

Accelerating Ocean Species Discovery and Laying the Foundations for the Future of Marine Biodiversity Research and Monitoring: Supplementary Material

1.0 Why Invest in Accelerating Species Discovery in the Ocean?

1.1 Societal Well-Being and Management of the Ocean

Biodiversity contributes to human health and well-being by providing food, underpinning livelihoods, producing oxygen, regulating climate, protecting millions of communities from extreme weather events, remediating pollution, supporting mental health and cultural practices, and providing novel metabolites that form a significant proportion of the pharmaceuticals we use to fight disease (Dasgupta, 2021). It has been estimated that benefits to society from the natural world are equal to or greater than global domestic product (OECD, 2019). Estimates of the contribution of ocean ecosystems to people have varied widely, with estimates of “gross marine product” of at least \$2.5 trillion and a total asset base of the ocean being \$24 trillion (Hoegh-Guldberg et al., 2015) while another study has appraised the value of ocean ecosystem services at \$49.7 trillion per annum (out of a total of \$124.8 trillion; Costanza et al., 2014). These figures are, however, contested and also hide the societal value of the oceans in terms of wider benefits to people. For example, global marine capture fisheries landed about 78.8 million tonnes (MT) of fish in 2020 with a further 8.3MT coming from mariculture (FAO, 2022). The value of marine fisheries has been estimated at around \$100 billion per annum, supporting about 260 million livelihoods and providing about 2.9 billion people with 20% of their protein needs as well as critical micronutrients (Lam et al., 2016; Selig et al., 2018). Coastal and marine tourism depend on healthy marine ecosystems and constitute approximately 50 percent of all global tourism, valued at US\$4.6 trillion or 5.2 percent of global gross domestic product (Northrop et al., 2022). Income from tourism is particularly important for small island developing states (SIDs) and coastal communities (Northrop et al., 2022). It has been estimated that over 775 million people globally are highly dependent on marine ecosystems for nutrition, employment and coastal protection (Selig et al., 2018).

Alongside cultural, educational and historic knowledge and perceptions, understanding the variety and distribution of life on Earth is fundamental to appreciate its importance to human well-being and strengthening our connection with nature. It is also critical to manage which human activities take place, where and when, in order to ensure biodiversity is maintained for present and future generations. Increased knowledge of the diversity and distribution of life in the ocean can lead to improved conservation and ocean management outcomes at local, national, regional and international levels (Rabone et al., 2019). Networks of Marine Protected Areas (MPAs) are an obvious example, where knowledge of the diversity and distribution of species is critical to the effective application of conservation. This is particularly the case for threatened species (IUCN Red List species), although relatively few marine species have been assessed for the Red List and only a small fraction of these from deep-sea ecosystems, despite the protection it can offer (Sigwart et al., 2019). If MPAs are to protect a representative proportion of biodiversity, protection should include consideration of habitat, species and genetic diversity. *Ad hoc* designation of MPAs leads to poor conservation outcomes for biodiversity and threatened species (e.g. Klein et al., 2015; Asaad et al., 2018) and can have implications for social equity and community livelihoods and long-term well-being (Gill et al., 2019). Even where systematic planning is undertaken to inform the designation of MPAs, it often uses proxies such as terrain or habitat to infer “importance” and can be subject to

compromise resulting from negotiations during the MPA designation processes by stakeholders with specific economic or political interests (e.g. fisheries, tourism, oil extraction; Edgar et al., 2008; Stevenson et al., 2019) and rarely considers genetic interconnectedness among regions. The discovery of new habitats and biodiversity, including novel species, have informed the placement of MPAs and other conservation measures. An example is the recent discovery of mesophotic reef ecosystems on the Philippine Rise in 2014 (Nacorda et al., 2017), which led to the designation of a fully protected MPA and a wider area of controlled management for fisheries by the government of the Philippines in 2018. Similarly, efforts are underway to restore degraded sites in Sundarbans, the world's largest contiguous mangrove wetland which is an UNESCO World Heritage site and a RAMSAR site. These efforts are based on the findings from robust coastal biodiversity mapping exercises that have also integrated state-of-art approaches including use of environmental DNA (Chatterjee et al., 2019; Ghosh et al., 2022).

