The integration and application of genomic information in mangrove conservation

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Introduction

Mangroves comprise of tropical and subtropical intertidal plant communities. They provide essential ecosystem services (e.g., carbon sequestration and coastal protection) that are severely undermined by widespread habitat degradation and destruction and were predicted to be lost or impaired by the end of this century (Duke et al. 2007).

In the last decade, the emergence of conservation genomics—based on high-throughput next-generation sequencing (NGS) technologies—promised much affordably generated molecular data that could contribute significantly to the decision-making process in conservation. Compared with traditional non-NGS genotyping techniques (e.g., microsatellite), NGS circumvents tedious marker development; thus, it can be more readily applicable to nonmodel organisms. Furthermore, the ease of multiplexing and the possibility of outsourcing in certain (developing) countries enabled the genotyping of large numbers of samples and significantly lowered the entry cost. Such costs may be covered by medium-sized grants that prioritize wetland ecosystems and technical capacity building. Despite growing efforts in mangrove conservation, practitioners have not fully embraced genomic information.

We considered 3 major areas of opportunity in which NGS-based data may be particularly useful: clarifying species' identity, defining conservation units, and understanding adaptation. We call for a new focus to integrate findings from mangrove genomics to conservation planning. We focused on mangrove plant species, which form the structural foundation of the ecosystem.

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Clarifying Species Identity

A fundamental conservation practice is the identification of rare and endangered species to be designated for legal protection. Mangrove forests face serious risk of loss of plant species; 11 of the 70 known mangrove species worldwide are threatened (Polidoro et al. 2010). Most species have a widespread distribution that overlaps with several other congeneric relatives, providing ample opportunity for hybridization and introgression and thereby leading to confusing species identity. Thus, clarifying species identity is crucial for directing conservation efforts to priority species and ensuring efficacy.

The best demonstration of this is the recent discovery that *Bruguiera hainesii*—1 of 2 critically endangered mangroves—is a hybrid between *B. gymnorhiza* and *B. cylindrical* (Ono et al. 2016). This revelation raised questions about the conservation status of *B. hainesii* because the International Union for Conservation of Nature (IUCN) prioritizes only the conservation of species, not hybrids. Deprioritizing *B. hainesii* would allow attention to be channeled to other endangered mangrove species.

Genomic information can also be used to guide reforestation activities and prevent unintentional anthropogenic hybridization, which can lead to reduced reproductive output, reduced fitness, and extinction. There is compounding evidence of the prevalence of natural hybridization in *Rhizophora*, the genus that is widely used in replantings. Hybrids can be morphologically indistinguishable from the parent species; hence, their detection may rely on molecular techniques (e.g., Ng & Szmidt 2015). This underscores the importance of including genetic verification of species identity in reforestation planning. Incorporating molecular screening may be beyond the scope and means of community-based reforestation efforts. Therefore, such an undertaking could be spearheaded by large-scale nurseries that supply seedlings for replanting, either by establishing research collaboration or by outsourcing the sequencing work. We recommend managers be aware of potential hybridization and urge seedling suppliers to conduct molecular screening to determine their provenances.

Defining Conservation Units

Transboundary conservation is a challenge for species distributed across multiple political units, especially in assigning protection status and enforcing international law. The delineation of conservation units (CUs) could present an objective approach to conservation prioritization and provide a common ground for transboundary discussions. A key biological metrics for the definition of CUs is genetic connectivity, which can be used to identify biogeographic regions, meta-populations, and barriers to dispersal.

The IUCN Mangrove Specialist Group Statement recommends the development of interconnected and transboundary protected areas to conserve the biodiversity and functionality of the ecosystem. This way, a multispecies landscape-level approach to assess genetic connectivity could render more credibility to the delimitation of CUs and is particularly useful in designing reserve networks. The delimitation of CUs based on phylogeographic data can provide a basis for explicit genetic evaluation of potential sites. For example, mangroves occur in 274 of over 2000 sites listed under the Wetlands of International Importance (Ramsar List 2017). Based on crude CU delimitation data on *Rhizophora* (Fig. 1), the mangrove CUs in Oceania occur in few Ramsar sites, especially in the southwestern Pacific (1 Ramsar site in New Zealand). Because mangrove forests in Ramsar sites tend to have lower rates of deforestation than the global average (Hamilton & Casey 2016), prioritizing this region for the designation of new Ramsar sites could help conserve its unique genetic diversity. Gaps in Ramsar sites do not fully equate with gaps in mangrove conservation. However, such an approach could help identify mangrove areas in need of higher conservation status and support their inclusion in Ramsar sites, marine protected areas, UNESCO World Heritage sites, and country-level nature reserves (Fig. 1).

The prerequisite to realizing an ecologically meaningful delimitation of CUs is the availability of multispecies data on genetic connectivity (e.g., Fig. 1) and population demography. Such information is sufficiently comprehensive for only a few mangrove genera (e.g., *Rhizophora* and *Avicennia*) (Takayama et al. 2013; Mori et al. 2015). Therefore, rapid global phylogeographic assessment of understudied taxa is necessary. This is a major undertaking that requires international collaboration and large-scale genotyping, which could be achieved through funding dedicated to the mitigation of mangrove loss and ecosystem management (e.g., Blue Carbon Initiative).

