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# CONSULTANCY ON VME MAPPING

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## 1. Introduction

Vulnerable Marine Ecosystems (VMEs) are ecosystems at potential risk from the effects of fishing activities or other anthropogenic disturbances, as determined by the vulnerability of their components (e.g., species, communities, or habitats) (FAO, 2009). The United Nations require states and regional fisheries management organizations/agreements to implement measures to prevent significant adverse impacts on VMEs, which can include closing areas to fishing (UNGA, 2007). Several species and taxonomic groups have been identified as indicators of VMEs in particular ocean regions to assist management authorities in their protection. VME taxa possess traits that make them particularly vulnerable to disturbance (slow growth, late maturity, longevity, and fragility), and include species that can form structurally complex frameworks such as coral reefs, coral gardens, and sponge grounds—which provide three-dimensional structures that enhance local biodiversity and act as areas of functional significance (e.g., spawning, breeding, and nursery grounds for fish stocks and particular life-history stages, and habitat for rare, threatened or endangered species of the habitat) (FAO, 2009).

In the Southern Indian Ocean, the Southern Indian Ocean Fisheries Agreement (SIOFA) has recently taken a series of steps towards the protection of VMEs. SIOFA's management efforts have identified five Benthic Protected Areas (BPAs) where bottom-fishing trawling is not permitted and have adopted a list of VME indicator taxa following UNGA resolutions. For SIOFA to meet its management obligations (UNGA, 2007), it requires scientific advice informed by maps of where VMEs are known to occur, or likely to occur, in the Agreement Area. The aim of this consultancy is to map the biogeographical regions of indicator taxa of VME, and VME habitat, in the Southern Indian Ocean to improve knowledge of VMEs within SIOFA's management area and help inform additional management measures to mitigate risks to VMEs. We aim to achieve this through the Terms of Reference (ToR) and applied deliverables established for the consultancy (Table 1).

The SIOFA area encompasses a large area with a rich biodiversity, especially in terms of VME indicator taxa, with an observed species richness of 1921 species and an estimated total richness of 2906 species (updated from Ramiro-Sánchez et al., 2021). Occurrence records of VME indicator taxa are typically scarce and collected without standardised methodologies. In ToR1 and ToR2, we assess their accuracy, quality, and comprehensiveness to properly evaluate the uncertainties of any map that will be derived from them. In ToR2, we further engage in habitat suitability modelling for predicting distribution patterns of VME indicator taxa, as such models are considered useful for marine ecosystem management (Ross and Howell, 2013; Reiss et al., 2014). In ToR3, we develop several bioregionalization approaches that provide maps of the extent of VME-based bioregions.

Because interpreting at once the distribution of hundreds of species is complex and makes it difficult to derive management recommendations, biogeographers often engage in biogeographical classifications, also known as bioregionalization (Ebach and Parenti, 2015). Bioregionalizations partition the geographical space into biological and physical units based on the distribution of multiple species, communities, ecosystems, or other biological characteristics—these units are called biogeographical regions or bioregions. Bioregions are therefore a simplification (a model) of the true biogeographical distribution of biodiversity,

which is generally based on taxa that share similar distributions because of similar ecological and physical preferences and of a shared history (Lomolino et al., 2016; Leroy et al., 2019; Woolley et al., 2020). These bioregional classifications are an indispensable component of the planning and implementation process of protected areas (CBD, 2010).

There are many predictive approaches to map bioregions, which can be generally classified into three categories (Woolley et al. 2020). The first one consists in grouping biological features into bioregions first, and then spatially predict these bioregions (“group first, then predict”). The second one consists in spatially predicting all biological features first, and then group them with a clustering approach (“predict first, then group”). The last one consists in grouping and predicting bioregions in a single modelling approach (“analyze simultaneously”). Each method has its set of advantages and disadvantages that make them complementary in the information they provide; although, ultimately, the kind of data available will often limit the choice of method (Woolley et al., 2020).

In this progress report, we synthesise results for Terms of Reference 1 to 3 of this consultancy (Table 1) and update preliminary observations presented at the PAEWG Annual meeting in March 2021. We note that improvements of the models will continue until the end of the consultancy (ToR4) and thus, results shown here should be interpreted with caution.

*Table 1. Terms of reference and corresponding deliverables for the consultancy.*

Terms of Reference	Deliverables
<b>ToR1: Compile, clean and verify occurrence and environmental data</b>	Consolidated VME occurrence dataset. Consolidated environmental variables dataset. Maps of VME taxa occurrence.
<b>ToR2: Evaluate the quality of occurrence data and determine spatial scale and taxonomic resolution.</b>	Indicators of data quality. Maps of optimal resolutions of analysis. Maps of predicted VME taxa occurrences.
<b>ToR3: Develop and compare multiple bioregionalization schemes and approaches.</b>	Maps of bioregionalization based on occurrence data. Maps of bioregionalization based on taxa distribution models. Maps of bioregionalization based on generalised dissimilarity models or other appropriate modelling techniques.
<b>ToR4: Reporting</b>	Scientific reports to PAEWG and SC annual meetings, 30 days prior to meeting commencement date. Final report to PAEWG and SC.