

## **Workshop brief: Integrating genetics into the IMMA identification process**

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## **1. Background**

Genetic tools have the potential to be highly informative in the application of the IMMA criteria in a manner that complements and enhances existing approaches based on biodiversity metrics, habitat maps, satellite telemetry studies, and expert opinion. Therefore, genetic data and information should be afforded strong consideration in a systematic way during the process of identifying IMMAs.

Work to develop a standardized approach to integrate genetics into marine spatial planning has evolved over a series of meetings, discussions, and papers during the past five years:

- i. 2<sup>nd</sup> International Marine Conservation Congress (2012): *Developing a framework for interpreting genetic data alongside oceanographic information to support marine protection efforts*. Symposium. Related publications:
  - Mendez, M. *et al.* (2014). Marine Spatial Planning 2.0: Genes and satellites to conserve seascape dynamics. *Aquatic Conservation: Marine and Freshwater Ecosystems*, **24**, 742-744.
  - Kershaw, F. & Rosenbaum, HC. (2014). Ten years lost at sea: response to Manel and Holderegger. *Trends in Ecology & Evolution*, **29**, 69-70.
- ii. 3<sup>rd</sup> International Marine Protected Area Congress (2013): *Advancing the MPA toolbox: Using genetics and remote sensing to identify management units and understand connectivity across scales*. Presentation.
- iii. 3<sup>rd</sup> International Marine Conservation Congress (IMCC3): *Developing an approach for integrating genetics into MPA design and spatial planning processes*. Focus Group.
- iv. Kershaw, F. & Rosenbaum, HC. (2014). *Information document submitted to the regional expert workshop to test the draft criteria used in the identification of Important Marine Mammal Areas (IMMAs)*. ICMMPA3, 8<sup>th</sup> November, Stamford Grande Adelaide, Australia.

The 2015 SMM workshop began the development of a genetic toolkit specifically to inform the identification of IMMAs. The workshop brought together more than twenty marine mammal experts from across the community of practice, and represented a partnership between the IUCN-MMPATF, the Natural Resources Defense Council, the University of California - Santa Barbara, and the Wildlife Conservation Society.

## 2. Aim and objectives

The overarching aim of the workshop was to begin the development of a genetic toolkit to guide the use of genetics in the identification of IMMAs in a standardized way. To this end, the workshop addressed the following objectives:

- i. Identify the ways in which genetic data can inform the identification of IMMAs;
- ii. Conduct an expert evaluation of geospatial genetic data and supporting analytics for two prototype case studies: humpback whale and spinner dolphin; and
- iii. Compile a list of questions and considerations for future work, including subsequent workshops related to the development of the IMMA Toolkit.

## 3. Outcomes

The main outcomes of each of the workshops objectives are briefly summarized as follows:

### ***a. How genetic data can be used to inform the identification of IMMAs***

Participants highlighted that genetic tools are one of the primary means of delineating demographic population units and are useful for developing estimates of abundance, both of which form the basis of the IMMA criteria. Specific intersections between genetics and the IMMA criteria were also identified (Table 1).

*Table 1: How genetics can be used to inform each of the IMMA criteria.*

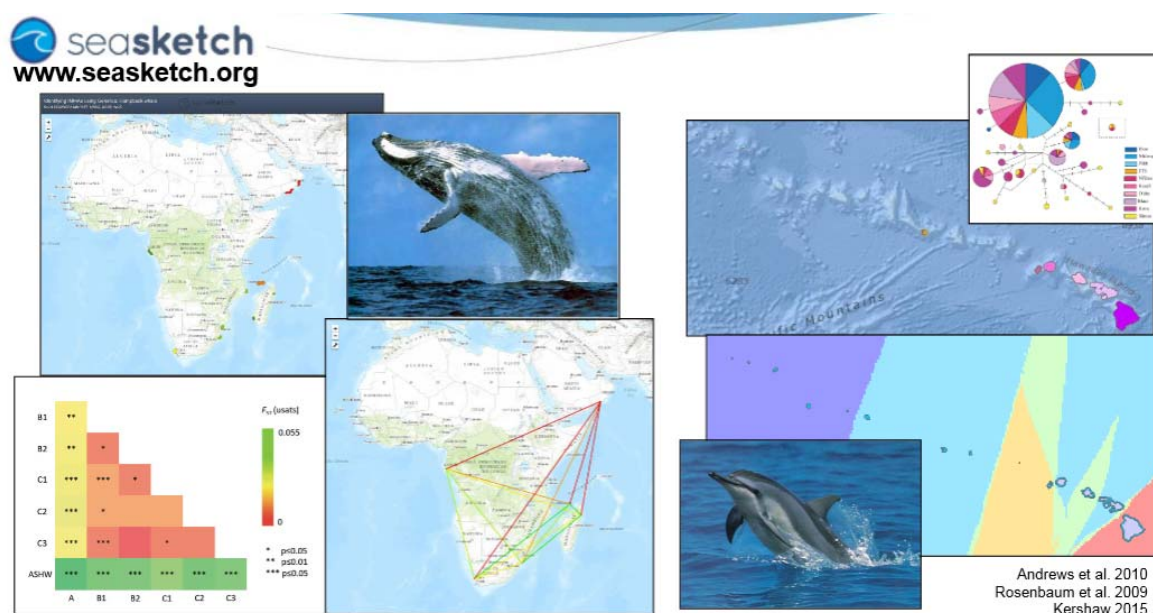
<b>A) Species or Population Vulnerability:</b> <ul style="list-style-type: none"><li>• Identification of species/stocks/populations; and</li><li>• Measuring status and trends (e.g. historic bottlenecks, effective population size, genetic diversity of species and populations.</li></ul>	<b>B) Distribution and abundance (sub-criterion B(i) small and resident populations):</b> <ul style="list-style-type: none"><li>• Number and distribution of populations;</li><li>• Population size;</li><li>• Site fidelity; and</li><li>• Changes in abundance through time.</li></ul>
<b>C) Key life cycle activities:</b> <ul style="list-style-type: none"><li>• Connectivity between different areas (e.g. breeding and feeding areas);</li><li>• Site fidelity;</li><li>• Sex-specific differences; and</li><li>• Mixing on migratory routes.</li></ul>	<b>D) Special Attributes:</b> <ul style="list-style-type: none"><li>• Evolutionary distinctive species (sub-criterion D(i) Distinctiveness);</li><li>• Highly isolated populations within a species (sub-criterion D(i) Distinctiveness); and</li><li>• Metrics of species diversity (sub-criterion D(ii) Diversity).</li></ul>

