AQUATIC CONSERVATION: MARINE AND FRESHWATER ECOSYSTEMS

Aquatic Conserv: Mar. Freshw. Ecosyst. (2014)
Published online in Wiley Online Library
(wileyonlinelibrary.com). DOI: 10.1002/aqc.2533

COMMENTARY AND CORRESPONDENCE

Marine Spatial Planning 2.0: genes and satellites to conserve seascape dynamics

 $\begin{array}{c} \text{MARTIN MENDEZ}^{a,b,*}, \text{ FRANCINE KERSHAW}^c, \text{ STEPHEN PALUMBI}^d, \text{ MALIN PINSKY}^e, \text{ CARLETON RAY}^f, \\ \text{HOWARD ROSENBAUM}^{a,b} \text{ and AJIT SUBRAMANIAM}^g \end{array}$

^aWildlife Conservation Society, Bronx, New York, USA

^bSackler Institute for Comparative Genomics, American Museum of Natural History, New York, USA

^cDepartment of Ecology, Evolution and Environmental Biology, Columbia University, New York, USA

^dDepartment of Biology, Hopkins Marine Station, Stanford University, CA, USA

^eDepartment of Ecology, Evolution, and Natural Resources, Rutgers University, New Brunswick, NJ, USA

^fDepartment of Environmental Sciences, University of Virginia, Charlottesville, VA, USA

^gLamont Doherty Earth Observatory, Columbia University, NY, USA

Received 27 June 2014; Revised 7 September 2014; Accepted 15 September 2014

Effective marine conservation requires protection and management of functional seascapes, but seascape-level conservation is challenging because it needs to capture complex physical and ecological features that characterize dynamic populations and their habitats. And since populations are spatially and temporally bounded by combinations of natural heterogeneities in the marine environment (environmental boundaries) and associated species' responses (population boundaries), marine protection mechanisms need to take such boundaries into account in a spatially and temporally explicit framework. Therefore, improved understanding of these population and environmental boundaries and the processes driving them over multiple scales is essential for developing effective marine spatial planning (MSP). This kind of comprehensive approach for MSP is especially relevant in the face of global climate change, as conservation targets will shift in space, and phenological relationships will be confounded, thereby diminishing the significance of the original conservation strategies.

Although traditionally it has been difficult to understand such boundaries and the spatial and temporal scales in which they operate, a suite of technologies and analytical approaches promises to dramatically improve our ability to integrate new boundary conditions into MSP. Existing tools in the fields of molecular ecology and oceanography allow spatially and temporally explicit analysis of population and environmental boundaries, and available models enable evaluations of alternative future climate scenarios. What is lacking is a formal analytical framework that sheds light on the potential relationships among these factors, allowing for their integration into MSP efforts. We suggest an analytical framework that

^{*}Correspondence to: M. Mendez, Wildlife Conservation Society, Bronx, New York 10460, USA. Email: mmendez@wcs.org

allows the integration of genetic data to identify populations in space and time, and remotely sensed oceanographic data to identify environmental boundaries. Such a framework would enable analysis of potential relationships between both types of boundaries and allow assessment of the potential effects of future environmental change. Specifically, this framework would make possible: (i) the identification of natural populations considering their actual spatial scale, which remains challenging for most species and especially for marine wildlife that is difficult to observe; (ii) identification of environmental breaks that delimit marine seascapes; (iii) the elucidation of ecological links between populations and their seascapes, which remain largely unexplored given the general of dialogue among marine ecologists, evolutionary biologists, and oceanographers; (iv) the exploration of potential change of seascape conditions and boundaries under a changing climate; and (v) the integration of these biological, environmental and anthropogenic issues to provide concrete recommendations for conservation and management.

On the one hand, genetic tools provide a great deal of information about species and populations, and should therefore become more integrated into MSP. Derived from the quantification of genetic diversity at different hierarchical levels in a spatially explicit context, these tools offer insights into the resolution of species and population units and their spatial patterns, estimations of population size, of gene flow between populations, and real-time estimations of dispersal. importance of genetics has, in fact, been highlighted in international policy mechanisms, such as the Convention on Biological Diversity (CBD), which recognizes that genetic tools represent important knowledge gaps in the identification of marine areas in need of protection (CBD, 2010), and for characterizing marine Ecologically and Biologically Significant Areas (EBSAs) (CBD, 2008). In practice, however, conservation and management initiatives with regard to MSP (e.g. choosing sites for marine protected areas) are generally devoid of genetic information (Laikre et al., 2010). Planning approaches remain primarily concerned with

the identification of ecological patterns based on mapping ecoregion-scale species richness, presence, abundance and/or movement information interpolated from observation data. What is lacking is an integration of the spatial distribution of actual biological units (populations) and the evolutionary processes that give rise to such units. Genetic tools are especially suited to understand these evolutionary processes and uncover different units at the species-population level.

On the other hand, gathering meaningful environmental data at scales that match the above-mentioned biological considerations, and at a spatial extent that enables capturing oceanographic processes, has been hindered by technological limitations until the recent development of high resolution remote-sensing including dedicated marine sensors, and new and evolving climate modelling techniques for the marine environment. Integration of genetic and broad-scale environmental data has been accordingly constrained, in large part by the lack of technology appropriate to the required scales of analyses, the high cost of such technologies, and limited institutional capacity. However, remote sensing now enables characterization of the marine environment at a level of detail sufficient to identify boundary conditions at regional scales. Climate models with spatial resolution relevant to studying population structure are beginning to become available. Capitalizing on existing technology and recent advances in genetics and remote sensing, we can now attempt a joint understanding of biological and environmental boundaries, their dynamic relationships and potential sensitivity to future climate change, and therefore integrate such knowledge into MSP.

In 2012, as we witnessed the failure to meet the target agreed at the World Summit of Sustainable Development a decade ago to establish a globally representative network of marine protected areas, a new Strategic Plan for Biodiversity by the Convention on Biological Diversity established new targets, including the protection of at least 10% of coastal and marine areas through effective marine protected areas (Aichi Target 11, URL: http://www.cbd.int/sp/targets/default.shtml). While we embrace these much needed conservation targets, we call for a focused and integrative scientific

approach that jointly addresses crucial biological and environmental issues related to the existence of population and seascape boundaries that are dynamic in time and space. Another target within the new Strategic Plan calls for significantly improving, sharing, transferring and applying 'the science base and technologies relating to biodiversity, its values, functioning, status and trend' (Aichi Target 19, URL: http://www.cbd.int/ sp/targets/default.shtml). New methods, such as we have described, allow for an integrated holistic characterization of marine environments and their biota in order to protect functional seascapes across multiple spatial and temporal scales. Specifically, such an approach facilitates the identification of population and habitat boundaries, enables a deeper understanding of wildlife-environment

interactions, and addresses the need for long-term resiliency to future environmental change.

REFERENCES

- CBD. 2008. Decision IX/20 Marine and Coastal biodiversity, adopted by the Conference of the Parties to the Convention on Biological Diversity at its Ninth Meeting, Bonn, 19–30 May 2008
- CBD. 2010. Report of the expert workshop on scientific and technical guidance on the use of biogeographic classification systems and identification of marine areas beyond national jurisdiction in need of protection. UNEP/CBD/SBSTTA/14/INF/4. Fourteenth meeting of SBSTTA, Nairobi, 10–21 May 2010.
- Laikre L, Allendorf FW, Aroner LC, Baker CS, Gregovich DP, Hansen MM, Jackson JA, Kendall KC, McKelvey K, Neel MC, et al. 2010. Neglect of genetic diversity in implementation of the Convention on Biological Diversity. Conservation Biology 24: 86–88.