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EDITED AND REVIEWED BY  
Rui Rosa,  
University of Lisbon, Portugal

\*CORRESPONDENCE  
Tomihiko Higuchi  
✉ [thiguchi@aori.u-tokyo.ac.jp](mailto:thiguchi@aori.u-tokyo.ac.jp)

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# Editorial: Sharing technical knowledge to understand the distribution patterns and migration history of marine organisms

Tomihiko Higuchi<sup>1\*</sup>, Ming-Tsung Chung<sup>2</sup>, Chisato Yoshikawa<sup>3</sup>  
and Yuki Minegishi<sup>4</sup>

<sup>1</sup>Department of Living Marine Resources, Atmosphere and Ocean Research Institute, The University of Tokyo, Kashiwa, Chiba, Japan, <sup>2</sup>Institute of Oceanography, National Taiwan University, Taipei, Taiwan, <sup>3</sup>Biogeochemistry Research Center, Research Institute for Marine Resources Utilization, Japan Agency of Marine-Earth Science and Technology (JAMSTEC), Yokosuka, Japan, <sup>4</sup>Otsuchi Coastal Research Center, Atmosphere and Ocean Research Institute, The University of Tokyo, Otsuchi, Iwate, Japan

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## Editorial on the Research Topic

[Sharing technical knowledge to understand the distribution patterns and migration history of marine organisms](#)

## 1 Introduction

Marine organisms contribute to many important biogeochemical processes while their ecological functions provide resources for human activity not only as food sources but also through natural products, and tourism. Despite their importance, the distribution patterns and migration history of many marine organisms are still unknown. Often even fish that are well-known for their importance to aquaculture and fisheries have unclear distribution patterns due to the difficulty of accessing their marine habitat. This Research Topic was aimed at collecting related research on the distribution patterns and migration history of marine organisms with recent technical advances and their combinations.

## 2 Fish otolith analysis

Recently, the reproduced migration history of the sardine has been reported by combining high-resolution otolith stable oxygen isotope ratio ( $\delta^{18}\text{O}$ ) analysis and numerical simulation (Sakamoto et al., 2019). This kind of method can be expected to apply to other species.

Hanson et al. suggested a comprehensive approach involving precise stable isotope sampling of otoliths, genetic identification, analysis of growth increments, and the use of a basic movement model. This integrated method aims to determine the whereabouts of individual wild Atlantic salmon. The research establishes an analytical framework for

predicting the ocean migratory paths by leveraging a natural data storage structure inherent to each salmon. This methodology proves particularly effective in uncovering the historical movements of species that are highly migratory or anadromous.

Gou et al. newly provide temperature-dependent fractionation in otolith  $\delta^{18}\text{O}$  of chum salmon based on a rearing experiment. Also, carbon isotope ( $\delta^{13}\text{C}$ ) in otolith was measured to examine the potential kinetic and metabolic effect of isotopic fractionations.  $\delta^{13}\text{C}$  in otolith can be a tool to estimate metabolic rate in the field (Chung et al., 2019).

### 3 Isotopes and iso-logging

The use of isotope analysis (iso-logging) for tracking highly migratory marine fish has gained prominence as a promising tool in recent years (e.g. Matsubayashi et al., 2020). However, the effectiveness of this method is frequently impeded by the absence of crucial information, such as spatial variations in isotope ratios across different habitats, commonly referred to as “isoscapes.”

Matsubayashi et al. conducted a study to assess the effectiveness of geostatistical analysis in creating isoscapes for  $\delta^{13}\text{C}$  and  $\delta^{15}\text{N}$  in the western Pacific. They aimed to estimate ontogenetic shifts in  $\delta^{13}\text{C}$  and  $\delta^{15}\text{N}$  values of skipjack tuna (*Katsuwonus pelamis*). The geostatistical model successfully generated isoscapes and accurately predicted ontogenetic shifts based on skipjack isotope ratios. The resulting isoscapes revealed that  $\delta^{13}\text{C}$  and  $\delta^{15}\text{N}$  could distinctly differentiate the latitudinal migration patterns of skipjack tuna in the Western Pacific. Yoshikawa et al. documented the development of nitrogen isoscapes for phytoplankton in the western North Pacific using a marine nitrogen isotope model. The simulated distributions of  $\delta^{15}\text{N}$  for nitrate, phytoplankton, and particulate organic nitrogen aligned well with observed  $\delta^{15}\text{N}$  values in the same region. The seamless nitrogen isoscapes can enhance the comprehension of the habitats of marine organisms and aid in the study of fish migration in the Western North Pacific.