### ***b. Expert evaluation of geospatial genetic data and supporting analytics***

Lack of access to and understanding of genetic data has previously been identified as a key reason why genetics is often overlooked in marine spatial planning processes. The development of geospatial genetic data layers, that can be viewed and mapped alongside other kinds of data (e.g., habitat and distribution maps, tracking or telemetry data), was therefore considered by the workshop organizers to be essential for the success of a genetic toolkit to support IMMA identification (and marine spatial planning more broadly).

Prior to the workshop, two prototype case studies demonstrating the geospatial mapping of genetic data were created in the marine spatial planning tool, SeaSketch ([www.seasketch.org](http://www.seasketch.org)), for expert evaluation by participants. Case studies were developed for a migratory baleen whale - humpback whales (<http://humpbacks.seasketch.org>) - and a coastal small cetacean - spinner dolphin (<http://spinners.seasketch.org>) - to explore how genetic data may need to be mapped and interpreted differently for species with different life histories and habitat preferences (Figure 1).

Through the completion of electronic questionnaires, participants were asked to evaluate the accessibility of the geospatial data layers, how they could be improved, and the associated caveats and uncertainties. Participants provided comments ranging from the accuracy of the biological representation of the data, ways in which to improve the ways in which the data is visualized, whether the data layers were understandable by non-geneticists, and suggestions for further types of genetic data and information that might be useful to include for identifying IMMAs.



*Figure 1: Examples of the geospatial genetic data layers and supporting analytics included in the prototype case studies subject to expert evaluation during the workshop. Left panel: humpback whale genetic diversity metrics (top left), pairwise  $F_{ST}$  matrix (bottom left), and magnitude of genetic connectivity (left-center). Right panel: Spinner dolphin haplotype network and corresponding key (top) and interpolated local  $F_{ST}$  (bottom).*

Participants also identified a range of caveats and uncertainties inherent in the data layers and analytics, including those related to sample size and location, spatial and temporal scale, statistical significance, and the type of genetic marker used. There was consensus among participants that expert synthesis of the genetic information, and the related caveats and uncertainties, in a standardized and accessible format is essential prior to its use for IMMA identification.

Feedback is still being collected on the data included in each of the case studies through a public expert consultation process that will be open until March 31<sup>st</sup>. The feedback will then be compiled and included in the genetics section of the IMMA Toolkit.

***c. Questions and considerations for future work, including subsequent workshops***

Looking towards the subsequent workshops and focus groups on integrating information on habitat and behavior into the IMMA Toolkit, the following key considerations were highlighted by the expert group:

- i. How can genetic data be integrated alongside the other data types being considered in the IMMA Toolkit (e.g., how do habitat areas align with genetically distinct populations, how can genetic connectivity and interchange measures be effectively compared with direct movement inferred from satellite telemetry data, etc.)? What are the spatial and temporal scales of each data type? How do they reinforce and complement one another?
- ii. How should the “distinctiveness” criterion be used in practice as there will not be a ‘one size fits all’ across species due to differing evolutionary histories. Are there similar considerations for other data types?
- iii. How can the data and information included in the IMMA Toolkit be tailored to meet management relevant scales? Is there a role for systematic conservation planning approaches and tools (e.g., MARXAN)? How might each of the different types of data be integrated into this process?
- iv. How can we align “management units” identified through the IMMA process and others with those of legal terminologies in the management and policy arena?