Sustainable management of marine living resources requires knowledge of the species occurring in an area (Glover et al 2018) and the carrying capacity of target populations of species to fishing mortality (e.g. Jennings et al., 2008; Glover et al 2018). Responses to management can be influenced by diverse aspects of species ecology, including population size, distribution, age structure, connectivity, life history and interactions with other species (Jennings et al., 2008; Ovenden et al., 2015). These responses can be specific to genetically distinct stocks or populations of a species, so a knowledge of intraspecific genetic and biological variation is important (e.g. Ovenden et al., 2015). An understanding of the wider impacts of exploitation on the ecosystems of target species, including the effects on non-target species, is also important to conserve biodiversity (e.g. Crowder et al., 2008; Ovenden et al., 2015; Clark et al., 2016). This is because exploitation methods, such as bottom trawling or long-lining, can cause significant mortality of non-target species through bycatch and habitat destruction leading to increased risk of species extinctions (e.g. seabirds such as albatrosses and petrels and pelagic sharks; e.g. Anderson et al., 2011; Pacoureau et al., 2021). Data on the distribution of species and habitats in the ocean supports sustainable management of living marine resources and the habitats and non-target species associated with them. This includes data on species presence, abundance, health, size distributions, diets, life-history traits, cellular and molecular responses to changing geochemical gradients, and other aspects of biology important to sustainable management.

The ocean is playing an increasing role in the direct economic activities of coastal States. An example of this is the rapid increase in ocean renewable energy installations in regions such as European waters (e.g. UK Government, 2021). Such development should conform to the principles of a blue economy, whereby they are economically viable, environmentally sustainable, and equitable to society (Bramley et al., 2021). Environmental sustainability means that blue economic activities should be at least neutral to biodiversity but, ideally, should be regenerative or restorative to marine species, habitats and ecosystems (Sala et al., 2013; Bramley et al., 2021). Knowledge of biodiversity is critical for the spatial management of human activities in the ocean to avoid harm to natural ecosystems. Moreover, such knowledge can be pivotal in removing bankability barriers that influence blue financing globally.

The conservation and sustainable use of marine biodiversity is integral to international treaty obligations under the United Nations Convention of the Law of the Sea (UNCLOS), the Convention on Biological Diversity and a range of other conventions, treaties and agreements (see Rogers et al., 2020) including the provisionally agreed international legally binding instrument under UNCLOS on the conservation and sustainable use of marine biological diversity of areas beyond national jurisdiction. At present, the ability of many States, especially low-income States, to meet their

national, regional and international policy commitments is hindered by insufficient knowledge and institutional capacity to document and obtain information on the biodiversity in their own waters and in areas beyond national jurisdiction, (e.g. Rogers et al., 2020, 2021a).

The current gaps in knowledge create challenges in setting baselines, monitoring how biodiversity is responding to changes in human activities and climate change (e.g. Edgar et al., 2023) and in evaluating if the policies and management plans implemented are proving effective. At present, we are effectively blind to how life in the ocean is responding to our intentional and unintentional actions and to rapidly changing environmental conditions. New molecular approaches, including environmental DNA (eDNA), environmental metabarcoding and environmental metagenomics, offer powerful technologies that will greatly assist in monitoring biodiversity (reviewed in Rogers et al., 2022a). However, for these technologies to be effective, DNA libraries that connect sequences to accurate species identifications with archived, vouchered and openly accessible materials are required. At present, existing quality-controlled barcoding libraries are insufficiently populated to be of general use in monitoring biodiversity using DNA sequencing approaches (Hestetun et al 2020; Rogers et al., 2022a). In addition, the accuracy of species identifications submitted to databases can also be questionable, an extreme example being where 100% of the sequences on GenBank were assigned to not only the wrong species of narcomedusae but to an organism in a completely different family (Lindsay et al., 2017). Moreover, there are many taxonomically intractable groups (e.g. free-living marine nematodes and members of the phylum Nemertea), which are widespread in many environments but are rarely represented in available sequence databases, limiting acceleration and quantification of the true extent of ocean biodiversity (e.g. Bhadury and Austen 2010; Kumar et al., 2015).