Understanding Adaptation

Present anthropogenic-driven global change could significantly affect the distribution and persistence of mangroves. Mangroves are expanding poleward in response to reduced frequency of extreme cold events (Cavanaugh et al. 2014). Microtidal areas with low sediment availability are becoming increasingly vulnerable to sea-level rise (Lovelock et al. 2015). Furthermore, because mangrove species have different salinity tolerances, the productivity and community assemblage may be altered by salinity changes in the system. Therefore, the future distribution of mangroves, especially those growing at the edge of their tolerances, will be highly dynamic.
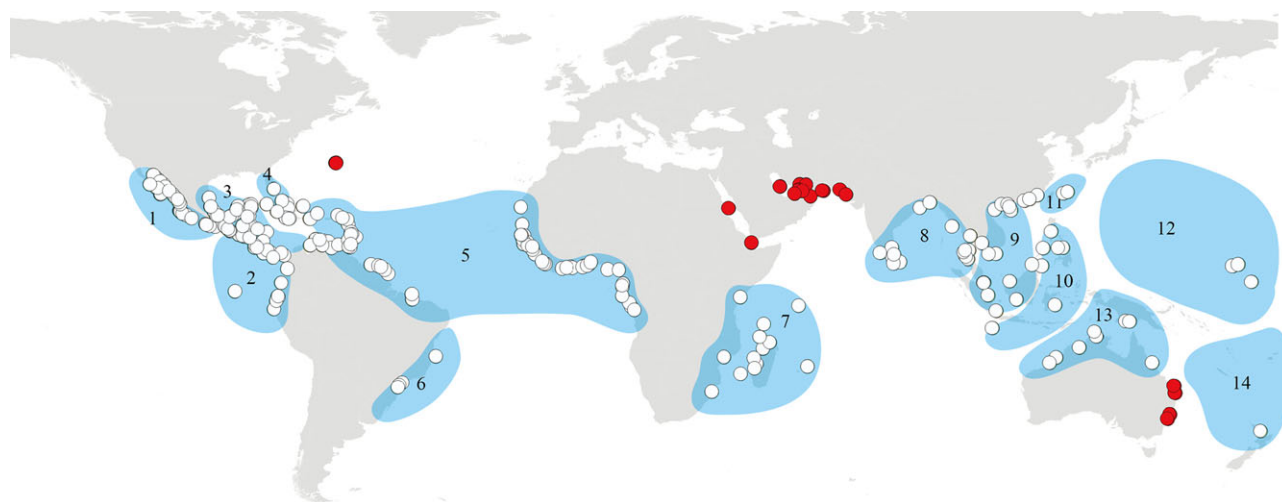
Figure 1. Putative conservation units (CUs) and Ramsar sites that contained mangroves (1, Gulf of California and northwestern Mexico; 2, Southeast Pacific; 3, Gulf of Mexico and Caribbean mainland; 4, Florida peninsula; 5, Caribbean islands, northern Brazil, and western Africa; 6, southern Brazil; 7, eastern Africa; 8, Bay of Bengal; 9, South China Sea; 10, Celebes Sea and Java Sea; 11, southern Japan; 12, northwestern Pacific; 13, Australia and New Guinea; 14, southwestern Pacific). The CUs are defined based on the genetic structure presented in 11 phylogeographic studies of the genus Rhizophora (see Supporting Information for the list of references). These putative CUs are not a policy recommendation, but merely a demonstration of conservation prioritization based on comparative phylogeography. Open circles denote Ramsar sites with mangrove forests that are included in a CU and filled circles denote Ramsar sites that lack mangrove genetic data and could not be assigned to a CU.

The vulnerability of mangroves to global change accentuates the importance of understanding their physiological and molecular responses to environmental stressors and identifying potential evolutionary outcomes under different scenarios. Due to the unique adaptation of mangroves to an intertidal environment, previous physiological studies have focused largely on their tolerances of salinity and flooding. There has been an increasing focus on cold tolerance in mangroves (Cook-Patton et al. 2015), although the molecular mechanism is yet to be explored. Studies of the molecular aspects of adaptive evolution in mangroves (Yang et al. 2015) lack empirical data on physiological responses and hence application to real-life conservation problems. Furthermore, intrapopulation epigenetic diversity may result from varying environmental stressors (Lira-Medeiros et al. 2010), indicating the importance of stress memory in mangroves. Thus, the integration of physiological and molecular data is necessary to fully understand adaptive potential and better predict future response of mangroves so managers and funders can optimize their inputs according to the predicted response of populations to environmental changes. This could also be an innovative way to support reserve design.

With the popularization of NGS, the regulatory mechanisms and phenotypic plasticity of acclimation can now be examined via a combination of common garden trials, stress treatments, transcriptome analysis, and epigenetics. This allows for quantification of the adaptive capacity of mangroves occurring under environmental

conditions near to their physiological limits and determination of whether mangroves can keep up with selective pressures and rate of environmental change. With this information, managers can potentially identify populations with limited capacity for adaptation and increase their evolutionary potential by promoting connectivity with other populations or by sourcing propagules from climatically diverse provenances. Managing evolutionary processes to avoid reduced effective population size and population isolation is crucial to adaptive responses and resilience of populations to a rapidly changing environment (Hoffmann & Sgro 2011).

Conclusion

Use of genetic information in mangrove conservation is crucial for its long-term effectiveness. Ultimately, it should aim to manage evolution (Hoffmann & Sgro 2011), whereby the adaptive and evolutionary potential of a species is preserved. Although significant developments have occurred in the fields of phylogeny and phylogeography, little has been translated into on-the-ground conservation. Considering the widespread distribution of mangroves and the urgency of their conservation, we call for an increase in technological transfer from academics to managers in the 3 major areas outlined above. We encourage researchers and conservation practitioners to bridge the gap by increasing interaction through forums

and meetings (e.g., IUCN Mangrove Specialist Group), applying published genetic and genomic data to conservation, and securing resources for genomics-guided projects and long-term commitment to the cause.

Acknowledgments

Supporting Information

A list of references used to generate Fig. 1 (Appendix S1) is available online. The authors are solely responsible for the content and functionality of these materials. Queries (other than absence of the material) should be directed to the corresponding author.

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