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Editorial: Integrated phylogeography and population genomics of coastal ecosystems

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Editorial on the Research Topic
Integrated phylogeography and population genomics of coastal ecosystems

Introduction

The Research Topic 'Integrated Phylogeography and Population Genomics of Coastal Ecosystems' is a collection of seven original articles that communicate new insights on the ecological and evolutionary processes influencing coastal populations, species, and ecosystems. These papers showcase how genetic and genomic tools may be useful to support evidence-based coastal conservation and management.

Coastal ecosystems are valuable environments occurring at the narrow interface between land and sea (Barbier et al., 2011; Costanza et al., 2014), which makes them susceptible to multiple potentially interacting threats from both ocean- and land-based human activities (Halpern et al., 2008). Thus, researchers and practitioners need a diverse set of tools and approaches to address complex conservation issues in coastal regions. For decades, the genetic information of coastal organisms –usually based on tens of neutral loci– has been used to delimit species boundaries, quantify connectivity among populations, describe population structure, and detect past demographic changes. In recent years, the increased availability of genomic resources has allowed one to expand the breadth of research questions, hence adding to the coastal ecosystem conservation toolbox. Both genetic and genomic resources come with their respective strengths and weaknesses. The former is usually more affordable for small-scale studies and less bioinformatically intensive, while the latter provides a wider representation of the genome and higher resolution of fine-scale genetic patterns. The choice of markers is thus highly context-specific and depends on the financial resource, technical capacity and conservation question of the issue at hand. This Research Topic features studies using both genetic and genomic resources.

One of the important applications of conservation genetics is in evaluating the importance and relevance of protected areas in conserving priority habitats and species. Using genetic tools based on mitochondrial genome regions, Hamamoto et al. studied the black sea cucumber (*Holothuria atra*) –a seafood species with rising demand– across the Ryukyu Islands, Southern Japan. They showed that the populations were genetically structured, with exclusive haplotypes in each of the studied island groups (Okinawajima, Kerama, and Sakishima islands groups). Additionally, the observed genetic diversity was higher within than beyond protected areas. These results suggest that the benefits conferred by the protection of natural parks, e.g. reduced fishing pressures, could support the maintenance of genetic diversity of *H. atra*, and likely of other harvested marine and coastal organisms.

The conservation management of coastal ecosystems can be informed by the biogeography and dispersal patterns of key species. Four articles in this Research Topic examined the influence of environmental factors on the genetic structure of coastal plant populations and the role of dispersal in defining conservation units. Two studies explicitly investigated the presence of genetic barriers and their implications on conservation. Triest et al. showed that lagoon complex promoted inbreeding in a euryhaline aquatic plant, *Ruppia brevipedunculata*, through local hydrodynamics that led to spatially structured gene pools and manmade physical structures from aquaculture that imposed barriers to dispersal. The insular nature of the lagoon complex thus highlights a dichotomous role, i.e. though the impediments to dispersal prevents genetic homogenization, they could create refugia and enhance genotypic diversity by preserving rare alleles. Working at a broader geographical scale, Triest et al. provided evidence for a distinctive genetic divide in *Avicennia marina* populations across a biogeographical barrier, the Malay Peninsula, which is congruent with previous work on its close relative, *Avicennia alba* (Wee et al., 2020). However, *A. marina* populations in the East Malay Peninsula were found to be introgressed with *A. alba* through chloroplast capture of the latter, suggesting a potential risk of cryptic ecological degradation. This highlights the need for detailed investigation on genetic structure when defining conservation units to avoid taxonomic errors or the conservation of a less typical and less functional species over a functional one.

Another crucial factor that determines the genetic structure in the seascape is long distance dispersal. Coastal geomorphology and ocean currents, both historical and contemporary, can influence the population structure of sea-dispersed coastal species. The plastomes of mangrove trees *Rhizophora mucronata* from the coastal regions in the Western Indian Ocean revealed several key historical events, including ancient refugia in the Seychelles and eastern Madagascar, range expansion from Northern Madagascar toward the African mainland coastline, and a unique bottleneck dispersal to the south of Delagoa Bight (Triest et al.). These events highlighted how long distance dispersal shaped the phylogeography of contemporary *R. mucronata* populations, and the importance of taking them into consideration when defining conservation units. On the other hand, contemporary dispersal events could also shed light on biodiversity management. Ngeve et al. genotyped *Rhizophora racemosa* drift propagules from the Cameroonian coastline, showing that although these propagules harboured higher levels of genetic diversity and private alleles, they were all genetically isolated from Cameroonian populations. This novel finding highlights the need for transboundary dialogue and intergovernmental efforts in coastal management.

Large-scale and transboundary conservation efforts may also benefit greatly from genetic data when it is integrated with environmental data through modelling. Using an ecological niche model that links abiotic variables with neutral genetic diversity of populations of *Avicennia germinans*, Ochoa-Zavala et al. showed that, overall, sites with high environmental suitability also presented high genetic variation (heterozygosity and allelic richness). This relationship highlighted not only that soil type and precipitation seasonality were good predictors of the distribution of genetic diversity but also the projection of genetic diversity itself in the geographic space, including regions where genetic information is scarce or non-existent. Complementarily, the use of ecological models also allows researchers and managers to anticipate how future conditions may threaten populations. Vidal Junior et al. used genomic-environmental association to predict adaptively driven vulnerability and observed that populations of *A. germinans* and *A. schaueriana* from higher-latitudes will likely be more vulnerable to climate-driven habitat loss compared to their equatorial counterparts. Coupling these findings with estimated site-specific accumulated deforestation illustrates that local and regional conservation strategies are key to protect coastal organisms and the ecosystems they form.

The contributions presented in this Research Topic provide a diverse compilation of approaches, methods, and coastal organisms. As a whole, they illustrate how conservation practitioners and managers may benefit from phylogeography and population genetics/genomics studies. We hope that this volume stimulates the translation of scientific evidence derived from molecular data into effective protection and conservation of coastal ecosystems.

Author contributions

GMM and AKSW drafted the Research Topic editorial. All authors listed have made a substantial, direct, and intellectual contribution to the work and approved it for publication.

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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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