1.2 Scientific Endeavour

Life began in the ocean and much of the legacy of nearly four billion years of evolution is recorded in the DNA of marine species. The discovery of extremophiles and chemosynthetic communities at deep-sea hydrothermal vents on the Galapagos Rift in 1977 changed humanity's perceptions of where life may be found elsewhere in the solar system and the universe beyond (Cable et al., 2021). The taxonomy and systematics of marine species is fundamental science. The ocean already presents some of the best-known examples of the links between environment and evolution at the genomic level (e.g. the evolution of antifreeze proteins in polar marine fish and other adaptations to extreme environments; Rogers, 2012). Sampling across the tree of life has been important in understanding how key genes involved in development and diversification of body plans, known as Homeobox genes, have evolved and function in invertebrates, fish and humans (e.g. Holland, 2013; Ferrier, 2016; Brauchle et al., 2018). A broader sampling of life in the ocean is critical to understanding the laws that drive evolutionary processes and how genomes can change across generations from simple nucleotide substitutions to changes at the level of chromosomes and in the expression of genes (Lewin et al., 2018). At a time when climate destabilisation is forcing rapid alterations in the Earth system, biodiversity science is key to resolving how marine ecosystems are responding to multiple stressors and assessing how genetic variation in marine life could support climate adaptation.

1.3 Marine Genetic Resources

Marine genetic resources are present in all marine life, including the physical genes and genomes (DNA and RNA), the information they encode (i.e., digital sequence information), and the products of these genes, including a wide range of molecules (e.g., enzymes, structural proteins, peptides and secondary metabolites), their derivatives, the biological processes they are a part of (e.g., biosynthetic pathways), and the physical structures they form that offer actual or potential value to humanity (Rabone et al., 2019; Rogers et al., 2021a). Marine genetic resources have been a source of

pharmaceuticals, nutraceuticals, personal care products, research tools (e.g. green fluorescent protein), industrial enzymes, modified aquaculture species and functional food products and can be applied in the management and conservation of marine species (Blasiak et al., 2020; Rogers et al., 2021a). For example, to date, 17 pharmaceutical drugs derived from marine organisms have been clinically approved, including treatments for cancer and drug resistant cancer cells, nosocomial infections, neuropathic pain, hypertriglyceridemia and viral agents such as *Herpes simplex* (www.marinepharmacology.org; Blasiak et al., 2020; Midwestern University, 2020). Another 24 marine-derived products are in clinical trials and a further 250 in preclinical investigations (Blasiak et al., 2020; Midwestern University, 2020). The anticancer drug Aplidin has also been found to be effective against the SARs Covid-2 virus (Tagliatalata-Scafati, 2021). Most of the approved pharmaceuticals have been derived from compounds extracted from marine invertebrates, many of which are derived from bacterial associates, with sponges being a particularly rich source (Blasiak et al., 2020), potentially partly because of their endosymbionts. Another example is Dolastatin-10, a key drug scaffold which originates from the tropical marine mollusc *Dolabella auricularia* (Gao et al 2021) and which has been found to have its origin through complex interactions between the mollusc and a cyanobacterium. The genetic basis of these interactions and geographic distribution of Dolastatin-10 are now being investigated from shallow tropical coastal biotopes of South Asia (Bhadury, 2023). Most importantly, genomic resources store biological information in a remarkably compact form that can be safely and inexpensively preserved for future analysis. Securely archiving genetic resources provides insurance globally against the irretrievable loss of data that might otherwise result from biodiversity loss and extinction. We have only just begun to explore the enormous potential of marine genetic resources and a large portion of these lie in the undescribed biodiversity of the ocean. These genetic resources could also pave the way to using synthetic biology approaches to address long-term societal needs.

2.0 The Moorea Biodiversity Project

The Moorea Biocode Project was initiated in 2006 with objectives to DNA-barcode the first entire tropical ecosystem including terrestrial and marine environments (Meyer et al., 2006). Alongside the barcodes, an additional objective was to create digital keys (morphological barcodes) dynamically linked to images and genetic data to enable the identification of individual species (Meyer et al., 2006). The aim of this was to create a unique model system for biodiversity science (Meyer, 2006) whereby it is possible to link the genomic information on biodiversity to physico-chemical, ecological, and socioeconomic data (Davies et al., 2014). Ultimately the intention was to be able to model the impacts of anthropogenic changes to ecosystems and ecosystem services through the creation of an Island Digital Ecosystem Avatar (IDEA; Davies et al., 2014; Cressey, 2015). The Moorea Biocode Project is set within the Genomic Observatories Network, itself part of the Genomic Standards Consortium and the Group on Earth Observations (GEO) through its Biodiversity Observation Network (GEO-BON).

