated with local adaptation processes under a highly structured differentiation pattern, while RDA indicated that both spatial distribution and environmental factors partially explained the genetic structure observed. The findings suggest that separation among Mediterranean sole populations is primarily driven by neutral processes, such as low connectivity due to spatial segregation and limited dispersal, but also highlight evidence of local adaptation. These results have important implications for the management and conservation of common sole populations in the Mediterranean, pointing to the need for a reassessment of stock units and a potential redefinition of fishery management strategies to better account for both genetic differentiation and local adaptation.

The study of Nota et al. focuses on the range expansion and increasing abundance of sea chubs (genus Kyphosus) in the Mediterranean Sea, a region known as a biodiversity hotspot. Due to seawater warming, the Mediterranean has become more accessible to thermophilic species, which pose significant threats to the local biodiversity. Among these, Kyphosus species, particularly Kyphosus vaigiensis and Kyphosus sectatrix, are enigmatic due to their high phenotypic similarity. This resemblance has caused frequent misidentifications, complicating species-level classifications. Despite the increasing presence of these fish in the Mediterranean, it remains unclear whether both species or only one is undergoing range extension and demographic growth. Prior to this study, 26 reports of Kyphosus individuals had been documented in the Mediterranean Sea across 24 different publications. The researchers provided 13 new records from various locations along the Mediterranean coast and reviewed the history of the genus in the region. To clarify the taxonomic uncertainty, they sequenced the complete mitochondrial genomes of two specimens and assessed their phylogenetic relationships with previously published Kyphosus mitochondrial DNA sequences from around the world. They also conducted detailed morphological and meristic analyses on one of the specimens. Their findings indicate that K. vaigiensis is the species currently expanding in the Mediterranean, while K. sectatrix remains rare and is only sporadically reported. The phylogenetic analysis suggests that K. vaigiensis individuals in the Mediterranean most likely originated from Atlantic populations, with no evidence supporting their introduction via the Red Sea or other anthropogenic vectors. The study also discusses the potential ecological and fishery impacts of this range expansion, highlighting the importance of continued monitoring and accurate species identification to better understand the ecological dynamics and management needs of these thermophilic invaders.

The future of research of Mediterranean coastal fish biology and ecology is at a critical juncture. As the region continues to grapple with the impacts of climate change, habitat degradation, biological invasions and overfishing, there is an urgent need for coordinated, interdisciplinary approaches to aid conservation and management efforts. The establishment and enforcement of MPAs, along with habitat restoration efforts, are essential for preserving critical fish habitats, such as seagrass meadows and rocky reefs. Additionally, various shallow coastal habitats serve as vital fish nurseries and are significantly affected by human activities, highlighting the need for stronger conservation efforts (Matić-Skoko et al., 2020). Adaptive management strategies that account for the effects of warming seas and ocean acidification are needed to protect vulnerable species.

# Author contributions

FT: Conceptualization, Data curation, Supervision, Validation, Writing – original draft, Writing – review & editing. BD: Data curation, Supervision, Validation, Writing – original draft, Writing – review & editing.

# **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.

The handling editor SK declared a past co-authorship with the author FT.

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