Ohno et al. investigated the inter-annual variations in the feeding habits and food sources of Japanese sardine and mackerel captured in the Kuroshio-Oyashio transition zone of the Western North Pacific by analyzing bulk stable isotopes ( $\delta^{13}\text{C}$  and  $\delta^{15}\text{N}$ ) and amino acid nitrogen isotopes ( $\delta^{15}\text{N}_{\text{AA}}$ ). These analytical methods supplied insights into distinctions in the structure of the food web, revealing that the variability in food sources stems from variations in migration area, depth, and feeding behaviors.

Jackel et al. indicated that the ecological significance of deep-sea squids in the Great Australian Bight, comparing them with other cephalopod species found in global, southern temperate, and polar squid distributions by using  $\delta^{13}\text{C}$  and  $\delta^{15}\text{N}$  stable isotopes, fatty acids, and energy content. This study underscored that, aside from enhancing our comprehension of the trophic ecology of deep-sea squids, the use of partial specimens highlighted the valuable ecological information that can be derived from a few samples.

### 4 Field survey and environmental DNA

Recent advancements in environmental DNA (eDNA) techniques have significantly enhanced the capacity to carry out ecological

monitoring across diverse locations. (e.g. Minegishi et al., 2019). Also, genetic analysis can be a powerful tool connectivity of organisms.

Kawakami et al. developed a novel species-specific qPCR assay targeting the eDNA of polar cod and collected the samples from various latitudinal points across their study area. The results align with existing information regarding the distribution and habitat of polar cod, indicating that eDNA can be considered a dependable tool, either as a substitute for or in conjunction with traditional methods.

Yu et al. investigated the distribution patterns of economically significant small pelagic fishes within the Kuroshio Current system (offshore of Japan) through the monitoring of eDNA. Utilizing generalized additive models (GAM), they examined the impact of environmental factors, including sea water temperature, salinity, and the presence of prey fish, on the occurrence and quantity of target fish eDNA. This study successfully unveiled intricate spatial distribution patterns of small pelagic fishes in the Kuroshio Current system, and hypothesized that predator-prey relationships play a role in influencing the distribution within small pelagic fish communities.

Marino et al. used a multidisciplinary approach to examine the connectivity of the marbled crab in the Adriatic and Ionian basins. Their investigation incorporated genetic analyses, Lagrangian simulations, and individual-based forward-time simulations to reveal both realized and potential connectivity among various locations. This study suggested that, when combined with representative sampling and the application of genome-wide approaches, this approach enables a more comprehensive understanding of the factors influencing oceanographic, demographic, and genetic connectivity.

As another survey, Henderson et al. utilized a dataset of tourist vessel locations in the southwest Atlantic sector of the Southern Ocean to ascertain the necessary number of tourist vessel voyages for reliable abundance estimates of baleen whales. Their findings demonstrated that surveys conducted from tourist vessels surpassed the performance of standardized line transect surveys in accurately reproducing simulated baleen whale abundances and distribution. These analyses indicate that tourist vessel-based surveys represent a viable method for estimating baleen whale abundance in remote regions.

## 5 Conclusions

A combination of several methods, such as isotope and/or genetic analysis, along with simulation and/or modeling, can bring new insights into the distribution patterns and migration history of marine organisms. Additionally, utilizing commercial ship voyages, such as cargo or tourist vessels, for survey can be expected to capture spatiotemporal trends. We believe that the research techniques proposed in this Research Topic can improve the ecological study of marine organisms in the near future.

### Author contributions

TH: Writing – original draft, Writing – review & editing. M-TC: Writing – original draft, Writing – review & editing. CY: Writing –

original draft, Writing – review & editing. YM: 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.

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