The Moorea Biocode Project and the wider Genomic Observatories Network has adopted a number of standardised approaches to ensure that environmental data are linked to both DNA barcode and other genomic data as well as to voucher specimens of the species that have been sequenced (Davies et al., 2014; Deck et al., 2017). It is important for the purposes of ecology and other areas of science to link physical samples and their associated genetic data with biological and ecological data at the point of collection (Deck et al., 2017). Whilst the standard genetic databases which are part of the INSDC encourage the submission of environmental metadata, this is not a requirement. To overcome this situation the Genomic Observatories Metadatabase (GeOMe, <http://www.geome-db.org/>) was established to link sequence data to organisms, their sampling localities and habitat

(Deck et al., 2017). GeOMe follows a set of customisable rules that ensure terminology is compliant to Darwin Core and MIxS standards (Yilmaz et al., 2011; Wieczorek et al., 2012; Deck et al., 2017). Each record is also assigned a unique identifier so it can be traced across multiple databases (Deck et al., 2017). Environmental samples and specimens of organisms are deposited at natural history museums, repositories and bio-banks to act as reference material for taxonomy and also as sources for future genome sequencing studies (Davies et al., 2014).

The systematic approach used by the Moorea Biocode Project has enabled a range of studies to be undertaken on biological communities prior to description and naming of taxa. An example has been food web studies undertaken on reef hawk fish and squirrel fish species through DNA barcode analysis of gut contents (Leray et al., 2012, 2015). Almost all (94%) of the prey found in the guts of these predatory fish had barcodes with >98% similarity to Biocode reference sequences and revealed new information on resource partitioning, feeding behaviours and the broader ecological consequences of feeding strategies (Leray et al., 2012, 2015).

3.0 Ocean Census Equity Principles

1. *Ocean Census* will be undertaken for the purposes of the discovery of ocean species and providing data for sustainable ecosystem-based ocean management and conservation for the benefit of biodiversity, ecosystems and humankind.
2. *Ocean Census*, its participants and activities will not discriminate on the grounds of age, disability, gender reassignment, marriage and civil partnership, pregnancy and maternity, race, religion or belief, sex or sexual orientation.
3. *Ocean Census* will work to level knowledge and develop capacity amongst all coastal states to undertake marine species discovery, biodiversity science and the management of their ocean biodiversity.
4. *Ocean Census* will be planned so that science is co-produced in full consultation with the relevant government, government departments and institutions of low- and middle-income countries and small-island nations, intergovernmental organisations, academic institutions and civil society including non-governmental organisations and indigenous communities local to the expedition.
5. *Ocean Census* will operate under the FAIR (data are Findable, Accessible, Interoperable and Reusable) and CARE principles (Collective benefit, Authority to Control, Responsibility and Ethics) for the production and subsequent use of data related to all aspects of its scientific work whilst respecting the rights of sovereign states in terms of authority and control of data originating from national waters and the species sampled therein.
6. Data collected as part of *Ocean Census* will be released according to FAIR principles as soon as is practically feasible and usually within 12 months of collection. Exceptionally, data can be released up to 24 months following its collection (e.g. if the data are important to the completion of a Ph.D. thesis). The only exceptions to this are if the release of data would endanger species or contravene the security of states or indigenous people. In line with Provision 4 states and indigenous people have authority and control over data collected in national waters.
7. *Ocean Census* and its participants will be compliant with international and national laws with respect to conservation, sampling, and transport of samples of species and all biological material associated with them including genetic materials. Examples of international treaties in respect of this provision include the Nagoya Protocol of the Convention on Biological Diversity and the Convention on International Trade in Endangered Species of Wild Fauna and Flora (CITES).

8. *Ocean Census* and all participants have a duty to ensure that all biological material, especially type material is archived in a secure manner indefinitely which also ensures its accessibility for future scientific research. It is acknowledged that some types of material may be destroyed during research (e.g. tissue subsamples, DNA) but this should not harm future prospects for scientific research on a species (e.g. samples are held in replicate). It is also recognised that some states may not have the facilities for secure storage of materials in which case an agreement (e.g. a Materials Transfer Agreement or MTA) on loan of material to a suitable institution in another country may be made on the understanding that once facilities are available in the country of origin they are returned.

9. *Ocean Census* will develop through an open network anchored through the *Ocean Census Biodiversity Centres* as well as the *Ocean Census Virtual Taxonomy Networks* (see below). Through these networks, knowledge, training and technology will be shared for furthering the purposes of species discovery and biodiversity monitoring globally.

10. *Ocean Census* will work to build the value-chain for marine biodiversity globally with an aim to a long-term transformation of ocean biodiversity science and monitoring ensuring a permanent legacy to the programme.

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